bioconda-recipes Documentation

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bioconda

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499ucsc-bedcommonregions 1143

500ucsc-bedcoverage 1145

501ucsc-bedextendranges 1147

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503ucsc-bedgraphpack 1151

504ucsc-bedgraphtobigwig 1153

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515ucsc-bigbedinfo 1175

516ucsc-bigbednameditems 1177

517ucsc-bigbedsummary 1179

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520ucsc-bigwigcat 1185

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523ucsc-bigwiginfo 1191

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525ucsc-bigwigsummary 1195

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527ucsc-bigwigtowig 1199

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Contents:

CHAPTER 1

age-metasv

1.1 Summary

optimal alignment of sequences with structural variants (SVs), modifiied for MetaSV integration

1.2 Home

https://github.com/marghoob/AGE/tree/simple-parseable-output

1.3 Versions

- 2015.01.29.3

1.4 License

CCPL (Creative Commons Public License)

1.5 Meta

```
package:
  name: age-metasv
  version: '2015.01.29.3'

source:
  fn: age-metasv-344429ccb.tar.gz
  url: https://github.com/marghoob/AGE/archive/344429ccb.tar.gz

build:
  number: 0

requirements:
  build:
  run:
```

```
test:
  commands:
    - age_align

about:
  home: https://github.com/marghoob/AGE/tree/simple-parseable-output
  license: CCPL (Creative Commons Public License)
  summary: optimal alignment of sequences with structural variants (SVs), modifiied for MetaSV integr
```

CHAPTER 2

ansible

2.1 Summary

Radically simple IT automation

2.2 Home

http://www.ansible.com/

2.3 Versions

- 1.9.4

2.4 License

GPLv3

2.5 Meta

```
package:
  name: ansible
  version: 1.9.4

# Updated version of ansible package from Barnaby Gray:
# https://github.com/barnybug/conda-recipes/tree/master/ansible

source:
  fn: ansible-1.9.4.tar.gz
  url: https://pypi.python.org/packages/source/a/ansible/ansible-1.9.4.tar.gz

build:
  skip: True # [not py27]

requirements:
```

```
  build:
    - python
    - setuptools
    - paramiko
    - jinja2
    - pyyaml
    - httplib2
    - pycrypto
    - six

  run:
    - python
    - setuptools
    - paramiko
    - jinja2
    - pyyaml
    - httplib2
    - pycrypto
    - six

test:
  imports:
    - ansible
    - ansible.constants
    - ansible.errors
    - ansible.playbook
    - ansible.utils
  commands:
    - ansible -h

about:
  home: http://www.ansible.com/
  license: GPLv3
  summary: Radically simple IT automation
```

CHAPTER 3

appdirs

3.1 Summary

A small Python module for determining appropriate platform-specific dirs, e.g. a "user data dir".

3.2 Home

http://github.com/ActiveState/appdirs

3.3 Versions

- 1.4.0

3.4 License

MIT License

3.5 Meta

```
package:
  name: appdirs
  version: "1.4.0"

source:
  fn: appdirs-1.4.0.tar.gz
  url: https://pypi.python.org/packages/source/a/appdirs/appdirs-1.4.0.tar.gz
  md5: 1d17b4c9694ab84794e228f28dc3275b

requirements:
  build:
    - python
    - setuptools

  run:
```

```
    - python

test:
  imports:
    - appdirs

about:
  home: http://github.com/ActiveState/appdirs
  license: MIT License
  summary: 'A small Python module for determining appropriate platform-specific dirs, e.g. a "user da
```

CHAPTER 4

argh

4.1 Summary

An unobtrusive argparse wrapper with natural syntax

4.2 Home

http://github.com/neithere/argh/

4.3 Versions

- 0.26.1

4.4 License

GNU Library or Lesser General Public License (LGPL)

4.5 Meta

```
package:
  name: argh
  version: "0.26.1"

source:
  fn: argh-0.26.1.tar.gz
  url: https://pypi.python.org/packages/source/a/argh/argh-0.26.1.tar.gz
  md5: 5a97ce2ae74bbe3b63194906213f1184
#  patches:
   # List any patch files here
   # - fix.patch

# build:
  # noarch_python: True
  # preserve_egg_dir: True
```

```
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - argh = argh:main
    #
    # Would create an entry point called argh that calls argh.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools

  run:
    - python

test:
  # Python imports
  imports:
    - argh

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  requires:
    - pytest
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: http://github.com/neithere/argh/
  license: GNU Library or Lesser General Public License (LGPL)
  summary: 'An unobtrusive argparse wrapper with natural syntax'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 5

arrow

5.1 Summary

Better dates and times for Python

5.2 Home

https://github.com/crsmithdev/arrow/

5.3 Versions

- 0.7.0

5.4 License

Apache License 2.0

5.5 Meta

```
package:
  name: arrow
  version: '0.7.0'

source:
  fn: arrow-0.7.0.tar.gz
  url: https://pypi.python.org/packages/source/a/arrow/arrow-0.7.0.tar.gz
  md5: 1597108362c5fa675dc5e0524ece4451

build:
  number: 0

requirements:
  build:
    - python
```

```
    - setuptools
    - python-dateutil

  run:
    - python
    - python-dateutil

test:
  imports:
    - arrow

about:
  home: https://github.com/crsmithdev/arrow/
  license: Apache License 2.0
  summary: Better dates and times for Python
```

CHAPTER 6

arvados-cli

6.1 Summary

Command line interface to Arvados, a free and open source platform for big data science

6.2 Home

http://doc.arvados.org/sdk/cli/index.html

6.3 Versions

- 0.1.20151207150126

6.4 License

Apache v2

6.5 Meta

```
package:
  name: arvados-cli
  version: "0.1.20151207150126"
build:
  number: 0
source:
  fn: arvados-cli-0.1.20151207150126.gem
  url: https://rubygems.org/downloads/arvados-cli-0.1.20151207150126.gem
requirements:
  build:
    - ruby
    - curl
  run:
    - ruby
    - curl
```

```
test:
  commands:
    - "arv --help 2>&1 | grep 'ARVADOS'"
about:
  home: http://doc.arvados.org/sdk/cli/index.html
  license: Apache v2
  summary: Command line interface to Arvados, a free and open source platform for big data science
```

CHAPTER 7

augustus

7.1 Summary

AUGUSTUS is a gene prediction program for eukaryotes written by Mario Stanke and Oliver Keller. It can be used as an ab initio program, which means it bases its prediction purely on the sequence. AUGUSTUS may also incorporate hints on the gene structure coming from extrinsic sources such as EST, MS/MS, protein alignments and synthenic genomic alignments.

7.2 Home

http://bioinf.uni-greifswald.de/augustus/

7.3 Versions

- 3.1

7.4 License

7.5 Meta

```
about:
  home: http://bioinf.uni-greifswald.de/augustus/
  license: ''
  summary: 'AUGUSTUS is a gene prediction program for eukaryotes written by Mario
    Stanke and Oliver Keller. It can be used as an ab initio program, which means
    it bases its prediction purely on the sequence. AUGUSTUS may also incorporate
    hints on the gene structure coming from extrinsic sources such as EST, MS/MS,
    protein alignments and synthenic genomic alignments.'
build:
  number: 0
package:
  name: augustus
  version: '3.1'
requirements:
  build: []
```

```
  run: []
source:
  fn: augustus-3.1.tar.gz
  sha256: 6db15a859537ccab8739e09c9c28f59c31dd9781e19d91f0d4489f60c7c15486
  url: http://bioinf.uni-greifswald.de/augustus/binaries/old/augustus-3.1.tar.gz
test:
  commands:
    - augustus --version
```

CHAPTER 8

autoconf

8.1 Summary

8.2 Home

http://www.gnu.org/software/autoconf/

8.3 Versions

- 2.69

8.4 License

GPL 3

8.5 Meta

```
package:
  name: autoconf
  version: 2.69

source:
  fn: autoconf-2.69.tar.gz
  url: http://ftp.gnu.org/gnu/autoconf/autoconf-2.69.tar.gz
  md5: 82d05e03b93e45f5a39b828dc9c6c29b

requirements:
  build:
    - m4
  run:
    - m4

test:
  commands:
    - autoconf --help
```

```
about:
  home: http://www.gnu.org/software/autoconf/
  license: GPL 3
```

CHAPTER 9

awscli

9.1 Summary

Universal Command Line Environment for AWS

9.2 Home

http://aws.amazon.com/cli/

9.3 Versions

- 1.8.3

9.4 License

Apache License 2.0

9.5 Meta

```
package:
  name: awscli
  version: '1.8.3'

source:
  fn: awscli-1.8.3.tar.gz
  url: https://pypi.python.org/packages/source/a/awscli/awscli-1.8.3.tar.gz
  md5: 9a603bcfe54afdb9184babe182e2cc54

build:
  number: 0

requirements:
  build:
    - python
```

```
    - setuptools
    - botocore
    - jmespath
    - bcdoc
    - colorama
    - docutils
    - rsa
  run:
    - python
    - botocore
    - jmespath
    - bcdoc
    - colorama
    - docutils
    - rsa

test:
  imports:
    - awscli

about:
  home: http://aws.amazon.com/cli/
  license: Apache License 2.0
  summary: Universal Command Line Environment for AWS
```

CHAPTER 10

bamtools

10.1 Summary

C++ API & command-line toolkit for working with BAM data

10.2 Home

https://github.com/pezmaster31/bamtools

10.3 Versions

- 2.4.0

10.4 License

MIT

10.5 Meta

```
package:
  name: bamtools
  version: '2.4.0'

source:
  fn: bamtools-2.4.0.tar.gz
  url: "https://github.com/pezmaster31/bamtools/archive/v2.4.0.tar.gz"
  sha256: "f1fe82b8871719e0fb9ed7be73885f5d0815dd5c7277ee33bd8f67ace961e13e"
  patches:
    # Install bamtools in lib instead of bamtools lib, thanks to homebrew-science:
    # https://github.com/Homebrew/homebrew-science/blob/master/bamtools.rb
    - bamtools_lib.diff

build:
  number: 1
```

```
requirements:
  build:
    - cmake
  run:

test:
  commands:
    - bamtools --help

about:
  home: https://github.com/pezmaster31/bamtools
  license: MIT
  summary: C++ API & command-line toolkit for working with BAM data
```

CHAPTER 11

barrnap

11.1 Summary

Barrnap predicts the location of 5S, 16S and 23S ribosomal RNA genes in Bacterial genome sequ It takes FASTA DNA sequence as input, and write GFF3 as output.

11.2 Home

https://github.com/tseemann/barrnap

11.3 Versions

- 0.7
- 0.3
- 0.2

11.4 License

GPL3

11.5 Meta

```
about:
  home: https://github.com/tseemann/barrnap
  license: GPL3
  summary: 'Barrnap predicts the location of 5S, 16S and 23S ribosomal RNA genes in
    Bacterial genome sequ It takes FASTA DNA sequence as input, and write GFF3 as
    output.'
build:
  number: 0
package:
  name: barrnap
```

```
  version: '0.7'
requirements:
  build: []
  run:
    - perl ==5.22.0
source:
  fn: 0.7.tar.gz
  sha256: ef2173e250f06cca7569c03404c9d4ab6a908ef7643e28901fbe9a732d20c09b
  url: https://github.com/tseemann/barrnap/archive/0.7.tar.gz
test:
  commands:
    - barrnap --help 2>&1 | grep Options > /dev/null
```

CHAPTER 12

bcbio-nextgen-vm

12.1 Summary

Run bcbio-nextgen genomic sequencing analyses using isolated containers and virtual machines

12.2 Home

https://github.com/chapmanb/bcbio-nextgen-vm

12.3 Versions

- 0.1.0a

12.4 License

MIT

12.5 Meta

```
package:
  name: bcbio-nextgen-vm
  version: '0.1.0a'

build:
  number: 69
  skip: True # [not py27]

source:
  fn: bcbio-nextgen-vm-8e55cc1.tar.gz
  url: https://github.com/chapmanb/bcbio-nextgen-vm/archive/8e55cc1.tar.gz

requirements:
  build:
    - python
```

```
    - setuptools

  run:
    - python
    - setuptools
    - bcbio-nextgen
    - elasticluster
    - nose
    - six

test:
  imports:
    - bcbiovm.version
  commands:
    - bcbio_vm.py -h

about:
  home: https://github.com/chapmanb/bcbio-nextgen-vm
  license: MIT
  summary: Run bcbio-nextgen genomic sequencing analyses using isolated containers and virtual machin
```

CHAPTER 13

bcbio-nextgen

13.1 Summary

Validated, scalable, community developed variant calling, RNA-seq and small RNA analysis

13.2 Home

https://github.com/chapmanb/bcbio-nextgen

13.3 Versions

- 0.9.6a

13.4 License

MIT

13.5 Meta

```
package:
  name: bcbio-nextgen
  version: '0.9.6a'

build:
  number: 2
  skip: True # [not py27]

source:
  #fn: bcbio-nextgen-0.9.5.tar.gz
  #url: https://pypi.python.org/packages/source/b/bcbio-nextgen/bcbio-nextgen-0.9.5.tar.gz
  fn: bcbio-nextgen-0341084.tar.gz
  url: https://github.com/chapmanb/bcbio-nextgen/archive/0341084.tar.gz

requirements:
```

```
  build:
    - python
    - setuptools
  run:
    - python
    - argparse [py26]
    - arrow
    - azure
    - bioblend
    - biopython
    - boto
    - click
    - cython
    - cyvcf2
    - fabric
    - fadapa
    - gffutils
    - ipyparallel
    - ipython-cluster-helper
    - joblib
    - logbook
    - lxml
    - matplotlib
    - msgpack-python
    - nose
    - numpy
    - openpyxl
    - openssl
    - pandas
    - path.py
    - patsy
    - pip
    - pycrypto
    - progressbar
    - psutil
    - python-dateutil
    - pybedtools
    - pysam
    - pyvcf
    - pyyaml
    - pyzmq
    - reportlab
    - requests
    - scikit-learn
    - scipy
    - seaborn
    - seqcluster
    - sh
    - sqlalchemy
    - statsmodels
    - tabulate
    - toolz
    - tornado

test:
  imports:
    - bcbio.distributed.ipython
    - bcbio.distributed.multi
```

```
    - bcbio.pipeline.main
    - bcbio.provenance.do
  commands:
    - bcbio_nextgen.py -h
    - bcbio_setup_genome.py -h
    - bcbio_prepare_samples.py -h

about:
  home: https://github.com/chapmanb/bcbio-nextgen
  license: MIT
  summary: Validated, scalable, community developed variant calling, RNA-seq and small RNA analysis
```

CHAPTER 14

bcbio-prioritize

14.1 Summary

Prioritize small variants, structural variants and coverage based on biological inputs

14.2 Home

https://github.com/chapmanb/bcbio.prioritize

14.3 Versions

- 0.0.5

14.4 License

MIT

14.5 Meta

```
package:
  name: bcbio-prioritize
  version: 0.0.5

source:
  fn: bcbio-prioritize
  url: https://github.com/chapmanb/bcbio.prioritize/releases/download/v0.0.5/bcbio-prioritize

build:
  number: 1

requirements:
  run:
    - java-jdk
```

```
test:
  commands:
    - bcbio-prioritize version

about:
  home: https://github.com/chapmanb/bcbio.prioritize
  license: MIT
  summary: Prioritize small variants, structural variants and coverage based on biological inputs
```

CHAPTER 15

bcbio-rnaseq

15.1 Summary

Report generation for bcbio-nextgen RNA-seq runs

15.2 Home

https://github.com/roryk/bcbio.rnaseq

15.3 Versions

- 1.0.4

15.4 License

MIT

15.5 Meta

```
package:
  name: bcbio-rnaseq
  version: 1.0.4

source:
  fn: bcbio-rnaseq
  url: https://github.com/roryk/bcbio.rnaseq/releases/download/v1.0.4/bcbio-rnaseq

build:
  number: 1

requirements:
  run:
    - java-jdk
    - r
```

```
test:
  commands:
    - bcbio-rnaseq --version

about:
  home: https://github.com/roryk/bcbio.rnaseq
  license: MIT
  summary: Report generation for bcbio-nextgen RNA-seq runs
```

CHAPTER 16

bcbio-variation-recall

16.1 Summary

Parallel merging, squaring off and ensemble calling for genomic variants

16.2 Home

https://github.com/chapmanb/bcbio.variation.recall

16.3 Versions

- 0.1.4

16.4 License

MIT

16.5 Meta

```
package:
  name: bcbio-variation-recall
  version: 0.1.4

source:
  fn: bcbio-variation-recall
  url: https://github.com/chapmanb/bcbio.variation.recall/releases/download/v0.1.4/bcbio-variation-re
  md5: 18c238c26ca06bfe8ee9b85fe921efe7

build:
  number: 2

requirements:
  run:
    - java-jdk
```

```
test:
  commands:
    - bcbio-variation-recall version

about:
  home: https://github.com/chapmanb/bcbio.variation.recall
  license: MIT
  summary: Parallel merging, squaring off and ensemble calling for genomic variants
```

CHAPTER 17

bcbio-variation

17.1 Summary

Toolkit to analyze genomic variation data, built on the GATK with Clojure

17.2 Home

https://github.com/chapmanb/bcbio.variation

17.3 Versions

- 0.2.6

17.4 License

MIT

17.5 Meta

```
package:
  name: bcbio-variation
  version: "0.2.6"

source:
  fn: bcbio.variation-0.2.6-standalone.jar
  url: https://github.com/chapmanb/bcbio.variation/releases/download/v0.2.6/bcbio.variation-0.2.6-sta

build:
  number: 0

requirements:
  run:
    - java-jdk >=7,<8
```

```
test:
  commands:
    - bcbio-variation variant-utils --help

about:
  home: https://github.com/chapmanb/bcbio.variation
  license: MIT
  summary: Toolkit to analyze genomic variation data, built on the GATK with Clojure
```

CHAPTER 18

bcbio_monitor

18.1 Summary

bcbio-monitor is an extension of bcbio-nextgen to visualize its progress

18.2 Home

https://github.com/guillermo-carrasco/bcbio-nextgen-monitor

18.3 Versions

- 1.0.2

18.4 License

MIT

18.5 Meta

```
package:
  name: bcbio_monitor
  version: "1.0.2"

source:
  fn: bcbio_monitor-1.0.2.tar.gz
  url: https://pypi.python.org/packages/source/b/bcbio_monitor/bcbio_monitor-1.0.2.tar.gz
  md5: 8f84cc4d99cfdf99d8bc78c651a45ed8
#  patches:
   # List any patch files here
   # - fix.patch

build:
  skip: True # [not py27]
  # noarch_python: True
```

```
  # preserve_egg_dir: True
  entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - bcbio_monitor = bcbio_monitor:main
    #
    # Would create an entry point called bcbio_monitor that calls bcbio_monitor.main()

    - bcbio_monitor = bcbio_monitor:main

  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools
    - flask 0.10.1
    - gevent 1.0
    - requests
    - py-graphviz
    - paramiko
    - pyyaml

  run:
    - python
    - flask 0.10.1
    - gevent 1.0
    - requests
    - py-graphviz
    - paramiko
    - pyyaml
    - pytz
    - dateutil

test:
  # Python imports
  imports:
    - bcbio_monitor
    - bcbio_monitor.config
    - bcbio_monitor.graph
    - bcbio_monitor.log
    - bcbio_monitor.parser

  commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.

    - bcbio_monitor --help

  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose
```

```
about:
  home: https://github.com/guillermo-carrasco/bcbio-nextgen-monitor
  license: MIT
  summary: 'bcbio-monitor is an extension of bcbio-nextgen to visualize its progress'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 19

bcbiogff

19.1 Summary

Read and write Generic Feature Format (GFF) with Biopython integration.

19.2 Home

https://github.com/chapmanb/bcbb/blob/master/gff

19.3 Versions

- 0.6.2

19.4 License

Biopython License Agreement

19.5 Meta

```
about:
  home: https://github.com/chapmanb/bcbb/blob/master/gff
  license: Biopython License Agreement
  summary: Read and write Generic Feature Format (GFF) with Biopython integration.
build:
  number: 0
package:
  name: bcbiogff
  version: 0.6.2
requirements:
  build:
  - python
  - six
  run:
  - python
```

```
  - six
  - biopython ==1.66
source:
  fn: bcbio-gff-0.6.2.tar.gz
  sha256: c682dc46a90e9fdb124ab5723797a5f71b2e3534542ceff9f6572b64b9814e68
  url: https://pypi.python.org/packages/source/b/bcbio-gff/bcbio-gff-0.6.2.tar.gz
test:
  imports:
    - BCBio.GFF
```

CHAPTER 20

bcbreport

20.1 Summary

Rmd templates for bcbio-nextgen analysis

20.2 Home

https://github.com/lpantano/bcbio.coverage

20.3 Versions

- 0.99.21

20.4 License

MIT License

20.5 Meta

```
package:
  name: bcbreport
  version: "0.99.21"
build:
  number: 1
source:
  git_url: https://github.com/lpantano/bcbio.coverage
  git_tag: cc9eb9c

requirements:
  build:
    - python
    - setuptools
  run:
    - python
```

```
test:
  imports:
    - bcbreport

about:
  home: https://github.com/lpantano/bcbio.coverage
  license: MIT License
  summary: Rmd templates for bcbio-nextgen analysis
```

CHAPTER 21

bcdoc

21.1 Summary

21.2 Home

https://github.com/boto/bcdoc

21.3 Versions

- 0.16.0

21.4 License

Apache License 2.0

21.5 Meta

```
package:
  name: bcdoc
  version: '0.16.0'

source:
  fn: bcdoc-0.16.0.tar.gz
  url: https://pypi.python.org/packages/source/b/bcdoc/bcdoc-0.16.0.tar.gz
  md5: e84b506c1c73e71b23d9be0aa00f6bec

build:
  number: 0

requirements:
  build:
    - python
    - setuptools
    - six
    - docutils
```

```
  run:
    - python
    - six
    - docutils

test:
  imports:
    - bcdoc

about:
  home: https://github.com/boto/bcdoc
  license: Apache License 2.0
```

CHAPTER 22

bcftools

22.1 Summary

BCFtools is a set of utilities that manipulate variant calls in the Variant Call Format (VCF) and its binary counterpart BCF. All commands work transparently with both VCFs and BCFs, both uncompressed and BGZF-compressed. Most commands accept VCF, bgzipped VCF and BCF with filetype detected automatically even when streaming from a pipe. Indexed VCF and BCF will work in all situations. Un-indexed VCF and BCF and streams will work in most, but not all situations.

22.2 Home

https://github.com/samtools/bcftools

22.3 Versions

- 1.3
- 1.2

22.4 License

MIT

22.5 Meta

```
about:
  home: https://github.com/samtools/bcftools
  license: MIT
  summary: BCFtools is a set of utilities that manipulate variant calls in the Variant
    Call Format (VCF) and its binary counterpart BCF. All commands work transparently
    with both VCFs and BCFs, both uncompressed and BGZF-compressed.  Most commands
    accept VCF, bgzipped VCF and BCF with filetype detected automatically even when
    streaming from a pipe. Indexed VCF and BCF will work in all situations. Un-indexed
    VCF and BCF and streams will work in most, but not all situations.
```

```
build:
  number: 0
package:
  name: bcftools
  version: '1.3'
requirements:
  build:
  - zlib ==1.2.8
  run:
  - zlib ==1.2.8
source:
  fn: bcftools-1.3.tar.bz2
  sha256: fc5332e49546d55120551b0d5fb690f79e4f2216b8492c7b53033cdaa4256a3d
  url: https://github.com/samtools/bcftools/releases/download/1.3/bcftools-1.3.tar.bz2
test:
  commands:
    - "bcftools -h > /dev/null"
    - bcftools --version
```

CHAPTER 23

bedtools

23.1 Summary

A powerful toolset for genome arithmetic

23.2 Home

http://bedtools.readthedocs.org/

23.3 Versions

- 2.25.0
- 2.22
- 2.20.1
- 2.19.1

23.4 License

GPL v2

23.5 Meta

```
package:
  name: bedtools
  version: "2.25.0"
source:
  fn: bedtools-2.25.0.tar.gz
  url: https://github.com/arq5x/bedtools2/releases/download/v2.25.0/bedtools-2.25.0.tar.gz
  sha256: d737ca42e7df76c5455d3e6e0562cdcb62336830eaad290fd4133a328a1ddacc
build:
    number: 1
requirements:
```

```
  build:
  run:
test:
  commands:
    - bedtools
about:
  home: http://bedtools.readthedocs.org/
  license: GPL v2
  summary: A powerful toolset for genome arithmetic
```

CHAPTER 24

bio-vcf

24.1 Summary

Smart VCF parser

24.2 Home

https://github.com/pjotrp/bioruby-vcf

24.3 Versions

- 0.9.2

24.4 License

MIT

24.5 Meta

```
package:
  name: bio-vcf
  version: "0.9.2"
build:
  number: 0
source:
  fn: bio-vcf-2063373.tar.gz
  url: https://github.com/pjotrp/bioruby-vcf/archive/2063373.tar.gz
requirements:
  build:
    - ruby
  run:
    - ruby
test:
  commands:
```

```
    - "bio-vcf --help | grep 'Usage: bio-vcf'"
about:
  home: https://github.com/pjotrp/bioruby-vcf
  license: MIT
  summary: Smart VCF parser
```

CHAPTER 25

bio_assembly_refinement

25.1 Summary

Assembly refinement tools, mostly useful for (but not limited to) pacbio bacterial assemblies

25.2 Home

https://github.com/nds/bio_assembly_refinement

25.3 Versions

- 0.5.0

25.4 License

GPLv3

25.5 Meta

```
package:
  name: bio_assembly_refinement
  version: "0.5.0"

source:
  fn: bio_assembly_refinement-0.5.0.tar.gz
  url: https://pypi.python.org/packages/source/b/bio_assembly_refinement/bio_assembly_refinement-0.5.
  md5: 93657bf827b05d033fd33215ace8e197
#  patches:
   # List any patch files here
   # - fix.patch

build:
  skip: True # [py27]
  # noarch_python: True
```

```
  # preserve_egg_dir: True
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - bio_assembly_refinement = bio_assembly_refinement:main
    #
    # Would create an entry point called bio_assembly_refinement that calls bio_assembly_refinement.m


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools
    - pyfastaq >=3.10.0
    - pymummer

  run:
    - python
    - pyfastaq >=3.10.0
    - pymummer

test:
  # Python imports
  imports:
    - bio_assembly_refinement

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  requires:
    - nose >=1.3
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: https://github.com/nds/bio_assembly_refinement
  license: GPLv3
  summary: 'Assembly refinement tools, mostly useful for (but not limited to) pacbio bacterial assemb

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 26

bioawk

26.1 Summary

BWK awk modified for biological data

26.2 Home

https://github.com/lh3/bioawk

26.3 Versions

- 1.0

26.4 License

Free software license (https://github.com/lh3/bioawk/blob/master/README.awk#L1)

26.5 Meta

```
package:
  name: bioawk
  version: "1.0"
source:
  fn: bioawk-1.0.tar.gz
  url: https://github.com/lh3/bioawk/archive/v1.0.tar.gz
  sha256: 5cbef3f39b085daba45510ff450afcf943cfdfdd483a546c8a509d3075ff51b5
build:
    number: 0
test:
  commands:
    - echo "hw" | bioawk '{print}' > /dev/null
about:
  home: https://github.com/lh3/bioawk
```

```
  license: Free software license (https://github.com/lh3/bioawk/blob/master/README.awk#L1)
  summary: BWK awk modified for biological data
```

CHAPTER 27

biobambam

27.1 Summary

Tools for early stage alignment file processing

27.2 Home

https://github.com/gt1/biobambam2

27.3 Versions

- 2.0.25

27.4 License

GPLv3

27.5 Meta

```
package:
  name: biobambam
  version: '2.0.25'
source:
  fn: biobambam2-2.0.25.tar.gz
  url: https://github.com/gt1/biobambam2/releases/download/2.0.25-release-20151105154334/biobambam2-2
build:
  number: 0
  binary_relocation: false
requirements:
  build:
  run:
test:
  commands:
    - bamsormadup --help
```

```
    - bamtofastq --help
about:
  home: https://github.com/gt1/biobambam2
  license: GPLv3
  summary: Tools for early stage alignment file processing
```

CHAPTER 28

bioblend

28.1 Summary

A Python library for interacting with CloudMan and the Galaxy API

28.2 Home

https://github.com/galaxy/bioblend

28.3 Versions

- 0.7.0

28.4 License

Academic Free License 3.0

28.5 Meta

```
package:
  name: bioblend
  version: '0.7.0'

source:
  fn: bioblend-0.7.0.tar.gz
  url: https://pypi.python.org/packages/source/b/bioblend/bioblend-0.7.0.tar.gz
  md5: 9b91e764de795e81ae7d136218b3b07e

build:
  number: 0

requirements:
  build:
    - python
```

```
    - setuptools
    - requests
    - requests-toolbelt
    - boto
    - pyyaml
    - six

  run:
    - python
    - requests
    - requests-toolbelt
    - boto
    - pyyaml
    - six

test:
  imports:
    - bioblend
    - bioblend.galaxy

about:
  home: https://github.com/galaxy/bioblend
  license: Academic Free License 3.0
  summary:  A Python library for interacting with CloudMan and the Galaxy API
```

CHAPTER 29

bioconductor-affy

29.1 Summary

The package contains functions for exploratory oligonucleotide array analysis. The dependence on tkWidgets only concerns few convenience functions. 'affy' is fully functional without it.

29.2 Home

http://bioconductor.org/packages/release/bioc/html/affy.html

29.3 Versions

- 1.48.0

29.4 License

LGPL (>= 2.0)

29.5 Meta

```
package:
  name: bioconductor-affy
  version: 1.48.0
source:
  fn: affy_1.48.0.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/affy_1.48.0.tar.gz
  md5: 12e56364b33d2c72547d170ffb7284fc
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
```

```
    - 'bioconductor-affyio >=1.13.3'
    - 'bioconductor-biobase >=2.5.5'
    - 'bioconductor-biocgenerics >=0.1.12'
    - bioconductor-biocinstaller
    - bioconductor-preprocesscore
    - bioconductor-zlibbioc
    - 'r >=2.8.0'
  run:
    - 'bioconductor-affyio >=1.13.3'
    - 'bioconductor-biobase >=2.5.5'
    - 'bioconductor-biocgenerics >=0.1.12'
    - bioconductor-biocinstaller
    - bioconductor-preprocesscore
    - bioconductor-zlibbioc
    - 'r >=2.8.0'
test:
  commands:
    - '$R -e "library(''affy'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/affy.html
  license: 'LGPL (>= 2.0)'
  summary: 'The package contains functions for exploratory oligonucleotide array analysis.
    The dependence on tkWidgets only concerns few convenience functions. ''affy''
    is fully functional without it.'
```

CHAPTER 30

bioconductor-affyio

30.1 Summary

Routines for parsing Affymetrix data files based upon file format information. Primary focus is on accessing the CEL and CDF file formats.

30.2 Home

http://bioconductor.org/packages/release/bioc/html/affyio.html

30.3 Versions

- 1.40.0

30.4 License

LGPL (>= 2)

30.5 Meta

```
package:
  name: bioconductor-affyio
  version: 1.40.0
source:
  fn: affyio_1.40.0.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/affyio_1.40.0.tar.gz
  md5: 7d6f9ffc936d768a3bbfd74942c9ab86
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
```

```
    - bioconductor-zlibbioc
    - 'r >=2.6.0'
  run:
    - bioconductor-zlibbioc
    - 'r >=2.6.0'
test:
  commands:
    - '$R -e "library(''affyio'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/affyio.html
  license: 'LGPL (>= 2)'
  summary: 'Routines for parsing Affymetrix data files based upon file format information.
    Primary focus is on accessing the CEL and CDF file formats.'
```

CHAPTER 31

bioconductor-annotate

31.1 Summary

Using R enviroments for annotation.

31.2 Home

http://bioconductor.org/packages/release/bioc/html/annotate.html

31.3 Versions

- 1.48.0

31.4 License

Artistic-2.0

31.5 Meta

```
package:
  name: bioconductor-annotate
  version: 1.48.0
source:
  fn: annotate_1.48.0.tar.gz
  url: https://bioarchive.galaxyproject.org/annotate_1.48.0.tar.gz
  md5: f42ea2231d1858f3d0f587cc44562898
build:
  number: 1
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
    - 'bioconductor-annotationdbi >=1.27.5'
```

```
    - bioconductor-biobase
    - 'bioconductor-biocgenerics >=0.13.8'
    - 'r >=2.10'
    - r-dbi
    - r-xml
    - r-xtable
  run:
    - 'bioconductor-annotationdbi >=1.27.5'
    - bioconductor-biobase
    - 'bioconductor-biocgenerics >=0.13.8'
    - 'r >=2.10'
    - r-dbi
    - r-xml
    - r-xtable
test:
  commands:
    - '$R -e "library(''annotate'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/annotate.html
  license: Artistic-2.0
  summary: 'Using R enviroments for annotation.'
```

CHAPTER 32

bioconductor-annotationdbi

32.1 Summary

Provides user interface and database connection code for annotation data packages using SQLite data storage.

32.2 Home

http://bioconductor.org/packages/release/bioc/html/AnnotationDbi.html

32.3 Versions

- 1.32.2

32.4 License

Artistic-2.0

32.5 Meta

```
package:
  name: bioconductor-annotationdbi
  version: 1.32.2
source:
  fn: AnnotationDbi_1.32.2.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/AnnotationDbi_1.32.2.tar.gz
  md5: ba140d55df3ee82d36c80b5ba5b22bae
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
    - 'bioconductor-biobase >=1.17.0'
```

```
    - 'bioconductor-biocgenerics >=0.15.10'
    - bioconductor-iranges
    - bioconductor-s4vectors
    - 'r >=2.7.0'
    - r-dbi
    - r-rsqlite
  run:
    - 'bioconductor-biobase >=1.17.0'
    - 'bioconductor-biocgenerics >=0.15.10'
    - bioconductor-iranges
    - bioconductor-s4vectors
    - 'r >=2.7.0'
    - r-dbi
    - r-rsqlite
test:
  commands:
    - '$R -e "library(''AnnotationDbi'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/AnnotationDbi.html
  license: Artistic-2.0
  summary: 'Provides user interface and database connection code for annotation data
    packages using SQLite data storage.'
```

CHAPTER 33

bioconductor-annotationforge

33.1 Summary

Provides code for generating Annotation packages and their databases. Packages produced are intended to be used with AnnotationDbi.

33.2 Home

http://bioconductor.org/packages/release/bioc/html/AnnotationForge.html

33.3 Versions

- 1.12.2

33.4 License

Artistic-2.0

33.5 Meta

```
package:
  name: bioconductor-annotationforge
  version: 1.12.2

source:
  fn: AnnotationForge_1.12.2.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/AnnotationForge_1.12.2.tar.gz
  md5: 23ec60f94fca10497bbfe1ecf3ab866f

build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
```

```
requirements:
  build:
    - 'bioconductor-annotationdbi >=1.31.19'
    - 'bioconductor-biobase >=1.17.0'
    - 'bioconductor-biocgenerics >=0.15.10'
    - bioconductor-org.hs.eg.db
    - bioconductor-s4vectors
    - 'r >=2.7.0'
    - r-dbi
    - r-rsqlite
  run:
    - 'bioconductor-annotationdbi >=1.31.19'
    - 'bioconductor-biobase >=1.17.0'
    - 'bioconductor-biocgenerics >=0.15.10'
    - bioconductor-org.hs.eg.db
    - bioconductor-s4vectors
    - 'r >=2.7.0'
    - r-dbi
    - r-rsqlite

test:
  commands:
    - '$R -e "library(''AnnotationForge'')"'

about:
  home: http://bioconductor.org/packages/release/bioc/html/AnnotationForge.html
  license: Artistic-2.0
  summary: 'Provides code for generating Annotation packages and their databases.  Packages produced
```

CHAPTER 34

bioconductor-basic4cseq

34.1 Summary

Basic4Cseq is an R/Bioconductor package for basic filtering, analysis and subsequent visualization of 4C-seq data. Virtual fragment libraries can be created for any BSGenome package, and filter functions for both reads and fragments and basic quality controls are included. Fragment data in the vicinity of the experiment's viewpoint can be visualized as a coverage plot based on a running median approach and a multi-scale contact profile.

34.2 Home

http://bioconductor.org/packages/release/bioc/html/Basic4Cseq.html

34.3 Versions

- 1.6.0

34.4 License

LGPL-3

34.5 Meta

```
package:
  name: bioconductor-basic4cseq
  version: 1.6.0
source:
  fn: Basic4Cseq_1.6.0.tar.gz
  url: https://bioarchive.galaxyproject.org/Basic4Cseq_1.6.0.tar.gz
  md5: 0a056c1a35f02918bfd165339fd6c00f
build:
  number: 0
  rpaths:
    - lib/R/lib/
```

```
    - lib/
requirements:
  build:
    - bioconductor-biostrings
    - bioconductor-bsgenome.ecoli.ncbi.20080805
    - bioconductor-genomicalignments
    - bioconductor-genomicranges
    - r
    - r-catools
    - r-rcircos
  run:
    - bioconductor-biostrings
    - bioconductor-bsgenome.ecoli.ncbi.20080805
    - bioconductor-genomicalignments
    - bioconductor-genomicranges
    - r
    - r-catools
    - r-rcircos
test:
  commands:
    - '$R -e "library(''Basic4Cseq'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/Basic4Cseq.html
  license: LGPL-3
  summary: 'Basic4Cseq is an R/Bioconductor package for basic filtering, analysis
    and subsequent visualization of 4C-seq data. Virtual fragment libraries can be
    created for any BSGenome package, and filter functions for both reads and fragments
    and basic quality controls are included. Fragment data in the vicinity of the
    experiment''s viewpoint can be visualized as a coverage plot based on a running
    median approach and a multi-scale contact profile.'
```

CHAPTER 35

bioconductor-biobase

35.1 Summary

Functions that are needed by many other packages or which replace R functions.

35.2 Home

http://bioconductor.org/packages/release/bioc/html/Biobase.html

35.3 Versions

- 2.30.0

35.4 License

Artistic-2.0

35.5 Meta

```
package:
  name: bioconductor-biobase
  version: 2.30.0
source:
  fn: Biobase_2.30.0.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/Biobase_2.30.0.tar.gz
  md5: 697d3b5504f899c38a5e6e784ca0e33f
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
    - 'bioconductor-biocgenerics >=0.3.2'
```

```
    - 'r >=2.10'
  run:
    - 'bioconductor-biocgenerics >=0.3.2'
    - 'r >=2.10'
test:
  commands:
    - '$R -e "library(''Biobase'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/Biobase.html
  license: Artistic-2.0
  summary: 'Functions that are needed by many other packages or which replace R functions.'
```

CHAPTER 36

bioconductor-biocgenerics

36.1 Summary

S4 generic functions needed by many Bioconductor packages.

36.2 Home

http://bioconductor.org/packages/release/bioc/html/BiocGenerics.html

36.3 Versions

- 0.16.1

36.4 License

Artistic-2.0

36.5 Meta

```
package:
  name: bioconductor-biocgenerics
  version: 0.16.1
source:
  fn: BiocGenerics_0.16.1.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/BiocGenerics_0.16.1.tar.gz
  md5: c2148ffd86fc6f1f819c7f68eb2c744f
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
    - r
```

```
  run:
    - r
test:
  commands:
    - '$R -e "library(''BiocGenerics'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/BiocGenerics.html
  license: Artistic-2.0
  summary: 'S4 generic functions needed by many Bioconductor packages.'
```

CHAPTER 37

bioconductor-biocinstaller

37.1 Summary

This package is used to install and update Bioconductor, CRAN, and (some) github packages.

37.2 Home

http://bioconductor.org/packages/release/bioc/html/BiocInstaller.html

37.3 Versions

- 1.20.1

37.4 License

Artistic-2.0

37.5 Meta

```
package:
  name: bioconductor-biocinstaller
  version: 1.20.1
source:
  fn: BiocInstaller_1.20.1.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/BiocInstaller_1.20.1.tar.gz
  md5: d6758faae696c9bbed2c5c43fcefdb00
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
    - 'r >=3.2.0'
```

```
  run:
    - 'r >=3.2.0'
test:
  commands:
    - '$R -e "library(''BiocInstaller'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/BiocInstaller.html
  license: Artistic-2.0
  summary: 'This package is used to install and update Bioconductor, CRAN, and (some)
    github packages.'
```

CHAPTER 38

bioconductor-biocparallel

38.1 Summary

This package provides modified versions and novel implementation of functions for parallel evaluation, tailored to use with Bioconductor objects.

38.2 Home

http://bioconductor.org/packages/release/bioc/html/BiocParallel.html

38.3 Versions

- 1.4.3

38.4 License

GPL-2 | GPL-3

38.5 Meta

```
package:
  name: bioconductor-biocparallel
  version: 1.4.3
source:
  fn: BiocParallel_1.4.3.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/BiocParallel_1.4.3.tar.gz
  md5: 7954a6ae6d148ac6f1179c47fde8d7d4
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
```

```
    - r
    - r-futile.logger
    - r-snow
  run:
    - r
    - r-futile.logger
    - r-snow
test:
  commands:
    - '$R -e "library(''BiocParallel'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/BiocParallel.html
  license: 'GPL-2 | GPL-3'
  summary: 'This package provides modified versions and novel implementation of functions
    for parallel evaluation, tailored to use with Bioconductor objects.'
```

CHAPTER 39

bioconductor-biocstyle

39.1 Summary

Provides standard formatting styles for Bioconductor PDF and HTML documents. Package vignettes illustrate use and functionality.

39.2 Home

http://bioconductor.org/packages/release/bioc/html/BiocStyle.html

39.3 Versions

- 1.8.0

39.4 License

Artistic-2.0

39.5 Meta

```
package:
  name: bioconductor-biocstyle
  version: 1.8.0
source:
  fn: BiocStyle_1.8.0.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/BiocStyle_1.8.0.tar.gz
  md5: f8fb61345f5c3044bde6d1f39126f8b8
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
```

```
    - r
  run:
    - r
test:
  commands:
    - '$R -e "library(''BiocStyle'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/BiocStyle.html
  license: Artistic-2.0
  summary: 'Provides standard formatting styles for Bioconductor PDF and HTML documents.
    Package vignettes illustrate use and functionality.'
```

CHAPTER 40

bioconductor-biomart

40.1 Summary

In recent years a wealth of biological data has become available in public data repositories. Easy access to these valuable data resources and firm integration with data analysis is needed for comprehensive bioinformatics data analysis. biomaRt provides an interface to a growing collection of databases implementing the BioMart software suite (http://www.biomart.org). The package enables retrieval of large amounts of data in a uniform way without the need to know the underlying database schemas or write complex SQL queries. Examples of BioMart databases are Ensembl, COSMIC, Uniprot, HGNC, Gramene, Wormbase and dbSNP mapped to Ensembl. These major databases give biomaRt users direct access to a diverse set of data and enable a wide range of powerful online queries from gene annotation to database mining.

40.2 Home

http://bioconductor.org/packages/release/bioc/html/biomaRt.html

40.3 Versions

- 2.26.1

40.4 License

Artistic-2.0

40.5 Meta

```
package:
  name: bioconductor-biomart
  version: 2.26.1
source:
  fn: biomaRt_2.26.1.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/biomaRt_2.26.1.tar.gz
  md5: 3adddc512c9763cf8527cc592e05204b
```

```
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
    - bioconductor-annotationdbi
    - r
    - r-rcurl
    - r-xml
  run:
    - bioconductor-annotationdbi
    - r
    - r-rcurl
    - r-xml
test:
  commands:
    - '$R -e "library(''biomaRt'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/biomaRt.html
  license: Artistic-2.0
  summary: 'In recent years a wealth of biological data has become available in public
    data repositories. Easy access to these valuable data resources and firm integration
    with data analysis is needed for comprehensive bioinformatics data analysis.  biomaRt
    provides an interface to a growing collection of databases implementing the BioMart
    software suite (http://www.biomart.org). The package enables retrieval of large
    amounts of data in a uniform way without the need to know the underlying database
    schemas or write complex SQL queries. Examples of BioMart databases are Ensembl,
    COSMIC, Uniprot, HGNC, Gramene, Wormbase and dbSNP mapped to Ensembl. These major
    databases give biomaRt users direct access to a diverse set of data and enable
    a wide range of powerful online queries from gene annotation to database mining.'
```

CHAPTER 41

bioconductor-biostrings

41.1 Summary

Memory efficient string containers, string matching algorithms, and other utilities, for fast manipulation of large biological sequences or sets of sequences.

41.2 Home

http://bioconductor.org/packages/release/bioc/html/Biostrings.html

41.3 Versions

- 2.38.3

41.4 License

Artistic-2.0

41.5 Meta

```
package:
  name: bioconductor-biostrings
  version: 2.38.3
source:
  fn: Biostrings_2.38.3.tar.gz
  url: https://bioconductor.org/packages/release/bioc/src/contrib/Biostrings_2.38.3.tar.gz
  md5: 6c7e9db1c84ac8f2614e38de0836c7fe
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
```

```
    - 'bioconductor-biocgenerics >=0.15.6'
    - 'bioconductor-iranges >=2.4.4'
    - 'bioconductor-s4vectors >=0.7.1'
    - 'bioconductor-xvector >=0.9.3'
    - 'r >=2.8.0'
  run:
    - 'bioconductor-biocgenerics >=0.15.6'
    - 'bioconductor-iranges >=2.4.4'
    - 'bioconductor-s4vectors >=0.7.1'
    - 'bioconductor-xvector >=0.9.3'
    - 'r >=2.8.0'
test:
  commands:
    - '$R -e "library(''Biostrings'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/Biostrings.html
  license: Artistic-2.0
  summary: 'Memory efficient string containers, string matching algorithms, and other
    utilities, for fast manipulation of large biological sequences or sets of sequences.'
```

CHAPTER 42

bioconductor-biovizbase

42.1 Summary

The biovizBase package is designed to provide a set of utilities, color schemes and conventions for genomic data. It serves as the base for various high-level packages for biological data visualization. This saves development effort and encourages consistency.

42.2 Home

http://bioconductor.org/packages/release/bioc/html/biovizBase.html

42.3 Versions

- 1.18.0

42.4 License

Artistic-2.0

42.5 Meta

```
package:
  name: bioconductor-biovizbase
  version: 1.18.0
source:
  fn: biovizBase_1.18.0.tar.gz
  url: https://bioarchive.galaxyproject.org/biovizBase_1.18.0.tar.gz
  md5: d678059b0ebe2a4478d31a3fa454ad67
build:
  number: 1
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
```

```
  build:
    - bioconductor-annotationdbi
    - bioconductor-biocgenerics
    - 'bioconductor-biostrings >=2.33.11'
    - 'bioconductor-genomeinfodb >=1.5.14'
    - 'bioconductor-genomicalignments >=1.1.16'
    - 'bioconductor-genomicfeatures >=1.21.19'
    - 'bioconductor-genomicranges >=1.17.19'
    - 'bioconductor-iranges >=1.99.28'
    - 'bioconductor-rsamtools >=1.17.28'
    - 'bioconductor-s4vectors >=0.2.4'
    - bioconductor-summarizedexperiment
    - 'bioconductor-variantannotation >=1.11.4'
    - 'r >=2.10'
    - r-dichromat
    - r-hmisc
    - r-rcolorbrewer
    - r-scales
  run:
    - bioconductor-annotationdbi
    - bioconductor-biocgenerics
    - 'bioconductor-biostrings >=2.33.11'
    - 'bioconductor-genomeinfodb >=1.5.14'
    - 'bioconductor-genomicalignments >=1.1.16'
    - 'bioconductor-genomicfeatures >=1.21.19'
    - 'bioconductor-genomicranges >=1.17.19'
    - 'bioconductor-iranges >=1.99.28'
    - 'bioconductor-rsamtools >=1.17.28'
    - 'bioconductor-s4vectors >=0.2.4'
    - bioconductor-summarizedexperiment
    - 'bioconductor-variantannotation >=1.11.4'
    - 'r >=2.10'
    - r-dichromat
    - r-hmisc
    - r-rcolorbrewer
    - r-scales
test:
  commands:
    - '$R -e "library(''biovizBase'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/biovizBase.html
  license: Artistic-2.0
  summary: 'The biovizBase package is designed to provide a set of utilities, color
    schemes and conventions for genomic data. It serves as the base for various high-level
    packages for biological data visualization. This saves development effort and
    encourages consistency.'
```

CHAPTER 43

bioconductor-bsgenome.ecoli.ncbi.20080805

43.1 Summary

Escherichia coli full genomes for several strains as provided by NCBI on 2008/08/05 and stored in Biostrings objects.

43.2 Home

http://bioconductor.org/packages/release/data/annotation/html/BSgenome.Ecoli.NCBI.20080805.html

43.3 Versions

- 1.3.1000

43.4 License

Artistic-2.0

43.5 Meta

```
package:
  name: bioconductor-bsgenome.ecoli.ncbi.20080805
  version: 1.3.1000
source:
  fn: BSgenome.Ecoli.NCBI.20080805_1.3.1000.tar.gz
  url: http://bioconductor.org/packages/release/data/annotation/src/contrib/BSgenome.Ecoli.NCBI.2008
  md5: c653e9cbee3faeb6fd5759b7575f234d
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
    - 'bioconductor-bsgenome >=1.33.5'
```

```
    - r
  run:
    - 'bioconductor-bsgenome >=1.33.5'
    - r
test:
  commands:
    - '$R -e "library(''BSgenome.Ecoli.NCBI.20080805'')"'
about:
  home: http://bioconductor.org/packages/release/data/annotation/html/BSgenome.Ecoli.NCBI.20080805.ht
  license: Artistic-2.0
  summary: 'Escherichia coli full genomes for several strains as provided by NCBI
    on 2008/08/05 and stored in Biostrings objects.'
```

CHAPTER 44

bioconductor-bsgenome.hsapiens.ucsc.hg19

44.1 Summary

Full genome sequences for Homo sapiens (Human) as provided by UCSC (hg19, Feb. 2009) and stored in Biostrings objects.

44.2 Home

http://bioconductor.org/packages/release/data/annotation/html/BSgenome.Hsapiens.UCSC.hg19.html

44.3 Versions

- 1.4.0

44.4 License

Artistic-2.0

44.5 Meta

```
package:
  name: bioconductor-bsgenome.hsapiens.ucsc.hg19
  version: 1.4.0

source:
  fn: BSgenome.Hsapiens.UCSC.hg19_1.4.0.tar.gz
  url: http://bioconductor.org/packages/release/data/annotation/src/contrib/BSgenome.Hsapiens.UCSC.hg
  md5: 672a988b28d8602afb2bd5595db7303b

build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
```

```
requirements:
  build:
    - 'bioconductor-bsgenome >=1.33.5'
    - r
  run:
    - 'bioconductor-bsgenome >=1.33.5'
    - r

test:
  commands:
    - '$R -e "library(''BSgenome.Hsapiens.UCSC.hg19'')"'

about:
  home: http://bioconductor.org/packages/release/data/annotation/html/BSgenome.Hsapiens.UCSC.hg19.htm
  license: Artistic-2.0
  summary: 'Full genome sequences for Homo sapiens (Human) as provided by UCSC (hg19, Feb. 2009) and
```

CHAPTER 45

bioconductor-bsgenome.mmusculus.ucsc.mm9

45.1 Summary

Full genome sequences for Mus musculus (Mouse) as provided by UCSC (mm9, Jul. 2007) and stored in Biostrings objects.

45.2 Home

http://bioconductor.org/packages/release/data/annotation/html/BSgenome.Mmusculus.UCSC.mm9.html

45.3 Versions

- 1.4.0

45.4 License

Artistic-2.0

45.5 Meta

```
package:
  name: bioconductor-bsgenome.mmusculus.ucsc.mm9
  version: 1.4.0

source:
  fn: BSgenome.Mmusculus.UCSC.mm9_1.4.0.tar.gz
  url: http://bioconductor.org/packages/release/data/annotation/src/contrib/BSgenome.Mmusculus.UCSC.m
  md5: 5a30ba2b4481a17e8e6979eb69eabf78

build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
```

```
requirements:
  build:
    - 'bioconductor-bsgenome >=1.33.5'
    - r
  run:
    - 'bioconductor-bsgenome >=1.33.5'
    - r

test:
  commands:
    - '$R -e "library(''BSgenome.Mmusculus.UCSC.mm9'')"'

about:
  home: http://bioconductor.org/packages/release/data/annotation/html/BSgenome.Mmusculus.UCSC.mm9.htm
  license: Artistic-2.0
  summary: 'Full genome sequences for Mus musculus (Mouse) as provided by UCSC (mm9, Jul. 2007) and s
```

CHAPTER 46

bioconductor-bsgenome

46.1 Summary

Infrastructure shared by all the Biostrings-based genome data packages

46.2 Home

http://bioconductor.org/packages/release/bioc/html/BSgenome.html

46.3 Versions

- 1.38.0

46.4 License

Artistic-2.0

46.5 Meta

```
package:
  name: bioconductor-bsgenome
  version: 1.38.0
source:
  fn: BSgenome_1.38.0.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/BSgenome_1.38.0.tar.gz
  md5: dd73af0d97993ca6122bf5383731d580
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
    - 'bioconductor-biocgenerics >=0.13.8'
```

```
    - 'bioconductor-biostrings >=2.35.3'
    - 'bioconductor-genomeinfodb >=1.3.19'
    - 'bioconductor-genomicranges >=1.19.23'
    - 'bioconductor-iranges >=2.1.33'
    - bioconductor-rsamtools
    - 'bioconductor-rtracklayer >=1.25.8'
    - 'bioconductor-s4vectors >=0.5.10'
    - bioconductor-xvector
    - 'r >=2.8.0'
  run:
    - 'bioconductor-biocgenerics >=0.13.8'
    - 'bioconductor-biostrings >=2.35.3'
    - 'bioconductor-genomeinfodb >=1.3.19'
    - 'bioconductor-genomicranges >=1.19.23'
    - 'bioconductor-iranges >=2.1.33'
    - bioconductor-rsamtools
    - 'bioconductor-rtracklayer >=1.25.8'
    - 'bioconductor-s4vectors >=0.5.10'
    - bioconductor-xvector
    - 'r >=2.8.0'
test:
  commands:
    - '$R -e "library(''BSgenome'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/BSgenome.html
  license: Artistic-2.0
  summary: 'Infrastructure shared by all the Biostrings-based genome data packages'
```

CHAPTER 47

bioconductor-bubbletree

47.1 Summary

CNV analysis in groups of tumor samples (Publication Pending).

47.2 Home

http://bioconductor.org/packages/release/bioc/html/BubbleTree.html

47.3 Versions

- 2.1.5

47.4 License

LGPL (>= 3)

47.5 Meta

```
package:
  name: bioconductor-bubbletree
  version: 2.1.5
source:
  fn: BubbleTree_2.1.5.tar.gz
  url: https://github.com/Bioconductor-mirror/BubbleTree/archive/a808167.tar.gz
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
    - bioconductor-biobase
    - 'bioconductor-biocgenerics >=0.7.5'
```

```
    - bioconductor-biocstyle
    - bioconductor-biovizbase
    - bioconductor-genomicranges
    - bioconductor-iranges
    - bioconductor-limma
    - 'r >=3.2.1'
    - r-dplyr
    - r-e1071
    - r-ggplot2
    - r-gridextra
    - r-gtable
    - r-gtools
    - r-magrittr
    - r-plyr
    - r-rainbow
    - r-rcolorbrewer
    - r-rgl
    - r-scales
    - r-writexls
  run:
    - bioconductor-biobase
    - 'bioconductor-biocgenerics >=0.7.5'
    - bioconductor-biocstyle
    - bioconductor-biovizbase
    - bioconductor-genomicranges
    - bioconductor-iranges
    - bioconductor-limma
    - 'r >=3.2.1'
    - r-dplyr
    - r-e1071
    - r-ggplot2
    - r-gridextra
    - r-gtable
    - r-gtools
    - r-magrittr
    - r-plyr
    - r-rainbow
    - r-rcolorbrewer
    - r-rgl
    - r-scales
    - r-writexls
test:
  commands:
    - '$R -e "library(''BubbleTree'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/BubbleTree.html
  license: 'LGPL (>= 3)'
  summary: 'CNV analysis in groups of tumor samples (Publication Pending).'
```

CHAPTER 48

bioconductor-category

48.1 Summary

A collection of tools for performing category analysis.

48.2 Home

http://bioconductor.org/packages/release/bioc/html/Category.html

48.3 Versions

- 2.36.0

48.4 License

Artistic-2.0

48.5 Meta

```
package:
  name: bioconductor-category
  version: 2.36.0

source:
  fn: Category_2.36.0.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/Category_2.36.0.tar.gz
  md5: 54d7d14521c22a8e16627b57974910ff

build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
```

```
requirements:
  build:
    - 'bioconductor-annotate >=1.15.6'
    - bioconductor-annotationdbi
    - bioconductor-biobase
    - 'bioconductor-biocgenerics >=0.13.8'
    - bioconductor-genefilter
    - bioconductor-go.db
    - bioconductor-graph
    - 'bioconductor-gseabase >=1.19.3'
    - bioconductor-rbgl
    - r
  run:
    - 'bioconductor-annotate >=1.15.6'
    - bioconductor-annotationdbi
    - bioconductor-biobase
    - 'bioconductor-biocgenerics >=0.13.8'
    - bioconductor-genefilter
    - bioconductor-go.db
    - bioconductor-graph
    - 'bioconductor-gseabase >=1.19.3'
    - bioconductor-rbgl
    - r

test:
  commands:
    - '$R -e "library(''Category'')"'

about:
  home: http://bioconductor.org/packages/release/bioc/html/Category.html
  license: Artistic-2.0
  summary: 'A collection of tools for performing category analysis.'
```

CHAPTER 49

bioconductor-chipcomp

49.1 Summary

ChIPComp detects differentially bound sharp binding sites across multiple conditions considering matching control.

49.2 Home

http://bioconductor.org/packages/release/bioc/html/ChIPComp.html

49.3 Versions

- 1.0.0

49.4 License

GPL

49.5 Meta

```
package:
  name: bioconductor-chipcomp
  version: 1.0.0

source:
  fn: ChIPComp_1.0.0.tar.gz
  url: https://bioarchive.galaxyproject.org/ChIPComp_1.0.0.tar.gz
  md5: 8f7972f826e866923a2691a3a634b01d

build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
```

```
requirements:
  build:
    - r >=3.2.0
    - bioconductor-genomicranges
    - bioconductor-iranges
    - bioconductor-rtracklayer
    - bioconductor-genomeinfodb
    - bioconductor-s4vectors
    - bioconductor-bsgenome.mmusculus.ucsc.mm9
    - bioconductor-biocgenerics
    - bioconductor-rsamtools
    - bioconductor-limma
    - bioconductor-bsgenome.hsapiens.ucsc.hg19

  run:
    - r >=3.2.0
    - bioconductor-genomicranges
    - bioconductor-iranges
    - bioconductor-rtracklayer
    - bioconductor-genomeinfodb
    - bioconductor-s4vectors
    - bioconductor-bsgenome.mmusculus.ucsc.mm9
    - bioconductor-biocgenerics
    - bioconductor-rsamtools
    - bioconductor-limma
    - bioconductor-bsgenome.hsapiens.ucsc.hg19

test:
  commands:
    - '$R -e "library(''ChIPComp'')"'

about:
  home: http://bioconductor.org/packages/release/bioc/html/ChIPComp.html
  license: GPL
  summary: 'ChIPComp detects differentially bound sharp binding sites across multiple conditions cons
```

CHAPTER 50

bioconductor-cn.mops

50.1 Summary

cn.mops (Copy Number estimation by a Mixture Of PoissonS) is a data processing pipeline for copy number variations and aberrations (CNVs and CNAs) from next generation sequencing (NGS) data. The package supplies functions to convert BAM files into read count matrices or genomic ranges objects, which are the input objects for cn.mops. cn.mops models the depths of coverage across samples at each genomic position. Therefore, it does not suffer from read count biases along chromosomes. Using a Bayesian approach, cn.mops decomposes read variations across samples into integer copy numbers and noise by its mixture components and Poisson distributions, respectively. cn.mops guarantees a low FDR because wrong detections are indicated by high noise and filtered out. cn.mops is very fast and written in C++.

50.2 Home

http://bioconductor.org/packages/release/bioc/html/cn.mops.html

50.3 Versions

- 1.16.2

50.4 License

LGPL (>= 2.0)

50.5 Meta

```
package:
  name: bioconductor-cn.mops
  version: 1.16.2
source:
  fn: cn.mops_1.16.2.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/cn.mops_1.16.2.tar.gz
  md5: a46119b3cf298fb773ca9f7aa8ef34ac
```

```
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
    - bioconductor-biobase
    - bioconductor-biocgenerics
    - bioconductor-genomicranges
    - bioconductor-iranges
    - bioconductor-rsamtools
    - 'r >=2.12'
  run:
    - bioconductor-biobase
    - bioconductor-biocgenerics
    - bioconductor-genomicranges
    - bioconductor-iranges
    - bioconductor-rsamtools
    - 'r >=2.12'
test:
  commands:
    - '$R -e "library(''cn.mops'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/cn.mops.html
  license: 'LGPL (>= 2.0)'
  summary: 'cn.mops (Copy Number estimation by a Mixture Of PoissonS) is a data processing
    pipeline for copy number variations and aberrations (CNVs and CNAs) from next
    generation sequencing (NGS) data. The package supplies functions to convert BAM
    files into read count matrices or genomic ranges objects, which are the input
    objects for cn.mops. cn.mops models the depths of coverage across samples at each
    genomic position. Therefore, it does not suffer from read count biases along chromosomes.
    Using a Bayesian approach, cn.mops decomposes read variations across samples into
    integer copy numbers and noise by its mixture components and Poisson distributions,
    respectively. cn.mops guarantees a low FDR because wrong detections are indicated
    by high noise and filtered out. cn.mops is very fast and written in C++.'
```

CHAPTER 51

bioconductor-complexheatmap

51.1 Summary

Complex heatmaps are efficient to visualize associations between different sources of data sets and reveal potential structures. Here the ComplexHeatmap package provides a highly flexible way to arrange multiple heatmaps and supports self-defined annotation graphics.

51.2 Home

http://bioconductor.org/packages/release/bioc/html/ComplexHeatmap.html

51.3 Versions

- 1.6.0

51.4 License

GPL (>= 2)

51.5 Meta

```
package:
  name: bioconductor-complexheatmap
  version: 1.6.0
source:
  fn: ComplexHeatmap_1.6.0.tar.gz
  url: https://bioarchive.galaxyproject.org/ComplexHeatmap_1.6.0.tar.gz
  md5: 326b74a2700c659cef63bb88884bd61f
build:
  number: 1
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
```

```
  build:
    - 'r >=3.1.2'
    - 'r-circlize >=0.3.1'
    - r-colorspace
    - 'r-dendextend >=1.0.1'
    - r-getoptlong
    - 'r-globaloptions >=0.0.6'
    - r-rcolorbrewer
  run:
    - 'r >=3.1.2'
    - 'r-circlize >=0.3.1'
    - r-colorspace
    - 'r-dendextend >=1.0.1'
    - r-getoptlong
    - 'r-globaloptions >=0.0.6'
    - r-rcolorbrewer
test:
  commands:
    - '$R -e "library(''ComplexHeatmap'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/ComplexHeatmap.html
  license: 'GPL (>= 2)'
  summary: 'Complex heatmaps are efficient to visualize associations between different
    sources of data sets and reveal potential structures. Here the ComplexHeatmap
    package provides a highly flexible way to arrange multiple heatmaps and supports
    self-defined annotation graphics.'
```

CHAPTER 52

bioconductor-csaw

52.1 Summary

Detection of differentially bound regions in ChIP-seq data with sliding windows, with methods for normalization and proper FDR control.

52.2 Home

http://bioconductor.org/packages/release/bioc/html/csaw.html

52.3 Versions

- 1.4.1

52.4 License

GPL-3

52.5 Meta

```
package:
  name: bioconductor-csaw
  version: 1.4.1
source:
  fn: csaw_1.4.1.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/csaw_1.4.1.tar.gz
  md5: 7ee43d43873dfa4f89d16d38563bd4b0
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
```

```
    - bioconductor-annotationdbi
    - bioconductor-edger
    - bioconductor-genomeinfodb
    - bioconductor-genomicalignments
    - bioconductor-genomicfeatures
    - bioconductor-genomicranges
    - bioconductor-iranges
    - bioconductor-limma
    - bioconductor-rsamtools
    - bioconductor-s4vectors
    - bioconductor-summarizedexperiment
    - 'r >=3.2.0'
  run:
    - bioconductor-annotationdbi
    - bioconductor-edger
    - bioconductor-genomeinfodb
    - bioconductor-genomicalignments
    - bioconductor-genomicfeatures
    - bioconductor-genomicranges
    - bioconductor-iranges
    - bioconductor-limma
    - bioconductor-rsamtools
    - bioconductor-s4vectors
    - bioconductor-summarizedexperiment
    - 'r >=3.2.0'
test:
  commands:
    - '$R -e "library(''csaw'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/csaw.html
  license: GPL-3
  summary: 'Detection of differentially bound regions in ChIP-seq data with sliding
    windows, with methods for normalization and proper FDR control.'
```

CHAPTER 53

bioconductor-dada2

53.1 Summary

Exact sample inference from Illumina amplicon data. Resolves real variants differing by as little as one nucleotide.

53.2 Home

http://bioconductor.org/packages/release/bioc/html/dada2.html

53.3 Versions

- 0.10.1

53.4 License

GPL-3

53.5 Meta

```
package:
  name: bioconductor-dada2
  version: 0.10.1
source:
  fn: master.zip
  url: https://github.com/benjjneb/dada2/archive/master.zip

build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
    - bioconductor-biobase
```

```
    - 'bioconductor-shortread >=1.24.0'
    - 'bioconductor-biocgenerics >=0.10.0'
    - 'bioconductor-biostrings >=2.32.1'
    - 'r >=3.1.0'
    - 'r-rcpp >=0.11.2'
    - 'r-data.table >=1.9.4'
    - 'r-foreach >=1.4.2'
    - 'r-ggplot2 >=1.0.0'
    - 'r-gridextra >=0.9'
    - 'r-reshape2 >=1.2.2'
  run:
    - bioconductor-biobase
    - 'bioconductor-shortread >=1.24.0'
    - 'bioconductor-biocgenerics >=0.10.0'
    - 'bioconductor-biostrings >=2.32.1'
    - 'r >=3.1.0'
    - 'r-rcpp >=0.11.2'
    - 'r-data.table >=1.9.4'
    - 'r-foreach >=1.4.2'
    - 'r-ggplot2 >=1.0.0'
    - 'r-gridextra >=0.9'
    - 'r-reshape2 >=1.2.2'
test:
  commands:
    - '$R -e "library(''dada2'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/dada2.html
  license: GPL-3
  summary: 'Exact sample inference from Illumina amplicon data. Resolves real variants differing by a
```

CHAPTER 54

bioconductor-degreport

54.1 Summary

Some nice figures for Differential Expression analysis.

54.2 Home

http://bioconductor.org/packages/release/bioc/html/DEGreport.html

54.3 Versions

- 1.7.2

54.4 License

LGPL (>= 3)

54.5 Meta

```
package:
  name: bioconductor-degreport
  version: 1.7.2
source:
  git_url: https://github.com/Bioconductor-mirror/DEGreport
build:
  number: 1
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
    - bioconductor-biobase
    - 'bioconductor-biocgenerics >=0.7.5'
    - r
```

```
    - r-ggplot2
    - r-nozzle.r1
    - r-plyr
    - bioconductor-edger
  run:
    - bioconductor-biobase
    - 'bioconductor-biocgenerics >=0.7.5'
    - r
    - r-ggplot2
    - r-nozzle.r1
    - r-plyr
    - bioconductor-edger
test:
  commands:
    - '$R -e "library(''DEGreport'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/DEGreport.html
  license: 'LGPL (>= 3)'
  summary: "Some nice figures for Differential Expression analysis."
```

CHAPTER 55

bioconductor-deseq

55.1 Summary

Estimate variance-mean dependence in count data from high-throughput sequencing assays and test for differential expression based on a model using the negative binomial distribution

55.2 Home

http://bioconductor.org/packages/release/bioc/html/DESeq.html

55.3 Versions

- 1.22.1

55.4 License

GPL (>= 3)

55.5 Meta

```
package:
  name: bioconductor-deseq
  version: 1.22.1
source:
  fn: DESeq_1.22.1.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/DESeq_1.22.1.tar.gz
  md5: c33cdeda38e731efd8f424502da1eaa6
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
```

```
    - 'bioconductor-biobase >=2.21.7'
    - 'bioconductor-biocgenerics >=0.7.5'
    - bioconductor-genefilter
    - bioconductor-geneplotter
    - r
    - r-locfit
    - r-rcolorbrewer
  run:
    - 'bioconductor-biobase >=2.21.7'
    - 'bioconductor-biocgenerics >=0.7.5'
    - bioconductor-genefilter
    - bioconductor-geneplotter
    - r
    - r-locfit
    - r-rcolorbrewer
test:
  commands:
    - '$R -e "library(''DESeq'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/DESeq.html
  license: 'GPL (>= 3)'
  summary: 'Estimate variance-mean dependence in count data from high-throughput sequencing
    assays and test for differential expression based on a model using the negative
    binomial distribution'
```

CHAPTER 56

bioconductor-deseq2

56.1 Summary

Estimate variance-mean dependence in count data from high-throughput sequencing assays and test for differential expression based on a model using the negative binomial distribution.

56.2 Home

http://bioconductor.org/packages/release/bioc/html/DESeq2.html

56.3 Versions

- 1.10.0

56.4 License

LGPL (>= 3)

56.5 Meta

```
package:
  name: bioconductor-deseq2
  version: 1.10.0
source:
  fn: DESeq2_1.10.0.tar.gz
  url: https://bioarchive.galaxyproject.org/DESeq2_1.10.0.tar.gz
  md5: 47d76b717b868244627ced415ecdb03d
build:
  number: 1
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
```

```
    - bioconductor-biobase
    - 'bioconductor-biocgenerics >=0.7.5'
    - bioconductor-biocparallel
    - bioconductor-genefilter
    - bioconductor-geneplotter
    - bioconductor-genomicranges
    - bioconductor-iranges
    - bioconductor-s4vectors
    - 'bioconductor-summarizedexperiment >=0.2.0'
    - r
    - r-ggplot2
    - r-hmisc
    - r-locfit
    - 'r-rcpp >=0.10.1'
    - 'r-rcpparmadillo >=0.3.4.4'
  run:
    - bioconductor-biobase
    - 'bioconductor-biocgenerics >=0.7.5'
    - bioconductor-biocparallel
    - bioconductor-genefilter
    - bioconductor-geneplotter
    - bioconductor-genomicranges
    - bioconductor-iranges
    - bioconductor-s4vectors
    - 'bioconductor-summarizedexperiment >=0.2.0'
    - r
    - r-ggplot2
    - r-hmisc
    - r-locfit
    - 'r-rcpp >=0.10.1'
    - 'r-rcpparmadillo >=0.3.4.4'
test:
  commands:
    - '$R -e "library(''DESeq2'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/DESeq2.html
  license: 'LGPL (>= 3)'
  summary: 'Estimate variance-mean dependence in count data from high-throughput sequencing
    assays and test for differential expression based on a model using the negative
    binomial distribution.'
```

CHAPTER 57

bioconductor-dexseq

57.1 Summary

The package is focused on finding differential exon usage using RNA-seq exon counts between samples with different experimental designs. It provides functions that allows the user to make the necessary statistical tests based on a model that uses the negative binomial distribution to estimate the variance between biological replicates and generalized linear models for testing. The package also provides functions for the visualization and exploration of the results.

57.2 Home

http://bioconductor.org/packages/release/bioc/html/DEXSeq.html

57.3 Versions

- 1.16.6

57.4 License

GPL (>= 3)

57.5 Meta

```
package:
  name: bioconductor-dexseq
  version: 1.16.6
source:
  fn: DEXSeq_1.16.6.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/DEXSeq_1.16.6.tar.gz
  md5: 54a02541abe6790f757c0740a28c4e2f
build:
  number: 0
  rpaths:
    - lib/R/lib/
```

```
    - lib/
requirements:
  build:
    - bioconductor-biobase
    - bioconductor-biocgenerics
    - bioconductor-biocparallel
    - bioconductor-biomart
    - 'bioconductor-deseq2 >=1.9.11'
    - bioconductor-genefilter
    - bioconductor-geneplotter
    - 'bioconductor-genomicranges >=1.19.6'
    - 'bioconductor-iranges >=2.1.10'
    - bioconductor-rsamtools
    - r
    - r-hwriter
    - r-rcolorbrewer
    - r-statmod
    - r-stringr
  run:
    - bioconductor-biobase
    - bioconductor-biocgenerics
    - bioconductor-biocparallel
    - bioconductor-biomart
    - 'bioconductor-deseq2 >=1.9.11'
    - bioconductor-genefilter
    - bioconductor-geneplotter
    - 'bioconductor-genomicranges >=1.19.6'
    - 'bioconductor-iranges >=2.1.10'
    - bioconductor-rsamtools
    - r
    - r-hwriter
    - r-rcolorbrewer
    - r-statmod
    - r-stringr
test:
  commands:
    - '$R -e "library(''DEXSeq'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/DEXSeq.html
  license: 'GPL (>= 3)'
  summary: 'The package is focused on finding differential exon usage using RNA-seq
    exon counts between samples with different experimental designs. It provides functions
    that allows the user to make the necessary statistical tests based on a model
    that uses the negative binomial distribution to estimate the variance between
    biological replicates and generalized linear models for testing. The package also
    provides functions for the visualization and exploration of the results.'
```

CHAPTER 58

bioconductor-diffbind

58.1 Summary

Compute differentially bound sites from multiple ChIP-seq experiments using affinity (quantitative) data. Also enables occupancy (overlap) analysis and plotting functions.

58.2 Home

http://bioconductor.org/packages/release/bioc/html/DiffBind.html

58.3 Versions

- 1.16.3

58.4 License

Artistic-2.0

58.5 Meta

```
package:
  name: bioconductor-diffbind
  version: 1.16.3

source:
  fn: DiffBind_1.16.3.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/DiffBind_1.16.3.tar.gz
  md5: 0a565fcb40c62f6c1a4ae21a289916a6

build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
```

```
requirements:
  build:
    - bioconductor-edger
    - bioconductor-genomicalignments
    - bioconductor-genomicranges
    - bioconductor-iranges
    - bioconductor-limma
    - bioconductor-summarizedexperiment
    - bioconductor-systempiper
    - bioconductor-zlibbioc
    - 'r >=3.2.2'
    - r-amap
    - r-gplots
    - r-locfit
    - r-rcolorbrewer
  run:
    - bioconductor-edger
    - bioconductor-genomicalignments
    - bioconductor-genomicranges
    - bioconductor-iranges
    - bioconductor-limma
    - bioconductor-summarizedexperiment
    - bioconductor-systempiper
    - bioconductor-zlibbioc
    - 'r >=3.2.2'
    - r-amap
    - r-gplots
    - r-locfit
    - r-rcolorbrewer

test:
  commands:
    - '$R -e "library(''DiffBind'')"'

about:
  home: http://bioconductor.org/packages/release/bioc/html/DiffBind.html
  license: Artistic-2.0
  summary: 'Compute differentially bound sites from multiple ChIP-seq experiments using affinity (qua
```

CHAPTER 59

bioconductor-dnacopy

59.1 Summary

Implements the circular binary segmentation (CBS) algorithm to segment DNA copy number data and identify genomic regions with abnormal copy number.

59.2 Home

http://bioconductor.org/packages/release/bioc/html/DNAcopy.html

59.3 Versions

- 1.44.0

59.4 License

GPL (>= 2)

59.5 Meta

```
package:
  name: bioconductor-dnacopy
  version: 1.44.0
source:
  fn: DNAcopy_1.44.0.tar.gz
  url: https://bioarchive.galaxyproject.org/DNAcopy_1.44.0.tar.gz
  md5: 63723005e489892ad311993076788857
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
```

```
    - r
  run:
    - r
test:
  commands:
    - '$R -e "library(''DNAcopy'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/DNAcopy.html
  license: 'GPL (>= 2)'
  summary: 'Implements the circular binary segmentation (CBS) algorithm to segment
    DNA copy number data and identify genomic regions with abnormal copy number.'
```

CHAPTER 60

bioconductor-edger

60.1 Summary

Differential expression analysis of RNA-seq expression profiles with biological replication. Implements a range of statistical methodology based on the negative binomial distributions, including empirical Bayes estimation, exact tests, generalized linear models and quasi-likelihood tests. As well as RNA-seq, it be applied to differential signal analysis of other types of genomic data that produce counts, including ChIP-seq, SAGE and CAGE.

60.2 Home

http://bioconductor.org/packages/release/bioc/html/edgeR.html

60.3 Versions

- 3.12.0

60.4 License

GPL (>=2)

60.5 Meta

```
package:
  name: bioconductor-edger
  version: 3.12.0
source:
  fn: edgeR_3.12.0.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/edgeR_3.12.0.tar.gz
  md5: d46e201e0ed0895d88609bde6a7272af
build:
  number: 0
  rpaths:
    - lib/R/lib/
```

```
    - lib/
requirements:
  build:
    - bioconductor-limma
    - 'r >=2.15.0'
  run:
    - bioconductor-limma
    - 'r >=2.15.0'
test:
  commands:
    - '$R -e "library(''edgeR'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/edgeR.html
  license: 'GPL (>=2)'
  summary: 'Differential expression analysis of RNA-seq expression profiles with biological
    replication. Implements a range of statistical methodology based on the negative
    binomial distributions, including empirical Bayes estimation, exact tests, generalized
    linear models and quasi-likelihood tests. As well as RNA-seq, it be applied to
    differential signal analysis of other types of genomic data that produce counts,
    including ChIP-seq, SAGE and CAGE.'
```

CHAPTER 61

bioconductor-fourcseq

61.1 Summary

FourCSeq is an R package dedicated to the analysis of (multiplexed) 4C sequencing data. The package provides a pipeline to detect specific interactions between DNA elements and identify differential interactions between conditions. The statistical analysis in R starts with individual bam files for each sample as inputs. To obtain these files, the package contains a python script (extdata/python/demultiplex.py) to demultiplex libraries and trim off primer sequences. With a standard alignment software the required bam files can be then be generated.

61.2 Home

http://bioconductor.org/packages/release/bioc/html/FourCSeq.html

61.3 Versions

- 1.4.0

61.4 License

GPL (>= 3)

61.5 Meta

```
package:
  name: bioconductor-fourcseq
  version: 1.4.0
source:
  fn: FourCSeq_1.4.0.tar.gz
  url: https://bioarchive.galaxyproject.org/FourCSeq_1.4.0.tar.gz
  md5: 1fa8c7291a9c0806ae9ada8e1f97e7f1
build:
  number: 1
  rpaths:
```

```
    - lib/R/lib/
    - lib/
requirements:
  build:
    - bioconductor-biobase
    - bioconductor-biostrings
    - 'bioconductor-deseq2 >=1.9.11'
    - bioconductor-genomicalignments
    - bioconductor-genomicranges
    - bioconductor-ggbio
    - bioconductor-rsamtools
    - bioconductor-rtracklayer
    - bioconductor-summarizedexperiment
    - 'r >=3.0'
    - r-fda
    - r-ggplot2
    - r-gtools
    - r-lsd
    - r-reshape2
  run:
    - bioconductor-biobase
    - bioconductor-biostrings
    - 'bioconductor-deseq2 >=1.9.11'
    - bioconductor-genomicalignments
    - bioconductor-genomicranges
    - bioconductor-ggbio
    - bioconductor-rsamtools
    - bioconductor-rtracklayer
    - bioconductor-summarizedexperiment
    - 'r >=3.0'
    - r-fda
    - r-ggplot2
    - r-gtools
    - r-lsd
    - r-reshape2
test:
  commands:
    - '$R -e "library(''FourCSeq'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/FourCSeq.html
  license: 'GPL (>= 3)'
  summary: 'FourCSeq is an R package dedicated to the analysis of (multiplexed) 4C
    sequencing data. The package provides a pipeline to detect specific interactions
    between DNA elements and identify differential interactions between conditions.
    The statistical analysis in R starts with individual bam files for each sample
    as inputs. To obtain these files, the package contains a python script (extdata/python/demultiple
    to demultiplex libraries and trim off primer sequences. With a standard alignment
    software the required bam files can be then be generated.'
```

CHAPTER 62

bioconductor-genefilter

62.1 Summary

Some basic functions for filtering genes

62.2 Home

http://bioconductor.org/packages/release/bioc/html/genefilter.html

62.3 Versions

- 1.52.0

62.4 License

Artistic-2.0

62.5 Meta

```
package:
  name: bioconductor-genefilter
  version: 1.52.0
source:
  fn: genefilter_1.52.0.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/genefilter_1.52.0.tar.gz
  md5: b7eeef0248b242ece1061193107c660f
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
    - bioconductor-annotate
```

```
    - bioconductor-annotationdbi
    - bioconductor-biobase
    - r
  run:
    - bioconductor-annotate
    - bioconductor-annotationdbi
    - bioconductor-biobase
    - r
test:
  commands:
    - '$R -e "library(''genefilter'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/genefilter.html
  license: Artistic-2.0
  summary: 'Some basic functions for filtering genes'
```

CHAPTER 63

bioconductor-geneplotter

63.1 Summary

Functions for plotting genomic data

63.2 Home

http://bioconductor.org/packages/release/bioc/html/geneplotter.html

63.3 Versions

- 1.48.0

63.4 License

Artistic-2.0

63.5 Meta

```
package:
  name: bioconductor-geneplotter
  version: 1.48.0
source:
  fn: geneplotter_1.48.0.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/geneplotter_1.48.0.tar.gz
  md5: 9f74bd0d9d500f158300ef7b0374df20
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
    - bioconductor-annotate
```

```
    - bioconductor-annotationdbi
    - bioconductor-biobase
    - bioconductor-biocgenerics
    - 'r >=2.10'
    - r-rcolorbrewer
  run:
    - bioconductor-annotate
    - bioconductor-annotationdbi
    - bioconductor-biobase
    - bioconductor-biocgenerics
    - 'r >=2.10'
    - r-rcolorbrewer
test:
  commands:
    - '$R -e "library(''geneplotter'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/geneplotter.html
  license: Artistic-2.0
  summary: 'Functions for plotting genomic data'
```

CHAPTER 64

bioconductor-genomeinfodb

64.1 Summary

Contains data and functions that define and allow translation between different chromosome sequence naming conventions (e.g., "chr1" versus "1"), including a function that attempts to place sequence names in their natural, rather than lexicographic, order.

64.2 Home

http://bioconductor.org/packages/release/bioc/html/GenomeInfoDb.html

64.3 Versions

- 1.6.1

64.4 License

Artistic-2.0

64.5 Meta

```
package:
  name: bioconductor-genomeinfodb
  version: 1.6.1
source:
  fn: GenomeInfoDb_1.6.1.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/GenomeInfoDb_1.6.1.tar.gz
  md5: 993d970ab69d0a739f15f9ab44658672
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
```

```
  build:
    - 'bioconductor-biocgenerics >=0.13.8'
    - 'bioconductor-iranges >=1.99.26'
    - 'bioconductor-s4vectors >=0.7.11'
    - 'r >=3.1'
  run:
    - 'bioconductor-biocgenerics >=0.13.8'
    - 'bioconductor-iranges >=1.99.26'
    - 'bioconductor-s4vectors >=0.7.11'
    - 'r >=3.1'
test:
  commands:
    - '$R -e "library(''GenomeInfoDb'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/GenomeInfoDb.html
  license: Artistic-2.0
  summary: 'Contains data and functions that define and allow translation between
    different chromosome sequence naming conventions (e.g., "chr1" versus "1"), including
    a function that attempts to place sequence names in their natural, rather than
    lexicographic, order.'
```

CHAPTER 65

bioconductor-genomicalignments

65.1 Summary

Provides efficient containers for storing and manipulating short genomic alignments (typically obtained by aligning short reads to a reference genome). This includes read counting, computing the coverage, junction detection, and working with the nucleotide content of the alignments.

65.2 Home

http://bioconductor.org/packages/release/bioc/html/GenomicAlignments.html

65.3 Versions

- 1.6.3

65.4 License

Artistic-2.0

65.5 Meta

```
package:
  name: bioconductor-genomicalignments
  version: 1.6.3
source:
  fn: GenomicAlignments_1.6.1.tar.gz
  url: https://bioconductor.org/packages/3.2/bioc/src/contrib/GenomicAlignments_1.6.3.tar.gz
  md5: 72db6a4c7212025323ef04f95806c4ba
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
```

```
  build:
    - 'bioconductor-biocgenerics >=0.15.3'
    - bioconductor-biocparallel
    - 'bioconductor-biostrings >=2.37.1'
    - 'bioconductor-genomeinfodb >=1.1.20'
    - 'bioconductor-genomicranges >=1.21.6'
    - 'bioconductor-iranges >=2.3.21'
    - 'bioconductor-rsamtools >=1.21.4'
    - 'bioconductor-s4vectors >=0.7.1'
    - 'bioconductor-summarizedexperiment >=0.3.1'
    - 'r >=2.10'
  run:
    - 'bioconductor-biocgenerics >=0.15.3'
    - bioconductor-biocparallel
    - 'bioconductor-biostrings >=2.37.1'
    - 'bioconductor-genomeinfodb >=1.1.20'
    - 'bioconductor-genomicranges >=1.21.6'
    - 'bioconductor-iranges >=2.3.21'
    - 'bioconductor-rsamtools >=1.21.4'
    - 'bioconductor-s4vectors >=0.7.1'
    - 'bioconductor-summarizedexperiment >=0.3.1'
    - 'r >=2.10'
test:
  commands:
    - '$R -e "library(''GenomicAlignments'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/GenomicAlignments.html
  license: Artistic-2.0
  summary: 'Provides efficient containers for storing and manipulating short genomic
    alignments (typically obtained by aligning short reads to a reference genome).
    This includes read counting, computing the coverage, junction detection, and working
    with the nucleotide content of the alignments.'
```

CHAPTER 66

bioconductor-genomicfeatures

66.1 Summary

A set of tools and methods for making and manipulating transcript centric annotations. With these tools the user can easily download the genomic locations of the transcripts, exons and cds of a given organism, from either the UCSC Genome Browser or a BioMart database (more sources will be supported in the future). This information is then stored in a local database that keeps track of the relationship between transcripts, exons, cds and genes. Flexible methods are provided for extracting the desired features in a convenient format.

66.2 Home

http://bioconductor.org/packages/release/bioc/html/GenomicFeatures.html

66.3 Versions

- 1.22.6

66.4 License

Artistic-2.0

66.5 Meta

```
package:
  name: bioconductor-genomicfeatures
  version: 1.22.6
source:
  fn: GenomicFeatures_1.22.6.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/GenomicFeatures_1.22.6.tar.gz
  md5: 545870dce3fd9d04726943cc8158c05b
build:
  number: 0
  rpaths:
```

```
    - lib/R/lib/
    - lib/
requirements:
  build:
    - 'bioconductor-annotationdbi >=1.27.9'
    - 'bioconductor-biobase >=2.15.1'
    - 'bioconductor-biocgenerics >=0.1.0'
    - 'bioconductor-biomart >=2.17.1'
    - 'bioconductor-biostrings >=2.23.3'
    - 'bioconductor-genomeinfodb >=1.5.16'
    - 'bioconductor-genomicranges >=1.21.32'
    - 'bioconductor-iranges >=2.3.21'
    - 'bioconductor-rtracklayer >=1.29.24'
    - 'bioconductor-s4vectors >=0.7.17'
    - bioconductor-xvector
    - r
    - 'r-dbi'
    - r-rcurl
    - 'r-rsqlite'
  run:
    - 'bioconductor-annotationdbi >=1.27.9'
    - 'bioconductor-biobase >=2.15.1'
    - 'bioconductor-biocgenerics >=0.1.0'
    - 'bioconductor-biomart >=2.17.1'
    - 'bioconductor-biostrings >=2.23.3'
    - 'bioconductor-genomeinfodb >=1.5.16'
    - 'bioconductor-genomicranges >=1.21.32'
    - 'bioconductor-iranges >=2.3.21'
    - 'bioconductor-rtracklayer >=1.29.24'
    - 'bioconductor-s4vectors >=0.7.17'
    - bioconductor-xvector
    - r
    - 'r-dbi'
    - r-rcurl
    - 'r-rsqlite'
test:
  commands:
    - '$R -e "library(''GenomicFeatures'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/GenomicFeatures.html
  license: Artistic-2.0
  summary: 'A set of tools and methods for making and manipulating transcript centric
    annotations. With these tools the user can easily download the genomic locations
    of the transcripts, exons and cds of a given organism, from either the UCSC Genome
    Browser or a BioMart database (more sources will be supported in the future).
    This information is then stored in a local database that keeps track of the relationship
    between transcripts, exons, cds and genes. Flexible methods are provided for extracting
    the desired features in a convenient format.'
```

CHAPTER 67

bioconductor-genomicranges

67.1 Summary

The ability to efficiently represent and manipulate genomic annotations and alignments is playing a central role when it comes to analyzing high-throughput sequencing data (a.k.a. NGS data). The GenomicRanges package defines general purpose containers for storing and manipulating genomic intervals and variables defined along a genome. More specialized containers for representing and manipulating short alignments against a reference genome, or a matrix-like summarization of an experiment, are defined in the GenomicAlignments and SummarizedExperiment packages respectively. Both packages build on top of the GenomicRanges infrastructure.

67.2 Home

http://bioconductor.org/packages/release/bioc/html/GenomicRanges.html

67.3 Versions

- 1.22.3

67.4 License

Artistic-2.0

67.5 Meta

```
package:
  name: bioconductor-genomicranges
  version: 1.22.3
source:
  fn: GenomicRanges_1.22.3.tar.gz
  url: https://bioconductor.org/packages/release/bioc/src/contrib/GenomicRanges_1.22.3.tar.gz
  md5: 9b39b784e91803b31fc861438ba3831e
build:
  number: 0
```

```
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
    - 'bioconductor-biocgenerics >=0.16.1'
    - 'bioconductor-genomeinfodb >=1.1.20'
    - 'bioconductor-iranges >=2.4.6'
    - 'bioconductor-s4vectors >=0.8.1'
    - bioconductor-xvector
    - 'r >=2.10'
  run:
    - 'bioconductor-biocgenerics >=0.16.1'
    - 'bioconductor-genomeinfodb >=1.1.20'
    - 'bioconductor-iranges >=2.4.6'
    - 'bioconductor-s4vectors >=0.8.1'
    - bioconductor-xvector
    - 'r >=2.10'
test:
  commands:
    - '$R -e "library(''GenomicRanges'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/GenomicRanges.html
  license: Artistic-2.0
  summary: 'The ability to efficiently represent and manipulate genomic annotations
    and alignments is playing a central role when it comes to analyzing high-throughput
    sequencing data (a.k.a. NGS data). The GenomicRanges package defines general purpose
    containers for storing and manipulating genomic intervals and variables defined
    along a genome. More specialized containers for representing and manipulating
    short alignments against a reference genome, or a matrix-like summarization of
    an experiment, are defined in the GenomicAlignments and SummarizedExperiment packages
    respectively. Both packages build on top of the GenomicRanges infrastructure.'
```

CHAPTER 68

bioconductor-geoquery

68.1 Summary

The NCBI Gene Expression Omnibus (GEO) is a public repository of microarray data. Given the rich and varied nature of this resource, it is only natural to want to apply BioConductor tools to these data. GEOquery is the bridge between GEO and BioConductor.

68.2 Home

http://bioconductor.org/packages/release/bioc/html/GEOquery.html

68.3 Versions

- 2.36.0

68.4 License

GPL-2

68.5 Meta

```
package:
  name: bioconductor-geoquery
  version: 2.36.0
source:
  fn: GEOquery_2.36.0.tar.gz
  url: https://bioarchive.galaxyproject.org/GEOquery_2.36.0.tar.gz
  md5: 1f7b6b82e259d994964f0ecde861dfa6
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
```

```
  build:
    - bioconductor-biobase
    - r
    - r-rcurl
    - r-xml
  run:
    - bioconductor-biobase
    - r
    - r-rcurl
    - r-xml
test:
  commands:
    - '$R -e "library(''GEOquery'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/GEOquery.html
  license: GPL-2
  summary: 'The NCBI Gene Expression Omnibus (GEO) is a public repository of microarray
    data.  Given the rich and varied nature of this resource, it is only natural to
    want to apply BioConductor tools to these data.  GEOquery is the bridge between
    GEO and BioConductor.'
```

CHAPTER 69

bioconductor-ggbio

69.1 Summary

The ggbio package extends and specializes the grammar of graphics for biological data. The graphics are designed to answer common scientific questions, in particular those often asked of high throughput genomics data. All core Bioconductor data structures are supported, where appropriate. The package supports detailed views of particular genomic regions, as well as genome-wide overviews. Supported overviews include ideograms and grand linear views. High-level plots include sequence fragment length, edge-linked interval to data view, mismatch pileup, and several splicing summaries.

69.2 Home

http://bioconductor.org/packages/release/bioc/html/ggbio.html

69.3 Versions

- 1.18.1

69.4 License

Artistic-2.0

69.5 Meta

```
package:
  name: bioconductor-ggbio
  version: 1.18.1
source:
  fn: ggbio_1.18.1.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/ggbio_1.18.1.tar.gz
  md5: f2161343a3e9c32196daa725e0bc367e
build:
  number: 0
```

```
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
    - bioconductor-biobase
    - bioconductor-biocgenerics
    - bioconductor-biostrings
    - 'bioconductor-biovizbase >=1.17.1'
    - bioconductor-bsgenome
    - 'bioconductor-genomeinfodb >=1.1.3'
    - 'bioconductor-genomicalignments >=1.1.16'
    - 'bioconductor-genomicfeatures >=1.17.13'
    - 'bioconductor-genomicranges >=1.21.10'
    - bioconductor-iranges
    - bioconductor-organismdbi
    - 'bioconductor-rsamtools >=1.17.28'
    - 'bioconductor-rtracklayer >=1.25.16'
    - bioconductor-s4vectors
    - bioconductor-summarizedexperiment
    - 'bioconductor-variantannotation >=1.11.4'
    - r
    - r-ggally
    - 'r-ggplot2 >=1.0.0'
    - r-gridextra
    - r-gtable
    - r-hmisc
    - r-reshape2
    - r-scales
  run:
    - bioconductor-biobase
    - bioconductor-biocgenerics
    - bioconductor-biostrings
    - 'bioconductor-biovizbase >=1.17.1'
    - bioconductor-bsgenome
    - 'bioconductor-genomeinfodb >=1.1.3'
    - 'bioconductor-genomicalignments >=1.1.16'
    - 'bioconductor-genomicfeatures >=1.17.13'
    - 'bioconductor-genomicranges >=1.21.10'
    - bioconductor-iranges
    - bioconductor-organismdbi
    - 'bioconductor-rsamtools >=1.17.28'
    - 'bioconductor-rtracklayer >=1.25.16'
    - bioconductor-s4vectors
    - bioconductor-summarizedexperiment
    - 'bioconductor-variantannotation >=1.11.4'
    - r
    - r-ggally
    - 'r-ggplot2 >=1.0.0'
    - r-gridextra
    - r-gtable
    - r-hmisc
    - r-reshape2
    - r-scales
test:
  commands:
    - '$R -e "library(''ggbio'')"'
about:
```

```
  home: http://bioconductor.org/packages/release/bioc/html/ggbio.html
  license: Artistic-2.0
  summary: 'The ggbio package extends and specializes the grammar of graphics for
    biological data. The graphics are designed to answer common scientific questions,
    in particular those often asked of high throughput genomics data. All core Bioconductor
    data structures are supported, where appropriate. The package supports detailed
    views of particular genomic regions, as well as genome-wide overviews. Supported
    overviews include ideograms and grand linear views. High-level plots include sequence
    fragment length, edge-linked interval to data view, mismatch pileup, and several
    splicing summaries.'
```

CHAPTER 70

bioconductor-go.db

70.1 Summary

A set of annotation maps describing the entire Gene Ontology assembled using data from GO

70.2 Home

http://bioconductor.org/packages/release/data/annotation/html/GO.db.html

70.3 Versions

- 3.2.2

70.4 License

Artistic-2.0

70.5 Meta

```
package:
  name: bioconductor-go.db
  version: 3.2.2

source:
  fn: GO.db_3.2.2.tar.gz
  url: http://bioconductor.org/packages/release/data/annotation/src/contrib/GO.db_3.2.2.tar.gz
  md5: efe8b3aba3534ccab0210d8def50f27d

build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
```

```
requirements:
  build:
    - 'bioconductor-annotationdbi >=1.31.18'
    - 'r >=2.7.0'
  run:
    - 'bioconductor-annotationdbi >=1.31.18'
    - 'r >=2.7.0'

test:
  commands:
    - '$R -e "library(''GO.db'')"'

about:
  home: http://bioconductor.org/packages/release/data/annotation/html/GO.db.html
  license: Artistic-2.0
  summary: 'A set of annotation maps describing the entire Gene Ontology assembled using data from GO
```

CHAPTER 71

bioconductor-gostats

71.1 Summary

A set of tools for interacting with GO and microarray data. A variety of basic manipulation tools for graphs, hypothesis testing and other simple calculations.

71.2 Home

http://bioconductor.org/packages/release/bioc/html/GOstats.html

71.3 Versions

- 2.36.0

71.4 License

Artistic-2.0

71.5 Meta

```
package:
  name: bioconductor-gostats
  version: 2.36.0

source:
  fn: GOstats_2.36.0.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/GOstats_2.36.0.tar.gz
  md5: 55afa051acac22a4acccba24c1c6c806

build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
```

```
requirements:
  build:
    - 'bioconductor-annotate >=1.13.2'
    - 'bioconductor-annotationdbi >=0.0.89'
    - bioconductor-annotationforge
    - 'bioconductor-biobase >=1.15.29'
    - 'bioconductor-category >=2.3.26'
    - 'bioconductor-go.db >=1.13.0'
    - 'bioconductor-graph >=1.15.15'
    - bioconductor-rbgl
    - 'r >=2.10'
  run:
    - 'bioconductor-annotate >=1.13.2'
    - 'bioconductor-annotationdbi >=0.0.89'
    - bioconductor-annotationforge
    - 'bioconductor-biobase >=1.15.29'
    - 'bioconductor-category >=2.3.26'
    - 'bioconductor-go.db >=1.13.0'
    - 'bioconductor-graph >=1.15.15'
    - bioconductor-rbgl
    - 'r >=2.10'

test:
  commands:
    - '$R -e "library(''GOstats'')"'

about:
  home: http://bioconductor.org/packages/release/bioc/html/GOstats.html
  license: Artistic-2.0
  summary: 'A set of tools for interacting with GO and microarray data. A variety of basic manipulati
```

CHAPTER 72

bioconductor-graph

72.1 Summary

A package that implements some simple graph handling capabilities.

72.2 Home

http://bioconductor.org/packages/release/bioc/html/graph.html

72.3 Versions

- 1.48.0

72.4 License

Artistic-2.0

72.5 Meta

```
package:
  name: bioconductor-graph
  version: 1.48.0
source:
  fn: graph_1.48.0.tar.gz
  url: https://bioarchive.galaxyproject.org/graph_1.48.0.tar.gz
  md5: 7933ce72bc5014060316b81035ef8273
  patches:            # [osx]
    - Makevars.patch  # [osx]
build:
  number: 1
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
```

```
  build:
    - 'bioconductor-biocgenerics >=0.13.11'
    - 'r >=2.10'
  run:
    - 'bioconductor-biocgenerics >=0.13.11'
    - 'r >=2.10'
test:
  commands:
    - '$R -e "library(''graph'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/graph.html
  license: Artistic-2.0
  summary: 'A package that implements some simple graph handling capabilities.'
```

CHAPTER 73

bioconductor-graphite

73.1 Summary

Graph objects from pathway topology derived from Biocarta, HumanCyc, KEGG, NCI, Panther, Reactome and SPIKE databases.

73.2 Home

http://bioconductor.org/packages/release/bioc/html/graphite.html

73.3 Versions

- 1.16.0

73.4 License

AGPL-3

73.5 Meta

```
package:
  name: bioconductor-graphite
  version: 1.16.0
source:
  fn: graphite_1.16.0.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/graphite_1.16.0.tar.gz
  md5: 7ecb6332bd14b90fd70990eefb614645
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
```

```
    - bioconductor-annotationdbi
    - bioconductor-biocgenerics
    - bioconductor-graph
    - 'r >=2.10'
    - r-rappdirs
  run:
    - bioconductor-annotationdbi
    - bioconductor-biocgenerics
    - bioconductor-graph
    - 'r >=2.10'
    - r-rappdirs
test:
  commands:
    - '$R -e "library(''graphite'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/graphite.html
  license: AGPL-3
  summary: 'Graph objects from pathway topology derived from Biocarta, HumanCyc, KEGG,
    NCI, Panther, Reactome and SPIKE databases.'
```

CHAPTER 74

bioconductor-gseabase

74.1 Summary

This package provides classes and methods to support Gene Set Enrichment Analysis (GSEA).

74.2 Home

http://bioconductor.org/packages/release/bioc/html/GSEABase.html

74.3 Versions

- 1.32.0

74.4 License

Artistic-2.0

74.5 Meta

```
package:
  name: bioconductor-gseabase
  version: 1.32.0

source:
  fn: GSEABase_1.32.0.tar.gz
  url: https://bioarchive.galaxyproject.org/GSEABase_1.32.0.tar.gz
  md5: 41d2e327fe2c603d409ea3ca4fdf1767

build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
```

```
requirements:
  build:
    - 'bioconductor-annotate >=1.45.3'
    - bioconductor-annotationdbi
    - 'bioconductor-biobase >=2.17.8'
    - 'bioconductor-biocgenerics >=0.13.8'
    - 'bioconductor-graph >=1.37.2'
    - 'r >=2.6.0'
    - r-xml
  run:
    - 'bioconductor-annotate >=1.45.3'
    - bioconductor-annotationdbi
    - 'bioconductor-biobase >=2.17.8'
    - 'bioconductor-biocgenerics >=0.13.8'
    - 'bioconductor-graph >=1.37.2'
    - 'r >=2.6.0'
    - r-xml

test:
  commands:
    - '$R -e "library(''GSEABase'')"'

about:
  home: http://bioconductor.org/packages/release/bioc/html/GSEABase.html
  license: Artistic-2.0
  summary: 'This package provides classes and methods to support Gene Set Enrichment Analysis (GSEA)
```

CHAPTER 75

bioconductor-gviz

75.1 Summary

Genomic data analyses requires integrated visualization of known genomic information and new experimental data. Gviz uses the biomaRt and the rtracklayer packages to perform live annotation queries to Ensembl and UCSC and translates this to e.g. gene/transcript structures in viewports of the grid graphics package. This results in genomic information plotted together with your data.

75.2 Home

http://bioconductor.org/packages/release/bioc/html/Gviz.html

75.3 Versions

- 1.14.2

75.4 License

Artistic-2.0

75.5 Meta

```
package:
  name: bioconductor-gviz
  version: 1.14.2
source:
  fn: Gviz_1.14.2.tar.gz
  url: https://bioconductor.org/packages/release/bioc/src/contrib/Gviz_1.14.2.tar.gz
  md5: 1578829f0f2a85a41cbb0d82cdbda6b0
build:
  number: 0
  rpaths:
    - lib/R/lib/
```

```
    - lib/
requirements:
  build:
    - 'bioconductor-s4vectors >=0.1.0'
    - 'bioconductor-iranges >=1.99.18'
    - 'bioconductor-genomicranges >=1.17.20'
    - 'bioconductor-xvector >=0.5.7'
    - 'bioconductor-rtracklayer >=1.25.13'
    - 'bioconductor-biomart >=2.11.0'
    - 'bioconductor-annotationdbi >=1.27.5'
    - 'bioconductor-biobase >=2.15.3'
    - 'bioconductor-genomicfeatures >=1.17.22'
    - 'bioconductor-bsgenome >=1.33.1'
    - 'bioconductor-biostrings >=2.33.11'
    - 'bioconductor-biovizbase >=1.13.8'
    - 'bioconductor-genomicalignments >=1.1.16'
    - 'bioconductor-genomeinfodb >=1.5.14'
    - 'bioconductor-biocgenerics >=0.11.3'
    - 'r >=2.10'
    - r-lattice
    - 'r-latticeextra >=0.6_26'
    - r-rcolorbrewer
    - r-matrixstats >=0.8.14
    - 'r-digest >=0.6.8'

  run:
    - 'bioconductor-s4vectors >=0.1.0'
    - 'bioconductor-iranges >=1.99.18'
    - 'bioconductor-genomicranges >=1.17.20'
    - 'bioconductor-xvector >=0.5.7'
    - 'bioconductor-rtracklayer >=1.25.13'
    - 'bioconductor-biomart >=2.11.0'
    - 'bioconductor-annotationdbi >=1.27.5'
    - 'bioconductor-biobase >=2.15.3'
    - 'bioconductor-genomicfeatures >=1.17.22'
    - 'bioconductor-bsgenome >=1.33.1'
    - 'bioconductor-biostrings >=2.33.11'
    - 'bioconductor-biovizbase >=1.13.8'
    - 'bioconductor-genomicalignments >=1.1.16'
    - 'bioconductor-genomeinfodb >=1.5.14'
    - 'bioconductor-biocgenerics >=0.11.3'
    - 'r >=2.10'
    - r-lattice
    - 'r-latticeextra >=0.6_26'
    - r-rcolorbrewer
    - r-matrixstats >=0.8.14
    - 'r-digest >=0.6.8'

test:
  commands:
    - '$R -e "library(''Gviz'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/Gviz.html
  license: Artistic-2.0
  summary: 'Genomic data analyses requires integrated visualization of known genomic
    information and new experimental data. Gviz uses the biomaRt and the rtracklayer
    packages to perform live annotation queries to Ensembl and UCSC and translates this
    to e.g. gene/transcript structures in viewports of the grid graphics package. This
```

```
    results in genomic information plotted together with your data.'
```

CHAPTER 76

bioconductor-iranges

76.1 Summary

The package provides efficient low-level and highly reusable S4 classes for storing ranges of integers, RLE vectors (Run-Length Encoding), and, more generally, data that can be organized sequentially (formally defined as Vector objects), as well as views on these Vector objects. Efficient list-like classes are also provided for storing big collections of instances of the basic classes. All classes in the package use consistent naming and share the same rich and consistent "Vector API" as much as possible.

76.2 Home

http://bioconductor.org/packages/release/bioc/html/IRanges.html

76.3 Versions

- 2.4.6

76.4 License

Artistic-2.0

76.5 Meta

```
package:
  name: bioconductor-iranges
  version: 2.4.6
source:
  fn: IRanges_2.4.6.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/IRanges_2.4.6.tar.gz
  md5: 8a55ec82f777f61a76b6c467af92b4f6
build:
  number: 0
  rpaths:
```

```
    - lib/R/lib/
    - lib/
requirements:
  build:
    - 'bioconductor-biocgenerics >=0.15.10'
    - 'bioconductor-s4vectors >=0.8.4'
    - 'r >=3.1.0'
  run:
    - 'bioconductor-biocgenerics >=0.15.10'
    - 'bioconductor-s4vectors >=0.8.4'
    - 'r >=3.1.0'
test:
  commands:
    - '$R -e "library(''IRanges'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/IRanges.html
  license: Artistic-2.0
  summary: 'The package provides efficient low-level and highly reusable S4 classes
    for storing ranges of integers, RLE vectors (Run-Length Encoding), and, more generally,
    data that can be organized sequentially (formally defined as Vector objects),
    as well as views on these Vector objects. Efficient list-like classes are also
    provided for storing big collections of instances of the basic classes. All classes
    in the package use consistent naming and share the same rich and consistent "Vector
    API" as much as possible.'
```

CHAPTER 77

bioconductor-limma

77.1 Summary

Data analysis, linear models and differential expression for microarray data.

77.2 Home

http://bioconductor.org/packages/release/bioc/html/limma.html

77.3 Versions

- 3.26.3

77.4 License

GPL (>=2)

77.5 Meta

```
package:
  name: bioconductor-limma
  version: 3.26.3
source:
  fn: limma_3.26.3.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/limma_3.26.3.tar.gz
  md5: 9543aec322a1177163cbd689800552d5
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
    - 'r >=2.3.0'
```

```
  run:
    - 'r >=2.3.0'
test:
  commands:
    - '$R -e "library(''limma'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/limma.html
  license: 'GPL (>=2)'
  summary: 'Data analysis, linear models and differential expression for microarray
    data.'
```

CHAPTER 78

bioconductor-mmdiff

78.1 Summary

This package detects statistically significant difference between read enrichment profiles in different ChIP-Seq samples. To take advantage of shape differences it uses Kernel methods (Maximum Mean Discrepancy, MMD).

78.2 Home

http://bioconductor.org/packages/release/bioc/html/MMDiff.html

78.3 Versions

- 1.10.0

78.4 License

Artistic-2.0

78.5 Meta

```
package:
  name: bioconductor-mmdiff
  version: 1.10.0

source:
  fn: MMDiff_1.10.0.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/MMDiff_1.10.0.tar.gz
  md5: 79a1f6646081d5c09621a80a26945516

build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
```

```
requirements:
  build:
    - 'r >=2.14.0'
    - bioconductor-genomicranges
    - bioconductor-diffbind
    - r-gmd
    - bioconductor-rsamtools
    - bioconductor-iranges
    - bioconductor-biobase
  run:
    - 'r >=2.14.0'
    - bioconductor-genomicranges
    - bioconductor-diffbind
    - r-gmd
    - bioconductor-rsamtools
    - bioconductor-iranges
    - bioconductor-biobase

test:
  commands:
    - '$R -e "library(''MMDiff'')"'

about:
  home: http://bioconductor.org/packages/release/bioc/html/MMDiff.html
  license: Artistic-2.0
  summary: 'This package detects statistically significant difference between read enrichment profile
```

CHAPTER 79

bioconductor-multtest

79.1 Summary

Non-parametric bootstrap and permutation resampling-based multiple testing procedures (including empirical Bayes methods) for controlling the family-wise error rate (FWER), generalized family-wise error rate (gFWER), tail probability of the proportion of false positives (TPPFP), and false discovery rate (FDR). Several choices of bootstrap-based null distribution are implemented (centered, centered and scaled, quantile-transformed). Single-step and step-wise methods are available. Tests based on a variety of t- and F-statistics (including t-statistics based on regression parameters from linear and survival models as well as those based on correlation parameters) are included. When probing hypotheses with t-statistics, users may also select a potentially faster null distribution which is multivariate normal with mean zero and variance covariance matrix derived from the vector influence function. Results are reported in terms of adjusted p-values, confidence regions and test statistic cutoffs. The procedures are directly applicable to identifying differentially expressed genes in DNA microarray experiments.

79.2 Home

http://bioconductor.org/packages/release/bioc/html/multtest.html

79.3 Versions

- 2.26.0

79.4 License

LGPL

79.5 Meta

```
package:
  name: bioconductor-multtest
  version: 2.26.0
source:
  fn: multtest_2.26.0.tar.gz
```

```
  url: http://bioconductor.org/packages/release/bioc/src/contrib/multtest_2.26.0.tar.gz
  md5: 77592f4a4f61628d00bb356da06b6179
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
    - bioconductor-biobase
    - bioconductor-biocgenerics
    - 'r >=2.10'
  run:
    - bioconductor-biobase
    - bioconductor-biocgenerics
    - 'r >=2.10'
test:
  commands:
    - '$R -e "library(''multtest'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/multtest.html
  license: LGPL
  summary: 'Non-parametric bootstrap and permutation resampling-based multiple testing
    procedures (including empirical Bayes methods) for controlling the family-wise
    error rate (FWER), generalized family-wise error rate (gFWER), tail probability
    of the proportion of false positives (TPPFP), and false discovery rate (FDR).  Several
    choices of bootstrap-based null distribution are implemented (centered, centered
    and scaled, quantile-transformed). Single-step and step-wise methods are available.
    Tests based on a variety of t- and F-statistics (including t-statistics based
    on regression parameters from linear and survival models as well as those based
    on correlation parameters) are included.  When probing hypotheses with t-statistics,
    users may also select a potentially faster null distribution which is multivariate
    normal with mean zero and variance covariance matrix derived from the vector influence
    function.  Results are reported in terms of adjusted p-values, confidence regions
    and test statistic cutoffs. The procedures are directly applicable to identifying
    differentially expressed genes in DNA microarray experiments.'
```

CHAPTER 80

bioconductor-org.hs.eg.db

80.1 Summary

Genome wide annotation for Human, primarily based on mapping using Entrez Gene identifiers.

80.2 Home

http://bioconductor.org/packages/release/data/annotation/html/org.Hs.eg.db.html

80.3 Versions

- 3.2.3

80.4 License

Artistic-2.0

80.5 Meta

```
package:
  name: bioconductor-org.hs.eg.db
  version: 3.2.3

source:
  fn: org.Hs.eg.db_3.2.3.tar.gz
  url: http://bioconductor.org/packages/release/data/annotation/src/contrib/org.Hs.eg.db_3.2.3.tar.gz
  md5: 4ab2503483f881513d7edc525e9a84ed

build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
```

```
requirements:
  build:
    - 'bioconductor-annotationdbi >=1.31.19'
    - 'r >=2.7.0'
  run:
    - 'bioconductor-annotationdbi >=1.31.19'
    - 'r >=2.7.0'

test:
  commands:
    - '$R -e "library(''org.Hs.eg.db'')"'

about:
  home: http://bioconductor.org/packages/release/data/annotation/html/org.Hs.eg.db.html
  license: Artistic-2.0
  summary: 'Genome wide annotation for Human, primarily based on mapping using Entrez Gene identifier
```

CHAPTER 81

bioconductor-organismdbi

81.1 Summary

The package enables a simple unified interface to several annotation packages each of which has its own schema by taking advantage of the fact that each of these packages implements a select methods.

81.2 Home

http://bioconductor.org/packages/release/bioc/html/OrganismDbi.html

81.3 Versions

- 1.12.0

81.4 License

Artistic-2.0

81.5 Meta

```
package:
  name: bioconductor-organismdbi
  version: 1.12.0
source:
  fn: OrganismDbi_1.12.0.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/OrganismDbi_1.12.0.tar.gz
  md5: da7f7314abf2dfbcf4acfe9b2a36ac0f
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
```

```
    - 'bioconductor-annotationdbi >=1.31.19'
    - bioconductor-biobase
    - 'bioconductor-biocgenerics >=0.15.10'
    - bioconductor-biocinstaller
    - 'bioconductor-genomicfeatures >=1.21.12'
    - bioconductor-genomicranges
    - bioconductor-graph
    - bioconductor-iranges
    - bioconductor-rbgl
    - bioconductor-s4vectors
    - 'r >=2.14.0'
    - r-rsqlite
  run:
    - 'bioconductor-annotationdbi >=1.31.19'
    - bioconductor-biobase
    - 'bioconductor-biocgenerics >=0.15.10'
    - bioconductor-biocinstaller
    - 'bioconductor-genomicfeatures >=1.21.12'
    - bioconductor-genomicranges
    - bioconductor-graph
    - bioconductor-iranges
    - bioconductor-rbgl
    - bioconductor-s4vectors
    - 'r >=2.14.0'
    - r-rsqlite
test:
  commands:
    - '$R -e "library(''OrganismDbi'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/OrganismDbi.html
  license: Artistic-2.0
  summary: 'The package enables a simple unified interface to several annotation packages
    each of which has its own schema by taking advantage of the fact that each of
    these packages implements a select methods.'
```

CHAPTER 82

bioconductor-phyloseq

82.1 Summary

phyloseq provides a set of classes and tools to facilitate the import, storage, analysis, and graphical display of microbiome census data.

82.2 Home

http://bioconductor.org/packages/release/bioc/html/phyloseq.html

82.3 Versions

- 1.14.0

82.4 License

AGPL-3

82.5 Meta

```
package:
  name: bioconductor-phyloseq
  version: 1.14.0
source:
  fn: phyloseq_1.14.0.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/phyloseq_1.14.0.tar.gz
  md5: ef118832d7a14e2e43db10e687afc871
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
```

```
    - bioconductor-biobase
    - 'bioconductor-biocgenerics >=0.14.0'
    - 'bioconductor-biostrings >=2.28.0'
    - 'bioconductor-multtest >=2.16.0'
    - 'r >=3.1.0'
    - 'r-ade4 >=1.7.2'
    - 'r-ape >=3.1.1'
    - 'r-biom >=0.3.9'
    - 'r-data.table >=1.9.4'
    - 'r-foreach >=1.4.2'
    - 'r-ggplot2 >=1.0.0'
    - 'r-igraph >=0.7.0'
    - 'r-plyr >=1.8'
    - 'r-reshape2 >=1.2.2'
    - 'r-scales >=0.2.3'
    - 'r-vegan >=2.0.10'
    - gmp
  run:
    - bioconductor-biobase
    - 'bioconductor-biocgenerics >=0.14.0'
    - 'bioconductor-biostrings >=2.28.0'
    - 'bioconductor-multtest >=2.16.0'
    - 'r >=3.1.0'
    - 'r-ade4 >=1.7.2'
    - 'r-ape >=3.1.1'
    - 'r-biom >=0.3.9'
    - 'r-data.table >=1.9.4'
    - 'r-foreach >=1.4.2'
    - 'r-ggplot2 >=1.0.0'
    - 'r-igraph >=0.7.0'
    - 'r-plyr >=1.8'
    - 'r-reshape2 >=1.2.2'
    - 'r-scales >=0.2.3'
    - 'r-vegan >=2.0.10'
    - gmp
test:
  commands:
    - '$R -e "library(''phyloseq'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/phyloseq.html
  license: AGPL-3
  summary: 'phyloseq provides a set of classes and tools to facilitate the import, storage, analysis,
```

CHAPTER 83

bioconductor-preprocesscore

83.1 Summary

A library of core preprocessing routines

83.2 Home

http://bioconductor.org/packages/release/bioc/html/preprocessCore.html

83.3 Versions

- 1.32.0

83.4 License

LGPL (>= 2)

83.5 Meta

```
package:
  name: bioconductor-preprocesscore
  version: 1.32.0
source:
  fn: preprocessCore_1.32.0.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/preprocessCore_1.32.0.tar.gz
  md5: 6372f96b0aff5b4487ff459eae9175c8
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
    - r
```

```
  run:
    - r
test:
  commands:
    - '$R -e "library(''preprocessCore'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/preprocessCore.html
  license: 'LGPL (>= 2)'
  summary: 'A library of core preprocessing routines'
```

CHAPTER 84

bioconductor-rbgl

84.1 Summary

A fairly extensive and comprehensive interface to the graph algorithms contained in the BOOST library.

84.2 Home

http://bioconductor.org/packages/release/bioc/html/RBGL.html

84.3 Versions

- 1.46.0

84.4 License

Artistic-2.0

84.5 Meta

```
package:
  name: bioconductor-rbgl
  version: 1.46.0
source:
  fn: RBGL_1.46.0.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/RBGL_1.46.0.tar.gz
  md5: 382d3a0c6f33f9b07a63f4f20b631fca
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
    - bioconductor-graph
```

```
    - r
  run:
    - bioconductor-graph
    - r
test:
  commands:
    - '$R -e "library(''RBGL'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/RBGL.html
  license: Artistic-2.0
  summary: 'A fairly extensive and comprehensive interface to the graph algorithms
    contained in the BOOST library.'
```

CHAPTER 85

bioconductor-regioner

85.1 Summary

regioneR offers a statistical framework based on customizable permutation tests to assess the association between genomic region sets and other genomic features.

85.2 Home

http://bioconductor.org/packages/release/bioc/html/regioneR.html

85.3 Versions

- 1.2.0

85.4 License

Artistic-2.0

85.5 Meta

```
package:
  name: bioconductor-regioner
  version: 1.2.0
source:
  fn: regioneR_1.2.0.tar.gz
  url: https://bioarchive.galaxyproject.org/regioneR_1.2.0.tar.gz
  md5: dec27cbbeae3410aa2181a267c05a494
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
```

```
    - bioconductor-bsgenome
    - bioconductor-genomicranges
    - bioconductor-rtracklayer
    - r
    - r-memoise
  run:
    - bioconductor-bsgenome
    - bioconductor-genomicranges
    - bioconductor-rtracklayer
    - r
    - r-memoise
test:
  commands:
    - '$R -e "library(''regioneR'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/regioneR.html
  license: Artistic-2.0
  summary: 'regioneR offers a statistical framework based on customizable permutation
    tests to assess the association between genomic region sets and other genomic
    features.'
```

CHAPTER 86

bioconductor-rhdf5

86.1 Summary

This R/Bioconductor package provides an interface between HDF5 and R. HDF5's main features are the ability to store and access very large and/or complex datasets and a wide variety of metadata on mass storage (disk) through a completely portable file format. The rhdf5 package is thus suited for the exchange of large and/or complex datasets between R and other software package, and for letting R applications work on datasets that are larger than the available RAM.

86.2 Home

http://bioconductor.org/packages/release/bioc/html/rhdf5.html

86.3 Versions

- 2.14.0

86.4 License

Artistic-2.0

86.5 Meta

```
package:
  name: bioconductor-rhdf5
  version: 2.14.0
source:
  fn: rhdf5_2.14.0.tar.gz
  url: https://bioarchive.galaxyproject.org/rhdf5_2.14.0.tar.gz
  md5: 6634f431c3359bb7c859539785a5aa1d
build:
  number: 1
  rpaths:
```

```
    - lib/R/lib/
    - lib/
requirements:
  build:
    - bioconductor-zlibbioc
    - r
  run:
    - bioconductor-zlibbioc
    - r
test:
  commands:
    - '$R -e "library(''rhdf5'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/rhdf5.html
  license: Artistic-2.0
  summary: 'This R/Bioconductor package provides an interface between HDF5 and R.
    HDF5''s main features are the ability to store and access very large and/or complex
    datasets and a wide variety of metadata on mass storage (disk) through a completely
    portable file format. The rhdf5 package is thus suited for the exchange of large
    and/or complex datasets between R and other software package, and for letting
    R applications work on datasets that are larger than the available RAM.'
```

CHAPTER 87

bioconductor-rsamtools

87.1 Summary

This package provides an interface to the 'samtools', 'bcftools', and 'tabix' utilities (see 'LICENCE') for manipulating SAM (Sequence Alignment / Map), FASTA, binary variant call (BCF) and compressed indexed tab-delimited (tabix) files.

87.2 Home

http://bioconductor.org/packages/release/bioc/html/Rsamtools.html

87.3 Versions

- 1.22.0

87.4 License

Artistic-2.0 | file LICENSE

87.5 Meta

```
package:
  name: bioconductor-rsamtools
  version: 1.22.0
source:
  fn: Rsamtools_1.22.0.tar.gz
  url: https://bioarchive.galaxyproject.org/Rsamtools_1.22.0.tar.gz
  md5: 6643603c4570b7b8fbdb52c49e98c801
build:
  number: 1
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
```

```
  build:
    - 'bioconductor-biocgenerics >=0.1.3'
    - bioconductor-biocparallel
    - 'bioconductor-biostrings >=2.37.1'
    - 'bioconductor-genomeinfodb >=1.1.3'
    - 'bioconductor-genomicranges >=1.21.6'
    - 'bioconductor-iranges >=2.3.7'
    - 'bioconductor-s4vectors >=0.7.11'
    - 'bioconductor-xvector >=0.9.1'
    - bioconductor-zlibbioc
    - r
    - r-bitops
  run:
    - 'bioconductor-biocgenerics >=0.1.3'
    - bioconductor-biocparallel
    - 'bioconductor-biostrings >=2.37.1'
    - 'bioconductor-genomeinfodb >=1.1.3'
    - 'bioconductor-genomicranges >=1.21.6'
    - 'bioconductor-iranges >=2.3.7'
    - 'bioconductor-s4vectors >=0.7.11'
    - 'bioconductor-xvector >=0.9.1'
    - bioconductor-zlibbioc
    - r
    - r-bitops
test:
  commands:
    - '$R -e "library(''Rsamtools'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/Rsamtools.html
  license: 'Artistic-2.0 | file LICENSE'
  summary: 'This package provides an interface to the ''samtools'', ''bcftools'',
    and ''tabix'' utilities (see ''LICENCE'') for manipulating SAM (Sequence Alignment
    / Map), FASTA, binary variant call (BCF) and compressed indexed tab-delimited
    (tabix) files.'
```

CHAPTER 88

bioconductor-rtracklayer

88.1 Summary

Extensible framework for interacting with multiple genome browsers (currently UCSC built-in) and manipulating annotation tracks in various formats (currently GFF, BED, bedGraph, BED15, WIG, BigWig and 2bit built-in). The user may export/import tracks to/from the supported browsers, as well as query and modify the browser state, such as the current viewport.

88.2 Home

http://bioconductor.org/packages/release/bioc/html/rtracklayer.html

88.3 Versions

- 1.30.1

88.4 License

Artistic-2.0

88.5 Meta

```
package:
  name: bioconductor-rtracklayer
  version: 1.30.1
source:
  fn: rtracklayer_1.30.1.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/rtracklayer_1.30.1.tar.gz
  md5: 5e2311cb886a68e7ad407218e70b5952
build:
  number: 0
  rpaths:
    - lib/R/lib/
```

```
    - lib/
requirements:
  build:
    - 'bioconductor-biocgenerics >=0.13.8'
    - 'bioconductor-biostrings >=2.37.1'
    - 'bioconductor-genomeinfodb >=1.3.14'
    - 'bioconductor-genomicalignments >=1.5.4'
    - 'bioconductor-genomicranges >=1.21.20'
    - 'bioconductor-iranges >=2.3.7'
    - 'bioconductor-rsamtools >=1.17.8'
    - 'bioconductor-s4vectors >=0.7.11'
    - 'bioconductor-xvector >=0.9.4'
    - bioconductor-zlibbioc
    - 'r >=2.10'
    - 'r-rcurl >=1.4-2'
    - 'r-xml >=1.98-0'
  run:
    - 'bioconductor-biocgenerics >=0.13.8'
    - 'bioconductor-biostrings >=2.37.1'
    - 'bioconductor-genomeinfodb >=1.3.14'
    - 'bioconductor-genomicalignments >=1.5.4'
    - 'bioconductor-genomicranges >=1.21.20'
    - 'bioconductor-iranges >=2.3.7'
    - 'bioconductor-rsamtools >=1.17.8'
    - 'bioconductor-s4vectors >=0.7.11'
    - 'bioconductor-xvector >=0.9.4'
    - bioconductor-zlibbioc
    - 'r >=2.10'
    - 'r-rcurl >=1.4-2'
    - 'r-xml >=1.98-0'
test:
  commands:
    - '$R -e "library(''rtracklayer'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/rtracklayer.html
  license: Artistic-2.0
  summary: 'Extensible framework for interacting with multiple genome browsers (currently
    UCSC built-in) and manipulating annotation tracks in various formats (currently
    GFF, BED, bedGraph, BED15, WIG, BigWig and 2bit built-in). The user may export/import
    tracks to/from the supported browsers, as well as query and modify the browser
    state, such as the current viewport.'
```

CHAPTER 89

bioconductor-s4vectors

89.1 Summary

The S4Vectors package defines the Vector and List virtual classes and a set of generic functions that extend the semantic of ordinary vectors and lists in R. Package developers can easily implement vector-like or list-like objects as concrete subclasses of Vector or List. In addition, a few low-level concrete subclasses of general interest (e.g. DataFrame, Rle, and Hits) are implemented in the S4Vectors package itself (many more are implemented in the IRanges package and in other Bioconductor infrastructure packages).

89.2 Home

http://bioconductor.org/packages/release/bioc/html/S4Vectors.html

89.3 Versions

- 0.8.7

89.4 License

Artistic-2.0

89.5 Meta

```
package:
  name: bioconductor-s4vectors
  version: 0.8.7
source:
  fn: S4Vectors_0.8.7.tar.gz
  url: https://bioconductor.org/packages/release/bioc/src/contrib/S4Vectors_0.8.7.tar.gz
  md5: de3f00f7a2e3af7a6dfac03f01b767ae
build:
  number: 0
  rpaths:
```

```
    - lib/R/lib/
    - lib/
requirements:
  build:
    - 'bioconductor-biocgenerics >=0.15.10'
    - 'r >=3.1.0'
  run:
    - 'bioconductor-biocgenerics >=0.15.10'
    - 'r >=3.1.0'
test:
  commands:
    - '$R -e "library(''S4Vectors'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/S4Vectors.html
  license: Artistic-2.0
  summary: 'The S4Vectors package defines the Vector and List virtual classes and
    a set of generic functions that extend the semantic of ordinary vectors and lists
    in R. Package developers can easily implement vector-like or list-like objects
    as concrete subclasses of Vector or List. In addition, a few low-level concrete
    subclasses of general interest (e.g. DataFrame, Rle, and Hits) are implemented
    in the S4Vectors package itself (many more are implemented in the IRanges package
    and in other Bioconductor infrastructure packages).'
```

CHAPTER 90

bioconductor-shortread

90.1 Summary

This package implements sampling, iteration, and input of FASTQ files. The package includes functions for filtering and trimming reads, and for generating a quality assessment report. Data are represented as DNAStringSet-derived objects, and easily manipulated for a diversity of purposes. The package also contains legacy support for early single-end, ungapped alignment formats.

90.2 Home

http://bioconductor.org/packages/release/bioc/html/ShortRead.html

90.3 Versions

- 1.28.0

90.4 License

Artistic-2.0

90.5 Meta

```
package:
  name: bioconductor-shortread
  version: 1.28.0
source:
  fn: ShortRead_1.28.0.tar.gz
  url: https://bioarchive.galaxyproject.org/ShortRead_1.28.0.tar.gz
  md5: 94fdda7c3c1d398626e135fa613062f0
build:
  number: 0
  rpaths:
    - lib/R/lib/
```

```
    - lib/
requirements:
  build:
    - bioconductor-biobase
    - bioconductor-biocparallel
    - 'bioconductor-biocgenerics >=0.11.3'
    - 'bioconductor-biostrings >=2.37.1'
    - 'bioconductor-genomeinfodb >=1.1.19'
    - 'bioconductor-genomicalignments >=1.5.4'
    - 'bioconductor-genomicranges >=1.21.6'
    - 'bioconductor-iranges >=2.3.7'
    - 'bioconductor-rsamtools >=1.21.4'
    - 'bioconductor-s4vectors >=0.7.1'
    - bioconductor-zlibbioc
    - r
    - r-hwriter
    - r-latticeextra
  run:
    - bioconductor-biobase
    - bioconductor-biocparallel
    - 'bioconductor-biocgenerics >=0.11.3'
    - 'bioconductor-biostrings >=2.37.1'
    - 'bioconductor-genomeinfodb >=1.1.19'
    - 'bioconductor-genomicalignments >=1.5.4'
    - 'bioconductor-genomicranges >=1.21.6'
    - 'bioconductor-iranges >=2.3.7'
    - 'bioconductor-rsamtools >=1.21.4'
    - 'bioconductor-s4vectors >=0.7.1'
    - bioconductor-zlibbioc
    - r
    - r-hwriter
    - r-latticeextra
test:
  commands:
    - '$R -e "library(''ShortRead'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/ShortRead.html
  license: Artistic-2.0
  summary: 'This package implements sampling, iteration, and input of FASTQ files.
    The package includes functions for filtering and trimming reads, and for generating
    a quality assessment report. Data are represented as DNAStringSet-derived objects,
    and easily manipulated for a diversity of purposes.  The package also contains
    legacy support for early single-end, ungapped alignment formats.'
```

CHAPTER 91

bioconductor-summarizedexperiment

91.1 Summary

The SummarizedExperiment container contains one or more assays, each represented by a matrix-like object of numeric or other mode. The rows typically represent genomic ranges of interest and the columns represent samples.

91.2 Home

http://bioconductor.org/packages/release/bioc/html/SummarizedExperiment.html

91.3 Versions

- 1.0.2

91.4 License

Artistic-2.0

91.5 Meta

```
package:
  name: bioconductor-summarizedexperiment
  version: 1.0.2
source:
  fn: SummarizedExperiment_1.0.1.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/SummarizedExperiment_1.0.2.tar.gz
  md5: ce5b5d0aa2868f754bc8d136ebd2e6cd
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
```

```
    - bioconductor-biobase
    - 'bioconductor-biocgenerics >=0.15.3'
    - bioconductor-genomeinfodb
    - 'bioconductor-genomicranges >=1.22.1'
    - bioconductor-iranges
    - 'bioconductor-s4vectors >=0.7.11'
    - 'r >=3.2'
  run:
    - bioconductor-biobase
    - 'bioconductor-biocgenerics >=0.15.3'
    - bioconductor-genomeinfodb
    - 'bioconductor-genomicranges >=1.22.1'
    - bioconductor-iranges
    - 'bioconductor-s4vectors >=0.7.11'
    - 'r >=3.2'
test:
  commands:
    - '$R -e "library(''SummarizedExperiment'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/SummarizedExperiment.html
  license: Artistic-2.0
  summary: 'The SummarizedExperiment container contains one or more assays, each represented
    by a matrix-like object of numeric or other mode. The rows typically represent
    genomic ranges of interest and the columns represent samples.'
```

CHAPTER 92

bioconductor-sva

92.1 Summary

The sva package contains functions for removing batch effects and other unwanted variation in high-throughput experiment. Specifically, the sva package contains functions for the identifying and building surrogate variables for high-dimensional data sets. Surrogate variables are covariates constructed directly from high-dimensional data (like gene expression/RNA sequencing/methylation/brain imaging data) that can be used in subsequent analyses to adjust for unknown, unmodeled, or latent sources of noise. The sva package can be used to remove artifacts in three ways: (1) identifying and estimating surrogate variables for unknown sources of variation in high-throughput experiments (Leek and Storey 2007 PLoS Genetics,2008 PNAS), (2) directly removing known batch effects using ComBat (Johnson et al. 2007 Biostatistics) and (3) removing batch effects with known control probes (Leek 2014 biorXiv). Removing batch effects and using surrogate variables in differential expression analysis have been shown to reduce dependence, stabilize error rate estimates, and improve reproducibility, see (Leek and Storey 2007 PLoS Genetics, 2008 PNAS or Leek et al. 2011 Nat. Reviews Genetics).

92.2 Home

http://bioconductor.org/packages/release/bioc/html/sva.html

92.3 Versions

- 3.18.0

92.4 License

Artistic-2.0

92.5 Meta

```
package:
  name: bioconductor-sva
  version: 3.18.0
source:
```

```
  fn: sva_3.18.0.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/sva_3.18.0.tar.gz
  md5: 9560d608d9e0d8f538420850272f3ff3
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
    - bioconductor-genefilter
    - 'r >=2.8'
  run:
    - bioconductor-genefilter
    - 'r >=2.8'
test:
  commands:
    - '$R -e "library(''sva'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/sva.html
  license: Artistic-2.0
  summary: 'The sva package contains functions for removing batch effects and other
    unwanted variation in high-throughput experiment. Specifically, the sva package
    contains functions for the identifying and building surrogate variables for high-dimensional
    data sets. Surrogate variables are covariates constructed directly from high-dimensional
    data (like gene expression/RNA sequencing/methylation/brain imaging data) that
    can be used in subsequent analyses to adjust for unknown, unmodeled, or latent
    sources of noise. The sva package can be used to remove artifacts in three ways:
    (1) identifying and estimating surrogate variables for unknown sources of variation
    in high-throughput experiments (Leek and Storey 2007 PLoS Genetics,2008 PNAS),
    (2) directly removing known batch effects using ComBat (Johnson et al. 2007 Biostatistics)
    and (3) removing batch effects with known control probes (Leek 2014 biorXiv).
    Removing batch effects and using surrogate variables in differential expression
    analysis have been shown to reduce dependence, stabilize error rate estimates,
    and improve reproducibility, see (Leek and Storey 2007 PLoS Genetics, 2008 PNAS
    or Leek et al. 2011 Nat. Reviews Genetics).'
```

CHAPTER 93

bioconductor-systempiper

93.1 Summary

R package for building and running automated end-to-end analysis workflows for a wide range of next generation sequence (NGS) applications such as RNA-Seq, ChIP-Seq, VAR-Seq and Ribo-Seq. Important features include a uniform workflow interface across different NGS applications, automated report generation, and support for running both R and command-line software, such as NGS aligners or peak/variant callers, on local computers or compute clusters. Efficient handling of complex sample sets and experimental designs is facilitated by a consistently implemented sample annotation infrastructure. Instructions for using systemPipeR are given in the Overview Vignette (HTML). The remaining Vignettes, linked below, are workflow templates for common NGS use cases.

93.2 Home

http://bioconductor.org/packages/release/bioc/html/systemPipeR.html

93.3 Versions

- 1.4.7

93.4 License

Artistic-2.0

93.5 Meta

```
package:
  name: bioconductor-systempiper
  version: 1.4.7

source:
  fn: systemPipeR_1.4.7.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/systemPipeR_1.4.7.tar.gz
  md5: 501b1bd634eb4844864f881056b9b471
```

```
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/

requirements:
  build:
    - bioconductor-annotate
    - bioconductor-biocgenerics
    - bioconductor-biostrings
    - bioconductor-deseq2
    - bioconductor-edger
    - bioconductor-genomicfeatures
    - bioconductor-genomicranges
    - bioconductor-go.db
    - bioconductor-gostats
    - bioconductor-limma
    - bioconductor-rsamtools
    - bioconductor-shortread
    - bioconductor-summarizedexperiment
    - bioconductor-variantannotation
    - r
    - r-batchjobs
    - r-ggplot2
    - r-pheatmap
    - r-rjson
  run:
    - bioconductor-annotate
    - bioconductor-biocgenerics
    - bioconductor-biostrings
    - bioconductor-deseq2
    - bioconductor-edger
    - bioconductor-genomicfeatures
    - bioconductor-genomicranges
    - bioconductor-go.db
    - bioconductor-gostats
    - bioconductor-limma
    - bioconductor-rsamtools
    - bioconductor-shortread
    - bioconductor-summarizedexperiment
    - bioconductor-variantannotation
    - r
    - r-batchjobs
    - r-ggplot2
    - r-pheatmap
    - r-rjson

test:
  commands:
    - '$R -e "library(''systemPipeR'')"'

about:
  home: http://bioconductor.org/packages/release/bioc/html/systemPipeR.html
  license: Artistic-2.0
  summary: 'R package for building and running automated end-to-end analysis workflows for a wide ran
```

CHAPTER 94

bioconductor-variantannotation

94.1 Summary

Annotate variants, compute amino acid coding changes, predict coding outcomes

94.2 Home

http://bioconductor.org/packages/release/bioc/html/VariantAnnotation.html

94.3 Versions

- 1.16.4

94.4 License

Artistic-2.0

94.5 Meta

```
package:
  name: bioconductor-variantannotation
  version: 1.16.4
source:
  fn: VariantAnnotation_1.16.4.tar.gz
  url: http://bioconductor.org/packages/release/bioc/src/contrib/VariantAnnotation_1.16.4.tar.gz
  md5: 03f51aaa15fa2824154a5e328b2b209c
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
    - 'bioconductor-annotationdbi >=1.27.9'
```

```
    - bioconductor-biobase
    - 'bioconductor-biocgenerics >=0.15.3'
    - 'bioconductor-biostrings >=2.33.5'
    - 'bioconductor-bsgenome >=1.37.6'
    - 'bioconductor-genomeinfodb >=1.1.3'
    - 'bioconductor-genomicfeatures >=1.19.17'
    - 'bioconductor-genomicranges >=1.19.47'
    - 'bioconductor-iranges >=2.3.25'
    - 'bioconductor-rsamtools >=1.19.52'
    - 'bioconductor-rtracklayer >=1.25.16'
    - 'bioconductor-s4vectors >=0.7.11'
    - 'bioconductor-summarizedexperiment >=0.3.1'
    - 'bioconductor-xvector >=0.5.6'
    - bioconductor-zlibbioc
    - 'r >=2.8.0'
    - r-dbi
  run:
    - 'bioconductor-annotationdbi >=1.27.9'
    - bioconductor-biobase
    - 'bioconductor-biocgenerics >=0.15.3'
    - 'bioconductor-biostrings >=2.33.5'
    - 'bioconductor-bsgenome >=1.37.6'
    - 'bioconductor-genomeinfodb >=1.1.3'
    - 'bioconductor-genomicfeatures >=1.19.17'
    - 'bioconductor-genomicranges >=1.19.47'
    - 'bioconductor-iranges >=2.3.25'
    - 'bioconductor-rsamtools >=1.19.52'
    - 'bioconductor-rtracklayer >=1.25.16'
    - 'bioconductor-s4vectors >=0.7.11'
    - 'bioconductor-summarizedexperiment >=0.3.1'
    - 'bioconductor-xvector >=0.5.6'
    - bioconductor-zlibbioc
    - 'r >=2.8.0'
    - r-dbi
test:
  commands:
    - '$R -e "library(''VariantAnnotation'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/VariantAnnotation.html
  license: Artistic-2.0
  summary: 'Annotate variants, compute amino acid coding changes, predict coding outcomes'
```

CHAPTER 95

bioconductor-xvector

95.1 Summary

Memory efficient S4 classes for storing sequences "externally" (behind an R external pointer, or on disk).

95.2 Home

http://bioconductor.org/packages/release/bioc/html/XVector.html

95.3 Versions

- 0.10.0

95.4 License

Artistic-2.0

95.5 Meta

```
package:
  name: bioconductor-xvector
  version: 0.10.0
source:
  fn: XVector_0.10.0.tar.gz
  url: https://bioarchive.galaxyproject.org/XVector_0.10.0.tar.gz
  md5: 792a52c3c9218c630733e232f3c19f46
build:
  number: 1
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
    - 'bioconductor-biocgenerics >=0.11.3'
```

```
    - 'bioconductor-iranges >=2.3.7'
    - 'bioconductor-s4vectors >=0.7.1'
    - bioconductor-zlibbioc
    - 'r >=2.8.0'
  run:
    - 'bioconductor-biocgenerics >=0.11.3'
    - 'bioconductor-iranges >=2.3.7'
    - 'bioconductor-s4vectors >=0.7.1'
    - bioconductor-zlibbioc
    - 'r >=2.8.0'
test:
  commands:
    - '$R -e "library(''XVector'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/XVector.html
  license: Artistic-2.0
  summary: 'Memory efficient S4 classes for storing sequences "externally" (behind
    an R external pointer, or on disk).'
```

CHAPTER 96

bioconductor-zlibbioc

96.1 Summary

This package uses the source code of zlib-1.2.5 to create libraries for systems that do not have these available via other means (most Linux and Mac users should have system-level access to zlib, and no direct need for this package). See the vignette for instructions on use.

96.2 Home

http://bioconductor.org/packages/release/bioc/html/zlibbioc.html

96.3 Versions

- 1.16.0

96.4 License

Artistic-2.0 + file LICENSE

96.5 Meta

```
package:
  name: bioconductor-zlibbioc
  version: 1.16.0
source:
  fn: zlibbioc_1.16.0.tar.gz
  url: https://bioarchive.galaxyproject.org/zlibbioc_1.16.0.tar.gz
  md5: cebad9e6ac7b3bd96fc6650aa72f61d8
build:
  number: 1
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
```

```
  build:
    - r
  run:
    - r
test:
  commands:
    - '$R -e "library(''zlibbioc'')"'
about:
  home: http://bioconductor.org/packages/release/bioc/html/zlibbioc.html
  license: 'Artistic-2.0 + file LICENSE'
  summary: 'This package uses the source code of zlib-1.2.5 to create libraries for
    systems that do not have these available via other means (most Linux and Mac users
    should have system-level access to zlib, and no direct need for this package).
    See the vignette for instructions on use.'
```

CHAPTER 97

biom-format

97.1 Summary

Biological Observation Matrix (BIOM) format

97.2 Home

http://www.biom-format.org

97.3 Versions

- 2.1.5
- 2.1.4

97.4 License

BSD License

97.5 Meta

```
package:
  name: biom-format
  version: "2.1.5"

source:
  fn: biom-format-2.1.5.tar.gz
  url: https://pypi.python.org/packages/source/b/biom-format/biom-format-2.1.5.tar.gz
  md5: 30964772b5eb9a84d407d1ed33a064c0


build:
  # noarch_python: True
  preserve_egg_dir: True
```

```
  entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - biom-format = biom-format:main
    #
    # Would create an entry point called biom-format that calls biom-format.main()

    - biom=biom.cli:cli

  number: 0
  skip: True    # [py3k]

requirements:
  build:
    - python
    - setuptools
    - pyqi ==0.3.2
    - click
    - numpy >=1.3.0
    - future >=0.14.3
    - scipy >=0.13.0

  run:
    - python
    - setuptools
    - click
    - pyqi ==0.3.2
    - numpy >=1.3.0
    - future >=0.14.3
    - scipy >=0.13.0

test:
  # Python imports
  imports:
    - biom
    - biom.cli

  commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.
    - biom --help

about:
  home: http://www.biom-format.org
  license: BSD License
  summary: 'Biological Observation Matrix (BIOM) format'
```

CHAPTER 98

blast-legacy [linux64]

98.1 Summary

The Basic Local Alignment Search Tool (BLAST) finds regions of local similarity between sequences.

98.2 Home

http://blast.ncbi.nlm.nih.gov

98.3 Versions

- 2.2.22

98.4 License

Public Domain

98.5 Meta

```
package:
  name: blast-legacy [linux64]
  version: 2.2.22

source:
  fn: blast-2.2.22-x64-linux.tar.gz
  url: ftp://ftp.ncbi.nlm.nih.gov/blast/executables/release/2.2.22/blast-2.2.22-x64-linux.tar.gz
  md5: 84e900b276a6e956dbbff9e6321155cf

build:
  number: 0

test:
  commands:
    - bl2seq --help | grep bl2seq > /dev/null
```

```
    - blastall --help | grep blastall > /dev/null
    - blastclust --help | grep blastclust > /dev/null
    - blastpgp --help | grep blastpgp > /dev/null
    - copymat --help | grep copymat > /dev/null
    - fastacmd --help | grep fastacmd > /dev/null
    - formatdb --help | grep formatdb > /dev/null
    - formatrpsdb --help | grep formatrpsdb > /dev/null
    - impala --help | grep impala > /dev/null
    - makemat --help | grep makemat > /dev/null
    - megablast --help | grep megablast > /dev/null
    - rpsblast --help | grep rpsblast > /dev/null
    - seedtop --help | grep seedtop > /dev/null


about:
  home: http://blast.ncbi.nlm.nih.gov
  license: Public Domain
  summary: The Basic Local Alignment Search Tool (BLAST) finds regions of local similarity between se
```

CHAPTER 99

blast

99.1 Summary

BLAST+ is a new suite of BLAST tools that utilizes the NCBI C++ Toolkit.

99.2 Home

http://blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE_TYPE=BlastDocs

99.3 Versions

- 2.2.31

99.4 License

Public Domain

99.5 Meta

```
package:
    name: blast
    version: 2.2.31
source:
    fn: ncbi-blast-2.2.31+-src.tar.gz # [linux]
    url: ftp://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/2.2.31/ncbi-blast-2.2.31+-src.tar.gz #
    md5: f32bd2d2c66205c53c6981f94e1a0d54 # [linux]
    fn: ncbi-blast-2.2.31+-universal-macosx.tar.gz # [osx]
    url: ftp://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/2.2.31/ncbi-blast-2.2.31+-universal-macc
    md5: 316555fef19749fe90455b7def03634e # [osx]
build:
    number: 1
requirements:
  build:
    - boost # [linux]
```

```
  run:
    - boost # [linux]
test:
    commands:
        - blastn -help > /dev/null
about:
    home: http://blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE_TYPE=BlastDocs
    license: Public Domain
    summary: BLAST+ is a new suite of BLAST tools that utilizes the NCBI C++ Toolkit.
```

CHAPTER 100

blat [linux64]

100.1 Summary

BLAT is a bioinformatics software tool which performs rapid mRNA/DNA and cross-species protein alignments.

100.2 Home

https://genome.ucsc.edu/FAQ/FAQblat.html

100.3 Versions

- 35

100.4 License

Free for academic, nonprofit and personal use

100.5 Meta

```
package:
  name: blat [linux64]
  version: 35

source:
  fn: blatSrc35.zip
  url: https://users.soe.ucsc.edu/~kent/src/blatSrc35.zip
  md5: 16e546b8843b85e0b0f2fa603cd78724

build:
  number: 0

requirements:
  build:
    - libpng
```

```
    - zlib
  run:
    - libpng
    - zlib
about:
  home: https://genome.ucsc.edu/FAQ/FAQblat.html
  license: Free for academic, nonprofit and personal use
  summary: BLAT is a bioinformatics software tool which performs rapid mRNA/DNA and cross-species pro

# vim:set ts=8 sw=2
```

CHAPTER 101

bleach

101.1 Summary

An easy whitelist-based HTML-sanitizing tool.

101.2 Home

http://github.com/jsocol/bleach

101.3 Versions

- 1.4.2

101.4 License

Apache Software License

101.5 Meta

```
package:
  name: bleach
  version: "1.4.2"

source:
  fn: bleach-1.4.2.tar.gz
  url: https://pypi.python.org/packages/source/b/bleach/bleach-1.4.2.tar.gz
  md5: 6a8f4d8afed000e2aea14c3aa02a1ea9
#  patches:
   # List any patch files here
   # - fix.patch

# build:
  # noarch_python: True
  # preserve_egg_dir: True
```

```
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - bleach = bleach:main
    #
    # Would create an entry point called bleach that calls bleach.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools
    - six
    - html5lib >=0.999

  run:
    - python
    - six
    - html5lib >=0.999

test:
  # Python imports
  imports:
    - bleach
    - bleach.tests

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  requires:
    - nose >=1.3
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: http://github.com/jsocol/bleach
  license: Apache Software License
  summary: 'An easy whitelist-based HTML-sanitizing tool.'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 102

bmfilter

102.1 Summary

bmfilter is part of BMTagger aka Best Match Tagger, for removing human reads from metagenomics datasets

102.2 Home

ftp://ftp.ncbi.nlm.nih.gov/pub/agarwala/bmtagger/

102.3 Versions

- 3.101

102.4 License

Public Domain

102.5 Meta

```
package:
    name: bmfilter
    version: 3.101
source:
    fn: bmtools.tar.gz # [linux]
    url: ftp://ftp.ncbi.nlm.nih.gov/pub/agarwala/bmtagger/bmtools.tar.gz # [linux]
    md5: 719474a0e3b54449cbe06f6e442994dd # [linux]
    fn: bmfilter # [osx]
    url: ftp://ftp.ncbi.nlm.nih.gov/pub/agarwala/bmtagger/mac-os/bmfilter # [osx]
build:
    number: 1
requirements:
  build:
    #- blast
    #- srprism
```

```
  run:
    #- blast
    #- srprism
test:
    commands:
        - "bmfilter -h &> /dev/null"
about:
    home: ftp://ftp.ncbi.nlm.nih.gov/pub/agarwala/bmtagger/
    license: Public Domain
    summary: "bmfilter is part of BMTagger aka Best Match Tagger, for removing human reads from metag
```

CHAPTER 103

bmtagger

103.1 Summary

BMTagger aka Best Match Tagger is for removing human reads from metagenomics datasets

103.2 Home

ftp://ftp.ncbi.nlm.nih.gov/pub/agarwala/bmtagger/

103.3 Versions

- 3.101

103.4 License

Public Domain

103.5 Meta

```
package:
    name: bmtagger
    version: 3.101
source:
    fn: bmtools.tar.gz # [linux]
    url: ftp://ftp.ncbi.nlm.nih.gov/pub/agarwala/bmtagger/bmtools.tar.gz # [linux]
    md5: 719474a0e3b54449cbe06f6e442994dd # [linux]
    fn: bmtagger.sh # [osx]
    url: ftp://ftp.ncbi.nlm.nih.gov/pub/agarwala/bmtagger/mac-os/bmtagger.sh # [osx]
build:
    number: 1
requirements:
  build:
    #- gcc
    - blast
```

```
    - srprism
    - bmfilter
    - bmtool
    - extract_fullseq
  run:
    #- libgcc
    - blast
    - srprism
    - bmfilter
    - bmtool
    - extract_fullseq
test:
    commands:
        - "bmtagger.sh -V &> /dev/null" # [linux]
        # to test on mac you need gnugetopt installed from homebrew / macports
about:
    home: ftp://ftp.ncbi.nlm.nih.gov/pub/agarwala/bmtagger/
    license: Public Domain
    summary: BMTagger aka Best Match Tagger is for removing human reads from metagenomics datasets
```

CHAPTER 104

bmtool

104.1 Summary

bmtool is part of BMTagger aka Best Match Tagger, for removing human reads from metagenomics datasets

104.2 Home

ftp://ftp.ncbi.nlm.nih.gov/pub/agarwala/bmtagger/

104.3 Versions

- 3.101

104.4 License

Public Domain

104.5 Meta

```
package:
    name: bmtool
    version: 3.101
source:
    fn: bmtools.tar.gz # [linux]
    url: ftp://ftp.ncbi.nlm.nih.gov/pub/agarwala/bmtagger/bmtools.tar.gz # [linux]
    md5: 719474a0e3b54449cbe06f6e442994dd # [linux]
    fn: bmtool # [osx]
    url: ftp://ftp.ncbi.nlm.nih.gov/pub/agarwala/bmtagger/mac-os/bmtool # [osx]
build:
    number: 1
requirements:
  build:
    # - blast
    # - srprism
```

```
  run:
    #- blast
    #- srprism
test:
    commands:
        - "bmtool -h &> /dev/null"
about:
    home: ftp://ftp.ncbi.nlm.nih.gov/pub/agarwala/bmtagger/
    license: Public Domain
    summary: "bmtool is part of BMTagger aka Best Match Tagger, for removing human reads from metagen
```

CHAPTER 105

botocore

105.1 Summary

105.2 Home

https://github.com/boto/botocore

105.3 Versions

- 1.3.6

105.4 License

Apache License 2.0

105.5 Meta

```
package:
  name: botocore
  version: '1.3.6'

source:
  fn: botocore-1.3.6.tar.gz
  url: https://pypi.python.org/packages/source/b/botocore/botocore-1.3.6.tar.gz
  md5: 0d88c01a33f278db51e23ff9b8223bb6

build:
  number: 0

requirements:
  build:
    - python
    - setuptools
    - jmespath
    - python-dateutil
```

```
    - docutils

  run:
    - python
    - jmespath
    - python-dateutil
    - docutils

test:
  imports:
    - botocore

about:
  home: https://github.com/boto/botocore
  license: Apache License 2.0
```

CHAPTER 106

bottle

106.1 Summary

Fast and simple WSGI-framework for small web-applications.

106.2 Home

http://bottlepy.org/

106.3 Versions

- 0.12.9

106.4 License

MIT License

106.5 Meta

```
# copied from https://anaconda.org/synthicity/bottle

package:
  name: bottle
  version: '0.12.9'

source:
  fn: bottle-0.12.9.tar.gz
  url: https://pypi.python.org/packages/source/b/bottle/bottle-0.12.9.tar.gz
  md5: f5850258a86224a791171e8ecbb66d99

requirements:
  build:
    - python
```

```
  run:
    - python

test:
  # Python imports
  imports:
    - bottle

about:
  home: http://bottlepy.org/
  license:  MIT License
  summary: 'Fast and simple WSGI-framework for small web-applications.'
```

CHAPTER 107

bowtie

107.1 Summary

An ultrafast memory-efficient short read aligner

107.2 Home

http://bowtie-bio.sourceforge.net/index.shtml

107.3 Versions

- 1.1.2

107.4 License

GPLv3

107.5 Meta

```
about:
    home: 'http://bowtie-bio.sourceforge.net/index.shtml'
    license: GPLv3
    summary: An ultrafast memory-efficient short read aligner
package:
    name: bowtie
    version: 1.1.2
requirements:
    build:
        - python
    run:
        - python
test:
    commands:
        - (bowtie --version 2>&1) > /dev/null
```

```
source:
  fn: bowtie-1.1.2-linux-x86_64.zip
  url: http://sourceforge.net/projects/bowtie-bio/files/bowtie/1.1.2/bowtie-1.1.2-linux-x86_64.zip
  md5: c61f748e45bccae69f6e1de25eec9aae
```

CHAPTER 108

bowtie2

108.1 Summary

Fast and sensitive read alignment

108.2 Home

http://bowtie-bio.sourceforge.net/bowtie2/index.shtml

108.3 Versions

- 2.2.6
- 2.2.5

108.4 License

GPLv3

108.5 Meta

```
about:
    home: 'http://bowtie-bio.sourceforge.net/bowtie2/index.shtml'
    license: GPLv3
    summary: Fast and sensitive read alignment
package:
    name: bowtie2
    version: 2.2.6
requirements:
    build:
        - python
    run:
        - python
test:
```

```
    commands:
        - (bowtie2 --version 2>&1) > /dev/null

source:
  fn: bowtie2-2.2.6-linux-x86_64.zip
  url: http://sourceforge.net/projects/bowtie-bio/files/bowtie2/2.2.6/bowtie2-2.2.6-linux-x86_64.zip
  md5: 074884c2989437491685cfdec649d424
```

CHAPTER 109

burrito-fillings

109.1 Summary

burrito-fillings: burrito application controllers for bioinformatics

109.2 Home

https://github.com/biocore/burrito-fillings

109.3 Versions

- 0.1.1

109.4 License

BSD License

109.5 Meta

```
package:
  name: burrito-fillings
  version: "0.1.1"

source:
  fn: burrito-fillings-0.1.1.tar.gz
  url: https://pypi.python.org/packages/source/b/burrito-fillings/burrito-fillings-0.1.1.tar.gz
  md5: ea65051e674aedfad8bbfdfa63f2c4d8

build:
  number: 0

requirements:
  build:
    - python
```

```
    - setuptools
    - scikit-bio ==0.2.3
    - burrito ==0.9.1

  run:
    - python
    - scikit-bio ==0.2.3
    - burrito ==0.9.1

test:
  # Python imports
  imports:
    - bfillings

about:
  home: https://github.com/biocore/burrito-fillings
  license: BSD License
  summary: 'burrito-fillings: burrito application controllers for bioinformatics'
```

CHAPTER 110

burrito

110.1 Summary

Framework for wrapping and controlling command-line applications.

110.2 Home

https://github.com/biocore/burrito

110.3 Versions

- 0.9.1

110.4 License

BSD License

110.5 Meta

```
package:
  name: burrito
  version: "0.9.1"

source:
  fn: burrito-0.9.1.tar.gz
  url: https://pypi.python.org/packages/source/b/burrito/burrito-0.9.1.tar.gz
  md5: ef2b0bee1e8c037a535627a33e304d61

build:
  number: 0

requirements:
  build:
    - python
```

```
    - setuptools
    - future

  run:
    - python
    - future

test:
  # Python imports
  imports:
    - burrito

about:
  home: https://github.com/biocore/burrito
  license: BSD License
  summary: 'Framework for wrapping and controlling command-line applications.'
```

CHAPTER 111

bwa

111.1 Summary

The BWA read mapper.

111.2 Home

http://bio-bwa.sourceforge.net

111.3 Versions

- 0.7.12

111.4 License

MIT

111.5 Meta

```
package:
  name: bwa
  version: "0.7.12"
build:
  number: 1
source:
  fn: bwa-0.7.12.tar.bz2
  url: https://github.com/lh3/bwa/archive/0.7.12.tar.gz
  #url: http://downloads.sourceforge.net/project/bio-bwa/bwa-0.7.12.tar.bz2
requirements:
  build:
  run:
about:
  home: http://bio-bwa.sourceforge.net
```

```
  license: MIT
  summary: The BWA read mapper.
```

CHAPTER 112

bwakit

112.1 Summary

A self-consistent installation-free package of scripts and precompiled binaries, providing an end-to-end solution to read mapping

112.2 Home

https://github.com/lh3/bwa/tree/master/bwakit

112.3 Versions

- 0.7.12

112.4 License

GPLv3

112.5 Meta

```
package:
  name: bwakit
  version: '0.7.12'

source:
  fn: bwakit-0.7.12_x64-linux.tar.bz2
  url: http://downloads.sourceforge.net/project/bio-bwa/bwakit/bwakit-0.7.12_x64-linux.tar.bz2

build:
  number: 0

requirements:
  build:
  run:
```

```
test:
  commands:
    - "run-bwamem 2>&1 | grep 'Usage:   run-bwamem'"

about:
  home: https://github.com/lh3/bwa/tree/master/bwakit
  license: GPLv3
  summary: A self-consistent installation-free package of scripts and precompiled binaries, providing
```

CHAPTER 113

bx-python

113.1 Summary

Toolkit to enable rapid implementation of genome scale analyses.

113.2 Home

http://bitbucket.org/james_taylor/bx-python/wiki/Home

113.3 Versions

- 0.7.3
- 0.7.2
- 0.7.1

113.4 License

MIT

113.5 Meta

```
package:
  name: bx-python
  version: '0.7.3'

source:
  #hg_url: https://bitbucket.org/james_taylor/bx-python
  fn: bx-python-0.7.3.tar.gz
  url: https://pypi.python.org/packages/source/b/bx-python/bx-python-0.7.3.tar.gz
  md5: d8c50c01c9e421bae0bbdbfa00fef6e4

build:
  number: 1
```

```
  skip: True # [not py27]

requirements:
  build:
    - python
    - setuptools
    - cython
    - nose
    - numpy x.x

  run:
    - python
    - setuptools
    - numpy x.x

test:
  imports:
    - bx.align.sitemask
    - bx.tabular
    - bx.intervals
    - bx.align
    - bx.bbi
    - bx.bbi.bigwig_file
    - bx.cookbook
    - bx.arrays
    - bx.motif.io
    - bx.seq
    - bx.intervals.operations
    - bx.pwm
    - bx.misc
    - bx.motif
    - bx.phylo
    - bx.motif.logo
    - bx_extras
    - bx.align.tools
    - bx
    - bx.intseq

  requires:
    # Put any additional test requirements here.  For example
    - nose

about:
  home: http://bitbucket.org/james_taylor/bx-python/wiki/Home
  license: MIT
  summary: Toolkit to enable rapid implementation of genome scale analyses.
```

CHAPTER 114

byobu

114.1 Summary

Byobu is a GPLv3 open source text-based window manager and terminal multiplexer.

114.2 Home

http://byobu.co/

114.3 Versions

- 5.98

114.4 License

GPLv3

114.5 Meta

```
package:
  name: byobu
  version: "5.98"

source:
  fn: byobu_5.98.orig.tar.gz
  url: https://launchpad.net/byobu/trunk/5.98/+download/byobu_5.98.orig.tar.gz
  md5: 2e09c9d2f9e3b6e2953bd581b027239c

build:
  number: 1

requirements:
  build:
    - newt
```

```
    - ncurses
    - libevent
    - tmux
  run:
    - newt
    - ncurses
    - libevent
    - tmux

test:
  commands:
    - byobu -c "echo 'hello world'"

about:
  home: http://byobu.co/
  license: GPLv3
  summary: Byobu is a GPLv3 open source text-based window manager and terminal multiplexer.
```

CHAPTER 115

cage

115.1 Summary

Changepoint Analysis for Efficient Variant Calling

115.2 Home

https://github.com/adambloniarz/CAGe

115.3 Versions

- 2016.01.24

115.4 License

Apache v2

115.5 Meta

```
package:
  name: cage
  version: '2016.01.24'

source:
  git_url: https://github.com/adambloniarz/CAGe.git
  git_rev: b8aec7e

build:
  number: 0

requirements:
  build:
    - bamtools
    - sqlite
```

```
  run:
    - python
    - bamtools
    - sqlite

test:
  commands:
    - cage --version
    - bamdump --help
    # - cage-classify.py --help

about:
  home: https://github.com/adambloniarz/CAGe
  license: Apache v2
  summary: Changepoint Analysis for Efficient Variant Calling
```

CHAPTER 116

cancerit-allelecount

116.1 Summary

Support code for NGS copy number algorithms

116.2 Home

https://github.com/cancerit/alleleCount

116.3 Versions

- 2.1.2

116.4 License

GPLv3

116.5 Meta

```
package:
  name: cancerit-allelecount
  version: '2.1.2'
source:
  fn: alleleCount-v2.1.2.tar.gz
  url: https://github.com/cancerit/alleleCount/archive/v2.1.2.tar.gz
build:
  number: 0
requirements:
  build:
  run:
test:
  commands:
    - 'alleleCounter -h'
about:
```

```
  home: https://github.com/cancerit/alleleCount
  license: GPLv3
  summary: Support code for NGS copy number algorithms
```

CHAPTER 117

cd-hit

117.1 Summary

Clusters and compares protein or nucleotide sequences

117.2 Home

http://weizhongli-lab.org/cd-hit/

117.3 Versions

- 4.6.4

117.4 License

GPL v2

117.5 Meta

```
package:
  name: cd-hit
  version: "4.6.4"

source:
  fn: cd-hit-v4.6.4-2015-0603.tar.gz
  url: https://github.com/weizhongli/cdhit/releases/download/V4.6.4/cd-hit-v4.6.4-2015-0603.tar.gz
  sha1: e4315377a2cf04648abe6d6ac1f988029a603581

build:
  number: 1

about:
  home: http://weizhongli-lab.org/cd-hit/
```

```
  license: GPL v2
  summary: Clusters and compares protein or nucleotide sequences
```

CHAPTER 118

cdbtools [linux64]

118.1 Summary

CDB (Constant DataBase) indexing and retrieval tools for FASTA files

118.2 Home

http://compbio.dfci.harvard.edu/tgi

118.3 Versions

- 0.99

118.4 License

Public Domain

118.5 Meta

```
package:
  name: cdbtools [linux64]
  version: 0.99

source:
  fn:  cdbfasta.tar.gz
  url: ftp://occams.dfci.harvard.edu/pub/bio/tgi/software/cdbfasta/cdbfasta.tar.gz
  md5: ed07e474d67e0e79e7e89f9f43ee96df

  patches:
    - zlib.patch

build:
  number: 0
```

```
requirements:
  build:
    - zlib
  run:
    - zlib

test:
  commands:
    - cdbfasta -v
    - cdbyank -v

about:
  home: http://compbio.dfci.harvard.edu/tgi
  license: Public Domain
  summary: CDB (Constant DataBase) indexing and retrieval tools for FASTA files

# vim:set ts=8 sw=2
```

CHAPTER 119

chanjo

119.1 Summary

Coverage analysis tool for clinical sequencing

119.2 Home

http://www.chanjo.co/

119.3 Versions

- 3.1.1

119.4 License

MIT

119.5 Meta

```
package:
  name: chanjo
  version: "3.1.1"

source:
  fn: chanjo-3.1.1.tar.gz
  url: https://pypi.python.org/packages/source/c/chanjo/chanjo-3.1.1.tar.gz
  md5: 23a691d5e6f23e99901d77493e8597e6

build:
  preserve_egg_dir: True
  entry_points:
    - chanjo = chanjo.__main__:root_command

  # If this is a new build for the same version, increment the build
```

```
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - click
    - setuptools
    - toolz
    - path.py
    - pyyaml
    - sqlalchemy >=0.8.2

  run:
    - python
    - click
    - setuptools
    - toolz
    - path.py
    - pyyaml
    - sqlalchemy >=0.8.2
    - sambamba

test:
  # Python imports
  imports:
    - chanjo
    - chanjo.annotate
    - chanjo.annotate.sambamba
    - chanjo.bootstrap
    - chanjo.cli
    - chanjo.config
    - chanjo.demo
    - chanjo.load
    - chanjo.parse
    - chanjo.parse.bed
    - chanjo.parse.sambamba
    - chanjo.sex
    - chanjo.store

  commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.

    - chanjo --help

  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  requires:
    - pytest

about:
  home: http://www.chanjo.co/
  license: MIT
  license_file: LICENSE
  summary: 'Coverage analysis tool for clinical sequencing'
```

```
# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 120

chromhmm

120.1 Summary

ChromHMM is software for learning and characterizing chromatin states. ChromHMM can integrate multiple chromatin datasets such as ChIP-seq data of various histone modifications to discover de novo the major re-occuring combinatorial and spatial patterns of marks.

120.2 Home

http://compbio.mit.edu/ChromHMM/

120.3 Versions

- 1.11

120.4 License

GPLv3

120.5 Meta

```
package:
  name: chromhmm
  version: 1.11

source:
  fn: ChromHMM.zip
  url: http://compbio.mit.edu/ChromHMM/ChromHMM.zip
  md5: bc114f31467a8b40b1d18d46e83c834a

build:
  detect_binary_files_with_prefix: True
  number: 0
```

```
requirements:
  run:
    - java-jdk

test:
  commands:
    - "ChromHMM.sh -Xmx512M BinarizeBam | grep -q 'usage BinarizeBam'"

about:
  home: http://compbio.mit.edu/ChromHMM/
  license: GPLv3
  summary: 'ChromHMM is software for learning and characterizing chromatin states. ChromHMM can integ
```

CHAPTER 121

circlator

121.1 Summary

circlator: a tool to circularise genome assemblies

121.2 Home

https://github.com/sanger-pathogens/circlator

121.3 Versions

- 1.1.2

121.4 License

GNU General Public License v3 (GPLv3)

121.5 Meta

```
package:
  name: circlator
  version: "1.1.2"

source:
  fn: circlator-1.1.2.tar.gz
  url: https://pypi.python.org/packages/source/c/circlator/circlator-1.1.2.tar.gz
  md5: 55a7ed5ab1795d04ba04cc0e80f67695
#  patches:
   # List any patch files here
   # - fix.patch

build:
  skip: True # [py27]
  # noarch_python: True
```

```
  # preserve_egg_dir: True
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - circlator = circlator:main
    #
    # Would create an entry point called circlator that calls circlator.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools
    - openpyxl
    - pyfastaq >=3.10.0
    - pysam >=0.8.1
    - pymummer >=0.6.1
    - bio_assembly_refinement >=0.4.0

  run:
    - python
    - openpyxl
    - pyfastaq >=3.10.0
    - pysam >=0.8.1
    - pymummer >=0.6.1
    - bio_assembly_refinement >=0.4.0
    - bwa
    - prodigal
    - samtools
    - spades

test:
  # Python imports
  imports:
    - circlator
    - circlator.tasks

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  requires:
    - nose >=1.3
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: https://github.com/sanger-pathogens/circlator
  license: GNU General Public License v3 (GPLv3)
```

```
  summary: 'circlator: a tool to circularise genome assemblies'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 122

clark

122.1 Summary

Fast, accurate and versatile k-mer based classification system

122.2 Home

http://clark.cs.ucr.edu/

122.3 Versions

- 1.2.2_b

122.4 License

GPL3

122.5 Meta

```
package:
  name: clark
  version: "1.2.2_b"

build:
  number: 0

source:
  fn: CLARKV1.2.2-b.tar.gz
  url: http://clark.cs.ucr.edu/Download/CLARKV1.2.2-b.tar.gz
  md5: 74a7a8836eb6b43276997bdc473e0757

requirements:
  build:
  - gcc
```

```
  run:
  - libgcc

test:
  commands:
    - CLARK --help 2>&1 | grep k-spectrum > /dev/null

about:
  home: http://clark.cs.ucr.edu/
  license: GPL3
  license_file: LICENSE_GNU_GPL.txt
  summary: Fast, accurate and versatile k-mer based classification system
```

CHAPTER 123

clearcut [linux64]

123.1 Summary

The reference implementation for Relaxed Neighbor Joining (RNJ).

123.2 Home

http://www.mothur.org

123.3 Versions

- 1.0.9

123.4 License

BSD

123.5 Meta

```
package:
  name: clearcut [linux64]
  version: 1.0.9

source:
  fn: Clearcut.source.zip
  url: http://www.mothur.org/w/images/9/91/Clearcut.source.zip
  md5: c7c01922d75d5bb6e218d7a9adc72978

build:
  number: 0

test:
  commands:
     - clearcut -V
```

```
about:
  home: http://www.mothur.org
  license: BSD
  license_file: clearcut/LICENSE
  summary: The reference implementation for Relaxed Neighbor Joining (RNJ).
```

CHAPTER 124

clever-toolkit

124.1 Summary

The clever toolkit (CTK) is a suite of tools to analyze next-generation sequencing data and, in particular, to discover and genotype insertions and deletions from paired-end reads.

124.2 Home

https://bitbucket.org/tobiasmarschall/clever-toolkit

124.3 Versions

- 2.0rc3

124.4 License

GPLv3

124.5 Meta

```
package:
  name: clever-toolkit
  version: "2.0rc3"

source:
  fn: clever-toolkit-v2.0rc3.tar.gz
  url: https://bitbucket.org/tobiasmarschall/clever-toolkit/downloads/clever-toolkit-v2.0rc3.tar.gz

requirements:
  build:
    - gcc
    - boost
    - cmake
    - zlib
```

```
  run:
    - libgcc
    - python
    - boost
    - zlib

test:
  commands:
    - clever --help > /dev/null
    - laser --help > /dev/null

about:
  home: https://bitbucket.org/tobiasmarschall/clever-toolkit
  license: GPLv3
  summary: The clever toolkit (CTK) is a suite of tools to analyze next-generation sequencing data ar
```

CHAPTER 125

click

125.1 Summary

A simple wrapper around optparse for powerful command line utilities.

125.2 Home

http://github.com/mitsuhiko/click

125.3 Versions

- 6.2

125.4 License

BSD License

125.5 Meta

```
package:
  name: click
  version: "6.2"

source:
  fn: click-6.2.tar.gz
  url: https://pypi.python.org/packages/source/c/click/click-6.2.tar.gz
  md5: 83252a8095397b1f5f710fdd58b484d9
#  patches:
   # List any patch files here
   # - fix.patch

# build:
  # noarch_python: True
  # preserve_egg_dir: True
```

```
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - click = click:main
    #
    # Would create an entry point called click that calls click.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools

  run:
    - python

test:
  # Python imports
  imports:
    - click

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: http://github.com/mitsuhiko/click
  license: BSD License
  summary: 'A simple wrapper around optparse for powerful command line utilities.'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 126

cnvkit

126.1 Summary

Copy number variant detection from targeted DNA sequencing

126.2 Home

https://github.com/etal/cnvkit

126.3 Versions

- 0.7.5

126.4 License

MIT

126.5 Meta

```
package:
  name: cnvkit
  version: '0.7.5'

source:
  fn: CNVkit-0.7.5.tar.gz
  url: https://pypi.python.org/packages/source/C/CNVkit/CNVkit-0.7.5.tar.gz

build:
  number: 0

requirements:
  build:
    - python
    - setuptools
```

```
  run:
    - python
    - atlas # [not osx]
    - numpy
    - scipy
    - pandas
    - matplotlib
    - biopython
    - reportlab
    - pysam
    - pyvcf
    - r-pscbs
    - r-cghflasso

test:
  imports:
    - cnvlib
  commands:
    - cnvkit.py -h

about:
  home: https://github.com/etal/cnvkit
  license: MIT
  summary: Copy number variant detection from targeted DNA sequencing
```

CHAPTER 127

cogent

127.1 Summary

COmparative GENomics Toolkit

127.2 Home

http://www.pycogent.org

127.3 Versions

- 1.5.3

127.4 License

GNU General Public License (GPL)

127.5 Meta

```
package:
  name: cogent
  version: !!str 1.5.3

source:
  fn: cogent-1.5.3.tgz
  url: https://pypi.python.org/packages/source/c/cogent/cogent-1.5.3.tgz
  md5: ecdfa0bc89e0c04c9d4d39cac9984498

build:
 number: 0
 skip: True [py3k]

requirements:
  build:
```

```
    - python
    - numpy >=1.3
    - zlib
    - matplotlib >=1.1.0
    - mpi4py >=1.0
    - mysql-python >=1.2.2
    - sqlalchemy >=0.5

  run:
    - python
    - numpy >=1.3
    - zlib
    - matplotlib >=1.1.0
    - mpi4py >=1.0
    - mysql-python >=1.2.2
    - sqlalchemy >=0.5

test:
  imports:
    - cogent
    - cogent.align
    - cogent.align.weights
    - cogent.app
    - cogent.cluster
    - cogent.core
    - cogent.data
    - cogent.evolve
    - cogent.format
    - cogent.maths
    - cogent.maths.matrix
    - cogent.maths.spatial
    - cogent.maths.stats
    - cogent.maths.stats.cai
    - cogent.maths.unifrac
    - cogent.motif
    - cogent.parse
    - cogent.phylo
    - cogent.recalculation
    - cogent.seqsim
    - cogent.struct
    - cogent.util
    - cogent.db.ensembl

about:
  home: http://www.pycogent.org
  license:  GNU General Public License (GPL)
  summary: 'COmparative GENomics Toolkit'
```

CHAPTER 128

cpat

128.1 Summary

Coding Potential Assessment Tool

128.2 Home

http://dldcc-web.brc.bcm.edu/lilab/liguow/CGI/cpat/_build/html/index.html

128.3 Versions

- 1.2.2

128.4 License

GNU

128.5 Meta

```
package:
  name: cpat
  version: 1.2.2

build:
  number: 2
  skip: True # [not py27]

source:
  fn: CPAT-1.2.2.tar.gz
  url: http://sourceforge.net/projects/rna-cpat/files/CPAT-1.2.2.tar.gz
  md5: fc296ec5fbd8b8062fa8353458b89c62
  patches:
    - setup.py.patch
```

```
requirements:
  build:
    - python
    - setuptools
    - bx-python
    - cython
    - pysam
    - nose
    - numpy

  run:
    - python
    - setuptools
    - bx-python
    - pysam

test:
  commands:
    - cpat.py -h
    - make_hexamer_tab.py -h
    - make_logitModel.py -h

about:
  home: http://dldcc-web.brc.bcm.edu/lilab/liguow/CGI/cpat/_build/html/index.html
  license: GNU
  summary: Coding Potential Assessment Tool
```

CHAPTER 129

cramtools

129.1 Summary

A set of Java tools and APIs for efficient compression of sequence read data

129.2 Home

http://www.ebi.ac.uk/ena/software/cram-toolkit

129.3 Versions

- 3.0.b47

129.4 License

Apache v2.0

129.5 Meta

```
package:
  name: cramtools
  version: "3.0.b47"

source:
  fn: cramtools-3.0.jar
  url: https://github.com/enasequence/cramtools/raw/9f0569da1753ebcfd8410142cbd0dd7021b36db5/cramtool

build:
  number: 2

requirements:
  run:
    - java-jdk
```

```
test:
  commands:
    - cramtools -h

about:
  home: http://www.ebi.ac.uk/ena/software/cram-toolkit
  license: Apache v2.0
  summary: A set of Java tools and APIs for efficient compression of sequence read data
```

CHAPTER 130

crossmap

130.1 Summary

Convert genomic coordiates between assemblies

130.2 Home

http://crossmap.sourceforge.net

130.3 Versions

- 0.2.2

130.4 License

GPL

130.5 Meta

```
package:
  name: crossmap
  version: "0.2.2"
source:
  url: http://sourceforge.net/projects/crossmap/files/CrossMap-0.2.2.tar.gz
  fn: CrossMap-0.2.2.tar.gz
  patches:
    - setup_remove_deps.diff

build:
    number: 1

    # CrossMap is very particular about Python version.
    skip: True # [not py27]
```

```
requirements:
  build:
    - python
    - cython
    - numpy
    - setuptools
    - nose
    - pysam
    - bx-python
  run:
    - python
    - cython
    - numpy
    - setuptools
    - nose
    - pysam
    - bx-python

test:
  commands:
    - CrossMap.py bed
    - CrossMap.py vcf

about:
  home: http://crossmap.sourceforge.net
  license: GPL
  summary: "Convert genomic coordiates between assemblies"
```

CHAPTER 131

cufflinks

131.1 Summary

Transcriptome assembly and differential expression analysis for RNA-Seq.

131.2 Home

http://cole-trapnell-lab.github.io/cufflinks/

131.3 Versions

- 2.2.1

131.4 License

Boost Software License

131.5 Meta

```
about:
    home: 'http://cole-trapnell-lab.github.io/cufflinks/'
    license: Boost Software License
    summary: Transcriptome assembly and differential expression analysis for RNA-Seq.
package:
    name: cufflinks
    version: 2.2.1
requirements:
    build:
        - python
    run:
        - python
test:
    commands:
        - (cuffmerge --help 2>&1) | grep Options > /dev/null
```

```
source:
  fn: cufflinks-2.2.1.Linux_x86_64.tar.gz
  url: http://cole-trapnell-lab.github.io/cufflinks/assets/downloads/cufflinks-2.2.1.Linux_x86_64.tar
  patches:
        - cuffmerge.python3.patch # [py3k]
build:
  number: 1
```

CHAPTER 132

curl

132.1 Summary

curl is an open source command line tool and library for transferring data with URL syntax

132.2 Home

http://www.curl.haxx.se/

132.3 Versions

- 7.45.0

132.4 License

MIT

132.5 Meta

```
about:
  home: http://www.curl.haxx.se/
  license: MIT
  summary: curl is an open source command line tool and library for transferring data with URL syntax

build:
  number: 1
  binary_has_prefix_files:
    - lib/libcurl.so.4.4.0 # [not osx]
    - lib/libcurl.4.dylib # [not linux]

requirements:
  build:
    - openssl
    - zlib
```

```
  run:
    - openssl
    - zlib

package:
  name: curl
  version: 7.45.0

test:
  commands:
    - (curl --version 2>&1) > /dev/null

source:
  fn: curl-7.45.0.tar.gz
  sha256: 02c78c8060d587422e2826f622c729189b56084bba365140f13af3d402b6cb6b
  url: http://curl.haxx.se/download/curl-7.45.0.tar.gz
```

CHAPTER 133

cutadapt

133.1 Summary

trim adapters from high-throughput sequencing reads

133.2 Home

https://cutadapt.readthedocs.org/

133.3 Versions

- 1.9.1

133.4 License

MIT License

133.5 Meta

```
package:
  name: cutadapt
  version: "1.9.1"
source:
  fn: cutadapt-1.9.1.tar.gz
  url: https://pypi.python.org/packages/source/c/cutadapt/cutadapt-1.9.1.tar.gz
  md5: cc2e4d3da46a0d88b4ababe065d0021a
requirements:
  build:
    - python
  run:
    - python
test:
  imports:
    - cutadapt
```

```
    - cutadapt.scripts
about:
  home: https://cutadapt.readthedocs.org/
  license: MIT License
  summary: 'trim adapters from high-throughput sequencing reads'
```

CHAPTER 134

cyordereddict

134.1 Summary

Cython implementation of Python's collections.OrderedDict

134.2 Home

https://github.com/shoyer/cyordereddict

134.3 Versions

- 0.2.2

134.4 License

BSD License

134.5 Meta

```
# copied from https://anaconda.org/IOOS/cyordereddict

package:
    name: cyordereddict
    version: "0.2.2"

source:
    fn: cyordereddict-0.2.2.tar.gz
    url: https://pypi.python.org/packages/source/c/cyordereddict/cyordereddict-0.2.2.tar.gz
    md5: 6279eb0bf9819f0293ad5315b2d484d0

build:
    number: 0

requirements:
```

```
    build:
        - python
        - cython
    run:
        - python

test:
    imports:
        - cyordereddict
        - cyordereddict.benchmark

about:
    home: https://github.com/shoyer/cyordereddict
    license: BSD License
    summary: "Cython implementation of Python's collections.OrderedDict"
```

CHAPTER 135

cyvcf2

135.1 Summary

A cython wrapper around htslib built for fast parsing of Variant Call Format (VCF) files

135.2 Home

https://github.com/brentp/cyvcf2

135.3 Versions

- 0.2.5

135.4 License

MIT

135.5 Meta

```
package:
  name: cyvcf2
  version: '0.2.5'

source:
  fn: cyvcf2-0.2.5.tar.gz
  url: https://pypi.python.org/packages/source/c/cyvcf2/cyvcf2-0.2.5.tar.gz
  md5: b4151584ed2b55a02ace40d7f9723459

build:
  number: 0

requirements:
  build:
    - python
```

```
    - setuptools
    - cython
    - numpy

  run:
    - python
    - numpy
    - matplotlib
    - seaborn
    - pandas

test:
  imports:
    - cyvcf2

about:
  home: https://github.com/brentp/cyvcf2
  summary: A cython wrapper around htslib built for fast parsing of Variant Call Format (VCF) files
  license: MIT
```

CHAPTER 136

daligner

136.1 Summary

DALIGNER: Find all significant local alignments between reads

136.2 Home

https://github.com/thegenemyers/DALIGNER

136.3 Versions

- 1.0

136.4 License

Custom

136.5 Meta

```
package:
  name: daligner
  version: "1.0"

build:
  number: 0
source:
  fn: V1.0.tar.gz
  md5: f1b4c396ae062caa4c0e6423ba0725ef
  url: https://github.com/thegenemyers/DALIGNER/archive/V1.0.tar.gz


requirements:
  build:
    - gcc
```

```
  run:
    - libgcc
test:
    commands:
       - daligner 2>&1 | grep Usage > /dev/null

about:
  home: 'https://github.com/thegenemyers/DALIGNER'
  license: Custom
  license_file: README
  summary: "DALIGNER: Find all significant local alignments between reads"
```

CHAPTER 137

datamash

137.1 Summary

GNU Datamash is a command-line program which performs basic numeric,textual and statistical operations on input textual data files.

137.2 Home

http://www.gnu.org/software/datamash

137.3 Versions

- 1.0.6

137.4 License

GPL3

137.5 Meta

```
about:
  home: http://www.gnu.org/software/datamash
  license: GPL3
  summary: 'GNU Datamash is a command-line program which performs basic numeric,textual
    and statistical operations on input textual data files.'
build:
  number: 0
package:
  name: datamash
  version: 1.0.6
requirements:
  build: []
  run: []
source:
```

```
  fn: datamash-1.0.6.tar.gz
  sha256: 0154c25c45b5506b6d618ca8e18d0ef093dac47946ac0df464fb21e77b504118
  url: http://ftp.gnu.org/gnu/datamash/datamash-1.0.6.tar.gz
test:
  commands:
    - datamash --help &> /dev/null
```

CHAPTER 138

dazz_db

138.1 Summary

DAZZ_DB: The Dazzler Data Base

138.2 Home

https://github.com/thegenemyers/DAZZ_DB

138.3 Versions

- 1.0

138.4 License

Custom

138.5 Meta

```
package:
  name: dazz_db
  version: "1.0"

build:
  number: 0
source:
  fn: V1.0.tar.gz
  md5: 12496195e13cc2e6d61f2647ab2ea2eb
  url: https://github.com/thegenemyers/DAZZ_DB/archive/V1.0.tar.gz


requirements:
  build:
    - gcc
```

```
  run:
    - libgcc
test:
    commands:
       - fasta2DB 2>&1 | grep Usage > /dev/null

about:
  home: 'https://github.com/thegenemyers/DAZZ_DB'
  license: Custom
  license_file: README
  summary: "DAZZ_DB: The Dazzler Data Base"
```

CHAPTER 139

deeptools

139.1 Summary

A set of user-friendly tools for normalization and visualzation of deep-sequencing data

139.2 Home

https://github.com/fidelram/deepTools

139.3 Versions

- 2.0.1

139.4 License

GPL3

139.5 Meta

```
package:
  name: deeptools
  version: '2.0.1'

source:
  fn: deepTools-2.0.1.tar.gz
  url: https://pypi.python.org/packages/source/d/deepTools/deepTools-2.0.1.tar.gz
  md5: 985143b6d92ee934be93d0284a8fedfb

build:
  number: 0
  skip: True # [not py27]

requirements:
  build:
```

```
    - python
    - setuptools
    - numpy >=1.8.0
    - scipy >=0.15.0
    - matplotlib >=1.4.0
    - pysam >=0.8.2
    - bx-python >=0.7.2
  run:
    - python
    - pybigwig >=0.2.3
    - numpy >=1.8.0
    - scipy >=0.15.0
    - matplotlib >=1.4.0
    - pysam >=0.8.2
    - bx-python >=0.7.2

test:
  imports:
    - deeptools

  commands:
    - bamCompare --version

about:
  home: https://github.com/fidelram/deepTools
  license: GPL3
  summary: A set of user-friendly tools for normalization and visualzation of deep-sequencing data
```

CHAPTER 140

delly

140.1 Summary

Structural variant discovery by integrated paired-end and split-read analysis

140.2 Home

https://github.com/tobiasrausch/delly

140.3 Versions

- 0.7.2

140.4 License

GPLv3

140.5 Meta

```
package:
  name: delly
  version: '0.7.2'

source:
  git_url: https://github.com/tobiasrausch/delly.git
  git_rev: v0.7.2

build:
  number: 1

test:
  commands:
    - delly --help 2>&1 | grep delly
```

```
about:
  home: https://github.com/tobiasrausch/delly
  license: GPLv3
  summary: Structural variant discovery by integrated paired-end and split-read analysis
```

CHAPTER 141

diamond

141.1 Summary

Accelerated BLAST compatible local sequence aligner

141.2 Home

http://ab.inf.uni-tuebingen.de/software/diamond/

141.3 Versions

- 0.7.10

141.4 License

BSD

141.5 Meta

```
package:
  name: diamond
  version: "0.7.10"
source:
  git_url: https://github.com/bbuchfink/diamond/
  git_tag: v0.7.10
  patches:
    - cmake_patch
# We pin on gcc version to avoid gcc-5 dual ABI issues depending on boost.
requirements:
  build:
    - gcc >=4.8.5,<5 # [unix]
    - boost >=1.53.0
    - cmake
  run:
```

```
    - libgcc >=4.8.5,<5 # [unix]
    - boost >=1.53.0
test:
  commands:
    - diamond --help 2>&1 > /dev/null
about:
  home: http://ab.inf.uni-tuebingen.de/software/diamond/
  license: BSD
  summary: Accelerated BLAST compatible local sequence aligner
```

CHAPTER 142

dropbox

142.1 Summary

Official Dropbox API Client

142.2 Home

http://www.dropbox.com/developers

142.3 Versions

- 3.38

142.4 License

https://raw.githubusercontent.com/dropbox/dropbox-sdk-python/master/LICENSE

142.5 Meta

```
package:
  name: dropbox
  version: "3.38"

source:
  fn: dropbox-3.38.tar.gz
  url: https://pypi.python.org/packages/source/d/dropbox/dropbox-3.38.tar.gz
  md5: f528584e24e969eb716fcbee769d3cf5

build:
  number: 1

requirements:
  build:
    - python
```

```
    - setuptools
    - urllib3
    - requests >=2.5.1
    - six >=1.3.0

  run:
    - python
    - urllib3
    - requests >=2.5.1
    - six >=1.3.0

test:
  imports:
    - dropbox

about:
  home: http://www.dropbox.com/developers
  license: https://raw.githubusercontent.com/dropbox/dropbox-sdk-python/master/LICENSE
  summary: 'Official Dropbox API Client'
```

CHAPTER 143

dxua

143.1 Summary

command-line tool for uploading files to the DNAnexus Platform

143.2 Home

https://wiki.dnanexus.com/Downloads#Upload-Agent

143.3 Versions

- 1.5.11

143.4 License

Apache v2.0

143.5 Meta

```
about:
    home: 'https://wiki.dnanexus.com/Downloads#Upload-Agent'
    license: "Apache v2.0"
    summary: command-line tool for uploading files to the DNAnexus Platform
package:
    name: dxua
    version: 1.5.11
requirements:
    # build:
    #     - python
    # run:
    #     - python
test:
    commands:
        - "dxua --help &> /dev/null"
```

```
source:
  fn: dnanexus-upload-agent-1.5.11-linux.tar.gz #[linux64]
  url: https://wiki.dnanexus.com/images/files/dnanexus-upload-agent-1.5.11-linux.tar.gz #[linux64]
  md5: caf276a95f0ad61af3e09b9140e9357d #[linux64]

  fn: dnanexus-upload-agent-1.5.11-osx.zip #[osx]
  url: https://wiki.dnanexus.com/images/files/dnanexus-upload-agent-1.5.11-osx.zip #[osx]
  md5: 0102c0a5d2fa22a925c881972b79f33b #[osx]
```

CHAPTER 144

ea-utils

144.1 Summary

Command-line tools for processing biological sequencing data.

144.2 Home

https://code.google.com/p/ea-utils/

144.3 Versions

- 1.1.2.537

144.4 License

MIT

144.5 Meta

```
package:
  name: ea-utils
  version: 1.1.2.537

source:
  fn: ea-utils.1.1.2-537.tar.gz
  url: https://ea-utils.googlecode.com/files/ea-utils.1.1.2-537.tar.gz
  sha1: 688bddb1891ed186be0070d0d581816a35f7eb4e
  patches:
    - buildflags.patch

requirements:
  build:
    - gsl
```

```
test:
  commands:
    - fastq-stats -h > /dev/null


about:
  home: https://code.google.com/p/ea-utils/
  license: MIT
  summary: Command-line tools for processing biological sequencing data.
```

CHAPTER 145

eigen

145.1 Summary

Eigen is a C++ template library for linear algebra: matrices, vectors, numerical solvers, and related algorithms.

145.2 Home

http://eigen.tuxfamily.org

145.3 Versions

- 3.2
- 3.1.3
- 2.0.17

145.4 License

MPL2

145.5 Meta

```
about:
  home: http://eigen.tuxfamily.org
  license: MPL2
  summary: "Eigen is a C++ template library for linear algebra: matrices, vectors, numerical solvers,
build:
  number: 2
package:
  name: eigen
  version: '3.2'
requirements:
  build:
```

```
  - cmake ==3.2.3
  run:
  - cmake ==3.2.3
source:
  fn: 3.2.6.tar.bz2
  sha256: 8a3352f9a5361fe90e451a7305fb1896fc7f771dc16cc0edd8e6b157f52c343e
  url: https://bitbucket.org/eigen/eigen/get/3.2.6.tar.bz2
test:
  commands:
    - ls -l $PREFIX/include/ &> /dev/null
    - ls -l $PREFIX/share/ &> /dev/null
```

CHAPTER 146

elasticluster

146.1 Summary

Create, manage and setup computing clusters hosted on a public or private cloud infrastructure.

146.2 Home

https://github.com/gc3-uzh-ch/elasticluster

146.3 Versions

- 0.1.3bcbio

146.4 License

GPL

146.5 Meta

```
package:
  name: elasticluster
  version: '0.1.3bcbio'

source:
  fn: elasticluster-0.1.3bcbio_11.tar.gz
  #url: https://github.com/jwm/elasticluster/archive/abf3ab1.tar.gz
  url: https://github.com/chapmanb/elasticluster/archive//8d6d108.tar.gz

build:
  number: 11
  skip: True # [not py27]

requirements:
  build:
```

```
    - python
    - setuptools

  run:
    - python
    - ansible
    - azure
    - pycli
    - paramiko
    - voluptuous
    - configobj
    - boto
    - google-api-python-client
    - oauth2client
    - python-gflags

test:
  # Python imports
  imports:
    - elasticluster
    - elasticluster.conf
    - elasticluster.main
    - elasticluster.providers.ansible_provider
    - elasticluster.providers.ec2_boto

about:
  home: https://github.com/gc3-uzh-ch/elasticluster
  license: GPL
  summary: Create, manage and setup computing clusters hosted on a public or private cloud infrastruc
```

CHAPTER 147

emperor

147.1 Summary

Emperor a tool for the analysis and visualization of large microbial ecology datasets

147.2 Home

http://github.com/biocore/emperor

147.3 Versions

- 0.9.51

147.4 License

BSD License

147.5 Meta

```
package:
  name: emperor
  version: "0.9.51"

source:
  fn: emperor-0.9.51.tar.gz
  url: https://pypi.python.org/packages/source/e/emperor/emperor-0.9.51.tar.gz
  md5: 9b763cae89fe7b938b8acab4b39b92ba

build:
  number: 0
  skip: True [py3k]

requirements:
  build:
```

```
    - python
    - numpy >=1.7
    - qcli
    - scikit-bio >=0.2.1,<0.3.0

  run:
    - python
    - numpy >=1.7
    - qcli
    - scikit-bio >=0.2.1,<0.3.0

test:
  # Python imports
  imports:
    - emperor
    - emperor.qiime_backports

  commands:
    - make_emperor.py --version

about:
  home: http://github.com/biocore/emperor
  license: BSD License
  license_file: LICENSE.md
  summary: Emperor a tool for the analysis and visualization of large microbial ecology datasets
```

CHAPTER 148

epydoc

148.1 Summary

Edward Loper's API Documentation Generation Tool

148.2 Home

http://epydoc.sourceforge.net

148.3 Versions

- 3.0.1

148.4 License

MIT License

148.5 Meta

```
package:
  name: epydoc
  version: "3.0.1"

source:
  fn: epydoc-3.0.1.tar.gz
  url: https://pypi.python.org/packages/source/e/epydoc/epydoc-3.0.1.tar.gz
  md5: 36407974bd5da2af00bf90ca27feeb44
#  patches:
   # List any patch files here
   # - fix.patch

build:
  skip: True # [not py27]
  # noarch_python: True
```

```
  # preserve_egg_dir: True
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - epydoc = epydoc:main
    #
    # Would create an entry point called epydoc that calls epydoc.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python

  run:
    - python

test:
  # Python imports
  imports:
    - epydoc
    - epydoc.docwriter
    - epydoc.markup
    - epydoc.test

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: http://epydoc.sourceforge.net
  license: MIT License
  summary: "Edward Loper's API Documentation Generation Tool"

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 149

ete2

149.1 Summary

Phylogenetic tree analyses and exploration

149.2 Home

http://etetoolkit.org/

149.3 Versions

- 2.3.10

149.4 License

GPLv3

149.5 Meta

```
package:
  name: ete2
  version: '2.3.10'

source:
  fn: ete2-2.3.10.tar.gz
  url: https://pypi.python.org/packages/source/e/ete2/ete2-2.3.10.tar.gz
  md5: 87bf020c25c293e8e4e1b1e02a3dc2b1

build:
  number: 0
  skip: true # [not py27]

requirements:
  build:
```

```
    - python
    - setuptools
    - pyqt
    - numpy
    - lxml
    - mysql-python

  run:
    - python
    - setuptools
    - pyqt
    - numpy
    - lxml
    - mysql-python

test:
  imports:
    - ete2

about:
  home: http://etetoolkit.org/
  license: GPLv3
  summary: Phylogenetic tree analyses and exploration
```

CHAPTER 150

expat

150.1 Summary

Expat is an XML parser library written in C. It is a stream-oriented parser in which an application registers handlers for things the parser might find in the XML document (like start tags).

150.2 Home

http://www.libexpat.org/

150.3 Versions

- 2.1.0

150.4 License

MIT

150.5 Meta

```
about:
  home: http://www.libexpat.org/
  license: MIT
  summary: 'Expat is an XML parser library written in C. It is a stream-oriented parser
    in which an application registers handlers for things the parser might find in
    the XML document (like start tags).'
build:
  number: 0
package:
  name: expat
  version: 2.1.0
requirements:
  build: []
  run: []
```

```
source:
  fn: expat-2.1.0.tar.gz
  sha256: 823705472f816df21c8f6aa026dd162b280806838bb55b3432b0fb1fcca7eb86
  url: https://downloads.sourceforge.net/project/expat/expat/2.1.0/expat-2.1.0.tar.gz
test:
  commands:
  - xmlwf -h &> /dev/null
```

CHAPTER 151

extract_fullseq

151.1 Summary

extract_fullseq is part of BMTagger aka Best Match Tagger, for removing human reads from metagenomics datasets

151.2 Home

ftp://ftp.ncbi.nlm.nih.gov/pub/agarwala/bmtagger/

151.3 Versions

- 3.101

151.4 License

Public Domain

151.5 Meta

```
package:
    name: extract_fullseq
    version: 3.101
source:
    fn: bmtools.tar.gz # [linux]
    url: ftp://ftp.ncbi.nlm.nih.gov/pub/agarwala/bmtagger/bmtools.tar.gz # [linux]
    md5: 719474a0e3b54449cbe06f6e442994dd # [linux]
    fn: extract_fullseq # [osx]
    url: ftp://ftp.ncbi.nlm.nih.gov/pub/agarwala/bmtagger/mac-os/extract_fullseq # [osx]
build:
    number: 1
requirements:
  build:
    #- blast
    #- srprism
```

```
  run:
    #- blast
    #- srprism
#test:
#    commands:
#        - extract_fullseq # not so easy to test
about:
    home: ftp://ftp.ncbi.nlm.nih.gov/pub/agarwala/bmtagger/
    license: Public Domain
    summary: "extract_fullseq is part of BMTagger aka Best Match Tagger, for removing human reads fro
```

CHAPTER 152

fadapa

152.1 Summary

FAstqc DAta PArser - A minimal parser to parse FastQC output data

152.2 Home

https://github.com/fadapa/fadapa

152.3 Versions

- 0.3.1

152.4 License

uncopyrighted

152.5 Meta

```
package:
  name: fadapa
  version: "0.3.1"

source:
  fn: fadapa-0.3.1.tar.gz
  url: https://pypi.python.org/packages/source/f/fadapa/fadapa-0.3.1.tar.gz
  md5: 4924717f0a02c1fa9fb8985970d59bf0

build:
  number: 0

requirements:
  build:
    - python
```

```
    - setuptools
  run:
    - python

test:
  imports:
    - fadapa

about:
  home: https://github.com/fadapa/fadapa
  license: uncopyrighted
  summary: FAstqc DAta PArser - A minimal parser to parse FastQC output data
```

CHAPTER 153

fasta3

153.1 Summary

The FASTA package - protein and DNA sequence similarity searching and alignment programs

153.2 Home

http://faculty.virginia.edu/wrpearson/fasta

153.3 Versions

- 36.3.8

153.4 License

Apache 2.0

153.5 Meta

```
package:
    name: fasta3
    version: 36.3.8

source:
    fn: fasta-36.3.8.tar.gz
    url: http://faculty.virginia.edu/wrpearson/fasta/fasta36/fasta-36.3.8.tar.gz
    md5: 071c1a33534e3b47c9a680b87f2a73d7
    patches:
      - libpath.patch

build:
    number: 0

requirements:
```

```
    build:
       - zlib

    run:
        - zlib
test:
    commands:
      - fasta36 > /dev/null
      - fastf36 > /dev/null
      - fastm36 > /dev/null
      - fasts36 > /dev/null
      - fastx36 > /dev/null
      - fasty36 > /dev/null
      - ggsearch36 > /dev/null
      - glsearch36 > /dev/null
      - lalign36 > /dev/null
      - ssearch36 > /dev/null
      - tfastf36 > /dev/null
      - tfastm36 > /dev/null
      - tfasts36 > /dev/null
      - tfastx36 > /dev/null
      - tfasty36 > /dev/null

about:
    home: http://faculty.virginia.edu/wrpearson/fasta
    license: Apache 2.0
    summary: The FASTA package - protein and DNA sequence similarity searching and alignment programs
    license_file: LICENSE
```

CHAPTER 154

fastq-join

154.1 Summary

Similar to audy's stitch program, but in C, more efficient and supports some automatic benchmarking and tuning. It uses the same "squared distance for anchored alignment" as other tools.

154.2 Home

https://github.com/brwnj/fastq-join

154.3 Versions

- 1.3.1

154.4 License

MIT

154.5 Meta

```
package:
  name: fastq-join
  version: 1.3.1
build:
  number: 1
source:
  fn: fastq-join-1.3.1.tar.gz
  url: https://github.com/brwnj/fastq-join/archive/v1.3.1.tar.gz
requirements:
  build:
  run:
test:
    commands:
        - fastq-join -h
```

```
about:
  home: https://github.com/brwnj/fastq-join
  license: MIT
  summary: Similar to audy's stitch program, but in C, more efficient and supports some automatic ber
```

CHAPTER 155

fastq-multx

155.1 Summary

Demultiplexes a fastq. Capable of auto-determining barcode id's based on a master set fields. Keeps multiple reads in-sync during demultiplexing. Can verify that the reads are in-sync as well, and fail if they're not.

155.2 Home

https://github.com/brwnj/fastq-multx

155.3 Versions

- 1.3.0

155.4 License

MIT

155.5 Meta

```
package:
  name: fastq-multx
  version: 1.3.0
build:
  number: 1
source:
  fn: fastq-multx-1.3.0.tar.gz
  url: https://github.com/brwnj/fastq-multx/archive/v1.3.0.tar.gz
requirements:
  build:
  run:
test:
    commands:
        - fastq-multx -h
```

```
about:
  home: https://github.com/brwnj/fastq-multx
  license: MIT
  summary: Demultiplexes a fastq. Capable of auto-determining barcode id's based on a master set fiel
```

CHAPTER 156

fastq-screen

156.1 Summary

FastQ Screen allows you to screen a library of sequences in FastQ format against a set of sequence databases so you can see if the composition of the library matches with what you expect

156.2 Home

http://www.bioinformatics.babraham.ac.uk/projects/fastq_screen/

156.3 Versions

- 0.5.2

156.4 License

GPLv3

156.5 Meta

```
about:
  home: 'http://www.bioinformatics.babraham.ac.uk/projects/fastq_screen/'
  license: GPLv3
  summary: 'FastQ Screen allows you to screen a library of sequences in FastQ format against a set o

build:
  number: 0

requirements:
  build:
    - bowtie
    - bowtie2
    - perl >=5.22.0
    - perl-gdgraph
```

```
  run:
    - bowtie
    - bowtie2
    - perl >=5.22.0
    - perl-gdgraph
package:
  name: fastq-screen
  version: '0.5.2'
source:
  fn: fastq_screen_v0.5.2.tar.gz
  url: http://www.bioinformatics.babraham.ac.uk/projects/fastq_screen/fastq_screen_v0.5.2.tar.gz
  patches:
    - env-perl.patch
test:
  commands:
    - 'fastq_screen -h'
```

CHAPTER 157

fastqc

157.1 Summary

A quality control tool for high throughput sequence data.

157.2 Home

http://www.bioinformatics.babraham.ac.uk/projects/fastqc/

157.3 Versions

- 0.11.4

157.4 License

GPL

157.5 Meta

```
# this recipe was derived from the montilab channel.
about:
  home: 'http://www.bioinformatics.babraham.ac.uk/projects/fastqc/'
  license: GPL
  summary: 'A quality control tool for high throughput sequence data.'

build:
  detect_binary_files_with_prefix: true
  number: 2

requirements:
  run:
    - java-jdk

package:
```

```
  name: fastqc
  version: 0.11.4

source:
  fn: fastqc_v0.11.4.zip
  url: http://www.bioinformatics.babraham.ac.uk/projects/fastqc/fastqc_v0.11.4.zip
  patches:
    - java_xms.patch

test:
  commands:
    - "fastqc -h"
```

CHAPTER 158

fasttree

158.1 Summary

FastTree infers approximately-maximum-likelihood phylogenetic trees from alignments of nucleotide or protein sequences

158.2 Home

http://www.microbesonline.org/fasttree/

158.3 Versions

- 2.1.8

158.4 License

GPL v2

158.5 Meta

```
package:
  name: fasttree
  version: '2.1.8'

source:
  fn: FastTree.c
  url: "http://www.microbesonline.org/fasttree/FastTree.c"
  md5: "c7e85689a26cabba241378d4f633c2fa"

build:
  number: 1

test:
  commands:
```

```
    - FastTree | cat

about:
  home: http://www.microbesonline.org/fasttree/
  license: "GPL v2"
  summary: "FastTree infers approximately-maximum-likelihood phylogenetic trees from alignments of nu
```

CHAPTER 159

fastx_toolkit

159.1 Summary

159.2 Home

https://github.com/agordon/fastx_toolkit

159.3 Versions

- 0.0.14

159.4 License

AGPL

159.5 Meta

```
package:
  name: fastx_toolkit
  version: 0.0.14

source:
    url: https://github.com/agordon/fastx_toolkit/releases/download/0.0.14/fastx_toolkit-0.0.14.tar.b
    fn: fastx_toolkit-0.0.14.tar.bz2

build:
  preserve_egg_dir: True
  number: 0

requirements:
  build:
    - cython
    - nose
    - libgtextutils
    #- pkg-config
```

```
  run:
    - cython
    - nose
    - libgtextutils
    #- pkg-config

test:
    commands:
      #- fastx_quality_stats -h  # This fails for some unknown reason, even though it prints the outp

about:
  home: https://github.com/agordon/fastx_toolkit
  license: AGPL
```

CHAPTER 160

fftw

160.1 Summary

The fastest Fourier transform in the west.

160.2 Home

http://fftw.org

160.3 Versions

- 3.3.4

160.4 License

GNU General Public License (GPL)

160.5 Meta

```
# Credits to jeanconn for the package https://binstar.org/jeanconn/fftw
package:
    name: fftw
    version: "3.3.4"

source:
    fn: fftw-3.3.4.tar.gz
    url: http://www.fftw.org/fftw-3.3.4.tar.gz
    md5: 2edab8c06b24feeb3b82bbb3ebf3e7b3

# Note: tests are run when building the package, they are not accessible
# in the installed package.

build:
  number: 0
```

```
about:
    home: http://fftw.org
    license: GNU General Public License (GPL)
    summary: 'The fastest Fourier transform in the west.'
```

CHAPTER 161

filechunkio

161.1 Summary

FileChunkIO represents a chunk of an OS-level file containing bytes data

161.2 Home

http://bitbucket.org/fabian/filechunkio

161.3 Versions

- 1.6

161.4 License

MIT license

161.5 Meta

```
package:
  name: filechunkio
  version: "1.6"

source:
  fn: filechunkio-1.6.tar.gz
  url: https://pypi.python.org/packages/source/f/filechunkio/filechunkio-1.6.tar.gz
  md5: c168a11ad94cd2ec42a219f0f8869a7b
#  patches:
   # List any patch files here
   # - fix.patch

# build:
  # noarch_python: True
  # preserve_egg_dir: True
```

```
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - filechunkio = filechunkio:main
    #
    # Would create an entry point called filechunkio that calls filechunkio.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python

  run:
    - python

test:
  # Python imports
  imports:
    - filechunkio

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: http://bitbucket.org/fabian/filechunkio
  license: MIT license
  summary: 'FileChunkIO represents a chunk of an OS-level file containing bytes data'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 162

fisher

162.1 Summary

Fast Fisher's Exact Test

162.2 Home

http://github.com/brentp/fishers_exact_test

162.3 Versions

- 0.1.4

162.4 License

BSD License

162.5 Meta

```
package:
  name: fisher
  version: "0.1.4"

source:
  fn: fisher-0.1.4.tar.gz
  url: https://pypi.python.org/packages/source/f/fisher/fisher-0.1.4.tar.gz
  md5: bfc763b7333a1f428e4c447dd8a85968

build:
  skip: True #  [not py27]
  number: 0

requirements:
  build:
```

```
    - python
    - numpy

  run:
    - python
    - numpy

test:
  # Python imports
  imports:
    - fisher

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: http://github.com/brentp/fishers_exact_test
  license: BSD License
  summary: "Fast Fisher's Exact Test"

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 163

flash

163.1 Summary

Merge mates from fragments that are shorter than twice the read length

163.2 Home

https://ccb.jhu.edu/software/FLASH/

163.3 Versions

- 1.2.11

163.4 License

GPLv3+

163.5 Meta

```
package:
  name: flash
  version: '1.2.11'
about:
  home: https://ccb.jhu.edu/software/FLASH/
  license: GPLv3+
  summary: 'Merge mates from fragments that are shorter than twice the read length'
source:
  fn: FLASH-1.2.11.tar.gz
  md5: e4d355023a766afaaab2d62f912b605c
  url: http://downloads.sourceforge.net/project/flashpage/FLASH-1.2.11.tar.gz
test:
  commands:
    - flash -v > /dev/null
```

CHAPTER 164

freebayes

164.1 Summary

Bayesian haplotype-based polymorphism discovery and genotyping

164.2 Home

https://github.com/ekg/freebayes

164.3 Versions

- 1.0.2

164.4 License

MIT

164.5 Meta

```
package:
  name: freebayes
  version: '1.0.2'

source:
  git_url: https://github.com/ekg/freebayes.git
  git_rev: 0cb2697

build:
  number: 0

requirements:
  build:
    - cmake
  run:
```

```
test:
  commands:
    - freebayes --version

about:
  home: https://github.com/ekg/freebayes
  license: MIT
  summary: Bayesian haplotype-based polymorphism discovery and genotyping
```

CHAPTER 165

ftputil

165.1 Summary

High-level FTP client library (virtual file system and more)

165.2 Home

http://ftputil.sschwarzer.net/

165.3 Versions

- 3.2

165.4 License

BSD License

165.5 Meta

```
package:
  name: ftputil
  version: "3.2"

source:
  fn: ftputil-3.2.tar.gz
  url: https://pypi.python.org/packages/source/f/ftputil/ftputil-3.2.tar.gz
  md5: e714790766b753bfdd712955bf3584f8

requirements:
  build:
    - python

  run:
    - python
```

```
test:
  imports:
    - ftputil

about:
  home: http://ftputil.sschwarzer.net/
  license: BSD License
  summary: 'High-level FTP client library (virtual file system and more)'
```

CHAPTER 166

functools32

166.1 Summary

Backport of the functools module from Python 3.2.3 for use on 2.7 and PyPy.

166.2 Home

https://github.com/MiCHiLU/python-functools32

166.3 Versions

- 3.2.3.2

166.4 License

PSF license

166.5 Meta

```
package:
  name: functools32
  version: "3.2.3.2"

source:
  fn: functools32-3.2.3-2.tar.gz
  url: https://pypi.python.org/packages/source/f/functools32/functools32-3.2.3-2.tar.gz

build:
  skip: True  # [not py27]

requirements:
  build:
    - python
```

```
  run:
    - python

test:
  # Python imports
  imports:
    - functools32

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: https://github.com/MiCHiLU/python-functools32
  license: PSF license
  summary: 'Backport of the functools module from Python 3.2.3 for use on 2.7 and PyPy.'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 167

gat

167.1 Summary

Genomic annotation tool

167.2 Home

https://github.com/AndreasHeger/gat

167.3 Versions

- 1.2.2

167.4 License

MIT

167.5 Meta

```
package:
  name: gat
  version: 1.2.2

source:
  fn: gat-1.2.2.tar.gz
  url: https://pypi.python.org/packages/source/g/gat/gat-1.2.2.tar.gz
  md5: 604478439c1431b3deb12b9ebaff0aca

build:
  number: 0
  skip: True  # [not py27]

requirements:
  build:
```

```
    - python
    - setuptools >=1.1
    - cython >=0.19
    - numpy >=1.7
    - scipy >=0.11
    - matplotlib >=1.3.0

  run:
    - python
    - setuptools >=1.1
    - cython >=0.19
    - numpy >=1.7
    - scipy >=0.11
    - matplotlib >=1.3.0

test:
  imports:
    - gat

  commands:
    - gat-run.py -h

about:
  summary: 'Genomic annotation tool'
  license: MIT
  home: https://github.com/AndreasHeger/gat
```

CHAPTER 168

gatk-framework

168.1 Summary

The core MIT-licensed Genome Analysis Toolkit (GATK) framework, free for all uses

168.2 Home

https://github.com/chapmanb/gatk

168.3 Versions

- 3.4.46

168.4 License

MIT

168.5 Meta

```
about:
  home: https://github.com/chapmanb/gatk
  license: MIT
  summary: The core MIT-licensed Genome Analysis Toolkit (GATK) framework, free for all uses

package:
  name: gatk-framework
  version: '3.4.46'

build:
  number: 3

source:
  fn: gatk-framework-3.4-46.tar.gz
  url: https://github.com/chapmanb/gatk/releases/download/v3.4-46-framework/gatk-framework-3.4-46.tar
```

```
requirements:
  run:
    - java-jdk >=7,<8

test:
    commands:
      - gatk-framework --version
```

CHAPTER 169

gemini

169.1 Summary

a lightweight db framework for disease and population genetics.

169.2 Home

https://github.com/arq5x/gemini

169.3 Versions

- 0.18.0

169.4 License

MIT License

169.5 Meta

```
package:
  name: gemini
  version: "0.18.0"
build:
  number: 8
  skip: True # [not py27]
source:
  fn: gemini-3f96226.tar.gz
  url: https://github.com/arq5x/gemini/archive/3f96226.tar.gz
  #fn: gemini-0.18.0.tar.gz
  #url: https://pypi.python.org/packages/source/g/gemini/gemini-0.18.0.tar.gz
  md5: c3071a77037785ddc8d5e4ae40f203ee

requirements:
  build:
```

```
    - python
    - setuptools
    - bcolz
    - bottle
    - bx-python
    - cyordereddict
    - cython
    - cyvcf2
    - geneimpacts
    - inheritance
    - ipyparallel
    - ipython-cluster-helper
    - jinja2
    - networkx
    - numexpr
    - numpy
    - openpyxl
    - pandas
    - pybedtools
    - pysam
    - pyyaml
    - scipy
    - unidecode
  run:
    - python
    - bcolz
    - bottle
    - bx-python
    - cyordereddict
    - cython
    - cyvcf2
    - geneimpacts
    - inheritance
    - ipyparallel
    - ipython-cluster-helper
    - jinja2
    - networkx
    - numexpr
    - numpy
    - openpyxl
    - pandas
    - pybedtools
    - pysam
    - pyyaml
    - scipy
    - unidecode
    - grabix

test:
  commands:
    - gemini -h
  imports:
    - gemini

about:
  home: https://github.com/arq5x/gemini
  license: MIT License
  summary: a lightweight db framework for disease and population genetics.
```

CHAPTER 170

geneimpacts

170.1 Summary

prioritize effects of variant annotations from VEP, SnpEff, et al.

170.2 Home

https://github.com/brentp/geneimpacts

170.3 Versions

- 0.0.5

170.4 License

MIT

170.5 Meta

```
package:
  name: geneimpacts
  version: '0.0.5'

source:
  fn: geneimpacts-0.0.5.tar.gz
  url: https://pypi.python.org/packages/source/g/geneimpacts/geneimpacts-0.0.5.tar.gz
  md5: 0e28b124418f6e3d9dd58b683df70e2a

build:
  number: 0
  skip: True # [not py27]

requirements:
  build:
```

```
    - python
    - setuptools
  run:
    - python

test:
  imports:
    - geneimpacts

about:
  home: https://github.com/brentp/geneimpacts
  summary: prioritize effects of variant annotations from VEP, SnpEff, et al.
  license: MIT
```

CHAPTER 171

genepop

171.1 Summary

The Genepop population genetics package.

171.2 Home

http://kimura.univ-montp2.fr/~rousset/Genepop.htm

171.3 Versions

- 4.5.1

171.4 License

CeCILL

171.5 Meta

```
package:
  name: genepop
  version: "4.5.1"
build:
  number: 0
source:
  fn: sources.tar.gz
  url: http://kimura.univ-montp2.fr/~rousset/sources.tar.gz
requirements:
  build:
  run:
about:
  home: http://kimura.univ-montp2.fr/~rousset/Genepop.htm
  license: CeCILL
  summary: The Genepop population genetics package.
```

CHAPTER 172

gffutils

172.1 Summary

Work with GFF and GTF files in a flexible database framework

172.2 Home

https://github.com/daler/gffutils

172.3 Versions

- 0.8.7.1

172.4 License

MIT

172.5 Meta

```
package:
  name: gffutils
  version: "0.8.7.1"

source:
  fn: gffutils-0.8.7.1.tar.gz
  url: https://pypi.python.org/packages/source/g/gffutils/gffutils-0.8.7.1.tar.gz
  md5: 99e1c97d52b3ee38870431f8606d8985

requirements:
  build:
    - python
    - setuptools
    - pyfaidx
    - six
```

```
    - argh
    - argcomplete
    - simplejson

  run:
    - python
    - pyfaidx
    - six
    - argh
    - argcomplete
    - simplejson

test:
  imports:
    - gffutils

  commands:
    - gffutils-cli -h

about:
  home: "https://github.com/daler/gffutils"
  license: MIT
  summary: 'Work with GFF and GTF files in a flexible database framework'
```

CHAPTER 173

gfold

173.1 Summary

Find differentially expressed genes from RNA-seq data with few replicates using generalized fold changes.

173.2 Home

http://compbio.tongji.edu.cn/~fengjx/GFOLD/gfold.html

173.3 Versions

- 1.1.4

173.4 License

MIT

173.5 Meta

```
package:
  name: gfold
  version: "1.1.4"

source:
  fn: gfold.V1.1.4.tar.gz
  url: https://bitbucket.org/feeldead/gfold/downloads/gfold.V1.1.4.tar.gz

requirements:
  build:
    - gsl
  run:
    - gsl

test:
```

```
  commands:
    - gfold &> /dev/null

about:
  home: http://compbio.tongji.edu.cn/~fengjx/GFOLD/gfold.html
  license: MIT
  summary: Find differentially expressed genes from RNA-seq data with few replicates using generalize
```

CHAPTER 174

ghc

174.1 Summary

GHC is a state-of-the-art, open source, compiler and interactive environment for the functional language Haskell.

174.2 Home

https://www.haskell.org/ghc/

174.3 Versions

- 6.8.3

174.4 License

BSD

174.5 Meta

```
package:
  name: ghc
  version: 6.8.3

source:
  fn: ghc-6.8.3-x86_64-unknown-linux.tar.bz2 # [linux64]
  url: https://www.haskell.org/ghc/dist/6.8.3/ghc-6.8.3-x86_64-unknown-linux.tar.bz2 # [linux64]
  sha1: e8869f7df7465f1db913ce070e95fb22cc9309e9 # [linux64]

build:
  number: 0

requirements:
  build:
    - gmp
```

```
  run:
    - gmp

test:
  commands:
    - ghc --help > /dev/null

about:
  home: https://www.haskell.org/ghc/
  license: BSD
  summary: "GHC is a state-of-the-art, open source, compiler and interactive environment for the func
```

CHAPTER 175

ghostscript

175.1 Summary

An interpreter for the PostScript language and for PDF.

175.2 Home

http://ghostscript.com/

175.3 Versions

- 9.18

175.4 License

Affero GPL

175.5 Meta

```
package:
  name: ghostscript
  version: 9.18

source:
  fn: ghostscript-9.18.tar.gz
  url: http://downloads.ghostscript.com/public/ghostscript-9.18.tar.gz
  sha1: 761c9c25b9f5fe01197bd1510f527b3c1b6eb9de

build:
  number: 0

requirements:
  build:
    - gcc
```

```
test:
  commands:
    - gs --version > /dev/null

about:
  home: http://ghostscript.com/
  summary: An interpreter for the PostScript language and for PDF.
  license: Affero GPL
  license_file: LICENSE
```

CHAPTER 176

glimmer

176.1 Summary

Glimmer is a system for finding genes in microbial DNA

176.2 Home

https://ccb.jhu.edu/software/glimmer/index.shtml

176.3 Versions

- 3.02

176.4 License

Custom

176.5 Meta

```
package:
  name: glimmer
  version: 3.02

about:
  home: https://ccb.jhu.edu/software/glimmer/index.shtml
  license: Custom
  license_file: LICENSE
  summary: Glimmer is a system for finding genes in microbial DNA

source:
  fn: glimmer302b.tar.gz
  url: https://ccb.jhu.edu/software/glimmer/glimmer302b.tar.gz
  md5: 344d012ae12596de905866fe9eb7f16c
```

```
build:
  number: 1

test:
  commands:
    - glimmer3 | cat
```

CHAPTER 177

glpk

177.1 Summary

The GLPK (GNU Linear Programming Kit) package is intended for solving large-scale linear programming (LP), mixed integer programming (MIP), and other related problems. It is a set of routines written in ANSI C and organized in the form of a callable library.

177.2 Home

https://www.gnu.org/software/glpk/

177.3 Versions

- 4.56

177.4 License

GNU General Public License 3.0

177.5 Meta

```
# copied from https://anaconda.org/mcg/glpk

package:
  name: glpk
  version: 4.56

source:
  fn: glpk-4.56.tar.gz
  url: http://ftp.gnu.org/gnu/glpk/glpk-4.56.tar.gz

requirements:
  build:
  run:
```

```
build:
  number: 0

about:
  home: https://www.gnu.org/software/glpk/
  license: 'GNU General Public License 3.0'
  summary: 'The GLPK (GNU Linear Programming Kit) package is intended for solving large-scale linear
```

CHAPTER 178

gmap

178.1 Summary

Genomic mapping and alignment program for mRNA and EST sequences

178.2 Home

http://research-pub.gene.com/gmap/

178.3 Versions

- 2015.09.10

178.4 License

Non-commercial

178.5 Meta

```
package:
  name: gmap
  version: "2015.09.10"
source:
  fn: gmap-gsnap-2015-09-10.tar.gz
  url: http://research-pub.gene.com/gmap/src/gmap-gsnap-2015-09-10.tar.gz
  sha1: c175c0d45ee7d79036fc08e357a66ab327dcb14f
requirements:
  build:
  run:
about:
  home: http://research-pub.gene.com/gmap/
  license: Non-commercial
  summary: Genomic mapping and alignment program for mRNA and EST sequences
build:
```

```
  binary_has_prefix_files:
    - bin/atoiindex
    - bin/cmetindex
    - bin/gmap
    - bin/gmapl
    - bin/gsnap
    - bin/gsnapl
    - bin/mpi_gsnap
    - bin/snpindex
    - bin/uniqscan
    - bin/uniqscanl
  has_prefix_files:
    - bin/gff3_introns
    - bin/gff3_splicesites
    - bin/gmap_build
    - bin/gmap_uncompress
    - bin/gtf_introns
    - bin/gtf_splicesites
```

CHAPTER 179

gnuplot

179.1 Summary

Gnuplot, plotting from command line

179.2 Home

https://github.com/gnuplot/gnuplot

179.3 Versions

- 4.6.0

179.4 License

Gnuplot License + others

179.5 Meta

```
package:
  name: gnuplot
  version: "4.6.0"
build:
  number: 1
source:
  git_url: https://github.com/gnuplot/gnuplot.git
  git_rev: Release_4_6_0
  patches:
    - fix-automake.patch
    - fix-proto-int.patch
requirements:
  build:
    - autoconf
    - m4
```

```
  run:
about:
  home: https://github.com/gnuplot/gnuplot
  license: Gnuplot License + others
  summary: Gnuplot, plotting from command line
test:
  files:
    - test-data.txt
  commands:
    - gnuplot -e "set terminal dumb; set style histogram; p 'test-data.txt'"
```

CHAPTER 180

google-api-python-client

180.1 Summary

180.2 Home

https://github.com/google/google-api-python-client/

180.3 Versions

- 1.3.2

180.4 License

Apache 2.0

180.5 Meta

```
package:
  name: google-api-python-client
  version: '1.3.2'

source:
  fn: google-api-python-client-1.3.2.tar.gz
  url: https://pypi.python.org/packages/source/g/google-api-python-client/google-api-python-client-1
  md5: d17fc4919724b0da29651086f5b72458

build:
  skip: True #[not py27]
  number: 0

requirements:
  build:
    - python
    - setuptools
```

```
  run:
    - python
    - httplib2
    - oauth2client
    - uritemplate

test:
  imports:
    - apiclient
    - apiclient.discovery

about:
  home: https://github.com/google/google-api-python-client/
  license: Apache 2.0
```

CHAPTER 181

grabix

181.1 Summary

a wee tool for random access into BGZF files.

181.2 Home

https://github.com/arq5x/grabix

181.3 Versions

- 0.1.6
- 0.1.3

181.4 License

MIT

181.5 Meta

```
package:
  name: grabix
  version: "0.1.6"
build:
  number: 0
source:
  fn: grabix-0.1.6.tar.gz
  url: https://github.com/arq5x/grabix/archive/0.1.6.tar.gz
requirements:
  build:
  run:
test:
  commands:
```

```
    - grabix
about:
  home: https://github.com/arq5x/grabix
  summary: a wee tool for random access into BGZF files.
  license: MIT
```

CHAPTER 182

graphmap

182.1 Summary

A highly sensitive and accurate mapper for long, error-prone reads

182.2 Home

https://github.com/isovic/graphmap

182.3 Versions

- 0.22.1

182.4 License

MIT

182.5 Meta

```
package:
  name: graphmap
  version: "0.22.1"

build:
  number: 0

source:
  fn: 0.22.1.tar.gz
  url: https://github.com/isovic/graphmap/archive/0.22.1.tar.gz
  md5: 339ccbc170f6309a5fd7da7d10e3b581

  patches:
    - makefile.patch
```

```
requirements:
  build:
  - gcc

  run:
  - libgcc

test:
  commands:
    - graphmap -h  > /dev/null

about:
  home: https://github.com/isovic/graphmap
  license: MIT
  license_file: LICENCE
  summary: A highly sensitive and accurate mapper for long, error-prone reads
```

CHAPTER 183

graphviz

183.1 Summary

Graph Visualization Software

183.2 Home

http://www.graphviz.org/

183.3 Versions

- 2.38.0

183.4 License

Eclipse Public License v1.0

183.5 Meta

```
package:
  name: graphviz
  version: "2.38.0"

source:
  fn: graphviz-2.38.0.tar.gz
  url: http://www.graphviz.org/pub/graphviz/stable/SOURCES/graphviz-2.38.0.tar.gz
  md5: 5b6a829b2ac94efcd5fa3c223ed6d3ae
  patches:
     - gvconfig_libdir.patch

build:
  number: 3
  binary_relocation: true
```

```
requirements:
  build:
    - libpng
    - libtiff
    - freetype
    - jpeg
    - zlib
  run:
    - libpng
    - libtiff
    - freetype
    - jpeg
    - zlib

test:
  commands:
    - dot -V

about:
  home: http://www.graphviz.org/
  license: Eclipse Public License v1.0
  summary: Graph Visualization Software
```

CHAPTER 184

hall-lab-svtools

184.1 Summary

Tools for processing and analyzing structural variants.

184.2 Home

https://github.com/hall-lab/svtools

184.3 Versions

- 0.1.1

184.4 License

184.5 Meta

```
package:
  name: hall-lab-svtools
  version: "0.1.1"

source:
  fn: svtools-3731a7c6e19.tar.gz
  url: https://github.com/hall-lab/svtools/archive/3731a7c6e19.tar.gz
  md5: c6ba71cd3a7f02b0c58d1d13a48c02db

build:
  skip: True # [not py27]

requirements:
  build:
    - python
    - setuptools

  run:
```

```
    - python

test:
  commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.

    - vcftobedpe -h

  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

about:
  home: https://github.com/hall-lab/svtools
  summary: 'Tools for processing and analyzing structural variants.'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 185

hifive

185.1 Summary

Python library for normalizing and analyzing HiC and 5C data

185.2 Home

https://github.com/bxlab/hifive

185.3 Versions

- 1.2.1

185.4 License

MIT

185.5 Meta

```
package:
  name: hifive
  version: "1.2.1"

source:
  fn: hifive-1.2.1.tar.gz
  url: https://pypi.python.org/packages/source/h/hifive/hifive-1.2.1.tar.gz
  md5: 352aa34feca6eb7275f71cb5d7ba3392

build:
  skip: True  # [not py27]
  number: 0

requirements:
  build:
```

```
    - python
    - setuptools
    - numpy
    - scipy
    - h5py
    - cython
    - setuptools_cython

  run:
    - python
    - numpy
    - scipy
    - h5py
    - cython
    - setuptools_cython

    # these are listed as optional
    - pyx ==0.12.1  # 0.12.1 is the latest pyx version supported on PY2
    - pysam
    - pil
    - mpi4py
    #- mlpy  # used for hifive.hic.learn_fend_3D_modol, but conda build currently fails


test:
  # Python imports
  imports:
    - hifive
    - hifive.commands
    - hifive.libraries

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  requires:
    - nose
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: https://github.com/bxlab/hifive
  license: MIT
  summary: 'Python library for normalizing and analyzing HiC and 5C data'
```

CHAPTER 186

hisat2

186.1 Summary

graph-based alignment of next generation sequencing reads to a population of genomes

186.2 Home

https://ccb.jhu.edu/software/hisat2/index.shtml

186.3 Versions

- 2.0.1beta

186.4 License

GPLv3

186.5 Meta

```
about:
    home: 'https://ccb.jhu.edu/software/hisat2/index.shtml'
    license: GPLv3
    summary: graph-based alignment of next generation sequencing reads to a population of genomes
package:
    name: hisat2
    version: 2.0.1beta
requirements:
    build:
        - python
    run:
        - python
test:
    commands:
        - hisat2 --version
```

```
source:
  fn: hisat2-2.0.1-beta-Linux_x86_64.zip #[linux]
  url: ftp://ftp.ccb.jhu.edu/pub/infphilo/hisat2/downloads/hisat2-2.0.1-beta-Linux_x86_64.zip #[linux
  md5: f2fa54657ccc52eb3a70938197cca607 #[linux]

  fn: hisat2-2.0.1-beta-OSX_x86_64.zip #[osx]
  url: ftp://ftp.ccb.jhu.edu/pub/infphilo/hisat2/downloads/hisat2-2.0.1-beta-OSX_x86_64.zip #[osx]
  md5: 24a848f93b439b4466ba0fbe51956951 #[osx]
```

CHAPTER 187

hmmer

187.1 Summary

Biosequence analysis using profile hidden Markov models

187.2 Home

http://hmmer.janelia.org/

187.3 Versions

- 3.1b2

187.4 License

GPL3

187.5 Meta

```
package:
  name: hmmer
  version: "3.1b2"

source:
  fn: hmmer-3.1b2.tar.gz
  url: http://selab.janelia.org/software/hmmer3/3.1b2/hmmer-3.1b2.tar.gz
  md5: c8c141018bc0ccd7fc37b33f2b945d5f

build:
  number: 0

requirements:
  build:
    - gcc
```

```
  run:

test:
  commands:
    - alimask -h

about:
  summary: Biosequence analysis using profile hidden Markov models
  home: http://hmmer.janelia.org/
  license: GPL3
  license_file: LICENSE
```

CHAPTER 188

hmmlearn

188.1 Summary

Hidden Markov Models in Python, with scikit-learn like API

188.2 Home

https://github.com/hmmlearn/hmmlearn

188.3 Versions

- 20151031

188.4 License

BSD

188.5 Meta

```
package:
  name: hmmlearn
  version: '20151031'

source:
  fn: hmmlearn-dd67a47.tar.gz
  url: https://github.com/hmmlearn/hmmlearn/archive/dd67a47.tar.gz

build:
  number: 0

requirements:
  build:
    - python
    - setuptools
```

```
    - cython
    - numpy
    - scipy
    - scikit-learn

  run:
    - python
    - setuptools
    - numpy
    - scipy
    - scikit-learn

test:
  imports:
    - hmmlearn.hmm

about:
  home: https://github.com/hmmlearn/hmmlearn
  license: BSD
  summary: Hidden Markov Models in Python, with scikit-learn like API
```

CHAPTER 189

htseq

189.1 Summary

A framework to process and analyze data from high-throughput sequencing (HTS) assays

189.2 Home

http://www-huber.embl.de/users/anders/HTSeq/

189.3 Versions

- 0.6.1p1
- 0.6.1

189.4 License

GNU General Public License (GPL)

189.5 Meta

```
package:
  name: htseq
  version: !!str 0.6.1p1

source:
  fn: HTSeq-0.6.1p1.tar.gz
  url: https://pypi.python.org/packages/source/H/HTSeq/HTSeq-0.6.1p1.tar.gz
  md5: c44d7b256281a8a53b6fe5beaeddd31c

build:
  preserve_egg_dir: True
  number: 0
  skip: True # [not py27]
```

```
requirements:
  build:
    - python
    - setuptools
    - numpy

  run:
    - python
    - numpy
    - setuptools
    - matplotlib

test:
  # Python imports
  imports:
    - HTSeq._HTSeq_internal
    - HTSeq.StepVector
    - HTSeq._version
    - HTSeq.scripts.qa
    - HTSeq.scripts.count


  commands:
    - htseq-count -h
    - htseq-qa -h

about:
  home: http://www-huber.embl.de/users/anders/HTSeq/
  license:  GNU General Public License (GPL)
  summary: 'A framework to process and analyze data from high-throughput sequencing (HTS) assays'
```

CHAPTER 190

htslib

190.1 Summary

C library for high-throughput sequencing data formats

190.2 Home

https://github.com/samtools/htslib

190.3 Versions

- 1.3

190.4 License

MIT

190.5 Meta

```
package:
  name: htslib
  version: "1.3"
build:
  number: 0
source:
  fn: htslib-1.3.tar.bz2
  url: https://github.com/samtools/htslib/releases/download/1.3/htslib-1.3.tar.bz2
  md5: 39d475730a66401e4d45398c95c414f7
requirements:
  build:
  run:
about:
  home: https://github.com/samtools/htslib
```

```
  license: MIT
  summary: C library for high-throughput sequencing data formats
```

CHAPTER 191

httplib2

191.1 Summary

A comprehensive HTTP client library.

191.2 Home

https://github.com/jcgregorio/httplib2

191.3 Versions

- 0.9.2

191.4 License

MIT License

191.5 Meta

```
package:
  name: httplib2
  version: "0.9.2"

source:
  fn: httplib2-0.9.2.tar.gz
  url: https://pypi.python.org/packages/source/h/httplib2/httplib2-0.9.2.tar.gz
  md5: bd1b1445b3b2dfa7276b09b1a07b7f0e
#  patches:
   # List any patch files here
   # - fix.patch

# build:
  # noarch_python: True
  # preserve_egg_dir: True
```

```
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - httplib2 = httplib2:main
    #
    # Would create an entry point called httplib2 that calls httplib2.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools

  run:
    - python

test:
  # Python imports
  imports:
    - httplib2

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: https://github.com/jcgregorio/httplib2
  license: MIT License
  summary: 'A comprehensive HTTP client library.'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 192

httpretty

192.1 Summary

HTTP client mock for Python

192.2 Home

http://github.com/gabrielfalcao/httpretty

192.3 Versions

- 0.8.10

192.4 License

MIT License

192.5 Meta

```
package:
  name: httpretty
  version: "0.8.10"

source:
  fn: httpretty-0.8.10.tar.gz
  url: https://pypi.python.org/packages/source/h/httpretty/httpretty-0.8.10.tar.gz
  md5: 9c130b16726cbf85159574ae5761bce7

requirements:
  build:
    - python
    - setuptools

  run:
```

```
    - python

test:
  # Python imports
  imports:
    - httpretty

  requires:
    - coverage >=3.7.1
    - httplib2 >=0.9
    - mock >=1.0.1
    - nose >=1.3.0
    - requests >=2.5.1
    - sure >=1.2.3
    - tornado >=4.0.2
    - urllib3 >=1.7.1

about:
  home: http://github.com/gabrielfalcao/httpretty
  license: MIT License
  summary: 'HTTP client mock for Python'
```

CHAPTER 193

hubward-all

193.1 Summary

Meta-package for hubward including bedtools and UCSC tools

193.2 Home

193.3 Versions

- 0.2.1

193.4 License

The license for this meta-package is MIT; individual tools vary

193.5 Meta

```
package:
  name: hubward-all
  version: "0.2.1"
build:
  number: 0
requirements:
  run:
    - hubward
    - ucsc-bedtobigbed
    - ucsc-bedgraphtobigwig
    - ucsc-wigtobigwig
    - ucsc-bigbedtobed
    - ucsc-fetchchromsizes
    - ucsc-liftover
    - ucsc-bigwigtobedgraph
    - ucsc-bigwigtowig
    - bedtools
    - crossmap
```

```
about:
  summary: "Meta-package for hubward including bedtools and UCSC tools"
  license: "The license for this meta-package is MIT; individual tools vary"
```

CHAPTER 194

hubward

194.1 Summary

Manage the visualization of large amounts of other people's [often messy] genomics data

194.2 Home

https://github.com/daler/hubward

194.3 Versions

- 0.2.2

194.4 License

BSD License

194.5 Meta

```
package:
  name: hubward
  version: "0.2.2"

source:
  fn: hubward-0.2.2.tar.gz
  url: https://pypi.python.org/packages/source/h/hubward/hubward-0.2.2.tar.gz
  md5: 335a36f6eb5e38bfb5f9d0f518aba2f7
#  patches:
   # List any patch files here
   # - fix.patch

build:
  skip: True  # [py3k]
  number: 1
```

```
  # noarch_python: True
  # preserve_egg_dir: True
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - hubward = hubward:main
    #
    # Would create an entry point called hubward that calls hubward.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools
    - argh
    - colorama
    - jsonschema
    - pyyaml
    - pybedtools
    - bleach
    - matplotlib
    - numpy
    - fabric
    - trackhub
    - docutils
    - pycurl
    - pyaml
    - functools32

  run:
    - python
    - argh
    - colorama
    - jsonschema
    - pyyaml
    - pybedtools
    - bleach
    - matplotlib
    - numpy
    - fabric
    - trackhub
    - docutils
    - pycurl
    - pyaml
    - functools32

test:
  # Python imports
  imports:
    - hubward

  commands:
    - hubward -h
```

```
  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: https://github.com/daler/hubward
  license: BSD License
  summary: "Manage the visualization of large amounts of other people's [often messy] genomics data"

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 195

igblast

195.1 Summary

A tool for analyzing immunoglobulin (IG) and T cell receptor (TR) sequences.

195.2 Home

http://www.ncbi.nlm.nih.gov/projects/igblast/

195.3 Versions

- 1.4.0

195.4 License

Public Domain

195.5 Meta

```
package:
  name: igblast
  version: "1.4.0"
source:
  fn: ncbi-igblast-1.4.0-x64-linux.tar.gz
  url: ftp://ftp.ncbi.nih.gov/blast/executables/igblast/release/1.4.0/ncbi-igblast-1.4.0-x64-linux.ta
about:
  home: http://www.ncbi.nlm.nih.gov/projects/igblast/
  license: Public Domain
  summary: A tool for analyzing immunoglobulin (IG) and T cell receptor (TR) sequences.
build:
  number: 4
requirements:
  run:
    - perl >=5.8.8
```

```
test:
  commands:
    - igblastn -h
```

CHAPTER 196

igvtools

196.1 Summary

command line tools for IGV

196.2 Home

http://www.broadinstitute.org/igv/

196.3 Versions

- 2.3.48

196.4 License

196.5 Meta

```
package:
  name: igvtools
  version: 2.3.48

source:
  fn: "igvtools_2.3.48.zip"
  url: "http://www.broadinstitute.org/igv/projects/downloads/igvtools_2.3.48.zip"

build:
  number: 1

requirements:
  run:
    - java-jdk

test:
  commands:
    - igvtools help
```

```
about:
  home: http://www.broadinstitute.org/igv/
  summary: command line tools for IGV
```

CHAPTER 197

infernal [linux64]

197.1 Summary

Infernal ("INFERence of RNA ALignment") is for searching DNA sequence databases for RNA structure and sequence similarities.

197.2 Home

http://infernal.janelia.org/

197.3 Versions

- 1.1.1
- 1.0.2

197.4 License

GPLv3

197.5 Meta

```
package:
  name: infernal [linux64]
  version: 1.1.1

source:
  fn: infernal-1.1.1.tar.gz
  url: http://selab.janelia.org/software/infernal/infernal-1.1.1.tar.gz
  md5: c5bff318f78c194a0d9b2a6bf1abb169

build:
  number: 0
```

```
test:
  commands:
     - cmalign -h  > /dev/null
     - cmbuild -h  > /dev/null
     - cmcalibrate -h  > /dev/null
     - cmconvert -h  > /dev/null
     - cmemit -h  > /dev/null
     - cmfetch -h  > /dev/null
     - cmpress -h  > /dev/null
     - cmscan -h  > /dev/null
     - cmsearch -h  > /dev/null
     - cmstat -h  > /dev/null

about:
  home: http://infernal.janelia.org/
  license: GPLv3
  license_file: COPYRIGHT
  summary: Infernal ("INFERence of RNA ALignment") is for searching DNA sequence databases for RNA st
```

CHAPTER 198

infinity

198.1 Summary

All-in-one infinity value for Python. Can be compared to any object.

198.2 Home

https://github.com/kvesteri/infinity

198.3 Versions

- 1.3

198.4 License

BSD License

198.5 Meta

```
package:
  name: infinity
  version: "1.3"

source:
  fn: infinity-1.3.tar.gz
  url: https://pypi.python.org/packages/source/i/infinity/infinity-1.3.tar.gz
  md5: 0aa8feadec140b7d091bac142411e6d9

requirements:
  build:
    - python
    - setuptools

  run:
```

```
    - python

test:
  imports:
    - infinity

about:
  home: https://github.com/kvesteri/infinity
  license: BSD License
  summary: 'All-in-one infinity value for Python. Can be compared to any object.'
```

CHAPTER 199

inheritance

199.1 Summary

inheritance models for mendelian diseases

199.2 Home

https://github.com/brentp/inheritance

199.3 Versions

- 0.0.5

199.4 License

MIT

199.5 Meta

```
package:
  name: inheritance
  version: 0.0.5

source:
  fn: inheritance-0.0.5.tar.gz
  url: https://pypi.python.org/packages/source/i/inheritance/inheritance-0.0.5.tar.gz#
  md5: fb2627f0dd56f0432f127fd903dcf164

build:
  number: 0

requirements:
  build:
    - python
```

```
    - setuptools
  run:
    - python

test:
  imports:
    - inheritance

about:
  home: https://github.com/brentp/inheritance
  summary: inheritance models for mendelian diseases
  license: MIT
```

CHAPTER 200

intervals

200.1 Summary

Python tools for handling intervals (ranges of comparable objects).

200.2 Home

https://github.com/kvesteri/intervals

200.3 Versions

- 0.6.0

200.4 License

BSD License

200.5 Meta

```
package:
  name: intervals
  version: "0.6.0"

source:
  fn: intervals-0.6.0.tar.gz
  url: https://pypi.python.org/packages/source/i/intervals/intervals-0.6.0.tar.gz
  md5: 633ea6469430f8529afe472a08c4e64a

requirements:
  build:
    - python
    - setuptools
    - infinity >=0.1.3
```

```
  run:
    - python
    - infinity >=0.1.3

test:
  imports:
    - intervals

about:
  home: https://github.com/kvesteri/intervals
  license: BSD License
  summary: 'Python tools for handling intervals (ranges of comparable objects).'
```

CHAPTER 201

intervalstats

201.1 Summary

Tool for assessing similarity between sets of intervals

201.2 Home

http://sonorus.princeton.edu/IntervalStats/

201.3 Versions

- 1.01

201.4 License

unknown

201.5 Meta

```
package:
  name: intervalstats
  version: 1.01
source:
  fn: IntervalStats.tar.gz
  url: http://sonorus.princeton.edu/IntervalStats/IntervalStats.tar.gz
  md5: eb056302e48e1b8042dea4d26a43e885
build:
  number: 0

test:
  commands:
    - IntervalStats -h
about:
  home: http://sonorus.princeton.edu/IntervalStats/
```

```
  license: unknown
  summary: Tool for assessing similarity between sets of intervals
```

CHAPTER 202

ipython-cluster-helper

202.1 Summary

Tool to easily start up an IPython cluster on different schedulers

202.2 Home

https://github.com/roryk/ipython-cluster-helper

202.3 Versions

- 0.5.1

202.4 License

MIT

202.5 Meta

```
package:
  name: ipython-cluster-helper
  version: 0.5.1

source:
  fn: ipython-cluster-helper-0.5.1.tar.gz
  url: https://pypi.python.org/packages/source/i/ipython-cluster-helper/ipython-cluster-helper-0.5.1

build:
  skip: True # [not py27]

requirements:
  build:
    - python
    - setuptools
```

```
    - netifaces

  run:
    - python
    - setuptools
    - ipyparallel
    - pyzmq
    - netifaces

test:
  imports:
    - cluster_helper.cluster

about:
  home: https://github.com/roryk/ipython-cluster-helper
  license: MIT
  summary: Tool to easily start up an IPython cluster on different schedulers
```

CHAPTER 203

jamm

203.1 Summary

JAMM is a peak finder for NGS datasets (ChIP-Seq, ATAC-Seq, DNase-Seq..etc.) that can integrate replicates and assign peak boundaries accurately.

203.2 Home

https://github.com/mahmoudibrahim/JAMM

203.3 Versions

- 1.0.7.2

203.4 License

GPL

203.5 Meta

```
package:
  name: jamm
  version: 1.0.7.2

source:
  fn: v1.0.7.2.zip
  url: https://github.com/mahmoudibrahim/JAMM/archive/v1.0.7.2.zip
  md5: 0902ea81e0559a8804c49dd7b1f02efd
  patches:
    - setpath.patch

build:
  number: 1
```

```
requirements:

  run:
    - r >=3
    - perl
    - r-signal
    - r-mclust >=4

test:

  commands:
    - JAMM.sh | grep JAMM > /dev/null
    - SignalGenerator.sh | grep JAMM > /dev/null

about:
  home: https://github.com/mahmoudibrahim/JAMM
  license: GPL
  license_file: LICENSE
  summary: JAMM is a peak finder for NGS datasets (ChIP-Seq, ATAC-Seq, DNase-Seq..etc.) that can inte
```

CHAPTER 204

java-jdk

204.1 Summary

The Zulu OpenJDK build.

204.2 Home

http://www.azulsystems.com/products/zulu

204.3 Versions

- 8.0.45
- 7.0.91

204.4 License

GPL

204.5 Meta

```
# Taken from the birdhouse channel

package:
  name: java-jdk
  version: 8.0.45

test:
  commands:
    - java -version

about:
  home: http://www.azulsystems.com/products/zulu
```

```
  license: GPL
  summary: The Zulu OpenJDK build.
```

CHAPTER 205

jellyfish

205.1 Summary

Jellyfish is a tool for fast, memory-efficient counting of k-mers in DNA. A k-mer is a substring of length k, and counting the occurrences of all such substrings is a central step in many analyses of DNA sequence

205.2 Home

http://www.genome.umd.edu/jellyfish.html

205.3 Versions

- 2.2.3
- 1.1.11

205.4 License

GPLv3

205.5 Meta

```
package:
  name: jellyfish
  version: "2.2.3"
source:
  fn: v2.2.3.tar.gz
  url: https://github.com/gmarcais/Jellyfish/archive/v2.2.3.tar.gz
  md5: a63398ce1cbde0eddcb3493f5b84a9b7
requirements:
  build:
    - yaggo >=1.5.8
  run:
test:
```

```
  commands:
    - jellyfish --version 2>&1 > /dev/null
about:
  home: http://www.genome.umd.edu/jellyfish.html
  license: GPLv3
  summary: Jellyfish is a tool for fast, memory-efficient counting of k-mers in DNA. A k-mer is a sub
```

CHAPTER 206

jmespath

206.1 Summary

206.2 Home

https://github.com/jmespath/jmespath.py

206.3 Versions

- 0.9.0

206.4 License

MIT

206.5 Meta

```
package:
  name: jmespath
  version: '0.9.0'

source:
  fn: jmespath-0.9.0.tar.gz
  url: https://pypi.python.org/packages/source/j/jmespath/jmespath-0.9.0.tar.gz
  md5: 471b7d19bd153ac11a21d4fb7466800c

build:
  number: 0

requirements:
  build:
    - python
    - setuptools

  run:
```

```
    - python

test:
  imports:
    - jmespath

about:
  home: https://github.com/jmespath/jmespath.py
  license: MIT
```

CHAPTER 207

joblib

207.1 Summary

Lightweight pipelining: using Python functions as pipeline jobs.

207.2 Home

http://packages.python.org/joblib/

207.3 Versions

- 0.9.3

207.4 License

BSD License

207.5 Meta

```
package:
  name: joblib
  version: '0.9.3'

source:
  fn: joblib-0.9.3.tar.gz
  url: https://pypi.python.org/packages/source/j/joblib/joblib-0.9.3.tar.gz
  md5: b90652daf3f5458e1d65b9b9d0f74756

build:
  number: 0

requirements:
  build:
    - python
```

```
    - setuptools

  run:
    - python

test:
  imports:
    - joblib
    - joblib.test
  requires:
    - nose

about:
  home: http://packages.python.org/joblib/
  license: BSD License
  summary: 'Lightweight pipelining: using Python functions as pipeline jobs.'
```

CHAPTER 208

julia

208.1 Summary

A high-performance dynamic programming language for data science

208.2 Home

http://julialang.org/

208.3 Versions

- 0.3.11

208.4 License

MIT

208.5 Meta

```
package:
  name: julia
  version: "0.3.11"
source:
  fn: julia-0.3.11_483dbf5279.tar.gz
  url: https://github.com/JuliaLang/julia/releases/download/v0.3.11/julia-0.3.11_483dbf5279.tar.gz
  sha256: 9953cdd8e0b2b3dd52bfe787830133ac30177d0ffd98f049fc18e6228419b1b3
build:
  rpaths:
    - lib/julia/
about:
  home: http://julialang.org/
  license: MIT
  license_file: LICENSE.md
  summary: A high-performance dynamic programming language for data science
```

CHAPTER 209

kallisto

209.1 Summary

Quantifying abundances of transcripts from RNA-Seq data, or more generally of target sequences using high-throughput sequencing reads.

209.2 Home

http://pachterlab.github.io/kallisto

209.3 Versions

- 0.42.4

209.4 License

Custom

209.5 Meta

```
about:
    home: "http://pachterlab.github.io/kallisto"
    license: Custom
    summary: Quantifying abundances of transcripts from RNA-Seq data, or more generally of target seq
package:
    name: kallisto
    version: 0.42.4
build:
    number: 1
requirements:
    build:
        - hdf5
        - cmake
        - zlib
```

```
    run:
        - hdf5
test:
    commands:
        - kallisto | grep Usage > /dev/null
source:
  fn: kallisto-0.42.4.tar.gz
  url: https://github.com/pachterlab/kallisto/archive/v0.42.4.tar.gz
```

CHAPTER 210

khmer

210.1 Summary

khmer is a library and suite of command line tools for working with DNA sequence. It is primarily aimed at short-read sequencing data such as that produced by the Illumina platform. khmer takes a k-mer-centric approach to sequence analysis, hence the name.

210.2 Home

https://khmer.readthedocs.org/

210.3 Versions

- 2.0

210.4 License

BSD-3-Clause

210.5 Meta

```
about:
  home: https://khmer.readthedocs.org/
  license: BSD-3-Clause
  summary: 'khmer is a library and suite of command line tools for working with DNA
    sequence. It is primarily aimed at short-read sequencing data such as that produced
    by the Illumina platform. khmer takes a k-mer-centric approach to sequence analysis,
    hence the name.'
build:
  number: 0
package:
  name: khmer
  version: '2.0'
requirements:
```

```
  build:
  - python
  - bz2file ==0.98
  - screed ==0.9
  run:
  - python
  - bz2file ==0.98
  - screed ==0.9
source:
  fn: khmer-2.0.tar.gz
  sha256: 6a8c6809b50adaf2d7d7307eefcca173f4b536329562530400fb1c88a12e6071
  url: https://pypi.python.org/packages/source/k/khmer/khmer-2.0.tar.gz
test:
  imports:
    - khmer
    - khmer.kfile
    - khmer.khmer_args
    - khmer.utils
```

CHAPTER 211

knot

211.1 Summary

Detection of knots in protein folds.

211.2 Home

http://mathbio.nimr.mrc.ac.uk/wiki/Software#KNOT

211.3 Versions

- 1.0.0

211.4 License

GPL

211.5 Meta

```
package:
  name: knot
  version: "1.0.0"

source:
  fn: KNOT-1.0.0.tgz
  url: http://mathbio.nimr.mrc.ac.uk/download/KNOT/KNOT-1.0.0.tgz
  md5: 2556876109bae506fe171a45902db0b6

build:
  number: 1

test:
  commands:
    - which knot
```

```
    - "knot || [[ $? == 139 ]]"

about:
  home: http://mathbio.nimr.mrc.ac.uk/wiki/Software#KNOT
  summary: Detection of knots in protein folds.
  license: GPL
```

CHAPTER 212

kraken

212.1 Summary

Kraken is a system for assigning taxonomic labels to short DNA sequences, usually obtained through metagenomic studies.

212.2 Home

http://ccb.jhu.edu/software/kraken/

212.3 Versions

- 0.10.5beta

212.4 License

GPLv3

212.5 Meta

```
package:
  name: kraken
  version: "0.10.5beta"
source:
  git_url: https://github.com/DerrickWood/kraken.git
  git_tag: v0.10.5-beta
build:
  has_prefix_files:
    - libexec/kraken
    - libexec/kraken-build
    - libexec/kraken-filter
    - libexec/kraken-mpa-report
    - libexec/kraken-report
    - libexec/kraken-translate
```

```
test:
  commands:
    - kraken --version 2>&1 > /dev/null
about:
  home: http://ccb.jhu.edu/software/kraken/
  license: GPLv3
  summary: Kraken is a system for assigning taxonomic labels to short DNA sequences, usually obtained
```

CHAPTER 213

last

213.1 Summary

LAST finds similar regions between sequences, and aligns them. It is designed for comparing large datasets to each other (e.g. vertebrate genomes and/or large numbers of DNA reads).

213.2 Home

http://last.cbrc.jp/

213.3 Versions

- 638

213.4 License

GPLv3

213.5 Meta

```
about:
    home: 'http://last.cbrc.jp/'
    license: GPLv3
    summary: "LAST finds similar regions between sequences, and aligns them. It is designed for compa
package:
  name: last
  version: '638'
source:
  fn: last-638.zip
  md5: 6c5edd2706934bfe7b3224073b79463b
  url: http://last.cbrc.jp/last-638.zip
build:
  number: 4
requirements:
```

```
  build:
    - python
  run:
    - python
test:
    commands:
        - "lastal -V &> /dev/null"
        - "lastdb -V &> /dev/null"
        - "last-split -V &> /dev/null"
        - "last-pair-probs -V &> /dev/null"
        - "last-merge-batches -V &> /dev/null"
        - "maf-convert -h &> /dev/null"
```

CHAPTER 214

libdb

214.1 Summary

The Berkeley DB embedded database system.

214.2 Home

http://www.oracle.com/technology/software/products/berkeley-db/index.html

214.3 Versions

- 6.1.26

214.4 License

AGPLv3

214.5 Meta

```
package:
  name: libdb
  version: "6.1.26"

source:
  fn: db-6.1.26.tar.gz
  url: http://download.oracle.com/berkeley-db/db-6.1.26.tar.gz

requirements:
  build:
    - gcc
  run:
    - libgcc

about:
```

```
  home: http://www.oracle.com/technology/software/products/berkeley-db/index.html
  license: AGPLv3
  summary: The Berkeley DB embedded database system.
```

CHAPTER 215

libgd

215.1 Summary

215.2 Home

http://libgd.github.io/

215.3 Versions

- 2.1.1

215.4 License

Custom OSS

215.5 Meta

```
package:
  name: libgd
  version: 2.1.1

requirements:
  build:
    - zlib
    - freetype
    - jpeg
    - libpng
    - libtiff
  run:
    - zlib
    - freetype
    - jpeg
    - libpng
    - libtiff
```

```
source:
  fn: libgd-2.1.1.tar.gz
  url: https://github.com/libgd/libgd/releases/download/gd-2.1.1/libgd-2.1.1.tar.gz

about:
    home: http://libgd.github.io/
    license: Custom OSS
```

CHAPTER 216

libgtextutils

216.1 Summary

216.2 Home

https://github.com/agordon/libgtextutils

216.3 Versions

- 0.7

216.4 License

AGPL

216.5 Meta

```
package:
  name: libgtextutils
  version: 0.7

source:
    url: https://github.com/agordon/libgtextutils/releases/download/0.7/libgtextutils-0.7.tar.gz
    fn: libgtextutils-0.7.tar.gz

build:
  preserve_egg_dir: True
  number: 0

requirements:
  build:
    - cython
    - nose
    #- pkg-config
```

```
  run:
    - cython
    - nose
    #- pkg-config


about:
  home: https://github.com/agordon/libgtextutils
  license: AGPL
```

CHAPTER 217

libmagic

217.1 Summary

Implementation of the file(1) command

217.2 Home

http://www.darwinsys.com/file/

217.3 Versions

- 5.25

217.4 License

https://raw.githubusercontent.com/file/file/master/COPYING

217.5 Meta

```
package:
  name: libmagic
  version: 5.25

source:
  fn: autoconf-2.69.tar.gz
  # mirror ftp://ftp.astron.com/pub/file/file-5.25.tar.gz
  url: https://fossies.org/linux/misc/file-5.25.tar.gz
  sha256: 3735381563f69fb4239470b8c51b876a80425348b8285a7cded8b61d6b890eca

requirements:
  build:
    #- m4
  run:
    #- m4
```

```
test:
  commands:
    - "file --help &> /dev/null"

about:
  home: http://www.darwinsys.com/file/
  summary: "Implementation of the file(1) command"
  license: "https://raw.githubusercontent.com/file/file/master/COPYING"
```

CHAPTER 218

libsvm

218.1 Summary

LIBSVM is an integrated software for support vector classification, (C-SVC,nu-SVC), regression (epsilon-SVR, nu-SVR) and distribution estimation(one-class SVM). It supports multi-class classification.http://www.csie.ntu.edu.tw/~cjlin/libsvm/

218.2 Home

218.3 Versions

- 3.16

218.4 License

218.5 Meta


```
about:
  home: ''
  license: ''
  summary: LIBSVM is an integrated software for support vector classification, (C-SVC,nu-SVC),
    regression (epsilon-SVR, nu-SVR) and distribution estimation(one-class SVM). It
    supports multi-class classification.http://www.csie.ntu.edu.tw/~cjlin/libsvm/
build:
  number: 0
package:
  name: libsvm
  version: '3.16'
requirements:
  build: []
  run: []
source:
  git_rev: 041496b61214aff1beba02c8f2957e80bd90c234
  git_url: https://github.com/cjlin1/libsvm.git
test:
  commands:
```

```
  - "svm-train | grep 'Usage' > /dev/null"
  - "svm-predict | grep 'Usage' > /dev/null"
```

CHAPTER 219

libxml2

219.1 Summary

Libxml2 is the XML C parser and toolkit developed for the Gnome project (but usable outside of the Gnomeplatform), it is free software available under the MIT License. XML itself is a metalanguage to design markuplanguages, i.e. text language where semantic and structure are added to the content using extra "markup"information enclosed between angle brackets. HTML is the most well-known markup language. Though the libraryis written in C a variety of language bindings make it available in other environments.

219.2 Home

http://xmlsoft.org/

219.3 Versions

- 2.9.3
- 2.9.1

219.4 License

MIT

219.5 Meta

```
about:
  home: http://xmlsoft.org/
  license: MIT
  summary: Libxml2 is the XML C parser and toolkit developed for the Gnome project
    (but usable outside of the Gnomeplatform), it is free software available under
    the MIT License. XML itself is a metalanguage to design markuplanguages, i.e.
    text language where semantic and structure are added to the content using extra
    "markup"information enclosed between angle brackets. HTML is the most well-known
    markup language. Though the libraryis written in C a variety of language bindings
```

```
    make it available in other environments.

build:
  number: 0

package:
  name: libxml2
  version: 2.9.3

test:
  files:
    - test.xml
  commands:
    - xmllint test.xml

requirements:
  build:
    - zlib                    [unix]
  run:
    - zlib                    [unix]

source:
  fn: libxml2_2.9.3_src_all.tar.gz
  sha256: 4de9e31f46b44d34871c22f54bfc54398ef124d6f7cafb1f4a5958fbcd3ba12d
  url: https://depot.galaxyproject.org/software/libxml2/libxml2_2.9.3_src_all.tar.gz
```

CHAPTER 220

lofreq

220.1 Summary

A fast and sensitive variant-caller for inferring SNVs and indels from next-generation sequencing data

220.2 Home

http://csb5.github.io/lofreq/

220.3 Versions

- 2.1.2

220.4 License

MIT

220.5 Meta

```
package:
  name: lofreq
  version: '2.1.2'
source:
  fn: lofreq_star-2.1.2.tgz
  url: http://downloads.sourceforge.net/project/lofreq/lofreq_star-2.1.2.tar.gz # [linux]
  url: http://downloads.sourceforge.net/project/lofreq/lofreq_star-2.1.2_macosx.tgz # [osx]
build:
  number: 0
  script: "mkdir -p $PREFIX/bin; chmod a+x bin/*; cp bin/* $PREFIX/bin" # [osx]
  skip: True # [not py27]
requirements:
  build:
    - python
  run:
```

```
    - python
test:
  commands:
    - 'lofreq version'
about:
  home: http://csb5.github.io/lofreq/
  license: MIT
  summary: A fast and sensitive variant-caller for inferring SNVs and indels from next-generation seq
```

CHAPTER 221

logbook

221.1 Summary

A logging replacement for Python

221.2 Home

http://logbook.pocoo.org/

221.3 Versions

- 0.12.2

221.4 License

BSD

221.5 Meta

```
# migrated from https://anaconda.org/asmeurer/logbook

package:
  name: logbook
  version: "0.12.2"

source:
  fn: Logbook-0.12.2.tar.gz
  url: https://pypi.python.org/packages/source/L/Logbook/Logbook-0.12.2.tar.gz
  md5: aec29d6ea167f9d4e7edcb951a24c86c

build:
  number: 0

requirements:
```

```
  build:
    - python
    - setuptools
  run:
    - python

test:
  imports:
    - logbook

about:
  home: http://logbook.pocoo.org/
  license: BSD
  summary: 'A logging replacement for Python'
```

CHAPTER 222

lumpy-sv

222.1 Summary

a general probabilistic framework for structural variant discovery

222.2 Home

https://github.com/arq5x/lumpy-sv

222.3 Versions

- 0.2.12

222.4 License

MIT

222.5 Meta

```
package:
  name: lumpy-sv
  version: 0.2.12
source:
  git_url: https://github.com/arq5x/lumpy-sv.git
  git_rev: 74e2945
  #fn: lumpy-sv-0.2.11.tar.gz
  #url: https://github.com/arq5x/lumpy-sv/releases/download/0.2.11/lumpy-sv-0.2.11.tar.gz
build:
  number: 0
  skip: True # [not py27]
requirements:
  build:
  run:
    - python
```

```
    - samtools
test:
    commands:
      - 'lumpy 2>&1 | grep -q structural'
      - 'lumpyexpress 2>&1 | grep -q lumpyexpress'
about:
    home: https://github.com/arq5x/lumpy-sv
    license: MIT
    summary: a general probabilistic framework for structural variant discovery
```

CHAPTER 223

m4

223.1 Summary

223.2 Home

http://www.gnu.org/software/m4/

223.3 Versions

- 1.4.17

223.4 License

GPL3

223.5 Meta

```
package:
  name: m4
  version: 1.4.17

source:
  fn: m4-1.4.17.tar.gz
  url: http://ftp.gnu.org/gnu/m4/m4-1.4.17.tar.gz
  md5: a5e9954b1dae036762f7b13673a2cf76

test:
  commands:
    - m4 --help
    - m4 --version

about:
  home: http://www.gnu.org/software/m4/
  license: GPL3
```

CHAPTER 224

macs2

224.1 Summary

MACS – Model-based Analysis of ChIP-Seq

224.2 Home

https://github.com/taoliu/MACS/

224.3 Versions

- 2.1.0

224.4 License

BSD New

224.5 Meta

```
about:
  home: https://github.com/taoliu/MACS/
  license: BSD New
  summary: MACS -- Model-based Analysis of ChIP-Seq
package:
  name: macs2
  version: 2.1.0
requirements:
  build:
    - python >=2.7,<3
    - numpy
  run:
    - python >=2.7,<3
    - numpy
test:
```

```
  requires:
    - python >=2.7,<3
    - numpy
  commands:
    - macs2 --version 2>&1 > /dev/null
source:
  fn: MACS2-2.1.0.20150731.tar.gz
  url: https://pypi.python.org/packages/source/M/MACS2/MACS2-2.1.0.20150731.tar.gz
  md5: 026a210b967e28e10e220d61744c82f0
```

CHAPTER 225

mafft

225.1 Summary

Multiple alignment program for amino acid or nucleotide sequences based on fast Fourier transform

225.2 Home

http://mafft.cbrc.jp/alignment/software/

225.3 Versions

- 7.221

225.4 License

BSD

225.5 Meta

```
about:
    home: 'http://mafft.cbrc.jp/alignment/software/'
    license: BSD
    summary: Multiple alignment program for amino acid or nucleotide sequences based on fast Fourier
package:
  name: mafft
  version: '7.221'
source:
  fn: mafft-7.221-without-extensions-src.tgz
  md5: 6b05a64d2ccfce1fd203a6a52776d401
  url: http://mafft.cbrc.jp/alignment/software/mafft-7.221-without-extensions-src.tgz
  patches:
    - osx-makefile.patch # [osx]
    - linux-makefile.patch # [linux]
test:
```

```
    commands:
        - mafft --version
```

CHAPTER 226

mageck-vispr

226.1 Summary

MAGeCK-VISPR is a comprehensive quality control, analysis and visualization workflow for CRISPR/Cas9 screens based on MAGeCK, VISPR, Snakemake, FastQC and cutadapt.

226.2 Home

https://bitbucket.org/liulab/mageck-vispr

226.3 Versions

- 0.4.7

226.4 License

MIT License

226.5 Meta

```
package:
  name: mageck-vispr
  version: "0.4.7"

source:
  git_url: https://bitbucket.org/liulab/mageck-vispr.git
  git_rev: v0.4.7

build:
  skip: True  # [py27]
  entry_points:
    - mageck-vispr = mageck_vispr.cli:main

requirements:
```

```
  build:
    - python
    - setuptools
    - snakemake
    - mageck >=0.5.3
    - vispr >=0.4.4
    - fastqc
    - cutadapt
    - jinja2
  run:
    - python
    - setuptools
    - snakemake
    - mageck >=0.5.3
    - vispr >=0.4.4
    - fastqc
    - cutadapt
    - jinja2

test:
  commands:
    - mageck-vispr --help > /dev/null

about:
  home: https://bitbucket.org/liulab/mageck-vispr
  license: MIT License
  summary: MAGeCK-VISPR is a comprehensive quality control, analysis and visualization workflow for C
```

CHAPTER 227

mageck

227.1 Summary

Model-based Analysis of Genome-wide CRISPR-Cas9 Knockout.

227.2 Home

http://mageck.sourceforge.net

227.3 Versions

- 0.5.3

227.4 License

BSD License

227.5 Meta

```
package:
  name: mageck
  version: "0.5.3"

source:
  git_url: https://bitbucket.org/liulab/mageck.git
  git_rev: v0.5.3

requirements:
  build:
    - python
    - numpy
    - scipy
  run:
    - python
```

```
    - numpy
    - scipy

test:
  commands:
    - mageck --help > /dev/null

about:
  home: http://mageck.sourceforge.net
  license: BSD License
  summary: Model-based Analysis of Genome-wide CRISPR-Cas9 Knockout.
```

CHAPTER 228

manta

228.1 Summary

Structural variant and indel caller for mapped sequencing data

228.2 Home

https://github.com/Illumina/manta

228.3 Versions

- 0.29.1

228.4 License

GPLv3

228.5 Meta

```
package:
  name: manta
  version: '0.29.1'
source:
  fn: manta-0.29.1.tar.bz2
  url: https://github.com/Illumina/manta/releases/download/v0.29.1/manta-0.29.1.centos5_x86_64.tar.bz
build:
  number: 0
  skip: True # [not py27]
requirements:
  build:
    - python
  run:
    - python
test:
```

```
  commands:
    - configManta.py -h
about:
  home: https://github.com/Illumina/manta
  license: GPLv3
  summary: Structural variant and indel caller for mapped sequencing data
```

CHAPTER 229

mapsplice

229.1 Summary

MapSplice is a software for mapping RNA-seq data to reference genome for splice junction discovery that depends only on reference genome, and not on any further annotations.

229.2 Home

229.3 Versions

- 2.2.0

229.4 License

Custom

229.5 Meta

```
package:
  name: mapsplice
  version: 2.2.0

source:
  fn: MapSplice-v2.2.0.zip
  url: http://protocols.netlab.uky.edu/~zeng/MapSplice-v2.2.0.zip
  md5: 171975d48d2ddcc111a314d926f3527a

  patches:
    - mapsplice.patch
    - samtools.patch

build:
  number: 1

requirements:
```

```
  build:
    - python
    - zlib
    - ncurses

  run:
    - python
    - zlib
    - ncurses

test:

 commands:
   - mapsplice.py -v 2>&1 |grep MapSplice > /dev/null

about:
  license: Custom
  summary: MapSplice is a software for mapping RNA-seq data to reference genome for splice junction c
  license_file: Copyright.txt
```

CHAPTER 230

mash

230.1 Summary

Fast sequence distance estimator that uses MinHash

230.2 Home

https://github.com/marbl/Mash

230.3 Versions

- 1.0.2

230.4 License

https://raw.githubusercontent.com/marbl/Mash/master/LICENSE.txt

230.5 Meta

```
package:
  name: mash
  version: '1.0.2'

source:
  fn: mash-OSX64-v1.0.2.tar.gz # [osx]
  md5: 0fe94bc691679b112f2273823c7b5c10 # [osx]
  url: https://github.com/marbl/Mash/releases/download/v1.0.2/mash-OSX64-v1.0.2.tar.gz # [osx]
  fn: mash-Linux64-v1.0.2.tar.gz # [linux64]
  md5: 243267c650ff92a1b4fee62d9d428ceb # [linux64]
  url: https://github.com/marbl/Mash/releases/download/v1.0.2/mash-Linux64-v1.0.2.tar.gz # [linux64]

build:
  number: 1
```

```
requirements:
  run:
    - libgcc
    - boost
    - zlib
    #- capnp
test:
  commands:
    - "mash -h &> /dev/null"

about:
  home: https://github.com/marbl/Mash
  license: "https://raw.githubusercontent.com/marbl/Mash/master/LICENSE.txt"
  summary: "Fast sequence distance estimator that uses MinHash"
```

CHAPTER 231

matplotlib-venn

231.1 Summary

Functions for plotting area-proportional two- and three-way Venn diagrams in matplotlib.

231.2 Home

https://github.com/konstantint/matplotlib-venn

231.3 Versions

- 0.11.1

231.4 License

MIT License

231.5 Meta

```
package:
  name: matplotlib-venn
  version: "0.11.1"

source:
  fn: matplotlib-venn-0.11.1.tar.gz
  url: https://pypi.python.org/packages/source/m/matplotlib-venn/matplotlib-venn-0.11.1.tar.gz

requirements:
  build:
    - python
    - setuptools
    - matplotlib
    - numpy
    - scipy
```

```
  run:
    - python
    - matplotlib
    - numpy
    - scipy

test:
  imports:
    - matplotlib_venn

  requires:
    - pytest
    - nose

about:
  home: https://github.com/konstantint/matplotlib-venn
  license: MIT License
  summary: 'Functions for plotting area-proportional two- and three-way Venn diagrams in matplotlib.
```

CHAPTER 232

megahit

232.1 Summary

MEGAHIT: An ultra-fast single-node solution for large and complex metagenomics assembly via succinct de Bruijn graph

232.2 Home

https://github.com/voutcn/megahit

232.3 Versions

- 1.0.3

232.4 License

GPL3

232.5 Meta

```
about:
  home: https://github.com/voutcn/megahit
  license: GPL3
  summary: 'MEGAHIT: An ultra-fast single-node solution for large and complex metagenomics assembly v
build:
  number: 0
package:
  name: megahit
  version: 1.0.3
requirements:
  build:
  - gcc     [not win]
  - gmp
  - zlib
```

```
  run:
  - libgcc
source:
  fn: v1.0.3.zip
  md5: 5e7c6562eda9bed6e9d6344ef795e56f
  url: https://github.com/voutcn/megahit/archive/v1.0.3.zip
test:
  commands:
  - megahit --help
```

CHAPTER 233

metaseq-all

233.1 Summary

Meta-package for metaseq including bedtools and UCSC tools

233.2 Home

233.3 Versions

- 0.5.6

233.4 License

The license for this meta-package is MIT; individual tools vary

233.5 Meta

```
package:
  name: metaseq-all
  version: "0.5.6"

build:
  number: 1
requirements:
  run:
    - metaseq
    - bedtools
    - samtools
    - ucsc-bedgraphtobigwig
    - ucsc-bedtobigbed
    - ucsc-bigbedtobed
    - ucsc-bigwigsummary

about:
```

```
  summary: "Meta-package for metaseq including bedtools and UCSC tools"
  license: "The license for this meta-package is MIT; individual tools vary"
```

CHAPTER 234

metaseq

234.1 Summary

Integrative analysis of high-thoughput sequencing data

234.2 Home

http://github.com/daler/metaseq

234.3 Versions

- 0.5.6

234.4 License

MIT License

234.5 Meta

```
package:
  name: metaseq
  version: "0.5.6"

source:
  fn: metaseq-0.5.6.tar.gz
  url: https://pypi.python.org/packages/source/m/metaseq/metaseq-0.5.6.tar.gz
  md5: f29575db23019a5cd1003bfccb599847
#  patches:
   # List any patch files here
   # - fix.patch

build:
  # noarch_python: True
  # preserve_egg_dir: True
```

```
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - metaseq = metaseq:main
    #
    # Would create an entry point called metaseq that calls metaseq.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  number: 0
  skip: True # [not py27]

requirements:
  build:
    - python
    - setuptools
    - scipy >=0.10.1
    - biopython
    - scikit-learn
    - bx-python >=0.7.1
    - cython
    - numpy >=1.8.0
    - matplotlib >=1.3.1
    - pandas >=0.13.1
    - pysam >=0.7
    - gffutils >=0.8.2
    - pyyaml >=3.10
    - pybedtools >=0.6.6
    - fisher

  run:
    - python
    - scipy >=0.10.1
    - biopython
    - scikit-learn
    - bx-python >=0.7.1
    - cython
    - numpy >=1.8.0
    - matplotlib >=1.3.1
    - pandas >=0.13.1
    - pysam >=0.7
    - gffutils >=0.8.2
    - pyyaml >=3.10
    - pybedtools >=0.6.6
    - fisher

test:
  # Python imports
  imports:
    - metaseq

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.
```

```
  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: http://github.com/daler/metaseq
  license: MIT License
  summary: 'Integrative analysis of high-thoughput sequencing data'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 235

metasv

235.1 Summary

An accurate and integrative structural-variant caller for next generation sequencing

235.2 Home

https://github.com/bioinform/metasv

235.3 Versions

- 0.4.0

235.4 License

MIT

235.5 Meta

```
package:
  name: metasv
  version: '0.4.0'

source:
  #fn: metasv-0.3.2a0.tar.gz
  #url: https://github.com/bioinform/metasv/archive/0.3.2a0.tar.gz

  fn: metasv-e499f09.tar.gz
  url: https://github.com/bioinform/metasv/archive/e499f09.tar.gz

build:
  number: 4
  skip: True # [not py27]
```

```
requirements:
  build:
    - python
    - setuptools
    - cython
    - pybedtools
    - pyvcf
    - pysam

  run:
    - python
    - pybedtools
    - pyvcf
    - pysam

test:
  commands:
    - run_metasv.py -h

about:
  home: https://github.com/bioinform/metasv
  summary: An accurate and integrative structural-variant caller for next generation sequencing
  license: MIT
```

CHAPTER 236

migmap

236.1 Summary

A wrapper for IgBlast V-(D)-J mapping tool designed to facilitate analysis immune receptor libraries profiled using high-throughput sequencing.

236.2 Home

https://github.com/mikessh/migmap

236.3 Versions

- 0.9.7

236.4 License

https://github.com/mikessh/migmap/blob/master/LICENSE

236.5 Meta

```
package:
  name: migmap
  version: "0.9.7"
source:
  fn: migmap-0.9.7.zip
  url: https://github.com/mikessh/migmap/releases/download/0.9.7/migmap-0.9.7.zip
about:
  home: https://github.com/mikessh/migmap
  license: https://github.com/mikessh/migmap/blob/master/LICENSE
  summary: >
    A wrapper for IgBlast V-(D)-J mapping tool
    designed to facilitate analysis immune receptor
    libraries profiled using high-throughput sequencing.
requirements:
```

```
  run:
    - igblast
    - java-jdk
```

CHAPTER 237

miniasm

237.1 Summary

Ultrafast de novo assembly for long noisy reads (though having no consensus step)

237.2 Home

https://github.com/lh3/miniasm

237.3 Versions

- 0.2

237.4 License

MIT

237.5 Meta

```
package:
  name: miniasm
  version: "0.2"

build:
  number: 0

source:
  fn: v0.2.tar.gz
  url: https://github.com/lh3/miniasm/archive/v0.2.tar.gz
  md5: e1f05eb352919b86c2b72832fecbac76


requirements:
  build:
```

```
  - gcc

  run:
  - libgcc

test:
  commands:
    - miniasm -V  > /dev/null

about:
  home: https://github.com/lh3/miniasm
  license: MIT
  license_file: LICENSE.txt
  summary: Ultrafast de novo assembly for long noisy reads (though having no consensus step)
```

CHAPTER 238

minimap

238.1 Summary

Experimental tool to find approximate mapping positions between long sequences

238.2 Home

https://github.com/lh3/minimap

238.3 Versions

- 0.2

238.4 License

MIT

238.5 Meta

```
package:
  name: minimap
  version: "0.2"

build:
  number: 0

source:
  fn: minimap_v0.2.tar.gz
  url: https://github.com/lh3/minimap/archive/v0.2.tar.gz
  md5: 15257d99648f486e86580d8a7accc96b

requirements:
  build:
  - gcc
```

```
  run:
  - libgcc

test:
  commands:
    - minimap -V  > /dev/null

about:
  home: https://github.com/lh3/minimap
  license: MIT
  license_file: LICENSE.txt
  summary: Experimental tool to find approximate mapping positions between long sequences
```

CHAPTER 239

mirdeep2

239.1 Summary

miRNA prediction

239.2 Home

https://github.com/lpantano/mirdeep2_core.git

239.3 Versions

- 2.0.0.7

239.4 License

academic

239.5 Meta

```
package:
  name: mirdeep2
  version: '2.0.0.7'

source:
  git_url: https://github.com/lpantano/mirdeep2_core.git
  git_rev: e875953

build:
  number: 2

requirements:
  run:
    - perl
    - perl-pdf-api2
```

```
about:
  home: https://github.com/lpantano/mirdeep2_core.git
  license: academic
  summary: miRNA prediction
```

CHAPTER 240

moreutils

240.1 Summary

a growing collection of the unix tools that nobody thought to write long ago when unix was young

240.2 Home

http://joeyh.name/code/moreutils/

240.3 Versions

- 0.5.7

240.4 License

GPLv2

240.5 Meta

```
package:
  name: moreutils
  version: '0.5.7'

source:
  fn: moreutils-0.5.7.tar.gz
  url: http://http.debian.net/debian/pool/main/m/moreutils/moreutils_0.57.orig.tar.gz

build:
  number: 1

requirements:
  build:
  run:
```

```
test:
  commands:
    - sponge -h

about:
  home: http://joeyh.name/code/moreutils/
  license: GPLv2
  summary: a growing collection of the unix tools that nobody thought to write long ago when unix was
```

CHAPTER 241

mosaik

241.1 Summary

MOSAIK is a stable, sensitive and open-source program for mapping second and third-generation sequencing reads to a reference genome.

241.2 Home

https://github.com/wanpinglee/MOSAIK

241.3 Versions

- 2.2.26

241.4 License

GPL 2.0+

241.5 Meta

```
about:
    home: 'https://github.com/wanpinglee/MOSAIK'
    license: 'GPL 2.0+'
    summary: "MOSAIK is a stable, sensitive and open-source program for mapping second and third-gene
package:
  name: mosaik
  version: '2.2.26'
source:
  fn: e04c806bb1410cf1dbd1534991c46d696aec6723.zip
  md5: 2fd32477444978ec7662df77226cc896
  url: https://github.com/wanpinglee/MOSAIK/archive/e04c806bb1410cf1dbd1534991c46d696aec6723.zip # p
  patches:
    - osx-makefile.patch # [osx]
    - linux.inc.patch # [linux]
```

```
test:
    commands:
        - "cd $SRC_DIR/demo && ls ../bin/ && bash Build.sh &> /dev/null && bash Align.sh &> /dev/null
build:
  number: 1
```

CHAPTER 242

mothur [linux64]

242.1 Summary

242.2 Home

http://www.mothur.org

242.3 Versions

- 1.36.1
- 1.25.0

242.4 License

GPL

242.5 Meta

```
package:
  name: mothur [linux64]
  version: 1.36.1

source:
  fn: v1.36.1.tar.gz
  url: https://github.com/mothur/mothur/archive/v1.36.1.tar.gz
  md5: 96e176b223468e4d0cda02859a4ac7aa
  patches:
    - Build-Flags.patch

build:
  number: 0

requirements:
  build:
```

```
    - zlib
    - ncurses
    - readline
    - boost
  run:
    - zlib
    - ncurses
    - readline
    - boost

test:
  commands:
     - mothur "#help()"
     - uchime --version

about:
  home: http://www.mothur.org
  license: GPL
```

CHAPTER 243

moto

243.1 Summary

A library that allows your python tests to easily mock out the boto library

243.2 Home

https://github.com/spulec/moto

243.3 Versions

- 0.4.14

243.4 License

Apache Software License

243.5 Meta

```
package:
  name: moto
  version: "0.4.14"

source:
  fn: moto-0.4.14.tar.gz
  url: https://pypi.python.org/packages/source/m/moto/moto-0.4.14.tar.gz
  md5: ce791928c59c67d699aba6eb58b9e253

build:
  entry_points:
    - moto_server = moto.server:main

requirements:
  build:
```

```
    - python
    - setuptools
    - jinja2
    - boto >=2.20.0
    - flask
    - httpretty >=0.6.1
    - requests
    - xmltodict
    - six
    - werkzeug

  run:
    - python
    - jinja2
    - boto >=2.20.0
    - flask
    - httpretty >=0.6.1
    - requests
    - xmltodict
    - six
    - werkzeug

test:
  # Python imports
  imports:
    - moto
    - moto.autoscaling
    - moto.cloudformation
    - moto.cloudwatch
    - moto.core
    - moto.datapipeline
    - moto.dynamodb
    - moto.dynamodb2
    - moto.ec2
    - moto.ec2.responses
    - moto.elb
    - moto.emr
    - moto.glacier
    - moto.iam
    - moto.kinesis
    - moto.kms
    - moto.rds
    - moto.rds2
    - moto.redshift
    - moto.route53
    - moto.s3
    - moto.s3bucket_path
    - moto.ses
    - moto.sns
    - moto.sqs
    - moto.sts

  commands:
    - moto_server --help

about:
  home: https://github.com/spulec/moto
  license: Apache Software License
```

```
summary: 'A library that allows your python tests to easily mock out the boto library'
```

CHAPTER 244

ms

244.1 Summary

Generates random independent samples according to a simple Wright-Fisher neutral model.

244.2 Home

http://home.uchicago.edu/rhudson1/source/mksamples.html

244.3 Versions

- 2014_03_04

244.4 License

Unknown

244.5 Meta

```
package:
  name: ms
  # No version numbers are supplied, so we use the last updated date in the
  # header of ms.c as the version number.
  version: "2014_03_04"

build:
  number: 0

requirements:
  build:
    - gcc

source:
  fn: ms.tar.gz
```

```
  url: https://webshare.uchicago.edu/users/rhudson1/Public/ms.folder/ms.tar.gz
  md5: ef693dcc424fd5293b0bea4c68953700

test:
  commands:
    - ms 2 1 -T > /dev/null

about:
  home: http://home.uchicago.edu/rhudson1/source/mksamples.html
  # No license information is provided in the source code or documentation
  license: Unknown
  summary: Generates random independent samples according to a simple Wright-Fisher neutral model.
```

CHAPTER 245

msms

245.1 Summary

MSMS is a program written in the C programming language to compute molecular surfaces.

245.2 Home

http://mgltools.scripps.edu/packages/MSMS/

245.3 Versions

- 2.6.1

245.4 License

Free for academic use.

245.5 Meta

```
package:
  name: msms
  version: "2.6.1"

source:
  fn: msms_i86_64Linux2_2.6.1.tar.gz
  url: http://mgltools.scripps.edu/downloads/tars/releases/MSMSRELEASE/REL2.6.1/msms_i86_64Linux2_2.6
  md5: 650d8c6fd49d9ce291f30ed530d5f313
  patches:
    - pdb_to_xyzr.patch
    - pdb_to_xyzrn.patch

build:
  number: 1
  has_prefix_files:
```

```
    - bin/pdb_to_xyzr
    - bin/pdb_to_xyzrn

test:
  commands:
    - msms -h

about:
  home: http://mgltools.scripps.edu/packages/MSMS/
  license: Free for academic use.
  summary: MSMS is a program written in the C programming language to compute molecular surfaces.
```

CHAPTER 246

msprime

246.1 Summary

A fast and accurate coalescent simulator.

246.2 Home

http://pypi.python.org/pypi/msprime

246.3 Versions

- 0.1.7

246.4 License

GNU Lesser General Public License v3 or later (LGPLv3+)

246.5 Meta

```
package:
  name: msprime
  version: "0.1.7"

source:
  fn: msprime-0.1.7.tar.gz
  url: https://pypi.python.org/packages/source/m/msprime/msprime-0.1.7.tar.gz
  md5: 4c87901df33245db534092ad5234bd0d
#  patches:
   # List any patch files here
   # - fix.patch

build:
  # noarch_python: True
  # preserve_egg_dir: True
```

```
  entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - msprime = msprime:main
    #
    # Would create an entry point called msprime that calls msprime.main()

    - mspms=msprime.cli:mspms_main
    - msp=msprime.cli:msp_main

  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  number: 1

requirements:
  build:
    - gcc
    - python
    - setuptools
    - setuptools_scm
    - svgwrite
    - hdf5
    - gsl

  run:
    - python
    - svgwrite
    - hdf5
    - gsl

test:
  # Python imports
  imports:
    - msprime

  commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.

    - msp --help > /dev/null
    - mspms 2 1 -T > /dev/null

  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: http://pypi.python.org/pypi/msprime
  license: GNU Lesser General Public License v3 or later (LGPLv3+)
  summary: 'A fast and accurate coalescent simulator.'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 247

mugsy [linux64]

247.1 Summary

Mugsy is a multiple whole genome aligner.

247.2 Home

http://mugsy.sourceforge.net

247.3 Versions

- 1.2.3

247.4 License

Artistic License 2.0

247.5 Meta

```
package:
  name: mugsy [linux64]
  version: 1.2.3

source:
  fn:  mugsy_x86-64-v1r2.3.tgz
  url: http://downloads.sourceforge.net/project/mugsy/mugsy_x86-64-v1r2.3.tgz
  md5: c4208cce45ff76f3fc7643764453617b
  patches:
    - perl-env.patch

build:
  number: 0

requirements:
```

```
  run:
    - perl

about:
  home: http://mugsy.sourceforge.net
  license: Artistic License 2.0
  summary: Mugsy is a multiple whole genome aligner.
  license_file: LICENSE
```

CHAPTER 248

mummer

248.1 Summary

MUMmer is a system for rapidly aligning entire genomes

248.2 Home

http://mummer.sourceforge.net/

248.3 Versions

- 3.23

248.4 License

The Artistic License

248.5 Meta

```
about:
    home: 'http://mummer.sourceforge.net/'
    license: "The Artistic License"
    summary: "MUMmer is a system for rapidly aligning entire genomes"
package:
  name: mummer
  version: '3.23'
source:
  fn: MUMmer3.23.tar.gz
  sha256: 1efad4f7d8cee0d8eaebb320a2d63745bb3a160bb513a15ef7af46f330af662f
  url: https://downloads.sourceforge.net/project/mummer/mummer/3.23/MUMmer3.23.tar.gz
requirements:
  build:
    - perl-threaded # [not osx]
  run:
```

```
    - perl-threaded # [not osx]
test:
    commands:
        - "mummer -h &> /dev/null"
```

CHAPTER 249

muscle

249.1 Summary

MUSCLE: multiple sequence alignment with high accuracy and high throughput

249.2 Home

http://www.drive5.com/muscle/

249.3 Versions

- 3.8.1551

249.4 License

http://www.drive5.com/muscle/manual/license.html

249.5 Meta

```
about:
    home: 'http://www.drive5.com/muscle/'
    license: "http://www.drive5.com/muscle/manual/license.html"
    summary: "MUSCLE: multiple sequence alignment with high accuracy and high throughput"
package:
  name: muscle
  version: '3.8.1551'
source:
  fn: muscle_src_3.8.1551.tar.gz
  md5: 1b7c9661f275a82d3cf708f923736bf8
  url: http://www.drive5.com/muscle/muscle_src_3.8.1551.tar.gz
  patches:
    - osx-makefile.patch # [osx]
build:
  number: 1
```

```
test:
    commands:
        - muscle -version
```

CHAPTER 250

mvicuna

250.1 Summary

M-Vicuna is a modularized version of VICUNA, a de novo assembly program targeting populations with high mutation rates

250.2 Home

https://www.broadinstitute.org/scientific-community/science/projects/viral-genomics/vicuna

250.3 Versions

- 1.0

250.4 License

https://www.broadinstitute.org/node/4238

250.5 Meta

```
about:
    home: 'https://www.broadinstitute.org/scientific-community/science/projects/viral-genomics/vicuna
    license: 'https://www.broadinstitute.org/node/4238'
    summary: 'M-Vicuna is a modularized version of VICUNA, a de novo assembly program targeting popul
package:
  name: mvicuna
  version: '1.0'
source:
  git_url: https://github.com/broadinstitute/mvicuna.git
build:
  number: 1
test:
    commands:
        - 'mvicuna -h | grep "Parameters" &> /dev/null'
```

CHAPTER 251

mygene

251.1 Summary

Python Client for MyGene.Info services.

251.2 Home

https://bitbucket.org/newgene/mygene

251.3 Versions

- 2.2.0

251.4 License

BSD License

251.5 Meta

```
package:
  name: mygene
  version: "2.2.0"

source:
  fn: mygene-2.2.0.tar.gz
  url: https://pypi.python.org/packages/source/m/mygene/mygene-2.2.0.tar.gz
  md5: 3ef36a7ed2b419ca812af2972d471905
#  patches:
   # List any patch files here
   # - fix.patch

# build:
  # noarch_python: True
  # preserve_egg_dir: True
```

```
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - mygene = mygene:main
    #
    # Would create an entry point called mygene that calls mygene.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools
    - httplib2 >=0.6

  run:
    - python
    - httplib2 >=0.6

test:
  # Python imports
  imports:
    - mygene

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: https://bitbucket.org/newgene/mygene
  license: BSD License
  summary: 'Python Client for MyGene.Info services.'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 252

mysql-connector-c

252.1 Summary

MySQL Connector/C, the C interface for communicating with MySQL servers.

252.2 Home

https://dev.mysql.com/downloads/connector/c/

252.3 Versions

- 6.1.6

252.4 License

LGPL

252.5 Meta

```
package:
  name: mysql-connector-c
  version: 6.1.6

source:
  fn: mysql-connector-c-6.1.6-linux-glibc2.5-x86_64.tar.gz
  url: https://dev.mysql.com/get/Downloads/Connector-C/mysql-connector-c-6.1.6-linux-glibc2.5-x86_64
  md5: 627d71c61dfad9048360c40ec822eac1

build:
  number: 1

# requirements:
  # build:
  # run:
```

```
test:
  commands:
    - mysql_config --version
    - my_print_defaults --version

about:
    home: https://dev.mysql.com/downloads/connector/c/
    license: LGPL
    summary: MySQL Connector/C, the C interface for communicating with MySQL servers.
```

CHAPTER 253

mysqlclient

253.1 Summary

Python interface to MySQL

253.2 Home

https://github.com/PyMySQL/mysqlclient-python

253.3 Versions

- 1.3.7

253.4 License

GNU General Public License (GPL)

253.5 Meta

```
package:
  name: mysqlclient
  version: "1.3.7"

source:
  fn: mysqlclient-1.3.7.tar.gz
  url: https://pypi.python.org/packages/source/m/mysqlclient/mysqlclient-1.3.7.tar.gz
  md5: 2ec5a96cbd9fd6ef343fa9b581a67fc4

build:
  number: 1

requirements:
  build:
    - python
```

```
    - mysql-connector-c
  run:
    - python
    - mysql-connector-c

test:
  imports:
    - MySQLdb

about:
  home: https://github.com/PyMySQL/mysqlclient-python
  license: GNU General Public License (GPL)
  summary: 'Python interface to MySQL'
```

CHAPTER 254

netifaces

254.1 Summary

254.2 Home

https://bitbucket.org/al45tair/netifaces

254.3 Versions

- 0.10.4

254.4 License

MIT

254.5 Meta

```
package:
  name: netifaces
  version: 0.10.4

build:
  number: 1

source:
  fn: netifaces-0.10.4.tar.gz
  url: https://pypi.python.org/packages/source/n/netifaces/netifaces-0.10.4.tar.gz
  md5: 36da76e2cfadd24cc7510c2c0012eb1e

requirements:
  build:
    - python
    - setuptools

  run:
```

```
    - python
    - setuptools

test:
  imports:
    - netifaces

about:
  home: https://bitbucket.org/al45tair/netifaces
  license: MIT
```

CHAPTER 255

newt

255.1 Summary

255.2 Home

https://fedorahosted.org/newt/

255.3 Versions

- 0.52.18

255.4 License

GPL

255.5 Meta

```
package:
  name: newt
  version: 0.52.18

source:
  fn: newt-0.52.18.tar.gz
  url: http://fedorahosted.org/releases/n/e/newt/newt-0.52.18.tar.gz
  md5: 685721bee1a318570704b19dcf31d268

build:
  number: 2

requirements:
  build:
    - popt
    - slang
    - python
  run:
```

```
    - popt
    - slang
    - python

test:
  commands:
    - whiptail --help
  imports:
    - snack

about:
  home: https://fedorahosted.org/newt/
  license: GPL
```

CHAPTER 256

ngs-sdk

256.1 Summary

NGS SDK Language Bindings

256.2 Home

https://github.com/ncbi/ngs

256.3 Versions

- 1.2.2

256.4 License

Public Domain

256.5 Meta

```
about:
  home: https://github.com/ncbi/ngs
  license: Public Domain
  summary: NGS SDK Language Bindings
package:
  name: ngs-sdk
  version: 1.2.2
source:
  fn: 1.2.2.tar.gz
  url: https://github.com/ncbi/ngs/archive/1.2.2.tar.gz
  md5: af6018ede86faddbf787057cd90297e1
```

CHAPTER 257

novoalign

257.1 Summary

Powerful tool designed for mapping of short reads onto a reference genome from Illumina, Ion Torrent, and 454 NGS platforms

257.2 Home

http://www.novocraft.com/products/novoalign/

257.3 Versions

- 3.03.02

257.4 License

Commercial (requires license for multithreaded use)

257.5 Meta

```
package:
  name: novoalign
  version: '3.03.02'
source:
  fn: novocraftV3.03.02.tar.gz
  url: http://www.novocraft.com/homebrew/novocraftV3.03.02.Linux2.6.tar.gz # [linux]
  url: http://www.novocraft.com/homebrew/novocraftV3.03.02.MacOSX.tar.gz # [osx]
build:
  number: 0
requirements:
  build:
  run:
test:
  commands:
```

```
    - 'novoalign 2>&1 | grep ^Novoalign'
about:
  home: http://www.novocraft.com/products/novoalign/
  license: Commercial (requires license for multithreaded use)
  summary: Powerful tool designed for mapping of short reads onto a reference genome from Illumina, I
```

CHAPTER 258

oauth2client

258.1 Summary

client library for OAuth 2.0

258.2 Home

https://github.com/google/oauth2client/

258.3 Versions

- 1.5.2

258.4 License

Apache 2.0

258.5 Meta

```
package:
  name: oauth2client
  version: '1.5.2'

source:
  fn: oauth2client-1.5.2.tar.gz
  url: https://pypi.python.org/packages/source/o/oauth2client/oauth2client-1.5.2.tar.gz
  md5: 842ab2fba8bce5b36d31f630ed80f17d

build:
  number: 0

requirements:
  build:
    - python
```

```
    - setuptools

  run:
    - python
    - httplib2
    - pyasn1
    - pyasn1-modules
    - rsa
    - six

test:
  imports:
    - oauth2client
    - oauth2client.client

about:
  home: https://github.com/google/oauth2client/
  license: Apache 2.0
  summary:  client library for OAuth 2.0
```

CHAPTER 259

oligotyping

259.1 Summary

The oligotyping and minimum entropy decomposition (MED) pipeline for the analysis of marker gene amplicons

259.2 Home

http://oligotyping.org

259.3 Versions

- 2.0

259.4 License

GNU General Public License v3 or later (GPLv3+)

259.5 Meta

```
package:
  name: oligotyping
  version: "2.0"

source:
  fn: oligotyping-2.0.tar.gz
  url: https://pypi.python.org/packages/source/o/oligotyping/oligotyping-2.0.tar.gz
  md5: 2159126a355bf3429418224ab17d5a56
#  patches:
   # List any patch files here
   # - fix.patch

build:
  skip: True # [not py27]
  # noarch_python: True
```

```
  # preserve_egg_dir: True
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - oligotyping = oligotyping:main
    #
    # Would create an entry point called oligotyping that calls oligotyping.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools
    - matplotlib
    - biopython
    - scipy
    - django

  run:
    - python
    - matplotlib
    - biopython
    - scipy
    - django
    - blast
    - r-vegan
    - r-ggplot2
    - r-gplots
    - r-gtools
    - r-reshape
    - r-optparse
    - r-pheatmap
    - r-rcolorbrewer
    - r-compute.es

test :
  # Python imports
  imports:
    - Oligotyping
    - Oligotyping.lib
    - Oligotyping.utils
    - Oligotyping.utils.html
    - Oligotyping.visualization

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  # requires:
```

```
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: http://oligotyping.org
  license: GNU General Public License v3 or later (GPLv3+)
  summary: 'The oligotyping and minimum entropy decomposition (MED) pipeline for the analysis of mark

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 260

oncofuse

260.1 Summary

Predicting oncogenic potential of gene fusions

260.2 Home

https://github.com/mikessh/oncofuse

260.3 Versions

- 1.1.0

260.4 License

Apache v2.0

260.5 Meta

```
package:
  name: oncofuse
  version: "1.1.0"

source:
  fn: oncofuse-1.1.0.zip
  url: https://github.com/mikessh/oncofuse/releases/download/1.1.0/oncofuse-1.1.0.zip

build:
  number: 1

requirements:
  run:
    - java-jdk
```

```
test:
  commands:
    - "oncofuse -h 2>&1 | grep '^usage: Oncofuse'"

about:
  home: https://github.com/mikessh/oncofuse
  license: Apache v2.0
  summary: Predicting oncogenic potential of gene fusions
```

CHAPTER 261

openbabel

261.1 Summary

Open Babel is a chemical toolbox designed to speak the many languages of chemical data. It's an open, collaborative project allowing anyone to search, convert, analyze, or store data from molecular modeling, chemistry, solid-state materials, biochemistry, or related areas.

261.2 Home

http://openbabel.org

261.3 Versions

- 2.3.2

261.4 License

GPL

261.5 Meta

```
about:
  home: http://openbabel.org
  license: GPL
  summary: 'Open Babel is a chemical toolbox designed to speak the many languages
    of chemical data. It''s an open, collaborative project allowing anyone to search,
    convert, analyze, or store data from molecular modeling, chemistry, solid-state
    materials, biochemistry, or related areas.'

build:
  skip: True # [not py27]
  number: 1

package:
```

```
  name: openbabel
  version: 2.3.2

requirements:
  build:
  - python
  - gcc
  - cmake
  - eigen
  - libxml2
  - zlib
  - cairo
  run:
  - python
  - libgcc

source:
  fn: openbabel-2.3.2.tar.gz
  sha256: 4eaca26679aa6cc85ebf96af19191472ac63ca442c36b0427b369c3a25705188
  url: http://downloads.sourceforge.net/project/openbabel/openbabel/2.3.2/openbabel-2.3.2.tar.gz

test:
  commands:
  - obabel --help
```

CHAPTER 262

optitype

262.1 Summary

Precision HLA typing from next-generation sequencing data

262.2 Home

https://github.com/FRED-2/OptiType

262.3 Versions

- 2015.10.20

262.4 License

BSD

262.5 Meta

```
package:
  name: optitype
  version: 2015.10.20
build:
  number: 1
  skip: True # [not py27]
source:
  fn: optitype-8961c1d.tar.gz
  url: https://github.com/FRED-2/OptiType/archive/8961c1d.tar.gz

requirements:
  build:
    - python
  run:
    - python
```

```
    - numpy
    - pyomo
    - hdf5
    - pytables
    - pandas
    - pysam
    - matplotlib
    - samtools
    - glpk
    - razers3

test:
  commands:
    - OptiTypePipeline.py -h

about:
  home: https://github.com/FRED-2/OptiType
  license: BSD
  summary: Precision HLA typing from next-generation sequencing data
```

CHAPTER 263

p7zip

263.1 Summary

p7zip is a quick port of 7z.exe and 7za.exe (command line version of 7zip, see www.7-zip.org) for Unix.

263.2 Home

http://sourceforge.net/projects/p7zip/

263.3 Versions

- 15.09

263.4 License

LGPLv2

263.5 Meta

```
package:
  name: p7zip
  version: "15.09"

build:
  number: 3

source:
  fn: p7zip_15.09_src_all.tar.bz2
  url: http://iweb.dl.sourceforge.net/project/p7zip/p7zip/15.09/p7zip_15.09_src_all.tar.bz2
  md5: ab69f4f13ba0ec57eca2cf4c9edd9678

test:
  commands:
    - touch xxx
```

```
    - 7z a xxx.7z xxx
    - 7za a xxx.7z xxx
    - 7zr a xxx.7z xxx

about:
  home: http://sourceforge.net/projects/p7zip/
  summary: p7zip is a quick port of 7z.exe and 7za.exe (command line version of 7zip, see www.7-zip.c
  license: LGPLv2
```

CHAPTER 264

parallel

264.1 Summary

GNU parallel is a shell tool for executing jobs in parallel using one or more computers.

264.2 Home

http://www.gnu.org/software/parallel/

264.3 Versions

- 20150922

264.4 License

GNU

264.5 Meta

```
# GNU Parallel
# updated to latest from https://github.com/ostrokach/conda-recipes-extra/tree/master/parallel

package:
  name: parallel
  version: 20150922

source:
  url: http://gnu.mirror.iweb.com/parallel/parallel-20150922.tar.bz2
  fn: parallel-20150922.tar.bz2

build:
  number: 0

requirements:
```

```
  build:
  run:

test:
  commands:
    - parallel --version

about:
  home: http://www.gnu.org/software/parallel/
  license: GNU
  summary: GNU parallel is a shell tool for executing jobs in parallel using one or more computers.
```

CHAPTER 265

pathtools

265.1 Summary

File system general utilities

265.2 Home

http://github.com/gorakhargosh/pathtools

265.3 Versions

- 0.1.2

265.4 License

MIT License

265.5 Meta

```
package:
  name: pathtools
  version: "0.1.2"

source:
  fn: pathtools-0.1.2.tar.gz
  url: https://pypi.python.org/packages/source/p/pathtools/pathtools-0.1.2.tar.gz
  md5: 9a1af5c605768ea5804b03b734ff0f82
#  patches:
   # List any patch files here
   # - fix.patch

# build:
  # noarch_python: True
  # preserve_egg_dir: True
```

```
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - pathtools = pathtools:main
    #
    # Would create an entry point called pathtools that calls pathtools.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools

  run:
    - python

test:
  # Python imports
  imports:
    - pathtools

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: http://github.com/gorakhargosh/pathtools
  license: MIT License
  summary: 'File system general utilities'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 266

pbgzip

266.1 Summary

Parallel Block GZIP

266.2 Home

https://github.com/nh13/pbgzip

266.3 Versions

- 2015.10.28

266.4 License

MIT/Expat

266.5 Meta

```
package:
  name: pbgzip
  version: 2015.10.28

source:
  fn: bgzip-6abda41a6.tar.gz
  url: https://github.com/nh13/pbgzip/archive/6abda41a6.tar.gz

build:
  number: 0

requirements:
  build:
  run:
```

```
test:
  commands:
    #- pbgzip -h

about:
  home: https://github.com/nh13/pbgzip
  summary: Parallel Block GZIP
  license: MIT/Expat
```

CHAPTER 267

peakranger

267.1 Summary

PeakRanger is a multi-purporse software suite for analyzing next-generation sequencing (NGS) data.

267.2 Home

http://ranger.sourceforge.net

267.3 Versions

- 1.18

267.4 License

Artistic License 2.0

267.5 Meta

```
package:
  name: peakranger
  version: 1.18

source:
  fn: PeakRanger-1.18-src.zip
  url: http://downloads.sourceforge.net/project/ranger/Source%20codes/PeakRanger-1.18-src.zip
  md5: 4b47352ee3200096f2ee8745a436b559
  patches:
    - makefile.patch

build:
  number: 0

requirements:
```

```
  build:
    - boost
    - zlib

  run:
    - boost
    - zlib
    - r

test:
  commands:
     - peakranger nr --version

about:
  home: http://ranger.sourceforge.net
  summary: PeakRanger is a multi-purporse software suite for analyzing next-generation sequencing (NG
  license: Artistic License 2.0
  license_file: COPYING
```

CHAPTER 268

peakzilla

268.1 Summary

Peakzilla identifies sites of enrichment and transcription factor binding sites from transcription factor ChIP-seq and ChIP-exo experiments at hight accuracy and resolution.

268.2 Home

http://stark.imp.ac.at/data/peakzilla

268.3 Versions

- 1.0

268.4 License

GPLv2

268.5 Meta

```
package:
  name: peakzilla
  version: 1.0

source:
  fn: master.zip
  url: https://github.com/steinmann/peakzilla/archive/master.zip
  md5: 38944abe797d7d25f7ecf39fa8bd8953
  patches:
    - indent.patch

build:
  number: 0
```

```
requirements:
  build:
    - python

  run:
    - python

test:
  commands:
     - peakzilla.py -h

about:
  home: http://stark.imp.ac.at/data/peakzilla
  summary:  Peakzilla identifies sites of enrichment and transcription factor binding sites from tran
  license: GPLv2
```

CHAPTER 269

pear

269.1 Summary

paired-end read merger

269.2 Home

http://sco.h-its.org/exelixis/web/software/pear/

269.3 Versions

- 0.9.6

269.4 License

Creative Commons Attribution-NonCommercial-ShareAlike 3.0 Unported

269.5 Meta

```
package:
  name: pear
  version: '0.9.6'
about:
  home: http://sco.h-its.org/exelixis/web/software/pear/
  license: 'Creative Commons Attribution-NonCommercial-ShareAlike 3.0 Unported'
  summary: 'paired-end read merger'
source:
  fn: pear-0.9.6-src.tar.gz
  md5: 5ed68d50c1620cd55c58681e38771799
  url: http://sco.h-its.org/exelixis/web/software/pear/files/pear-0.9.6-src.tar.gz
requirements:
  build:
    - pkgconfig
    - zlib
```

```
  run:
    - zlib
test:
  # 'pear -h' exits with error code 1 and there is no 'pear --version', so try
  # to actually merge something. That way, we can also test whether gzip support
  # is compiled in.
  files:
    - fwd.fastq.gz
    - rev.fastq.gz
  commands:
    - pear -f fwd.fastq.gz -r rev.fastq.gz -o out > /dev/null
```

CHAPTER 270

perl-app-cpanminus

270.1 Summary

get, unpack, build and install modules from CPAN

270.2 Home

https://github.com/miyagawa/cpanminus

270.3 Versions

- 1.7039

270.4 License

perl_5

270.5 Meta

```
# Migrated from https://github.com/dan-blanchard/conda-cpan-recipes

package:
  name: perl-app-cpanminus
  version: '1.7039'

source:
  fn: App-cpanminus-1.7039.tar.gz
  url: https://cpan.metacpan.org/authors/id/M/MI/MIYAGAWA/App-cpanminus-1.7039.tar.gz

build:
  number: 0

requirements:
  build:
```

```
    - perl

  run:
    - perl

test:
  imports:
    - App::cpanminus
  commands:
    - cpanm --help

about:
  home: https://github.com/miyagawa/cpanminus
  license: perl_5
  summary: 'get, unpack, build and install modules from CPAN'
```

CHAPTER 271

perl-archive-extract

271.1 Summary

A generic archive extracting mechanism

271.2 Home

https://metacpan.org/pod/Archive::Extract

271.3 Versions

- 0.76

271.4 License

Perl

271.5 Meta

```
package:
  name: perl-archive-extract
  version: '0.76'

source:
  fn: Archive-Extract-0.76.tar.gz
  url: https://cpan.metacpan.org/authors/id/B/BI/BINGOS/Archive-Extract-0.76.tar.gz

build:
  number: 0

requirements:
  build:
    - perl
    - perl-app-cpanminus
```

```
  run:
    - perl

about:
  home: https://metacpan.org/pod/Archive::Extract
  license: Perl
  summary: A generic archive extracting mechanism
```

CHAPTER 272

perl-archive-zip

272.1 Summary

Provide an interface to ZIP archive files

272.2 Home

https://metacpan.org/pod/Archive::Zip

272.3 Versions

- 1.55

272.4 License

Perl

272.5 Meta

```
package:
  name: perl-archive-zip
  version: '1.55'

source:
  fn: Archive-Zip-1.55.tar.gz
  url: https://cpan.metacpan.org/authors/id/P/PH/PHRED/Archive-Zip-1.55.tar.gz

build:
  number: 0

requirements:
  build:
    - perl
    - perl-app-cpanminus
```

```
    - perl-module-build
  run:
    - perl

about:
  home: https://metacpan.org/pod/Archive::Zip
  license: Perl
  summary: Provide an interface to ZIP archive files
```

CHAPTER 273

perl-bio-db-sam

273.1 Summary

Read SAM/BAM database files

273.2 Home

https://metacpan.org/pod/Bio::DB::Sam

273.3 Versions

- 1.41

273.4 License

Perl

273.5 Meta

```
package:
  name: perl-bio-db-sam
  version: '1.41'

source:
  fn: Bio-SamTools-1.41.tar.gz
  url: https://cpan.metacpan.org/authors/id/L/LD/LDS/Bio-SamTools-1.41.tar.gz

build:
  number: 0

requirements:
  build:
    - perl
    - perl-app-cpanminus
```

```
    - perl-module-build
    - perl-bioperl
  run:
    - perl
    - perl-bioperl

test:
  imports:
    - Bio::DB::Sam

about:
  home: https://metacpan.org/pod/Bio::DB::Sam
  license: Perl
  summary:  Read SAM/BAM database files
```

CHAPTER 274

perl-bioperl

274.1 Summary

BioPerl - Perl Modules for Biology

274.2 Home

https://metacpan.org/pod/distribution/BioPerl/BioPerl.pm

274.3 Versions

- 1.6.924

274.4 License

Perl

274.5 Meta

```
package:
  name: perl-bioperl
  version: '1.6.924'

source:
  fn: BioPerl-1.6.924.tar.gz
  url: https://cpan.metacpan.org/authors/id/C/CJ/CJFIELDS/BioPerl-1.6.924.tar.gz

build:
  number: 0

requirements:
  build:
    - perl
    - perl-app-cpanminus
```

```
    - perl-module-build
  run:
    - perl

about:
  home: https://metacpan.org/pod/distribution/BioPerl/BioPerl.pm
  license: Perl
  summary: BioPerl - Perl Modules for Biology
```

CHAPTER 275

perl-cgi

275.1 Summary

A generic file fetching mechanism

275.2 Home

https://metacpan.org/pod/distribution/CGI/lib/CGI.pod

275.3 Versions

- 4.22

275.4 License

GPL

275.5 Meta

```
package:
  name: perl-cgi
  version: '4.22'

source:
  fn: CGI-4.22.tar.gz
  url: https://cpan.metacpan.org/authors/id/L/LE/LEEJO/CGI-4.22.tar.gz

build:
  number: 0

requirements:
  build:
    - perl
    - perl-app-cpanminus
```

```
    - perl-module-build
  run:
    - perl

test:
  imports:
    - CGI

about:
  home: https://metacpan.org/pod/distribution/CGI/lib/CGI.pod
  license: GPL
  summary: A generic file fetching mechanism
```

CHAPTER 276

perl-compress-raw-zlib

276.1 Summary

Low-Level Interface to zlib compression library

276.2 Home

https://metacpan.org/pod/Compress::Raw::Zlib

276.3 Versions

- 2.069

276.4 License

Perl

276.5 Meta

```
package:
  name: perl-compress-raw-zlib
  version: '2.069'

source:
  fn: Compress-Raw-Zlib-2.069.tar.gz
  url: https://cpan.metacpan.org/authors/id/P/PM/PMQS/Compress-Raw-Zlib-2.069.tar.gz

build:
  number: 0

requirements:
  build:
    - perl
    - perl-app-cpanminus
```

```
    - perl-module-build
  run:
    - perl

about:
  home: https://metacpan.org/pod/Compress::Raw::Zlib
  license: Perl
  summary: Low-Level Interface to zlib compression library
```

CHAPTER 277

perl-data-uuid

277.1 Summary

Globally/Universally Unique Identifiers (GUIDs/UUIDs)

277.2 Home

https://metacpan.org/pod/Data::UUID

277.3 Versions

- 1.221

277.4 License

Perl

277.5 Meta

```
package:
  name: perl-data-uuid
  version: '1.221'

source:
  fn: Data-UUID-1.221.tar.gz
  url: https://cpan.metacpan.org/authors/id/R/RJ/RJBS/Data-UUID-1.221.tar.gz

build:
  number: 0

requirements:
  build:
    - gcc
    - perl
```

```
    - perl-app-cpanminus
    - perl-module-build
  run:
    - perl

test:
  imports:
    - Data::UUID

about:
  home: https://metacpan.org/pod/Data::UUID
  license: Perl
  summary: Globally/Universally Unique Identifiers (GUIDs/UUIDs)
```

CHAPTER 278

perl-db-file

278.1 Summary

Perl5 access to Berkeley DB version 1.x.

278.2 Home

https://metacpan.org/pod/Set::IntervalTree

278.3 Versions

- 1.835

278.4 License

perl_5

278.5 Meta

```
package:
  name: perl-db-file
  version: 1.835
source:
  fn: DB_File-1.835.tar.gz
  url: https://cpan.metacpan.org/authors/id/P/PM/PMQS/DB_File-1.835.tar.gz
build:
  number: 3
requirements:
  build:
    - perl
    - libdb
  run:
    - perl
    - libdb
```

```
test:
  imports:
    - DB_File
about:
  home: https://metacpan.org/pod/Set::IntervalTree
  license: perl_5
  summary: Perl5 access to Berkeley DB version 1.x.
```

CHAPTER 279

perl-dbd-mysql

279.1 Summary

MySQL driver for the Perl5 Database Interface (DBI)

279.2 Home

https://metacpan.org/pod/DBD::mysql

279.3 Versions

- 4.033

279.4 License

Perl

279.5 Meta

```
package:
  name: perl-dbd-mysql
  version: '4.033'

source:
  fn: DBD-mysql-4.033.tar.gz
  url: https://cpan.metacpan.org/authors/id/C/CA/CAPTTOFU/DBD-mysql-4.033.tar.gz

build:
  number: 0

requirements:
  build:
    - perl
    - perl-app-cpanminus
```

```
    - perl-module-build
    - perl-dbi
    - mysqlclient
  run:
    - perl
    - perl-dbi
    - mysqlclient

test:
  imports:
    - DBD::mysql

about:
  home: https://metacpan.org/pod/DBD::mysql
  license: Perl
  summary: MySQL driver for the Perl5 Database Interface (DBI)
```

CHAPTER 280

perl-dbi

280.1 Summary

Database independent interface for Perl

280.2 Home

https://metacpan.org/pod/DBI

280.3 Versions

- 1.634

280.4 License

Perl

280.5 Meta

```
package:
  name: perl-dbi
  version: '1.634'

source:
  fn: DBI-1.634.tar.gz
  url: https://cpan.metacpan.org/authors/id/T/TI/TIMB/DBI-1.634.tar.gz

build:
  number: 0

requirements:
  build:
    - perl
    - perl-app-cpanminus
```

```
    - perl-module-build
  run:
    - perl

about:
  home: https://metacpan.org/pod/DBI
  license: Perl
  summary: Database independent interface for Perl
```

CHAPTER 281

perl-encode-locale

281.1 Summary

Determine the locale encoding

281.2 Home

https://metacpan.org/pod/Encode::Locale

281.3 Versions

- 1.05

281.4 License

Perl

281.5 Meta

```
package:
  name: perl-encode-locale
  version: '1.05'

source:
  fn: Encode-Locale-1.05.tar.gz
  url: https://cpan.metacpan.org/authors/id/G/GA/GAAS/Encode-Locale-1.05.tar.gz

build:
  number: 0

requirements:
  build:
    - perl
    - perl-app-cpanminus
```

```
  run:
    - perl

about:
  home: https://metacpan.org/pod/Encode::Locale
  license: Perl
  summary: Determine the locale encoding
```

CHAPTER 282

perl-file-fetch

282.1 Summary

A generic file fetching mechanism

282.2 Home

https://metacpan.org/pod/File::Fetch

282.3 Versions

- 0.48

282.4 License

Perl

282.5 Meta

```
package:
  name: perl-file-fetch
  version: '0.48'

source:
  fn: File-Fetch-0.48.tar.gz
  url: https://cpan.metacpan.org/authors/id/B/BI/BINGOS/File-Fetch-0.48.tar.gz

build:
  number: 0

requirements:
  build:
    - perl
    - perl-app-cpanminus
```

```
    - perl-module-build
  run:
    - perl

test:
  imports:
    - File::Fetch

about:
  home: https://metacpan.org/pod/File::Fetch
  license: Perl
  summary: A generic file fetching mechanism
```

CHAPTER 283

perl-file-sharedir-install

283.1 Summary

Install shared files

283.2 Home

https://metacpan.org/pod/File::ShareDir::Install

283.3 Versions

- 0.10

283.4 License

Perl

283.5 Meta

```
package:
  name: perl-file-sharedir-install
  version: '0.10'

source:
  fn: File-ShareDir-Install-0.10.tar.gz
  url: https://cpan.metacpan.org/authors/id/G/GW/GWYN/File-ShareDir-Install-0.10.tar.gz

build:
  number: 0

requirements:
  build:
    - perl
    - perl-app-cpanminus
```

```
    - perl-module-build
  run:
    - perl

test:
  imports:
    - File::ShareDir::Install

about:
  home: https://metacpan.org/pod/File::ShareDir::Install
  license: Perl
  summary: Install shared files
```

CHAPTER 284

perl-file-sharedir

284.1 Summary

Locate per-dist and per-module shared files

284.2 Home

https://metacpan.org/pod/File::ShareDir

284.3 Versions

- 1.102

284.4 License

Perl

284.5 Meta

```
package:
  name: perl-file-sharedir
  version: '1.102'

source:
  fn: File-ShareDir-1.102.tar.gz
  url: https://cpan.metacpan.org/authors/id/R/RE/REHSACK/File-ShareDir-1.102.tar.gz

build:
  number: 0

requirements:
  build:
    - perl
    - perl-app-cpanminus
```

```
    - perl-module-build
  run:
    - perl

test:
  imports:
    - File::ShareDir

about:
  home: https://metacpan.org/pod/File::ShareDir
  license: Perl
  summary: Locate per-dist and per-module shared files
```

CHAPTER 285

perl-gd

285.1 Summary

Perl interface to the gd2 graphics library

285.2 Home

http://metacpan.org/pod/GD

285.3 Versions

- 2.56

285.4 License

perl_5

285.5 Meta

```
package:
  name: perl-gd
  version: "2.56"
source:
  fn: GD-2.56.tar.gz
  url: https://cpan.metacpan.org/authors/id/L/LD/LDS/GD-2.56.tar.gz
  md5: c4b3afd98b2c4ce3c2e1027d101a8f1e
requirements:
  build:
    - perl >=5.22.0
    - libgd
    - perl-module-build
  run:
    - perl >=5.22.0
    - libgd
```

```
test:
  imports:
    - GD
about:
  home: http://metacpan.org/pod/GD
  license: perl_5
  summary: 'Perl interface to the gd2 graphics library'
```

CHAPTER 286

perl-gdgraph

286.1 Summary

Produces charts with GD

286.2 Home

http://metacpan.org/pod/GDGraph

286.3 Versions

- 1.49

286.4 License

perl_5

286.5 Meta

```
package:
  name: perl-gdgraph
  version: "1.49"

source:
  fn: GDGraph-1.49.tar.gz
  url: https://cpan.metacpan.org/authors/id/R/RU/RUZ/GDGraph-1.49.tar.gz
  md5: 8bb270a30fea27491302b39b701b3d4e
#  patches:
   # List any patch files here
   # - fix.patch

# build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
```

```
  # number: 1

requirements:
  build:
    - perl >=5.22.0
    - perl-gdtextutil
    - perl-gd

  run:
    - perl >=5.22.0
    - perl-gd
    - perl-gdtextutil

test:
  # Perl 'use' tests
  imports:
    - GD::Graph

  # You can also put a file called run_test.pl (or run_test.py) in the recipe
  # that will be run at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: http://metacpan.org/pod/GDGraph
  license: perl_5
  summary: 'Produces charts with GD'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 287

perl-gdtextutil

287.1 Summary

Text utilities for use with GD

287.2 Home

http://metacpan.org/pod/GDTextUtil

287.3 Versions

- 0.86

287.4 License

unknown

287.5 Meta

```
package:
  name: perl-gdtextutil
  version: "0.86"

source:
  fn: GDTextUtil-0.86.tar.gz
  url: http://cpan.metacpan.org/authors/id/M/MV/MVERB/GDTextUtil-0.86.tar.gz
  md5: 941ad06eadc86b47f3a32da405665c41
#  patches:
   # List any patch files here
   # - fix.patch

# build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
```

```
  # number: 1

requirements:
  build:
    - perl >=5.22.0
    - perl-gd

  run:
    - perl >=5.22.0
    - perl-gd

test:
  # Perl 'use' tests
  imports:
    - GD::Text

  # You can also put a file called run_test.pl (or run_test.py) in the recipe
  # that will be run at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: http://metacpan.org/pod/GDTextUtil
  license: unknown
  summary: 'Text utilities for use with GD'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 288

perl-ipc-system-simple

288.1 Summary

Run commands simply, with detailed diagnostics

288.2 Home

https://metacpan.org/pod/IPC::System::Simple

288.3 Versions

- 1.25

288.4 License

Perl

288.5 Meta

```
package:
  name: perl-ipc-system-simple
  version: '1.25'

source:
  fn: IPC-System-Simple-1.25.tar.gz
  url: https://cpan.metacpan.org/authors/id/P/PJ/PJF/IPC-System-Simple-1.25.tar.gz

build:
  number: 0

requirements:
  build:
    - perl
    - perl-app-cpanminus
```

```
    - perl-module-build
  run:
    - perl

test:
  imports:
    - IPC::System::Simple

about:
  home: https://metacpan.org/pod/IPC::System::Simple
  license: Perl
  summary: Run commands simply, with detailed diagnostics
```

CHAPTER 289

perl-lwp-protocol-https

289.1 Summary

Provide https support for LWP::UserAgent

289.2 Home

https://metacpan.org/pod/LWP::Protocol::https

289.3 Versions

- 6.06

289.4 License

Perl

289.5 Meta

```
package:
  name: perl-lwp-protocol-https
  version: '6.06'

source:
  fn: LWP-Protocol-https-6.06.tar.gz
  url: https://cpan.metacpan.org/authors/id/M/MS/MSCHILLI/LWP-Protocol-https-6.06.tar.gz

build:
  number: 0

requirements:
  build:
    - perl
    - openssl
```

```
    - perl-app-cpanminus
    - perl-lwp-simple
    - perl-module-build
  run:
    - perl
    - openssl
    - perl-lwp-simple

test:
  imports:
    #- Net::SSLeay
    #- IO::Socket::SSL
    #- LWP::Simple

about:
  home: https://metacpan.org/pod/LWP::Protocol::https
  license: Perl
  summary: Provide https support for LWP::UserAgent
```

CHAPTER 290

perl-lwp-simple

290.1 Summary

simple procedural interface to LWP

290.2 Home

https://metacpan.org/pod/LWP::Simple

290.3 Versions

- 6.15

290.4 License

Perl

290.5 Meta

```
package:
  name: perl-lwp-simple
  version: '6.15'

source:
  fn: libwww-perl-6.15.tar.gz
  url: https://cpan.metacpan.org/authors/id/E/ET/ETHER/libwww-perl-6.15.tar.gz

build:
  number: 0

requirements:
  build:
    - perl
    - perl-app-cpanminus
```

```
    - perl-encode-locale
    - perl-module-build
  run:
    - perl
    - perl-encode-locale

test:
  imports:
    - LWP::Simple

about:
  home: https://metacpan.org/pod/LWP::Simple
  license: Perl
  summary: simple procedural interface to LWP
```

CHAPTER 291

perl-math-cdf

291.1 Summary

Generate probabilities and quantiles from several statistical probability functions

291.2 Home

http://metacpan.org/pod/Math-CDF

291.3 Versions

- 0.1

291.4 License

Public Domain

291.5 Meta

```
package:
  name: perl-math-cdf
  version: "0.1"

source:
  fn: Math-CDF-0.1.tar.gz
  url: http://cpan.metacpan.org/authors/id/C/CA/CALLAHAN/Math-CDF-0.1.tar.gz
  md5: 7866c7b6b9d27f0ce4b7637334478ab7

build:
  number: 0

requirements:
  build:
    - perl
```

```
    - gcc

  run:
    - perl

test:
  # Perl 'use' tests
  imports:
    - Math::CDF

about:
  home: http://metacpan.org/pod/Math-CDF
  license: Public Domain
  summary: 'Generate probabilities and quantiles from several statistical probability functions'
```

CHAPTER 292

perl-module-build

292.1 Summary

Build and install Perl modules

292.2 Home

http://metacpan.org/pod/Module-Build

292.3 Versions

- 0.4214

292.4 License

perl_5

292.5 Meta

```
package:
  name: perl-module-build
  version: "0.4214"

source:
  fn: Module-Build-0.4214.tar.gz
  url: https://cpan.metacpan.org/authors/id/L/LE/LEONT/Module-Build-0.4214.tar.gz
  md5: 7b7ca5a47bef48c50c8b5906ca3ac7fb
#  patches:
   # List any patch files here
   # - fix.patch

# build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
```

```
  # number: 1

requirements:
  build:
    - perl >=5.22.0

  run:
    - perl >=5.22.0

test:
  # Perl 'use' tests
  imports:
    - Module::Build
    - Module::Build::Base
    - Module::Build::Compat
    - Module::Build::Config
    - Module::Build::Cookbook
    - Module::Build::Dumper
    - Module::Build::Notes
    - Module::Build::PPMMaker
    - Module::Build::Platform::Default
    - Module::Build::Platform::MacOS
    - Module::Build::Platform::Unix
    - Module::Build::Platform::VMS
    - Module::Build::Platform::VOS
    - Module::Build::Platform::Windows
    - Module::Build::Platform::aix
    - Module::Build::Platform::cygwin
    - Module::Build::Platform::darwin
    - Module::Build::Platform::os2
    - Module::Build::PodParser

  # You can also put a file called run_test.pl (or run_test.py) in the recipe
  # that will be run at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: http://metacpan.org/pod/Module-Build
  license: perl_5
  summary: 'Build and install Perl modules'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 293

perl-pcap

293.1 Summary

NGS reference implementations and helper code for the IGCG/TCGA Pan-Cancer Analysis Project

293.2 Home

https://github.com/ICGC-TCGA-PanCancer/PCAP-core

293.3 Versions

- 1.11.1

293.4 License

GPLv3

293.5 Meta

```
package:
  name: perl-pcap
  version: '1.11.1'

source:
  fn: PCAP-v1.11.1.tar.gz
  url: https://github.com/ICGC-TCGA-PanCancer/PCAP-core/archive/v1.11.1.tar.gz

build:
  number: 0

requirements:
  build:
    - gcc
    - perl
```

```
    - perl-app-cpanminus
    - perl-file-sharedir-install
    - perl-module-build
    - perl-bio-db-sam
    - perl-bioperl
    - perl-gd
    - perl-ipc-system-simple
    - perl-sanger-cgp-vcf
    - perl-encode-locale
    - perl-lwp-simple
    - perl-xml-parser
  run:
    - perl
    - perl-bio-db-sam
    - perl-bioperl
    - perl-encode-locale
    - perl-gd
    - perl-ipc-system-simple
    - perl-sanger-cgp-vcf
    - perl-encode-locale
    - perl-lwp-simple
    - perl-xml-parser

test:
  imports:
    - PCAP

about:
  home: https://github.com/ICGC-TCGA-PanCancer/PCAP-core
  license: GPLv3
  summary: NGS reference implementations and helper code for the IGCG/TCGA Pan-Cancer Analysis Projec
```

CHAPTER 294

perl-pdf-api2

294.1 Summary

Facilitates the creation and modification of PDF files

294.2 Home

https://metacpan.org/pod/PDF::API2

294.3 Versions

- 2.025

294.4 License

Perl

294.5 Meta

```
package:
  name: perl-pdf-api2
  version: '2.025'

source:
  fn: PDF-API2-2.025.tar.gz
  url: https://cpan.metacpan.org/authors/id/S/SS/SSIMMS/PDF-API2-2.025.tar.gz

build:
  number: 0

requirements:
  build:
    - perl
    - perl-app-cpanminus
```

```
    - perl-module-build
  run:
    - perl

test:
  imports:
    - PDF::API2

about:
  home: https://metacpan.org/pod/PDF::API2
  license: Perl
  summary: Facilitates the creation and modification of PDF files
```

CHAPTER 295

perl-sanger-allelecount

295.1 Summary

Support code for NGS copy number algorithm

295.2 Home

https://github.com/cancerit/alleleCount

295.3 Versions

- 2.1.2

295.4 License

GPLv3

295.5 Meta

```
package:
  name: perl-sanger-allelecount
  version: '2.1.2'

source:
  fn: alleleCount-v2.1.2.tar.gz
  url: https://github.com/cancerit/alleleCount/archive/v2.1.2.tar.gz

build:
  number: 0

requirements:
  build:
    - gcc
    - perl
```

```
    - perl-app-cpanminus
    - perl-module-build
    - perl-sanger-cgp-vcf
    - perl-bio-db-sam
    - perl-bioperl
  run:
    - perl
    - perl-sanger-cgp-vcf
    - perl-bio-db-sam
    - perl-bioperl

test:
  imports:
    - Sanger::CGP::AlleleCount

about:
  home: https://github.com/cancerit/alleleCount
  license: GPLv3
  summary: Support code for NGS copy number algorithm
```

CHAPTER 296

perl-sanger-cgp-vcf

296.1 Summary

a set of common perl utilities for generating consistent Vcf headers

296.2 Home

https://github.com/cancerit/cgpVcf

296.3 Versions

- 1.3.1

296.4 License

GPLv3

296.5 Meta

```
package:
  name: perl-sanger-cgp-vcf
  version: '1.3.1'

source:
  fn: cgpVcf-v1.3.1.tar.gz
  url: https://github.com/cancerit/cgpVcf/archive/v1.3.1.tar.gz

build:
  number: 0

requirements:
  build:
    - gcc
    - perl
```

```
    - perl-app-cpanminus
    - perl-module-build
    - perl-data-uuid
    - perl-vcftools-vcf
  run:
    - perl
    - perl-data-uuid
    - perl-vcftools-vcf

test:
  imports:
    - Sanger::CGP::Vcf

about:
  home: https://github.com/cancerit/cgpVcf
  license: GPLv3
  summary: a set of common perl utilities for generating consistent Vcf headers
```

CHAPTER 297

perl-scalar-list-utils

297.1 Summary

Common Scalar and List utility subroutines

297.2 Home

http://metacpan.org/pod/Scalar-List-Utils

297.3 Versions

- 1.42

297.4 License

perl_5

297.5 Meta

```
package:
  name: perl-scalar-list-utils
  version: "1.42"

source:
  fn: Scalar-List-Utils-1.42.tar.gz
  url: https://cpan.metacpan.org/authors/id/P/PE/PEVANS/Scalar-List-Utils-1.42.tar.gz
  md5: a76768c6e0f92eefb6d4b3b779469c3d
#  patches:
   # List any patch files here
   # - fix.patch

# build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
```

```
  # number: 1

requirements:
  build:
    - perl

  run:
    - perl

test:
  # Perl 'use' tests
  imports:
    - Scalar::Util

about:
  home: http://metacpan.org/pod/Scalar-List-Utils
  license: perl_5
  summary: 'Common Scalar and List utility subroutines'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 298

perl-set-intervaltree

298.1 Summary

An interval tree implementation in PERL.

298.2 Home

https://metacpan.org/pod/Set::IntervalTree

298.3 Versions

- 0.1

298.4 License

perl_5

298.5 Meta

```
package:
  name: perl-set-intervaltree
  version: 0.10
source:
  fn: Set-IntervalTree-0.10.tar.gz
  url: http://search.cpan.org/CPAN/authors/id/B/BE/BENBOOTH/Set-IntervalTree-0.10.tar.gz
build:
  number: 1
requirements:
  build:
    - perl
  run:
    - perl
test:
  imports:
```

```
    - Set::IntervalTree
about:
  home: https://metacpan.org/pod/Set::IntervalTree
  license: perl_5
  summary: An interval tree implementation in PERL.
```

CHAPTER 299

perl-statistics-descriptive

299.1 Summary

Module of basic descriptive statistical functions

299.2 Home

https://metacpan.org/pod/Statistics::Descriptive

299.3 Versions

- 3.0609

299.4 License

Perl

299.5 Meta

```
package:
  name: perl-statistics-descriptive
  version: '3.0609'

source:
  fn: Statistics-Descriptive-3.0609.tar.gz
  url: https://cpan.metacpan.org/authors/id/S/SH/SHLOMIF/Statistics-Descriptive-3.0609.tar.gz

build:
  number: 0

requirements:
  build:
    - perl
    - perl-app-cpanminus
```

```
    - perl-module-build
  run:
    - perl

about:
  home: https://metacpan.org/pod/Statistics::Descriptive
  license: Perl
  summary: Module of basic descriptive statistical functions
```

CHAPTER 300

perl-sub-uplevel

300.1 Summary

apparently run a function in a higher stack frame

300.2 Home

https://github.com/dagolden/Sub-Uplevel

300.3 Versions

- 0.25

300.4 License

perl_5

300.5 Meta

```
package:
  name: perl-sub-uplevel
  version: "0.25"

source:
  fn: Sub-Uplevel-0.25.tar.gz
  url: https://cpan.metacpan.org/authors/id/D/DA/DAGOLDEN/Sub-Uplevel-0.25.tar.gz
  md5: 5d0752dbfa94d0c91b25a264f47f5675

build:
  number: 0

requirements:
  build:
    - perl
```

```
  run:
    - perl

test:
  # Perl 'use' tests
  imports:
    - Sub::Uplevel

about:
  home: https://github.com/dagolden/Sub-Uplevel
  license: perl_5
  summary: 'apparently run a function in a higher stack frame'
```

CHAPTER 301

perl-threaded

301.1 Summary

The Perl language.

301.2 Home

http://www.perl.org/

301.3 Versions

- 5.22.0

301.4 License

Perl

301.5 Meta

```
# Derived from the dan_blanchard channel.
package:
  name: perl-threaded
  version: 5.22.0

source:
  fn: perl-5.22.0.tar.gz
  url: http://www.cpan.org/src/5.0/perl-5.22.0.tar.gz
  md5: e32cb6a8dda0084f2a43dac76318d68d

build:
  number: 8

test:
  commands:
```

```
    - perl --help > /dev/null

about:
  home: http://www.perl.org/
  license: Perl
  summary: The Perl language.
```

CHAPTER 302

perl-time-hires

302.1 Summary

High resolution alarm, sleep, gettimeofday, interval timers

302.2 Home

https://metacpan.org/pod/Time::HiRes

302.3 Versions

- 1.9728

302.4 License

Perl

302.5 Meta

```
package:
  name: perl-time-hires
  version: '1.9728'

source:
  fn: Time-HiRes-1.9728.tar.gz
  url: https://cpan.metacpan.org/authors/id/R/RJ/RJBS/Time-HiRes-1.9728.tar.gz

build:
  number: 0

requirements:
  build:
    - perl
    - perl-app-cpanminus
```

```
    - perl-module-build
  run:
    - perl

test:
  imports:
    - Time::HiRes

about:
  home: https://metacpan.org/pod/Time::HiRes
  license: Perl
  summary: High resolution alarm, sleep, gettimeofday, interval timers
```

CHAPTER 303

perl-uri

303.1 Summary

Uniform Resource Identifiers (absolute and relative)

303.2 Home

http://metacpan.org/pod/URI

303.3 Versions

- 1.69

303.4 License

perl_5

303.5 Meta

```
package:
  name: perl-uri
  version: "1.69"

source:
  fn: URI-1.69.tar.gz
  url: https://cpan.metacpan.org/authors/id/E/ET/ETHER/URI-1.69.tar.gz
  md5: 3c56aee0300bce5a440ccbd558277ea0
#  patches:
   # List any patch files here
   # - fix.patch

# build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
```

```
  # number: 1

requirements:
  build:
    - perl
    - perl-scalar-list-utils

  run:
    - perl
    - perl-scalar-list-utils

test:
  imports:
    - URI

about:
  home: http://metacpan.org/pod/URI
  license: perl_5
  summary: 'Uniform Resource Identifiers (absolute and relative)'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 304

perl-vcftools-vcf

304.1 Summary

cpanm ready distribution of VCFtools Perl libraries

304.2 Home

https://github.com/vcftools/vcftools

304.3 Versions

- 0.953

304.4 License

LGPLv3

304.5 Meta

```
package:
  name: perl-vcftools-vcf
  version: '0.953'

source:
  fn: vcftools-0.1.14.tar.gz
  url: https://github.com/vcftools/vcftools/releases/download/v0.1.14/vcftools-0.1.14.tar.gz

build:
  number: 1

requirements:
  build:
    - perl
    - perl-app-cpanminus
```

```
    - perl-module-build
  run:
    - perl

test:
  imports:
    - Vcf

about:
  home: https://github.com/vcftools/vcftools
  license: LGPLv3
  summary: cpanm ready distribution of VCFtools Perl libraries
```

CHAPTER 305

perl-xml-parser

305.1 Summary

A perl module for parsing XML documents

305.2 Home

https://metacpan.org/pod/XML::Parser

305.3 Versions

- 2.44

305.4 License

Perl

305.5 Meta

```
package:
  name: perl-xml-parser
  version: '2.44'

source:
  fn: XML-Parser-2.44.tar.gz
  url: https://cpan.metacpan.org/authors/id/T/TO/TODDR/XML-Parser-2.44.tar.gz

build:
  number: 0

requirements:
  build:
    - gcc
    - perl
```

```
    - perl-app-cpanminus
    - perl-module-build
    - expat
  run:
    - perl
    - expat

test:
  imports:
    - XML::Parser

about:
  home: https://metacpan.org/pod/XML::Parser
  license: Perl
  summary: A perl module for parsing XML documents
```

CHAPTER 306

perl

306.1 Summary

The Perl language.

306.2 Home

http://www.perl.org/

306.3 Versions

- 5.22.0
- 5.18.1

306.4 License

Perl

306.5 Meta

```
# Derived from the dan_blanchard channel.
package:
  name: perl
  version: 5.22.0

source:
  fn: perl-5.22.0.tar.gz
  url: http://www.cpan.org/src/5.0/perl-5.22.0.tar.gz
  md5: e32cb6a8dda0084f2a43dac76318d68d

build:
  number: 9
```

```
requirements:
  build:
    - gcc

test:
  commands:
    - perl --help > /dev/null

about:
  home: http://www.perl.org/
  license: Perl
  summary: The Perl language.
```

CHAPTER 307

phonenumbers

307.1 Summary

Python version of Google's common library for parsing, formatting, storing and validating international phone numbers.

307.2 Home

https://github.com/daviddrysdale/python-phonenumbers

307.3 Versions

- 7.2.4

307.4 License

Apache Software License

307.5 Meta

```
package:
  name: phonenumbers
  version: "7.2.4"

source:
  fn: phonenumbers-7.2.4.tar.gz
  url: https://pypi.python.org/packages/source/p/phonenumbers/phonenumbers-7.2.4.tar.gz
  md5: 1a8dfeb4109189a580a17258ec259b4c

requirements:
  build:
    - python
    - setuptools
```

```
  run:
    - python

test:
  imports:
    - phonenumbers
    - phonenumbers.carrierdata
    - phonenumbers.data
    - phonenumbers.geodata
    - phonenumbers.shortdata
    - phonenumbers.tzdata

about:
  home: https://github.com/daviddrysdale/python-phonenumbers
  license: Apache Software License
  summary: "Python version of Google's common library for parsing, formatting, storing and validatin
```

CHAPTER 308

phylowgs

308.1 Summary

Application for inferring subclonal composition and evolution from whole-genome sequencing data

308.2 Home

https://github.com/morrislab/phylowgs

308.3 Versions

- 20150714

308.4 License

GPLv3

308.5 Meta

```
package:
  name: phylowgs
  version: '20150714'

source:
  fn: phylowgs-9a108f4.tar.gz
  url: https://github.com/morrislab/phylowgs/archive/9a108f4.tar.gz

build:
  number: 1
  skip: true # [not py27]

requirements:
  build:
    - python
```

```
    - setuptools
    - numpy
    - scipy
    - ete2
    - gsl

  run:
    - python
    - setuptools
    - numpy
    - scipy
    - ete2
    - gsl

#test:
#  commands:
#    - evolve.py -h

about:
  home: https://github.com/morrislab/phylowgs
  license: GPLv3
  summary:  Application for inferring subclonal composition and evolution from whole-genome sequencin
```

CHAPTER 309

picard

309.1 Summary

Java tools for working with NGS data in the BAM format

309.2 Home

http://broadinstitute.github.io/picard/

309.3 Versions

- 1.126

309.4 License

MIT

309.5 Meta

```
# Migrated from BioBuilds recipe
# https://anaconda.org/BioBuilds/picard

package:
  name: picard
  version: "1.126"

source:
  fn: picard-tools-1.126.zip
  url: https://github.com/broadinstitute/picard/releases/download/1.126/picard-tools-1.126.zip

build:
  number: 3

requirements:
```

```
  run:
    - java-jdk

test:
  commands:
    - "picard 2>&1 | grep 'USAGE: PicardCommandLine'"

about:
  home: "http://broadinstitute.github.io/picard/"
  license: MIT
  summary: "Java tools for working with NGS data in the BAM format"
```

CHAPTER 310

pindel

310.1 Summary

Pindel can detect breakpoints of large deletions, medium sized insertions, inversions, tandem duplications and other structural variants at single-based resolution from next-gen sequence data

310.2 Home

http://gmt.genome.wustl.edu/packages/pindel/index.html

310.3 Versions

- 0.2.5b8

310.4 License

GPLv3

310.5 Meta

```
package:
  name: pindel
  version: '0.2.5b8'
build:
  number: 0
source:
  fn: pindel-0.2.5b8.tar.gz
  url: https://github.com/genome/pindel/archive/v0.2.5b8.tar.gz

requirements:
  build:
    - htslib
  run:
    - htslib
```

```
test:
  commands:
    - "pindel -h 2>&1 | grep 'Pindel version'"
    - "pindel2vcf  --help | grep Example:"

about:
  home: http://gmt.genome.wustl.edu/packages/pindel/index.html
  license: GPLv3
  summary: Pindel can detect breakpoints of large deletions, medium sized insertions, inversions, tar
```

CHAPTER 311

platypus-variant

311.1 Summary

A Haplotype-Based Variant Caller For Next Generation Sequence Data

311.2 Home

http://www.well.ox.ac.uk/platypus

311.3 Versions

- 0.8.1

311.4 License

GPLv3

311.5 Meta

```
about:
  home: http://www.well.ox.ac.uk/platypus
  license: GPLv3
  summary: A Haplotype-Based Variant Caller For Next Generation Sequence Data
package:
  name: platypus-variant
  version: '0.8.1'
build:
  number: 0
  skip: True # [not py27]
source:
  fn: Platypus_0.8.1.tgz
  url: https://github.com/andyrimmer/Platypus/raw/master/release/AllReleases/Platypus_0.8.1.tgz
requirements:
  build:
```

```
    - python
    - htslib
  run:
    - python
    - htslib
test:
   commands:
     - platypus callVariants -h
```

CHAPTER 312

popt

312.1 Summary

312.2 Home

https://fedorahosted.org/newt/

312.3 Versions

- 1.16

312.4 License

GPL

312.5 Meta

```
package:
  name: popt
  version: 1.16

source:
  fn: popt-1.16.tar.gz
  url: ftp://anduin.linuxfromscratch.org/BLFS/popt/popt-1.16.tar.gz
  md5: 3743beefa3dd6247a73f8f7a32c14c33

# Tests included in build.sh
# test:
#   commands:
#     - "ldconfig -p | grep libpopt"

about:
  home: https://fedorahosted.org/newt/
  license: GPL
```

CHAPTER 313

poretools

313.1 Summary

poretools: a toolkit for working with nanopore sequencing data from Oxford Nanopore

313.2 Home

http://poretools.readthedocs.org/en/latest/

313.3 Versions

- 0.5.1

313.4 License

313.5 Meta

```
package:
    name: poretools
    version: "0.5.1"
source:
    git_url: https://github.com/arq5x/poretools

requirements:
    build:
        - python
        - watchdog >=0.8.3
        - rpy2 >=2.4.2
        - h5py >=2.0

    run:
        - python
        - hdf5 >=1.8.7
        - r >=3.0.0
        - rpy2 >=2.4.2
```

```
        - h5py >=2.0
        - watchdog >=0.8.3
        - qcli >=0.1.1

build:
    skip: True # [not py27]

test:
    commands:
        - poretools -v

about:
    home: http://poretools.readthedocs.org/en/latest/
    summary: "poretools: a toolkit for working with nanopore sequencing data from Oxford Nanopore"
```

CHAPTER 314

prinseq

314.1 Summary

PRINSEQ can be used to filter, reformat, or trim your genomic and metagenomic sequence data

314.2 Home

http://prinseq.sourceforge.net/

314.3 Versions

- 0.20.4

314.4 License

GPLv3

314.5 Meta

```
about:
    home: 'http://prinseq.sourceforge.net/'
    license: "GPLv3"
    summary: "PRINSEQ can be used to filter, reformat, or trim your genomic and metagenomic sequence
package:
  name: prinseq
  version: '0.20.4'
source:
  fn: prinseq-lite-0.20.4.tar.gz
  md5: 3be1a572073ebbbecfeba42a42853ff5
  url: http://iweb.dl.sourceforge.net/project/prinseq/standalone/prinseq-lite-0.20.4.tar.gz
requirements:
  run:
      - perl # [not osx]
test:
```

```
    commands:
        - prinseq-lite.pl -version
```

CHAPTER 315

prodigal

315.1 Summary

Prodigal (Prokaryotic Dynamic Programming Genefinding Algorithm) is a microbial (bacterial and archaeal) gene finding program

315.2 Home

http://prodigal.ornl.gov/

315.3 Versions

- 2.6.2

315.4 License

GPL v3

315.5 Meta

```
package:
  name: prodigal
  version: "2.6.2"
source:
  fn: Prodigal-2.6.2.zip
  url: https://github.com/hyattpd/Prodigal/archive/v2.6.2.zip
  sha256: 8fb270872a144bbf60dbf4035339183c0771379ecc8749f494993ce9c7235306
build:
    number: 2
requirements:
  build:
  run:
test:
  commands:
```

```
    - prodigal
about:
  home: http://prodigal.ornl.gov/
  license: GPL v3
  summary: Prodigal (Prokaryotic Dynamic Programming Genefinding Algorithm) is a microbial (bacterial
```

CHAPTER 316

protrac

316.1 Summary

piRNA detection

316.2 Home

http://www.smallrnagroup.uni-mainz.de/software.html

316.3 Versions

- 2.1

316.4 License

CC BY-NC 2.0

316.5 Meta

```
package:
  name: protrac
  version: '2.1'

source:
  fn: proTRAC_2.1.pl
  url: http://www.smallrnagroup.uni-mainz.de/software/proTRAC_2.1.pl

build:
  number: 0

requirements:
  run:
    - perl >=5.22.0
    - perl-gd
```

```
test:
  commands:
    - proTRAC_2.1.pl

about:
  home: http://www.smallrnagroup.uni-mainz.de/software.html
  license: CC BY-NC 2.0
  summary: piRNA detection
```

CHAPTER 317

py-graphviz

317.1 Summary

Simple Python interface for Graphviz

317.2 Home

http://github.com/xflr6/graphviz

317.3 Versions

- 0.4.8

317.4 License

MIT License

317.5 Meta

```
package:
  name: py-graphviz
  version: "0.4.8"

source:
  fn: graphviz-0.4.8.zip
  url: https://pypi.python.org/packages/source/g/graphviz/graphviz-0.4.8.zip
  md5: 9a36287847b1eb737b7ef4a519ad72dd
#  patches:
   # List any patch files here
   # - fix.patch

# build:
  # noarch_python: True
  # preserve_egg_dir: True
```

```
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - graphviz = graphviz:main
    #
    # Would create an entry point called graphviz that calls graphviz.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools

  run:
    - python

test:
  # Python imports
  imports:
    - graphviz

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: http://github.com/xflr6/graphviz
  license: MIT License
  summary: 'Simple Python interface for Graphviz'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 318

pyaml

318.1 Summary

PyYAML-based module to produce pretty and readable YAML-serialized data

318.2 Home

https://github.com/mk-fg/pretty-yaml

318.3 Versions

- 15.8.2

318.4 License

WTFPL

318.5 Meta

```
package:
  name: pyaml
  version: "15.8.2"

source:
  fn: pyaml-15.8.2.tar.gz
  url: https://pypi.python.org/packages/source/p/pyaml/pyaml-15.8.2.tar.gz
  md5: e3a39e02dffaf5f6efa8ccdd22745739
#  patches:
   # List any patch files here
   # - fix.patch

# build:
  # noarch_python: True
  # preserve_egg_dir: True
```

```
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - pyaml = pyaml:main
    #
    # Would create an entry point called pyaml that calls pyaml.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools
    - pyyaml

  run:
    - python
    - pyyaml

test:
  # Python imports
  imports:
    - pyaml
    - pyaml.tests

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: https://github.com/mk-fg/pretty-yaml
  license: WTFPL
  summary: 'PyYAML-based module to produce pretty and readable YAML-serialized data'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 319

pyasn1-modules

319.1 Summary

a small but growing collection of ASN.1 data structures expressed in Python terms using pyasn1 data model

319.2 Home

https://pypi.python.org/pypi/pyasn1-modules

319.3 Versions

- 0.0.8

319.4 License

BSD

319.5 Meta

```
package:
  name: pyasn1-modules
  version: '0.0.8'

source:
  fn: pyasn1-modules-0.0.8.tar.gz
  url: https://pypi.python.org/packages/source/p/pyasn1-modules/pyasn1-modules-0.0.8.tar.gz
  md5: 178129bc7fbf07215c25230c5f053f81

build:
  number: 0

requirements:
  build:
    - python
```

```
    - setuptools
    - pyasn1

  run:
    - python
    - pyasn1

test:
  imports:
    - pyasn1_modules

about:
  home: https://pypi.python.org/pypi/pyasn1-modules
  license: BSD
  summary: a small but growing collection of ASN.1 data structures expressed in Python terms using py
```

CHAPTER 320

pybedtools

320.1 Summary

Wraps BEDTools for use in Python and adds many additional features.

320.2 Home

https://github.com/daler/pybedtools

320.3 Versions

- 0.7.5

320.4 License

MIT

320.5 Meta

```
package:
  name: pybedtools
  version: '0.7.5'

source:
  url: https://pypi.python.org/packages/source/p/pybedtools/pybedtools-0.7.5.tar.gz
  fn: pybedtools-0.7.5.tar.gz
  md5: 3f150cd4f3ba66c315db3447a847ca37

build:
  number: 0

requirements:
  build:
    - python
```

```
    - six
    - pysam >=0.8.1
    - setuptools
    - pandas
    - cython

  run:
    - python
    - six
    - pysam >=0.8.1
    - pandas

test:
  imports:
    - pybedtools

about:
  home: https://github.com/daler/pybedtools
  license: MIT
  summary: Wraps BEDTools for use in Python and adds many additional features.
```

CHAPTER 321

pybigwig

321.1 Summary

A python extension written in C for quick access to bigWig files.

321.2 Home

https://github.com/dpryan79/pyBigWig

321.3 Versions

- 0.2.4
- 0.1.11

321.4 License

MIT

321.5 Meta

```
package:
  name: pybigwig
  version: '0.2.4'

source:
  #git_url: https://github.com/dpryan79/pyBigWig
  fn: pyBigWig-0.2.4.tar.gz
  sha256: e6515d3a2a127d1731fea83ebd81ba215ab9543f956ed0209e883c5d18dab73d
  url: https://pypi.python.org/packages/source/p/pyBigWig/pyBigWig-0.2.4.tar.gz

build:
  number: 0
```

```
requirements:
  build:
    - python
    - curl
  run:
    - python
    - curl
test:
  imports:
    - pyBigWig

  commands:
    - nosetests pyBigWigTest -s -v

  requires:
    - nose

about:
  home: https://github.com/dpryan79/pyBigWig
  license: MIT
  summary: A python extension written in C for quick access to bigWig files.
```

CHAPTER 322

pycli

322.1 Summary

Simple, object-oriented approach to Python CLI apps

322.2 Home

http://packages.python.org/pyCLI/

322.3 Versions

- 2.0.3

322.4 License

MIT

322.5 Meta

```
package:
  name: pycli
  version: "2.0.3"

source:
  fn: pyCLI-2.0.3.tar.gz
  url: https://pypi.python.org/packages/source/p/pyCLI/pyCLI-2.0.3.tar.gz
  md5: 89c487e7c8068ce05d63394d2ae7ebad

build:
  number: 0

requirements:
  build:
    - python
```

```
    - setuptools

  run:
    - python

test:
  # Python imports
  imports:
    - cli
    - cli._ext
    - cli.tests
    - cli.tests.functional

about:
  home: http://packages.python.org/pyCLI/
  license: MIT
  summary: 'Simple, object-oriented approach to Python CLI apps'
```

CHAPTER 323

pyfaidx

323.1 Summary

pyfaidx: efficient pythonic random access to fasta subsequences

323.2 Home

http://mattshirley.com

323.3 Versions

- 0.4.4

323.4 License

MIT License

323.5 Meta

```
package:
  name: pyfaidx
  version: "0.4.4"

source:
  fn: pyfaidx-0.4.4.tar.gz
  url: https://pypi.python.org/packages/source/p/pyfaidx/pyfaidx-0.4.4.tar.gz
  md5: b5fa82a27da4d8314a65ea8ab5b55cfd
#  patches:
   # List any patch files here
   # - fix.patch

build:
  # noarch_python: True
  # preserve_egg_dir: True
```

```
  entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - pyfaidx = pyfaidx:main
    #
    # Would create an entry point called pyfaidx that calls pyfaidx.main()

    - faidx = pyfaidx.cli:main

  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools
    - six

  run:
    - python
    - six

test:
  # Python imports
  imports:
    - pyfaidx

  commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.

    - faidx --help

  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: http://mattshirley.com
  license: MIT License
  summary: 'pyfaidx: efficient pythonic random access to fasta subsequences'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 324

pyfastaq

324.1 Summary

Script to manipulate FASTA and FASTQ files, plus API for developers

324.2 Home

https://github.com/sanger-pathogens/Fastaq

324.3 Versions

- 3.11.0

324.4 License

GNU General Public License v3 (GPLv3)

324.5 Meta

```
package:
  name: pyfastaq
  version: "3.11.0"

source:
  fn: pyfastaq-3.11.0.tar.gz
  url: https://pypi.python.org/packages/source/p/pyfastaq/pyfastaq-3.11.0.tar.gz
  md5: 9689ca1e1e3777fea7f5e830fa4c49aa
#  patches:
   # List any patch files here
   # - fix.patch

build:
  skip: True # [py27]
  # noarch_python: True
```

```
  # preserve_egg_dir: True
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - pyfastaq = pyfastaq:main
    #
    # Would create an entry point called pyfastaq that calls pyfastaq.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools

  run:
    - python

test:
  # Python imports
  imports:
    - pyfastaq
    - pyfastaq.runners

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  requires:
    - nose >=1.3
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: https://github.com/sanger-pathogens/Fastaq
  license: GNU General Public License v3 (GPLv3)
  summary: 'Script to manipulate FASTA and FASTQ files, plus API for developers'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 325

pyloh

325.1 Summary

Deconvolving tumor purity and ploidy by integrating copy number alterations and loss of heterozygosity

325.2 Home

https://github.com/uci-cbcl/PyLOH

325.3 Versions

- 1.4.1

325.4 License

GPL

325.5 Meta

```
package:
  name: pyloh
  version: '1.4.1'

source:
  fn: pyloh-1.4.1.tar.gz
  url: https://github.com/uci-cbcl/PyLOH/archive/1.4.1.tar.gz

build:
  number: 1

requirements:
  build:
    - python
    - setuptools
```

```
  run:
    - python
    - numpy
    - scipy
    - matplotlib
    - pysam

test:
  imports:
    - pyloh

about:
  home: https://github.com/uci-cbcl/PyLOH
  license: GPL
  summary: Deconvolving tumor purity and ploidy by integrating copy number alterations and loss of he
```

CHAPTER 326

pymummer

326.1 Summary

Wrapper for MUMmer

326.2 Home

https://github.com/sanger-pathogens/pymummer

326.3 Versions

- 0.6.1

326.4 License

GNU General Public License v3 (GPLv3)

326.5 Meta

```
package:
  name: pymummer
  version: "0.6.1"

source:
  fn: pymummer-0.6.1.tar.gz
  url: https://pypi.python.org/packages/source/p/pymummer/pymummer-0.6.1.tar.gz
  md5: 8fad530faa57f40ea82b9bb5dbf54892
#  patches:
   # List any patch files here
   # - fix.patch

build:
  skip: True # [py27]
  # noarch_python: True
```

```
  # preserve_egg_dir: True
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - pymummer = pymummer:main
    #
    # Would create an entry point called pymummer that calls pymummer.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools
    - pyfastaq >=3.10.0
    - mummer

  run:
    - python
    - pyfastaq >=3.10.0
    - mummer

test:
  # Python imports
  imports:
    - pymummer

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  requires:
    - nose >=1.3
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: https://github.com/sanger-pathogens/pymummer
  license: GNU General Public License v3 (GPLv3)
  summary: 'Wrapper for MUMmer'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 327

pynast

327.1 Summary

The Python Nearest Alignment Space Termination tool

327.2 Home

http://qiime.org/pynast

327.3 Versions

- 1.2.2

327.4 License

BSD License

327.5 Meta

```
package:
  name: pynast
  version: "1.2.2"

source:
  fn: pynast-1.2.2.tar.gz
  url: https://pypi.python.org/packages/source/p/pynast/pynast-1.2.2.tar.gz
  md5: 6f1744d8d3f333eb2dbe81026d4dcb1b

build:
   number: 0
   skip: True [py3k]

requirements:
  build:
```

```
    - python
    - numpy >=1.5.1
    - cogent >=1.5.3

  run:
    - python
    - numpy >=1.5.1
    - cogent >=1.5.3

test:
  # Python imports
  imports:
    - pynast

about:
  home: http://qiime.org/pynast
  license: BSD License
  summary: 'The Python Nearest Alignment Space Termination tool'
```

CHAPTER 328

pyomo

328.1 Summary

Pyomo: Python Optimization Modeling Objects

328.2 Home

http://pyomo.org

328.3 Versions

- 4.1.10527

328.4 License

BSD License

328.5 Meta

```
# Copied from https://anaconda.org/timcera/pyomo/

package:
  name: pyomo
  version: "4.1.10527"

source:
  fn: Pyomo-4.1.10527.tar.gz
  url: https://pypi.python.org/packages/source/P/Pyomo/Pyomo-4.1.10527.tar.gz
  md5: c7c6b933edd5fd667cafcffa04da5b82

build:
  skip: True # [not py27]

requirements:
```

```
  build:
    #- suds-jurko
    #- pyro4
    - pyutilib
    - python
    - setuptools
    - ply
    - nose
    - six >=1.6.1

  run:
    #- suds-jurko
    #- pyro4
    - pyutilib
    - python
    - ply
    - nose
    - six >=1.6.1

test:
  # Python imports
  imports:
    - pyomo
    - pyomo.bilevel
    - pyomo.bilevel.plugins
    - pyomo.bilevel.tests
    - pyomo.checker
    - pyomo.checker.plugins
    - pyomo.checker.plugins.checkers
    - pyomo.checker.plugins.checkers.model
    - pyomo.checker.plugins.checkers.py3k
    - pyomo.checker.plugins.checkers.sample
    - pyomo.checker.tests
    - pyomo.core
    - pyomo.core.base
    - pyomo.core.data
    - pyomo.core.plugins
    - pyomo.core.plugins.data
    - pyomo.core.plugins.transform
    - pyomo.core.preprocess
    - pyomo.core.tests
    - pyomo.core.tests.data
    - pyomo.core.tests.diet
    - pyomo.core.tests.examples
    - pyomo.core.tests.transform
    - pyomo.core.tests.unit
    - pyomo.dae
    - pyomo.dae.plugins
    - pyomo.dae.tests
    - pyomo.data
    - pyomo.environ
    - pyomo.environ.tests
    - pyomo.gdp
    - pyomo.gdp.plugins
    - pyomo.gdp.tests
    - pyomo.mpec
    - pyomo.mpec.plugins
    - pyomo.mpec.tests
```

```
    - pyomo.neos
    - pyomo.neos.plugins
    - pyomo.openopt
    - pyomo.openopt.plugins
    - pyomo.openopt.tests
    - pyomo.opt
    - pyomo.opt.base
    - pyomo.opt.blackbox
    - pyomo.opt.parallel
    - pyomo.opt.plugins
    - pyomo.opt.problem
    - pyomo.opt.results
    - pyomo.opt.solver
    - pyomo.opt.testing
    - pyomo.opt.tests
    - pyomo.opt.tests.base
    - pyomo.opt.tests.blackbox
    - pyomo.os
    - pyomo.os.plugins
    - pyomo.os.tests
    - pyomo.pysp
    - pyomo.pysp.plugins
    - pyomo.pysp.scenariotree
    - pyomo.pysp.tests
    - pyomo.pysp.tests.examples
    - pyomo.pysp.tests.unit
    - pyomo.pysp.util
    - pyomo.repn
    - pyomo.repn.plugins
    - pyomo.repn.plugins.ampl
    - pyomo.repn.tests
    - pyomo.repn.tests.ampl
    - pyomo.scripting
    - pyomo.scripting.plugins
    - pyomo.solvers
    - pyomo.solvers.plugins
    - pyomo.solvers.plugins.converter
    - pyomo.solvers.plugins.smanager
    - pyomo.solvers.plugins.solvers
    - pyomo.solvers.plugins.testdriver
    - pyomo.solvers.tests
    - pyomo.solvers.tests.io
    - pyomo.solvers.tests.io.fd
    - pyomo.solvers.tests.mip
    - pyomo.solvers.tests.pickling
    - pyomo.util
    - pyomo.util.tests
    - pyomo.version
    - pyomo.version.tests

about:
  home: http://pyomo.org
  license: BSD License
  summary: 'Pyomo: Python Optimization Modeling Objects'
```

CHAPTER 329

pyopt

329.1 Summary

329.2 Home

http://www.pyopt.org/index.html

329.3 Versions

- 1.2.0

329.4 License

LGPLv3

329.5 Meta

```
package:
    name: pyopt
    version: 1.2.0

source:
    fn: pyOpt-1.2.0.tar.gz
    url: http://www.pyopt.org/_downloads/pyOpt-1.2.0.tar.gz
    md5: 84f7574cb40919009312ad52d30109db
build:
    number: 0
    skip: True [py3k]

requirements:
    build:
        - python
        - numpy >=1.0
        - swig >=1.3
        - mpi4py
```

```
    run:
        - python
        - numpy >=1.0
        - mpi4py

about:
    home: http://www.pyopt.org/index.html
    license: LGPLv3
    license_file: LICENSE
```

CHAPTER 330

pyqi

330.1 Summary

pyqi: expose your interface

330.2 Home

http://bipy.github.io/pyqi

330.3 Versions

- 0.3.2

330.4 License

BSD License

330.5 Meta

```
package:
  name: pyqi
  version: "0.3.2"

source:
  fn: pyqi-0.3.2.tar.gz
  url: https://pypi.python.org/packages/source/p/pyqi/pyqi-0.3.2.tar.gz
  md5: 9507c06eeb22a816d963c860ad8e92ae

build:
  number: 0
  skip: True    [not py27]

requirements:
  build:
```

```
    - python
    - setuptools

  run:
    - python
    - setuptools

test:
  # Python imports
  imports:
    - pyqi

about:
  home: http://bipy.github.io/pyqi
  license: BSD License
  summary: 'pyqi: expose your interface'
```

CHAPTER 331

pysam

331.1 Summary

Pysam is a python module for reading and manipulating Samfiles. It's a lightweight wrapper of the samtools C-API. Pysam also includes an interface for tabix.

331.2 Home

https://github.com/pysam-developers/pysam

331.3 Versions

- 0.8.4

331.4 License

MIT

331.5 Meta

```
package:
  name: pysam
  version: 0.8.4

source:
  fn: pysam-0.8.4.tar.gz
  url: https://pypi.python.org/packages/source/p/pysam/pysam-0.8.4.tar.gz
  md5: 1357038e50e49b79ba02868ac2dbe2c1

build:
  number: 0

requirements:
  build:
```

```
    - python
    - setuptools
    - cython

  run:
    - python

test:
  imports:
    - pysam

about:
  home: https://github.com/pysam-developers/pysam
  license: MIT
  summary: Pysam is a python module for reading and manipulating Samfiles. It's a lightweight wrapper
```

CHAPTER 332

pysamstats

332.1 Summary

A Python utility for calculating statistics against genome position based on sequence alignments from a SAM, BAM or CRAM file.

332.2 Home

https://github.com/alimanfoo/pysamstats

332.3 Versions

- 0.24.0

332.4 License

MIT

332.5 Meta

```
package:
  name: pysamstats
  version: 0.24.0

source:
  fn: v0.24.0.tar.gz
  url: https://github.com/alimanfoo/pysamstats/archive/v0.24.0.tar.gz

build:
  number: 0

requirements:
  build:
    - python
```

```
    - cython
    - pysam >=0.8.4

  run:
    - python
    - pysam >=0.8.4

test:
  imports:
    - pysamstats
  commands:
    - pysamstats --help

about:
  home: https://github.com/alimanfoo/pysamstats
  license: MIT
  summary: A Python utility for calculating statistics against genome position based on sequence alig
```

CHAPTER 333

pysftp

333.1 Summary

A friendly face on SFTP

333.2 Home

https://bitbucket.org/dundeemt/pysftp

333.3 Versions

- 0.2.8

333.4 License

BSD License

333.5 Meta

```
package:
  name: pysftp
  version: "0.2.8"

source:
  fn: pysftp-0.2.8.tar.gz
  url: https://pypi.python.org/packages/source/p/pysftp/pysftp-0.2.8.tar.gz
  md5: 10bd5452aee5684871f434f5cfc8e07b
requirements:
  build:
    - python
    - setuptools
    - paramiko >=1.7.7

  run:
```

```
    - python
    - paramiko >=1.7.7

test:
  # Python imports
  imports:
    - pysftp

about:
  home: https://bitbucket.org/dundeemt/pysftp
  license: BSD License
  summary: 'A friendly face on SFTP'
```

CHAPTER 334

pytabix

334.1 Summary

fast random access to sorted files compressed with bgzip and indexed by tabix

334.2 Home

https://github.com/slowkow/pytabix

334.3 Versions

- 0.0.2

334.4 License

MIT

334.5 Meta

```
package:
  name: pytabix
  version: 0.0.2
build:
  number: 1
source:
  fn: pytabix-e4a6f81.tar.gz
  url: https://github.com/slowkow/pytabix/archive/e4a6f81.tar.gz

requirements:
  build:
    - python
    - setuptools

  run:
```

```
    - python
    - setuptools

test:
  imports:
    - tabix

about:
  home: https://github.com/slowkow/pytabix
  license: MIT
  summary: fast random access to sorted files compressed with bgzip and indexed by tabix
```

CHAPTER 335

pytest-cov

335.1 Summary

Pytest plugin for measuring coverage.

335.2 Home

https://github.com/pytest-dev/pytest-cov

335.3 Versions

- 2.2.0

335.4 License

BSD License

335.5 Meta

```
package:
  name: pytest-cov
  version: "2.2.0"

source:
  fn: pytest-cov-2.2.0.tar.gz
  url: https://pypi.python.org/packages/source/p/pytest-cov/pytest-cov-2.2.0.tar.gz
  md5: 65a5238cdcfaa8618e6607c94faecbd6
#  patches:
   # List any patch files here
   # - fix.patch

build:
  # noarch_python: True
  preserve_egg_dir: True
```

```
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - pytest-cov = pytest-cov:main
    #
    # Would create an entry point called pytest-cov that calls pytest-cov.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools
    - pytest >=2.6.0
    - coverage >=3.7.1

  run:
    - python
    - setuptools
    - pytest >=2.6.0
    - coverage >=3.7.1

test:
  # Python imports
  imports:
    - pytest_cov

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: https://github.com/pytest-dev/pytest-cov
  license: BSD License
  summary: 'Pytest plugin for measuring coverage.'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 336

pytest-timeout

336.1 Summary

py.test plugin to abort hanging tests

336.2 Home

http://bitbucket.org/pytest-dev/pytest-timeout/

336.3 Versions

- 1.0.0

336.4 License

MIT License

336.5 Meta

```
package:
  name: pytest-timeout
  version: "1.0.0"

source:
  fn: pytest-timeout-1.0.0.tar.gz
  url: https://pypi.python.org/packages/source/p/pytest-timeout/pytest-timeout-1.0.0.tar.gz
  md5: f9f162bd079689980b5614673ddfdae4
#  patches:
   # List any patch files here
   # - fix.patch

build:
  # noarch_python: True
  preserve_egg_dir: True
```

```
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - pytest-timeout = pytest-timeout:main
    #
    # Would create an entry point called pytest-timeout that calls pytest-timeout.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools
    - pytest >=2.8.0

  run:
    - python
    - setuptools
    - pytest >=2.8.0

# test:
  # Python imports
  # imports:

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: http://bitbucket.org/pytest-dev/pytest-timeout/
  license: MIT License
  summary: 'py.test plugin to abort hanging tests'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 337

python-dateutil

337.1 Summary

Extensions to the standard Python datetime module

337.2 Home

https://dateutil.readthedocs.org

337.3 Versions

- 2.3

337.4 License

BSD License

337.5 Meta

```
package:
  name: python-dateutil
  version: "2.3"

source:
  fn: python-dateutil-2.3.tar.gz
  url: https://pypi.python.org/packages/source/p/python-dateutil/python-dateutil-2.3.tar.gz
  md5: 14dae5a51d11802cc1e8828c5f797358
#  patches:
   # List any patch files here
   # - fix.patch

# build:
  # noarch_python: True
  # preserve_egg_dir: True
```

```
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - python-dateutil = python-dateutil:main
    #
    # Would create an entry point called python-dateutil that calls python-dateutil.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools
    - six

  run:
    - python
    - six

test:
  # Python imports
  imports:
    - dateutil
    - dateutil.zoneinfo

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: https://dateutil.readthedocs.org
  license: BSD License
  summary: 'Extensions to the standard Python datetime module'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 338

python-igraph

338.1 Summary

High performance graph data structures and algorithms

338.2 Home

http://pypi.python.org/pypi/python-igraph

338.3 Versions

- 0.7.1.post6

338.4 License

GNU General Public License (GPL)

338.5 Meta

```
package:
  name: python-igraph
  version: "0.7.1.post6"

source:
  fn: python-igraph-0.7.1.post6.tar.gz
  url: https://pypi.python.org/packages/source/p/python-igraph/python-igraph-0.7.1.post6.tar.gz
  md5: a4c0b5960735b36adb5d3a40031cb7c0

build:
  number: 1

requirements:
  build:
    - python
```

```
    - lxml
  run:
    - python
    - lxml

test:
  imports:
    - igraph
    - igraph.app
    - igraph.drawing
    - igraph.remote
    - igraph.test
    - igraph.vendor

about:
  home: http://pypi.python.org/pypi/python-igraph
  license: GNU General Public License (GPL)
  summary: 'High performance graph data structures and algorithms'
```

CHAPTER 339

python-levenshtein

339.1 Summary

Python extension for computing string edit distances and similarities.

339.2 Home

https://pypi.python.org/pypi/python-Levenshtein/

339.3 Versions

- 0.12.0

339.4 License

GPL

339.5 Meta

```
package:
  name: python-levenshtein
  version: 0.12.0

about:
  home: https://pypi.python.org/pypi/python-Levenshtein/
  license: GPL
  summary: Python extension for computing string edit distances and similarities.

source:
    url: https://pypi.python.org/packages/source/p/python-Levenshtein/python-Levenshtein-0.12.0.tar.g
    fn: python-Levenshtein-0.12.0.tar.gz

build:
  preserve_egg_dir: True
```

```
  number: 1

requirements:
  build:
    - cython
    - nose
    - python

  run:
    - cython
    - nose
    - python

test:
  requires:
    - nose
  imports:
    - Levenshtein
```

CHAPTER 340

python-magic

340.1 Summary

File type identification using libmagic

340.2 Home

http://github.com/ahupp/python-magic

340.3 Versions

- 0.4.10
- 0.4.6

340.4 License

MIT License

340.5 Meta

```
package:
  name: python-magic
  version: "0.4.10"

source:
  fn: python-magic-0.4.10.tar.gz
  url: https://pypi.python.org/packages/source/p/python-magic/python-magic-0.4.10.tar.gz
  md5: becc45e6b4e00d4e8a6bdf727c52bd27
#  patches:
   # List any patch files here
   # - fix.patch

build:
```

```
  number: 1

requirements:
  build:
    - python
    - setuptools
    - libmagic

  run:
    - python
    - libmagic

# test:
  # Python imports
  # imports:

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: http://github.com/ahupp/python-magic
  license: MIT License
  summary: 'File type identification using libmagic'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 341

python-wget

341.1 Summary

pure python download utility

341.2 Home

http://bitbucket.org/techtonik/python-wget/

341.3 Versions

- 3.2

341.4 License

Public Domain

341.5 Meta

```
package:
  name: python-wget
  version: "3.2"

source:
  fn: wget-3.2.zip
  url: https://pypi.python.org/packages/source/w/wget/wget-3.2.zip
  md5: fb7a04ee59a56bd8db974146df1d7a8b
#  patches:
   # List any patch files here
   # - fix.patch

# build:
  # noarch_python: True
  # preserve_egg_dir: True
```

```
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - wget = wget:main
    #
    # Would create an entry point called wget that calls wget.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python

  run:
    - python

# test:
  # Python imports
  # imports:

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: http://bitbucket.org/techtonik/python-wget/
  license: Public Domain
  summary: 'pure python download utility'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 342

pythonpy

342.1 Summary

the swiss army knife of the command line

342.2 Home

https://github.com/Russell91/pythonpy

342.3 Versions

- 0.4.2

342.4 License

Unknown

342.5 Meta

```
package:
  name: pythonpy
  version: '0.4.2'

source:
  fn: pythonpy-0.4.2.tar.gz
  url: https://pypi.python.org/packages/source/p/pythonpy/pythonpy-0.4.2.tar.gz
  md5: 9e4de105c594ecc04127a0fee088edc0

build:
  number: 0

requirements:
  build:
    - python
```

```
    - setuptools

  run:
    - python
    - setuptools

test:
  commands:
    - py -h

about:
  home: https://github.com/Russell91/pythonpy
  summary: the swiss army knife of the command line
  license: Unknown
```

CHAPTER 343

pyutilib

343.1 Summary

PyUtilib: A collection of Python utilities

343.2 Home

https://software.sandia.gov/trac/pyutilib

343.3 Versions

- 5.1.3556

343.4 License

BSD License

343.5 Meta

```
# copied from https://anaconda.org/timcera/pyutilib

package:
  name: pyutilib
  version: "5.1.3556"

source:
  fn: PyUtilib-5.1.3556.tar.gz
  url: https://pypi.python.org/packages/source/P/PyUtilib/PyUtilib-5.1.3556.tar.gz
  md5: fa6b4fba1e8c817d431e9c2aac8a27b5

build:
  skip: True # [not py27]

requirements:
```

```
  build:
    - python
    - setuptools
    - nose
    - six

  run:
    - python
    - nose
    - six

test:
  # Python imports
  imports:
    - pyutilib
    - pyutilib.autotest
    - pyutilib.autotest.tests
    - pyutilib.common
    - pyutilib.component
    - pyutilib.component.app
    - pyutilib.component.app.tests
    - pyutilib.component.config
    - pyutilib.component.config.tests
    - pyutilib.component.core
    - pyutilib.component.core.tests
    - pyutilib.component.executables
    - pyutilib.component.loader
    - pyutilib.component.loader.tests
    - pyutilib.dev
    - pyutilib.enum
    - pyutilib.enum.tests
    - pyutilib.excel
    - pyutilib.excel.tests
    - pyutilib.math
    - pyutilib.math.tests
    - pyutilib.misc
    - pyutilib.misc.tests
    - pyutilib.misc.tests.import_data
    - pyutilib.misc.tests.import_data.a
    - pyutilib.misc.tests.import_data.b
    - pyutilib.ply
    - pyutilib.pyro
    - pyutilib.services
    - pyutilib.subprocess
    - pyutilib.subprocess.tests
    - pyutilib.th
    - pyutilib.th.tests
    - pyutilib.workflow
    - pyutilib.workflow.tests

about:
  home: https://software.sandia.gov/trac/pyutilib
  license: BSD License
  summary: 'PyUtilib: A collection of Python utilities'
```

CHAPTER 344

pyvcf

344.1 Summary

A Variant Call Format reader for Python

344.2 Home

https://github.com/jamescasbon/PyVCF

344.3 Versions

- 0.6.8.dev0

344.4 License

BSD

344.5 Meta

```
package:
  name: pyvcf
  version: '0.6.8.dev0'

source:
  fn: PyVCF-ee0208a.tar.gz
  url: https://github.com/jamescasbon/PyVCF/archive/ee0208a.tar.gz
  #fn: PyVCF-0.6.7.tar.gz
  #url: https://pypi.python.org/packages/source/P/PyVCF/PyVCF-0.6.7.tar.gz

build:
  number: 0

requirements:
  build:
```

```
    - python
    - setuptools

  run:
    - python

test:
  # Python imports
  imports:
    - vcf.test
    - vcf

about:
  home: https://github.com/jamescasbon/PyVCF
  license: BSD
  summary: A Variant Call Format reader for Python
```

CHAPTER 345

pyx

345.1 Summary

Python package for the generation of PostScript, PDF, and SVG files

345.2 Home

http://pyx.sourceforge.net/

345.3 Versions

- 0.12.1

345.4 License

GNU General Public License (GPL)

345.5 Meta

```
package:
  name: pyx
  version: "0.12.1"

source:
  fn: PyX-0.12.1.tar.gz
  url: https://pypi.python.org/packages/source/P/PyX/pyx-0.12.1.tar.gz
  md5: 04263eb002553dae0e8a1d0eeb805ec1

build:
  number: 0
  skip: True  # [not py27]

requirements:
  build:
```

```
    - python

  run:
    - python

test:
  imports:
    - pyx
    - pyx.dvi
    - pyx.font
    - pyx.graph
    - pyx.graph.axis
    - pyx.metapost

about:
  home: http://pyx.sourceforge.net/
  license: GNU General Public License (GPL)
  summary: 'Python package for the generation of PostScript, PDF, and SVG files'
```

CHAPTER 346

qcli

346.1 Summary

qcli

346.2 Home

346.3 Versions

- 0.1.1

346.4 License

GPL

346.5 Meta

```
package:
  name: qcli
  version: "0.1.1"

source:
  fn: qcli-0.1.1.tar.gz
  url: https://pypi.python.org/packages/source/q/qcli/qcli-0.1.1.tar.gz
  md5: 25b7bc209c1e52be16efad295bd37ed4

  patches:
    - python3.patch [py3k]

build:
  number: 0

requirements:
  build:
    - python
```

```
  run:
    - python

test:
  # Python imports
  imports:
    - qcli

  commands:
    - qcli_make_rst -h
    - qcli_make_script -h

about:
  license: GPL
  summary: qcli
```

CHAPTER 347

qsignature

347.1 Summary

qsignature is a simple and highly effective method for detecting potential sample mix-ups using distance measurements between SNP

347.2 Home

http://sourceforge.net/p/adamajava/wiki/Home/

347.3 Versions

- 0.1pre

347.4 License

GPLv3

347.5 Meta

```
package:
  name: qsignature
  version: '0.1pre'

source:
  fn: qsignature-0.1pre.tar.bz2
  url: http://downloads.sourceforge.net/project/adamajava/qsignature.tar.bz2

build:
  number: 2

requirements:
  run:
    - java-jdk
```

```
test:
  commands:
    - qsignature org.qcmg.sig.SignatureGenerator -h

about:
  home: http://sourceforge.net/p/adamajava/wiki/Home/
  license: GPLv3
  summary: qsignature is a simple and highly effective method for detecting potential sample mix-ups
```

CHAPTER 348

qualimap

348.1 Summary

Quality control of alignment sequencing data and its derivatives like feature counts

348.2 Home

http://qualimap.bioinfo.cipf.es/

348.3 Versions

- 2.1.3

348.4 License

GPLv2

348.5 Meta

```
package:
  name: qualimap
  version: "2.1.3"

source:
  fn: qualimap_v2.1.3.zip
  url: https://bitbucket.org/kokonech/qualimap/downloads/qualimap_v2.1.3.zip

build:
  number: 1

requirements:
  run:
    - java-jdk
```

```
test:
  commands:
    - qualimap -h

about:
  home: http://qualimap.bioinfo.cipf.es/
  license: GPLv2
  summary: Quality control of alignment sequencing data and its derivatives like feature counts
```

CHAPTER 349

r-ade4

349.1 Summary

Multivariate data analysis and graphical display.

349.2 Home

http://pbil.univ-lyon1.fr/ADE-4, Mailing list: http://listes.univ-lyon1.fr/wws/info/adelist

349.3 Versions

- 1.7_2

349.4 License

GPL (>= 2)

349.5 Meta

```
package:
  name: r-ade4
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "1.7_2"

source:
  fn: ade4_1.7-2.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/ade4_1.7-2.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/ade4/ade4_1.7-2.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
```

```
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: waveslim, splancs, MASS, maptools, spdep, pixmap, ape, deldir, ade4TkGUI, adegraphics, sp
requirements:
  build:
    - r

  run:
    - r

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('ade4')" # [not win]
    - "\"%R%\" -e \"library('ade4')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: 'http://pbil.univ-lyon1.fr/ADE-4, Mailing list: http://listes.univ-lyon1.fr/wws/info/adelist

  license: GPL (>= 2)
  summary: Multivariate data analysis and graphical display.

# The original CRAN metadata for this package was:

# Package: ade4
# Version: 1.7-2
# Date: 2015-04-14
# Title: Analysis of Ecological Data : Exploratory and Euclidean Methods in Environmental Sciences
# Author: StÃ©phane Dray <stephane.dray@univ-lyon1.fr>, Anne-BÃ©atrice Dufour <anne-beatrice.dufour@u
# Maintainer: AurÃ©lie Siberchicot <aurelie.siberchicot@univ-lyon1.fr>
# Imports: methods
# Suggests: waveslim, splancs, MASS, maptools, spdep, pixmap, ape, deldir, ade4TkGUI, adegraphics, sp
# Depends: R (>= 2.10)
# Description: Multivariate data analysis and graphical display.
# License: GPL (>= 2)
# URL: http://pbil.univ-lyon1.fr/ADE-4, Mailing list: http://listes.univ-lyon1.fr/wws/info/adelist
# Encoding: UTF-8
# Repository: CRAN
# Repository/R-Forge/Project: ade4
```

```
# Repository/R-Forge/Revision: 799
# Repository/R-Forge/DateTimeStamp: 2015-04-14 07:38:21
# Date/Publication: 2015-04-14 13:47:39
# Packaged: 2015-04-14 07:45:42 UTC; rforge
# NeedsCompilation: yes

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 350

r-amap

350.1 Summary

Tools for Clustering and Principal Component Analysis (With robust methods, and parallelized functions).

350.2 Home

http://mulcyber.toulouse.inra.fr/projects/amap/

350.3 Versions

- 0.8_14

350.4 License

GPL

350.5 Meta

```
package:
  name: r-amap
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.8_14"

source:
  fn: amap_0.8-14.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/amap_0.8-14.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/amap/amap_0.8-14.tar.gz

build:
  number: 0
```

```
  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: Biobase
requirements:
  build:
    - r
    - gcc # [not win]

  run:
    - r
    - libgcc # [not win]

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('amap')" # [not win]
    - "\"%R%\" -e \"library('amap')\"" # [win]

about:
  home: http://mulcyber.toulouse.inra.fr/projects/amap/
  license: GPL
  summary: Tools for Clustering and Principal Component Analysis (With robust methods, and paralleliz
    functions).

# The original CRAN metadata for this package was:

# Package: amap
# Version: 0.8-14
# Date: 2014-12-17
# Title: Another Multidimensional Analysis Package
# Author: Antoine Lucas
# Maintainer: Antoine Lucas <antoinelucas@gmail.com>
# Depends: R (>= 2.10.0)
# Suggests: Biobase
# Description: Tools for Clustering and Principal Component Analysis (With robust methods, and paral
# License: GPL
# URL: http://mulcyber.toulouse.inra.fr/projects/amap/
# Packaged: 2014-12-17 18:09:00 UTC; antoine
# Repository: CRAN
# Date/Publication: 2014-12-17 23:26:42
# NeedsCompilation: yes

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 351

r-ash

351.1 Summary

David Scott's ASH routines ported from S-PLUS to R.

351.2 Home

351.3 Versions

- 1.0_15

351.4 License

GPL (>= 2)

351.5 Meta

```
package:
  name: r-ash
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "1.0_15"

source:
  fn: ash_1.0-15.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/ash_1.0-15.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/ash/ash_1.0-15.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
```

```
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/


requirements:
  build:
    - r

  run:
    - r

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('ash')" # [not win]
    - "\"%R%\" -e \"library('ash')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  #home:
  license: GPL (>= 2)
  summary: !!python/unicode 'David Scott''s ASH routines ported from S-PLUS to R.'


# The original CRAN metadata for this package was:

# Package: ash
# Version: 1.0-15
# Title: David Scott's ASH Routines
# Author: S original by David W. Scott R port by Albrecht Gebhardt <albrecht.gebhardt@aau.at> adopte
# Maintainer: Albrecht Gebhardt <albrecht.gebhardt@aau.at>
# Description: David Scott's ASH routines ported from S-PLUS to R.
# License: GPL (>= 2)
# Date: 2015-08-27
# NeedsCompilation: yes
# Packaged: 2015-08-31 21:39:59 UTC; alge
# Repository: CRAN
# Date/Publication: 2015-09-01 17:56:55

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 352

r-batchjobs

352.1 Summary

Provides Map, Reduce and Filter variants to generate jobs on batch computing systems like PBS/Torque, LSF, SLURM and Sun Grid Engine. Multicore and SSH systems are also supported. For further details see the project web page.

352.2 Home

https://github.com/tudo-r/BatchJobs

352.3 Versions

- 1.6

352.4 License

BSD_2_clause + file LICENSE

352.5 Meta

```
package:
  name: r-batchjobs
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "1.6"

source:
  fn: BatchJobs_1.6.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/BatchJobs_1.6.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/BatchJobs/BatchJobs_1.6.tar.gz

build:
  number: 0
```

```
  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: MASS, testthat
requirements:
  build:
    - r
    - r-bbmisc >=1.9
    - r-dbi
    - r-rsqlite >=1.0.0
    - r-brew
    - r-checkmate >=1.5.1
    - r-digest
    - r-fail >=1.2
    - r-sendmailr
    - r-stringr

  run:
    - r
    - r-bbmisc >=1.9
    - r-dbi
    - r-rsqlite >=1.0.0
    - r-brew
    - r-checkmate >=1.5.1
    - r-digest
    - r-fail >=1.2
    - r-sendmailr
    - r-stringr

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('BatchJobs')" # [not win]
    - "\"%R%\" -e \"library('BatchJobs')\"" # [win]

about:
  home: https://github.com/tudo-r/BatchJobs
  license: BSD_2_clause + file LICENSE
  summary: Provides Map, Reduce and Filter variants to generate jobs on batch computing systems
    like PBS/Torque, LSF, SLURM and Sun Grid Engine. Multicore and SSH systems are also
    supported. For further details see the project web page.

# The original CRAN metadata for this package was:

# Package: BatchJobs
# Title: Batch Computing with R
# Description: Provides Map, Reduce and Filter variants to generate jobs on batch computing systems
# Author: Bernd Bischl <bernd_bischl@gmx.net>, Michel Lang <michellang@gmail.com>, Henrik Bengtsson
# Maintainer: Bernd Bischl <bernd_bischl@gmx.net>
# URL: https://github.com/tudo-r/BatchJobs
# BugReports: https://github.com/tudo-r/BatchJobs/issues
# MailingList: batchjobs@googlegroups.com
# License: BSD_2_clause + file LICENSE
# Depends: R (>= 2.15.0), BBmisc (>= 1.9), methods
# Imports: brew, checkmate (>= 1.5.1), DBI, digest, fail (>= 1.2), parallel, RSQLite (>= 1.0.0), sen
# Suggests: MASS, testthat
```

```
# LazyData: yes
# ByteCompile: yes
# Version: 1.6
# Packaged: 2015-03-18 16:40:05 UTC; bischl
# NeedsCompilation: no
# Repository: CRAN
# Date/Publication: 2015-03-18 18:01:21

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 353

r-bbmisc

353.1 Summary

Miscellaneous helper functions for and from B. Bischl and some other guys at TU Dortmund, mainly for package development.

353.2 Home

https://github.com/berndbischl/BBmisc

353.3 Versions

- 1.9

353.4 License

BSD_3_clause + file LICENSE

353.5 Meta

```
package:
  name: r-bbmisc
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "1.9"

source:
  fn: BBmisc_1.9.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/BBmisc_1.9.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/BBmisc/BBmisc_1.9.tar.gz

build:
  number: 0
```

```
  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: testthat, microbenchmark, codetools
requirements:
  build:
    - r
    - r-checkmate
    - gcc # [not win]

  run:
    - r
    - r-checkmate
    - libgcc # [not win]

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('BBmisc')" # [not win]
    - "\"%R%\" -e \"library('BBmisc')\"" # [win]

about:
  home: https://github.com/berndbischl/BBmisc
  license: BSD_3_clause + file LICENSE
  summary: Miscellaneous helper functions for and from B. Bischl and some other guys at TU Dortmund,
    mainly for package development.

# The original CRAN metadata for this package was:

# Package: BBmisc
# Title: Miscellaneous Helper Functions for B. Bischl
# Description: Miscellaneous helper functions for and from B. Bischl and some other guys at TU Dortmu
# Authors@R: c(person("Bernd", "Bischl", email = "bernd_bischl@gmx.net", role = c("aut", "cre")), pe
# URL: https://github.com/berndbischl/BBmisc
# BugReports: https://github.com/berndbischl/BBmisc/issues
# License: BSD_3_clause + file LICENSE
# Encoding: UTF-8
# Imports: stats, checkmate
# Suggests: testthat, microbenchmark, codetools
# LazyData: yes
# ByteCompile: yes
# Version: 1.9
# Packaged: 2015-02-03 12:39:37 UTC; bischl
# Author: Bernd Bischl [aut, cre], Michel Lang [aut], Jakob Bossek [aut], Daniel Horn [aut], Jakob R
# Maintainer: Bernd Bischl <bernd_bischl@gmx.net>
# NeedsCompilation: yes
# Repository: CRAN
# Date/Publication: 2015-02-03 14:03:05

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 354

r-bio3d

354.1 Summary

Utilities to process, organize and explore protein structure, sequence and dynamics data. Features include the ability to read and write structure, sequence and dynamic trajectory data, perform sequence and structure database searches, data summaries, atom selection, alignment, superposition, rigid core identification, clustering, torsion analysis, distance matrix analysis, structure and sequence conservation analysis, normal mode analysis, principal component analysis of heterogeneous structure data, and correlation network analysis from normal mode and molecular dynamics data. In addition, various utility functions are provided to enable the statistical and graphical power of the R environment to work with biological sequence and structural data. Please refer to the URLs below for more information.

354.2 Home

http://thegrantlab.org/bio3d/, http://bitbucket.org/Grantlab/bio3d

354.3 Versions

- 2.2_3

354.4 License

GPL (>= 2)

354.5 Meta

```
package:
  name: r-bio3d
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "2.2_3"

source:
  fn: bio3d_2.2-3.tar.gz
```

```
  url:
    - http://cran.r-project.org/src/contrib/bio3d_2.2-3.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/bio3d/bio3d_2.2-3.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: XML, RCurl, lattice, ncdf, igraph, bigmemory, knitr, testthat (>= 0.9.1)
requirements:
  build:
    - r

  run:
    - r

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('bio3d')" # [not win]
    - "\"%R%\" -e \"library('bio3d')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: http://thegrantlab.org/bio3d/, http://bitbucket.org/Grantlab/bio3d
  license: GPL (>= 2)
  summary: Utilities to process, organize and explore protein structure, sequence and dynamics
    data.  Features include the ability to read and write structure, sequence and dynamic
    trajectory data, perform sequence and structure database searches, data summaries,
    atom selection, alignment, superposition, rigid core identification, clustering,
    torsion analysis, distance matrix analysis, structure and sequence conservation
    analysis, normal mode analysis, principal component analysis of heterogeneous structure
    data, and correlation network analysis from normal mode and molecular dynamics data.  In
    addition, various utility functions are provided to enable the statistical and graphical
    power of the R environment to work with biological sequence and structural data.  Please
    refer to the URLs below for more information.

# The original CRAN metadata for this package was:
```

```
# Package: bio3d
# Title: Biological Structure Analysis
# Version: 2.2-3
# Author: Barry Grant, Xin-Qiu Yao, Lars Skjaerven, Julien Ide
# VignetteBuilder: knitr
# Imports: parallel, grid, graphics, grDevices, stats, utils
# Suggests: XML, RCurl, lattice, ncdf, igraph, bigmemory, knitr, testthat (>= 0.9.1)
# Depends: R (>= 3.1.0)
# LazyData: yes
# Description: Utilities to process, organize and explore protein structure, sequence and dynamics da
# Maintainer: Barry Grant <bjgrant@umich.edu>
# License: GPL (>= 2)
# URL: http://thegrantlab.org/bio3d/, http://bitbucket.org/Grantlab/bio3d
# NeedsCompilation: no
# Packaged: 2015-09-04 17:42:13 UTC; xinqyao
# Repository: CRAN
# Date/Publication: 2015-09-04 21:49:41

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 355

r-biom

355.1 Summary

This is an R package for interfacing with the BIOM format.

355.2 Home

https://github.com/joey711/biom/, http://biom-format.org/

355.3 Versions

- 0.3.12

355.4 License

GPL-2

355.5 Meta

```
package:
  name: r-biom
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.3.12"

source:
  fn: biom_0.3.12.tar.gz
  url:
    - https://cran.r-project.org/src/contrib/biom_0.3.12.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
```

```
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: XML, RCurl, lattice, ncdf, igraph, bigmemory, knitr, testthat (>= 0.9.1)
requirements:
  build:
    - r
    - r-plyr
    - r-rjsonio
    - r-matrix

  run:
    - r
    - r-plyr
    - r-rjsonio
    - r-matrix

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('biom')" # [not win]
    - "\"%R%\" -e \"library('biom')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: https://github.com/joey711/biom/, http://biom-format.org/
  license: GPL-2
  summary: This is an R package for interfacing with the BIOM format.
```

CHAPTER 356

r-bit

356.1 Summary

bitmapped vectors of booleans (no NAs), coercion from and to logicals, integers and integer subscripts; fast boolean operators and fast summary statistics. With 'bit' vectors you can store true binary booleans {FALSE,TRUE} at the expense of 1 bit only, on a 32 bit architecture this means factor 32 less RAM and ~ factor 32 more speed on boolean operations. Due to overhead of R calls, actual speed gain depends on the size of the vector: expect gains for vectors of size > 10000 elements. Even for one-time boolean operations it can pay-off to convert to bit, the pay-off is obvious, when such components are used more than once. Reading from and writing to bit is approximately as fast as accessing standard logicals - mostly due to R's time for memory allocation. The package allows to work with pre-allocated memory for return values by calling .Call() directly: when evaluating the speed of C-access with pre-allocated vector memory, coping from bit to logical requires only 70% of the time for copying from logical to logical; and copying from logical to bit comes at a performance penalty of 150%. the package now contains further classes for representing logical selections: 'bitwhich' for very skewed selections and 'ri' for selecting ranges of values for chunked processing. All three index classes can be used for subsetting 'ff' objects (ff-2.1-0 and higher).

356.2 Home

http://ff.r-forge.r-project.org/

356.3 Versions

- 1.1_12

356.4 License

GPL-2

356.5 Meta

```
package:
  name: r-bit
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "1.1_12"

source:
  fn: bit_1.1-12.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/bit_1.1-12.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/bit/bit_1.1-12.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/


requirements:
  build:
    - r
    - gcc # [not win]

  run:
    - r
    - libgcc # [not win]

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('bit')" # [not win]
    - "\"%R%\" -e \"library('bit')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: http://ff.r-forge.r-project.org/
  license: GPL-2
  summary: 'bitmapped vectors of booleans (no NAs),  coercion from and to logicals, integers
    and integer subscripts;  fast boolean operators and fast summary statistics.  With
    ''bit'' vectors you can store true binary booleans {FALSE,TRUE} at the  expense
```

```
    of 1 bit only, on a 32 bit architecture this means factor 32 less  RAM and ~ factor
    32 more speed on boolean operations. Due to overhead of  R calls, actual speed gain
    depends on the size of the vector: expect gains  for vectors of size > 10000 elements.
    Even for one-time boolean operations  it can pay-off to convert to bit, the pay-off
    is obvious, when such  components are used more than once.  Reading from and writing
    to bit is approximately as fast as accessing  standard logicals - mostly due to
    R''s time for memory allocation. The package  allows to work with pre-allocated
    memory for return values by calling .Call()  directly: when evaluating the speed
    of C-access with pre-allocated vector  memory, coping from bit to logical requires
    only 70% of the time for copying  from logical to logical; and copying from logical
    to bit comes at a  performance penalty of 150%. the package now contains further
    classes for  representing logical selections: ''bitwhich'' for very skewed selections
    and  ''ri'' for selecting ranges of values for chunked processing. All three index  classes
    can be used for subsetting ''ff'' objects (ff-2.1-0 and higher).'


# The original CRAN metadata for this package was:

# Package: bit
# Type: Package
# Title: A class for vectors of 1-bit booleans
# Version: 1.1-12
# Date: 2012-01-17
# Author: Jens Oehlschlägel <Jens.Oehlschlaegel@truecluster.com>
# Maintainer: Jens Oehlschlägel <Jens.Oehlschlaegel@truecluster.com>
# Depends: R (>= 2.9.2)
# Description: bitmapped vectors of booleans (no NAs),  coercion from and to logicals, integers and
# License: GPL-2
# LazyLoad: yes
# ByteCompile: yes
# Encoding: latin1
# URL: http://ff.r-forge.r-project.org/
# Packaged: 2014-04-08 21:51:43 UTC; jens
# NeedsCompilation: yes
# Repository: CRAN
# Date/Publication: 2014-04-09 09:54:10

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 357

r-bit64

357.1 Summary

Package 'bit64' provides serializable S3 atomic 64bit (signed) integers that can be used in vectors, matrices, arrays and data.frames. Methods are available for coercion from and to logicals, integers, doubles, characters and factors as well as many elementwise and summary functions. Many fast algorithmic operations such as 'match' and 'order' support interactive data exploration and manipulation and optionally leverage caching.

357.2 Home

http://ff.r-forge.r-project.org/

357.3 Versions

- 0.9_5

357.4 License

GPL-2

357.5 Meta

```
package:
  name: r-bit64
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.9_5"

source:
  fn: bit64_0.9-5.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/bit64_0.9-5.tar.gz
```

```
    - http://cran.r-project.org/src/contrib/Archive/bit64/bit64_0.9-5.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/


requirements:
  build:
    - r
    - r-bit >=1.1_12
    - gcc # [not win]

  run:
    - r
    - r-bit >=1.1_12
    - libgcc # [not win]

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('bit64')" # [not win]
    - "\"%R%\" -e \"library('bit64')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: http://ff.r-forge.r-project.org/
  license: GPL-2
  summary: ' Package ''bit64'' provides serializable S3 atomic 64bit (signed) integers  that
    can be used in vectors, matrices, arrays and data.frames. Methods are  available
    for coercion from and to logicals, integers, doubles, characters  and factors as
    well as many elementwise and summary functions. Many fast  algorithmic operations
    such as ''match'' and ''order'' support interactive data exploration and manipulation
    and optionally leverage caching.'


# The original CRAN metadata for this package was:

# Package: bit64
```

```
# Type: Package
# Title: A S3 Class for Vectors of 64bit Integers
# Version: 0.9-5
# Date: 2015-06-24
# Author: Jens Oehlschlägel <Jens.Oehlschlaegel@truecluster.com>
# Maintainer: Jens Oehlschlägel <Jens.Oehlschlaegel@truecluster.com>
# Depends: R (>= 3.0.1), bit (>= 1.1-12), utils, methods, stats
# Description:  Package 'bit64' provides serializable S3 atomic 64bit (signed) integers  that can be
# License: GPL-2
# LazyLoad: yes
# ByteCompile: yes
# URL: http://ff.r-forge.r-project.org/
# Encoding: latin1
# Packaged: 2015-07-04 09:58:24 UTC; jo
# NeedsCompilation: yes
# Repository: CRAN
# Date/Publication: 2015-07-05 09:24:32

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 358

r-catools

358.1 Summary

Contains several basic utility functions including: moving (rolling, running) window statistic functions, read/write for GIF and ENVI binary files, fast calculation of AUC, LogitBoost classifier, base64 encoder/decoder, round-off-error-free sum and cumsum, etc.

358.2 Home

358.3 Versions

- 1.17.1

358.4 License

GPL-3

358.5 Meta

```
package:
  name: r-catools
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "1.17.1"

source:
  fn: caTools_1.17.1.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/caTools_1.17.1.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/caTools/caTools_1.17.1.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
```

```
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: MASS, rpart
requirements:
  build:
    - r
    - r-bitops
    - gcc # [not win]

  run:
    - r
    - r-bitops
    - libgcc # [not win]

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('caTools')" # [not win]
    - "\"%R%\" -e \"library('caTools')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  #home:
  license: GPL-3
  summary: !!python/unicode 'Contains several basic utility functions including: moving (rolling,
    running) window statistic functions, read/write for GIF and ENVI binary files, fast
    calculation of AUC, LogitBoost classifier, base64 encoder/decoder, round-off-error-free
    sum and cumsum, etc.'


# The original CRAN metadata for this package was:

# Package: caTools
# Type: Package
# Title: Tools: moving window statistics, GIF, Base64, ROC AUC, etc.
# Version: 1.17.1
# Date: 2014-04-21
# Author: Jarek Tuszynski <jaroslaw.w.tuszynski@saic.com>
# Maintainer: Harutyun Khachatryan <kh_harut@yahoo.com>
# Depends: R (>= 2.2.0)
# Imports: bitops
```

```
# Suggests: MASS, rpart
# Description: Contains several basic utility functions including: moving (rolling, running) window s
# License: GPL-3
# Packaged: 2014-09-09 21:05:06 UTC; ripley
# NeedsCompilation: yes
# Repository: CRAN
# Date/Publication: 2014-09-10 16:22:53

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 359

r-cghflasso

359.1 Summary

Spatial smoothing and hot spot detection using the fused lasso regression

359.2 Home

359.3 Versions

- 0.2_1

359.4 License

GPL (>= 2)

359.5 Meta

```
package:
  name: r-cghflasso
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.2_1"

source:
  fn: cghFLasso_0.2-1.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/cghFLasso_0.2-1.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/cghFLasso/cghFLasso_0.2-1.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
```

```
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/


requirements:
  build:
    - r

  run:
    - r

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('cghFLasso')" # [not win]
    - "\"%R%\" -e \"library('cghFLasso')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  #home:
  license: GPL (>= 2)
  summary: !!python/unicode 'Spatial smoothing and hot spot detection using the fused lasso regressio


# The original CRAN metadata for this package was:

# Package: cghFLasso
# Version: 0.2-1
# Date: 2009-06-01
# Title: Detecting hot spot on CGH array data with fused lasso regression.
# Author: Nicholas Austin Johnson <nickaj@stanford.edu>, Robert Tibshirani <tibs@stat.stanford.edu>,
# Maintainer: Pei Wang <pwang@fhcrc.org>
# Description: Spatial smoothing and hot spot detection using the fused lasso regression
# License: GPL (>= 2)
# Packaged: 2009-06-05 01:13:30 UTC; pwang
# Repository: CRAN
# Date/Publication: 2009-06-07 19:19:51
# NeedsCompilation: yes

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 360

r-chbutils

360.1 Summary

Useful utility functions used at the Harvard Chan School Bioinformatics core

360.2 Home

https://github.com/hbc/CHBUtils

360.3 Versions

- 0.1_2015_12_21

360.4 License

MIT

360.5 Meta

```
package:
  name: r-chbutils
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.1_2015_12_21"

source:
  fn: CHBUtils-0.1_2015_12_21.tar.gz
  url: https://github.com/hbc/CHBUtils/archive/d862e27f.tar.gz

build:
  number: 0
  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
```

```
    - lib/

requirements:
  build:
    - r
    - r-mvtnorm
    - r-rcolorbrewer

  run:
    - r
    - r-mvtnorm
    - r-rcolorbrewer

test:
  commands:
    - $R -e "library('CHBUtils')"

about:
  home: https://github.com/hbc/CHBUtils
  license: MIT
  summary: Useful utility functions used at the Harvard Chan School Bioinformatics core
```

CHAPTER 361

r-checkmate

361.1 Summary

Tests and assertions to perform frequent argument checks. A substantial part of the package was written in C to minimize any worries about execution time overhead.

361.2 Home

https://github.com/mllg/checkmate

361.3 Versions

- 1.6.3

361.4 License

BSD_3_clause + file LICENSE

361.5 Meta

```
package:
  name: r-checkmate
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "1.6.3"

source:
  fn: checkmate_1.6.3.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/checkmate_1.6.3.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/checkmate/checkmate_1.6.3.tar.gz

build:
  number: 0
```

```
  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: data.table, dplyr, ggplot2, knitr, microbenchmark, testthat
requirements:
  build:
    - r
    - gcc # [not win]

  run:
    - r
    - libgcc # [not win]

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('checkmate')" # [not win]
    - "\"%R%\" -e \"library('checkmate')\"" # [win]

about:
  home: https://github.com/mllg/checkmate
  license: BSD_3_clause + file LICENSE
  summary: Tests and assertions to perform frequent argument checks. A substantial part of the
    package was written in C to minimize any worries about execution time overhead.

# The original CRAN metadata for this package was:

# Package: checkmate
# Type: Package
# Title: Fast and Versatile Argument Checks
# Description: Tests and assertions to perform frequent argument checks. A substantial part of the pa
# Version: 1.6.3
# Author: Michel Lang <michellang@gmail.com>, Bernd Bischl <bernd_bischl@gmx.net>
# Maintainer: Michel Lang <michellang@gmail.com>
# URL: https://github.com/mllg/checkmate
# BugReports: https://github.com/mllg/checkmate/issues
# NeedsCompilation: yes
# ByteCompile: yes
# Encoding: UTF-8
# Depends: R (>= 3.0.0)
# Imports: utils
# Suggests: data.table, dplyr, ggplot2, knitr, microbenchmark, testthat
# License: BSD_3_clause + file LICENSE
# VignetteBuilder: knitr
# Packaged: 2015-10-23 11:08:45 UTC; lang
# Repository: CRAN
# Date/Publication: 2015-10-23 16:23:03

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 362

r-circlize

362.1 Summary

Circular layout is an efficient way for the visualization of huge amounts of information. Here the circlize package provides an implementation of circular layout generation in R as well as an enhancement of available software. The flexibility of this package is based on the usage of low-level graphics functions such that self-defined high-level graphics can be easily implemented by users for specific purposes. Together with the seamless connection between the powerful computational and visual environment in R, circlize gives users more convenience and freedom to design figures for better understanding complex patterns behind multi-dimensional data.

362.2 Home

https://github.com/jokergoo/circlize

362.3 Versions

- 0.3.3

362.4 License

GPL (>= 2)

362.5 Meta

```
package:
  name: r-circlize
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.3.3"

source:
  fn: circlize_0.3.3.tar.gz
  url:
```

```
    - http://cran.r-project.org/src/contrib/circlize_0.3.3.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/circlize/circlize_0.3.3.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: knitr, dendextend (>= 1.0.1)
requirements:
  build:
    - r
    - r-globaloptions >=0.0.6
    - r-colorspace
    - r-shape

  run:
    - r
    - r-globaloptions >=0.0.6
    - r-colorspace
    - r-shape

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('circlize')" # [not win]
    - "\"%R%\" -e \"library('circlize')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: https://github.com/jokergoo/circlize
  license: GPL (>= 2)
  summary: Circular layout is an efficient way for the visualization of huge  amounts of information.
    Here the circlize package provides an implementation  of circular layout generation
    in R as well as an enhancement of available  software. The flexibility of this package
    is based on the usage of low-level  graphics functions such that self-defined high-level
    graphics can be easily  implemented by users for specific purposes. Together with
    the seamless  connection between the powerful computational and visual environment
    in R,  circlize gives users more convenience and freedom to design figures for  better
    understanding complex patterns behind multi-dimensional data.
```

```
# The original CRAN metadata for this package was:

# Package: circlize
# Type: Package
# Title: Circular Visualization
# Version: 0.3.3
# Date: 2015-11-25
# Author: Zuguang Gu
# Maintainer: Zuguang Gu <z.gu@dkfz.de>
# Depends: R (>= 2.10.0), graphics
# Imports: GlobalOptions (>= 0.0.6), shape, grDevices, utils, stats, colorspace, methods, grid
# Suggests: knitr, dendextend (>= 1.0.1)
# VignetteBuilder: knitr
# Description: Circular layout is an efficient way for the visualization of huge  amounts of informat
# URL: https://github.com/jokergoo/circlize
# License: GPL (>= 2)
# Packaged: 2015-11-25 22:09:23 UTC; jokergoo
# Repository: CRAN
# Date/Publication: 2015-11-26 08:33:04
# NeedsCompilation: no

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 363

r-compute.es

363.1 Summary

This package contains several functions for calculating the most widely used effect sizes (ES), along with their variances, confidence intervals and p-values. The output includes ES's of d (mean difference), g (unbiased estimate of d), r (correlation coefficient), z' (Fisher's z), and OR (odds ratio and log odds ratio). In addition, NNT (number needed to treat), U3, CLES (Common Language Effect Size) and Cliff's Delta are computed. This package uses recommended formulas as described in The Handbook of Research Synthesis and Meta-Analysis (Cooper, Hedges, & Valentine, 2009).

363.2 Home

http://acdelre.weebly.com

363.3 Versions

- 0.2_4

363.4 License

GPL-2

363.5 Meta

```
package:
  name: r-compute.es
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.2_4"

source:
  fn: compute.es_0.2-4.tar.gz
  url:
```

```
    - http://cran.r-project.org/src/contrib/compute.es_0.2-4.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/compute.es/compute.es_0.2-4.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/


requirements:
  build:
    - r

  run:
    - r

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('compute.es')" # [not win]
    - "\"%R%\" -e \"library('compute.es')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: http://acdelre.weebly.com
  license: GPL-2
  summary: This package contains several functions for calculating the most widely used effect
    sizes (ES), along with their variances, confidence intervals and p-values.  The
    output includes ES's of d (mean difference), g (unbiased estimate of d), r (correlation
    coefficient), z' (Fisher's z), and OR (odds ratio and log odds ratio). In addition,
    NNT (number needed to treat), U3, CLES (Common Language Effect Size) and Cliff's
    Delta are computed. This package uses recommended formulas as described in The Handbook
    of Research Synthesis and Meta-Analysis (Cooper, Hedges, & Valentine, 2009).

# The original CRAN metadata for this package was:

# Package: compute.es
# Type: Package
# Title: Compute Effect Sizes
# Version: 0.2-4
```

```
# Date: 2014-09-16
# Author: AC Del Re
# Maintainer: AC Del Re <acdelre@gmail.com>
# Description: This package contains several functions for calculating the most widely used effect si
# Depends: R (>= 2.10.1)
# License: GPL-2
# URL: http://acdelre.weebly.com
# Packaged: 2014-09-16 18:30:53 UTC; acd
# NeedsCompilation: no
# Repository: CRAN
# Date/Publication: 2014-09-16 23:35:38

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 364

r-corrplot

364.1 Summary

The corrplot package is a graphical display of a correlation matrix, confidence interval. It also contains some algorithms to do matrix reordering.

364.2 Home

https://github.com/taiyun/corrplot

364.3 Versions

- 0.73

364.4 License

GPL

364.5 Meta

```
package:
  name: r-corrplot
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.73"

source:
  fn: corrplot_0.73.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/corrplot_0.73.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/corrplot/corrplot_0.73.tar.gz


  # You can add a hash for the file here, like md5 or sha1
```

```
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: seriation, knitr
requirements:
  build:
    - r

  run:
    - r

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('corrplot')" # [not win]
    - "\"%R%\" -e \"library('corrplot')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: https://github.com/taiyun/corrplot
  license: GPL
  summary: The corrplot package is a graphical display of a correlation matrix, confidence interval.
    It also contains some algorithms to do matrix reordering.

# The original CRAN metadata for this package was:

# Package: corrplot
# Type: Package
# Title: Visualization of a correlation matrix
# Version: 0.73
# Author: Taiyun Wei
# Suggests: seriation, knitr
# Maintainer: Taiyun Wei <weitaiyun@gmail.com>
# Description: The corrplot package is a graphical display of a correlation matrix, confidence interv
# License: GPL
# URL: https://github.com/taiyun/corrplot
# BugReports: https://github.com/taiyun/corrplot/issues
# VignetteBuilder: knitr
# Packaged: 2013-10-15 07:24:46 UTC; taiyun
# NeedsCompilation: no
```

```
# Repository: CRAN
# Date/Publication: 2013-10-15 10:04:07

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 365

r-dbchip

365.1 Summary

ChIP-seq differential binding

365.2 Home

http://pages.cs.wisc.edu/~kliang/DBChIP

365.3 Versions

- 1.1.6

365.4 License

GPL (>= 2)

365.5 Meta

```
package:
  name: r-dbchip
  version: "1.1.6"

source:
  fn: DBChIP_1.1.6.tar.gz
  url: http://pages.cs.wisc.edu/~kliang/DBChIP/DBChIP_1.1.6.tar.gz
  md5: f4b22bb2051ad6b2d33d4687754e8cee

build:
  number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
```

```
    - lib/

requirements:
  build:
    - r
    - bioconductor-deseq
    - bioconductor-edger

  run:
    - r
    - bioconductor-deseq
    - bioconductor-edger

test:
  commands:
    - $R -e "library('DBChIP')" # [not win]

about:
  home: http://pages.cs.wisc.edu/~kliang/DBChIP
  license: 'GPL (>= 2)'
  summary: 'ChIP-seq differential binding'
```

CHAPTER 366

r-dendextend

366.1 Summary

Offers a set of functions for extending dendrogram objects in R, letting you visualize and compare trees of hierarchical clusterings. You can (1) Adjust a tree's graphical parameters - the color, size, type, etc of its branches, nodes and labels. (2) Visually and statistically compare different dendrograms to one another.

366.2 Home

http://cran.r-project.org/package=dendextend, https://github.com/talgalili/dendextend/, http://www.r-statistics.com/tag/dendextend/, http://bioinformatics.oxfordjournals.org/content/early/2015/08/18/bioinformatics.btv428

366.3 Versions

- 1.1.2

366.4 License

GPL-2 | GPL-3

366.5 Meta

```
package:
  name: r-dendextend
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "1.1.2"

source:
  fn: dendextend_1.1.2.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/dendextend_1.1.2.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/dendextend/dendextend_1.1.2.tar.gz
```

```
  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: dendextendRcpp (>= 0.5.0), knitr, testthat, colorspace, ggplot2, plyr, ape, profdpm, mic
requirements:
  build:
    - r
    - r-magrittr >=1.0.1
    - r-whisker

  run:
    - r
    - r-magrittr >=1.0.1
    - r-whisker

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('dendextend')" # [not win]
    - "\"%R%\" -e \"library('dendextend')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: http://cran.r-project.org/package=dendextend, https://github.com/talgalili/dendextend/,
    http://www.r-statistics.com/tag/dendextend/, http://bioinformatics.oxfordjournals.org/content/ea
  license: GPL-2 | GPL-3
  summary: Offers a set of functions for extending dendrogram objects in R, letting you visualize
    and compare trees of hierarchical clusterings. You can (1) Adjust a tree's graphical
    parameters - the color, size, type, etc of its branches, nodes and labels. (2) Visually
    and statistically compare different dendrograms to one another.

# The original CRAN metadata for this package was:

# Package: dendextend
# Type: Package
# Title: Extending R's Dendrogram Functionality
# Version: 1.1.2
# Date: 2015-10-30
```

```
# Authors@R: c(person("Tal", "Galili", role = c("aut", "cre", "cph"), email = "tal.galili@gmail.com",
# Description: Offers a set of functions for extending dendrogram objects in R, letting you visualize
# Depends: R (>= 3.0.0)
# Imports: utils, stats, magrittr (>= 1.0.1), whisker
# Suggests: dendextendRcpp (>= 0.5.0), knitr, testthat, colorspace, ggplot2, plyr, ape, profdpm, mici
# Enhances: ggdendro, labeltodendro,dendroextras, data.table, rpart
# VignetteBuilder: knitr
# LazyData: true
# License: GPL-2 | GPL-3
# URL: http://cran.r-project.org/package=dendextend, https://github.com/talgalili/dendextend/, http:/
# BugReports: https://github.com/talgalili/dendextend/issues
# NeedsCompilation: no
# Packaged: 2015-10-31 08:55:48 UTC; junior
# Author: Tal Galili [aut, cre, cph] (http://www.r-statistics.com), Gavin Simpson [ctb], Gregory Jefi
# Maintainer: Tal Galili <tal.galili@gmail.com>
# Repository: CRAN
# Date/Publication: 2015-10-31 16:16:02

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 367

r-diagram

367.1 Summary

Visualises simple graphs (networks) based on a transition matrix, utilities to plot flow diagrams, visualising webs, electrical networks, ... Support for the books "A practical guide to ecological modelling - using R as a simulation platform" by Karline Soetaert and Peter M.J. Herman (2009). Springer. and the book "Solving Differential Equations in R" by Karline Soetaert, Jeff Cash and Francesca Mazzia. Springer. Includes demo(flowchart), demo(plotmat), demo(plotweb)

367.2 Home

367.3 Versions

- 1.6.3

367.4 License

GPL (>= 2)

367.5 Meta

```
package:
  name: r-diagram
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "1.6.3"

source:
  fn: diagram_1.6.3.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/diagram_1.6.3.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/diagram/diagram_1.6.3.tar.gz
```

```
  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/


requirements:
  build:
    - r
    - r-shape

  run:
    - r
    - r-shape

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('diagram')" # [not win]
    - "\"%R%\" -e \"library('diagram')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  #home:
  license: GPL (>= 2)
  summary: Visualises simple graphs (networks) based on a transition matrix, utilities to plot
    flow diagrams,  visualising webs, electrical networks, ...   Support for the books
    "A practical guide to ecological modelling - using R as a simulation platform" by
    Karline Soetaert and Peter M.J. Herman (2009). Springer. and the book "Solving Differential
    Equations in R" by Karline Soetaert, Jeff Cash and Francesca Mazzia. Springer. Includes
    demo(flowchart), demo(plotmat), demo(plotweb)

# The original CRAN metadata for this package was:

# Package: diagram
# Version: 1.6.3
# Date: 2014-11-01
# Title: Functions for visualising simple graphs (networks), plotting flow diagrams
# Author: Karline Soetaert <karline.soetaert@nioz.nl>
# Maintainer: Karline Soetaert <karline.soetaert@nioz.nl>
# Depends: R (>= 2.01) ,shape
```

```
# Description: Visualises simple graphs (networks) based on a transition matrix, utilities to plot f
# License: GPL (>= 2)
# LazyData: yes
# Packaged: 2014-11-01 08:46:06 UTC; rforge
# Repository: CRAN
# Repository/R-Forge/Project: diagram
# Repository/R-Forge/Revision: 69
# Repository/R-Forge/DateTimeStamp: 2014-11-01 08:26:03
# Date/Publication: 2014-11-06 15:08:17
# NeedsCompilation: no

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 368

r-discriminer

368.1 Summary

Functions for Discriminant Analysis and Classification purposes covering various methods such as descriptive, geometric, linear, quadratic, PLS, as well as qualitative discriminant analyses

368.2 Home

http://www.gastonsanchez.com

368.3 Versions

- 0.1_29

368.4 License

GPL-3

368.5 Meta

```
package:
  name: r-discriminer
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.1_29"

source:
  fn: DiscriMiner_0.1-29.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/DiscriMiner_0.1-29.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/DiscriMiner/DiscriMiner_0.1-29.tar.gz


  # You can add a hash for the file here, like md5 or sha1
```

```
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: MASS, FactoMineR
requirements:
  build:
    - r

  run:
    - r

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('DiscriMiner')" # [not win]
    - "\"%R%\" -e \"library('DiscriMiner')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: http://www.gastonsanchez.com
  license: GPL-3
  summary: Functions for Discriminant Analysis and Classification purposes covering various methods
    such as descriptive, geometric, linear, quadratic, PLS, as well as qualitative discriminant
    analyses

# The original CRAN metadata for this package was:

# Package: DiscriMiner
# Type: Package
# Title: Tools of the Trade for Discriminant Analysis
# Version: 0.1-29
# Date: 2013-11-14
# Authors@R: c( person("Gaston", "Sanchez", email = "gaston.stat@gmail.com", role = c("aut", "cre")),
# Depends: R (>= 2.15.0)
# Suggests: MASS, FactoMineR
# Description: Functions for Discriminant Analysis and Classification purposes covering various metho
# License: GPL-3
# URL: http://www.gastonsanchez.com
# LazyData: yes
# Collate: 'DiscriMiner-package.R' 'FRatio.R' 'betweenCov.R' 'betweenSS.R' 'binarize.R' 'classify.R'
```

```
# Packaged: 2013-11-14 19:52:13 UTC; Gaston
# Author: Gaston Sanchez [aut, cre], Charles Determan [ctb]
# Maintainer: Gaston Sanchez <gaston.stat@gmail.com>
# NeedsCompilation: no
# Repository: CRAN
# Date/Publication: 2013-11-15 00:52:30

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 369

r-docopt

369.1 Summary

Define a command-line interface by just giving it a description in the specific format.

369.2 Home

https://github.com/docopt/docopt.R

369.3 Versions

- 0.4.3.3

369.4 License

MIT + file LICENSE

369.5 Meta

```
package:
  name: r-docopt
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.4.3.3"

source:
  fn: docopt_0.4.3.3.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/docopt_0.4.3.3.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/docopt/docopt_0.4.3.3.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
```

```
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: testthat
requirements:
  build:
    - r
    - r-stringr

  run:
    - r
    - r-stringr

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('docopt')" # [not win]
    - "\"%R%\" -e \"library('docopt')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: https://github.com/docopt/docopt.R
  license: MIT + file LICENSE
  summary: Define a command-line interface by just giving it a description in the specific format.

# The original CRAN metadata for this package was:

# Package: docopt
# Type: Package
# Title: Command-Line Interface Specification Language
# Version: 0.4.3.3
# Date: 2015-05-03
# Author: Edwin de Jonge (edwindjonge@gmail.com)
# Maintainer: Edwin de Jonge <edwindjonge@gmail.com>
# Description: Define a command-line interface by just giving it a description in the specific format
# License: MIT + file LICENSE
# URL: https://github.com/docopt/docopt.R
# Imports: stringr
# Depends: methods
# Suggests: testthat
# Packaged: 2015-05-04 09:26:29 UTC; Edwin
```

```
# NeedsCompilation: no
# Repository: CRAN
# Date/Publication: 2015-05-04 12:06:41

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 370

r-dunn.test

370.1 Summary

Computes Dunn's test (1964) for stochastic dominance and reports the results among multiple pairwise comparisons after a Kruskal-Wallis test for stochastic dominance among k groups (Kruskal and Wallis, 1952). The interpretation of stochastic dominance requires an assumption that the CDF of one group does not cross the CDF of the other. 'dunn.test' makes k(k-1)/2 multiple pairwise comparisons based on Dunn's z-test-statistic approximations to the actual rank statistics. The null hypothesis for each pairwise comparison is that the probability of observing a randomly selected value from the first group that is larger than a randomly selected value from the second group equals one half; this null hypothesis corresponds to that of the Wilcoxon-Mann-Whitney rank-sum test. Like the rank-sum test, if the data can be assumed to be continuous, and the distributions are assumed identical except for a difference in location, Dunn's test may be understood as a test for median difference. 'dunn.test' accounts for tied ranks.

370.2 Home

370.3 Versions

- 1.3.1

370.4 License

GPL-2

370.5 Meta

```
package:
  name: r-dunn.test
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "1.3.1"

source:
  fn: dunn.test_1.3.1.tar.gz
  url:
```

```
    - http://cran.r-project.org/src/contrib/dunn.test_1.3.1.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/dunn.test/dunn.test_1.3.1.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/


requirements:
  build:
    - r

  run:
    - r

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('dunn.test')" # [not win]
    - "\"%R%\" -e \"library('dunn.test')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  #home:
  license: GPL-2
  summary: Computes Dunn's test (1964) for stochastic dominance and reports the results among
    multiple pairwise comparisons after a Kruskal-Wallis test for stochastic dominance
    among k groups (Kruskal and Wallis, 1952). The interpretation of stochastic dominance
    requires an assumption that the CDF of one group does not cross the CDF of the other.
    'dunn.test' makes k(k-1)/2 multiple pairwise comparisons based on Dunn's z-test-statistic
    approximations to the actual rank statistics. The null hypothesis for each pairwise
    comparison is that the probability of observing a randomly selected value from the
    first group that is larger than a randomly selected value from the second group
    equals one half; this null hypothesis corresponds to that of the Wilcoxon-Mann-Whitney
    rank-sum test. Like the rank-sum test, if the data can be assumed to be continuous,
    and the distributions are assumed identical except for a difference in location,
    Dunn's test may be understood as a test for median difference. 'dunn.test' accounts
    for tied ranks.
```

```
# The original CRAN metadata for this package was:

# Package: dunn.test
# Version: 1.3.1
# Date: 2015-10-08
# Title: Dunn's Test of Multiple Comparisons Using Rank Sums
# Author: Alexis Dinno <alexis.dinno@pdx.edu>
# Maintainer: Alexis Dinno <alexis.dinno@pdx.edu>
# Description: Computes Dunn's test (1964) for stochastic dominance and reports the results among mu
# License: GPL-2
# LazyData: no
# Encoding: UTF-8
# NeedsCompilation: no
# Packaged: 2015-10-08 15:16:34 UTC; Alexis
# Repository: CRAN
# Date/Publication: 2015-10-08 20:13:40

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 371

r-fail

371.1 Summary

More comfortable interface to work with R data or source files in a key-value fashion.

371.2 Home

https://github.com/mllg/fail

371.3 Versions

- 1.3

371.4 License

BSD_3_clause + file LICENSE

371.5 Meta

```
package:
  name: r-fail
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "1.3"

source:
  fn: fail_1.3.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/fail_1.3.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/fail/fail_1.3.tar.gz

build:
  number: 0
```

```
  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: testthat
requirements:
  build:
    - r
    - r-bbmisc
    - r-checkmate

  run:
    - r
    - r-bbmisc
    - r-checkmate

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('fail')" # [not win]
    - "\"%R%\" -e \"library('fail')\"" # [win]

about:
  home: https://github.com/mllg/fail
  license: BSD_3_clause + file LICENSE
  summary: More comfortable interface to work with R data or source files in a key-value fashion.

# The original CRAN metadata for this package was:

# Package: fail
# Type: Package
# Title: File Abstraction Interface Layer (FAIL)
# Description: More comfortable interface to work with R data or source files in a key-value fashion
# Version: 1.3
# Author: Michel Lang <michellang@gmail.com>
# Maintainer: Michel Lang <michellang@gmail.com>
# URL: https://github.com/mllg/fail
# License: BSD_3_clause + file LICENSE
# Imports: stats, utils, BBmisc, checkmate
# Suggests: testthat
# ByteCompile: yes
# NeedsCompilation: no
# Packaged: 2015-09-30 11:01:23 UTC; lang
# Repository: CRAN
# Date/Publication: 2015-10-01 00:21:25

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 372

r-fda

372.1 Summary

These functions were developed to support functional data analysis as described in Ramsay, J. O. and Silverman, B. W. (2005) Functional Data Analysis. New York: Springer. They were ported from earlier versions in Matlab and S-PLUS. An introduction appears in Ramsay, J. O., Hooker, Giles, and Graves, Spencer (2009) Functional Data Analysis with R and Matlab (Springer). The package includes data sets and script files working many examples including all but one of the 76 figures in this latter book. Matlab versions of the code and sample analyses are no longer distributed through CRAN, as they were when the book was published. For those, ftp from http://www.psych.mcgill.ca/misc/fda/downloads/FDAfuns/ There you find a set of .zip files containing the functions and sample analyses, as well as two .txt files giving instructions for installation and some additional information. The changes from Version 2.4.1 are fixes of bugs in density.fd and removal of functions create.polynomial.basis, polynompen, and polynomial. These were deleted because the monomial basis does the same thing and because there were errors in the code.

372.2 Home

http://www.functionaldata.org

372.3 Versions

- 2.4.4

372.4 License

GPL (>= 2)

372.5 Meta

```
package:
  name: r-fda
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
```

```
  version: "2.4.4"

source:
  fn: fda_2.4.4.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/fda_2.4.4.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/fda/fda_2.4.4.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: deSolve, R.matlab, quadprog, nlme, lattice, RCurl, zoo
requirements:
  build:
    - r
    - r-matrix # [not win]

  run:
    - r
    - r-matrix # [not win]

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('fda')" # [not win]
    - "\"%R%\" -e \"library('fda')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: http://www.functionaldata.org
  license: GPL (>= 2)
  summary: 'These functions were developed to support functional data analysis as described in
    Ramsay, J. O. and Silverman, B. W. (2005) Functional Data Analysis. New York: Springer.  They
    were ported from earlier versions in Matlab and S-PLUS.  An introduction appears
    in Ramsay, J. O., Hooker, Giles, and Graves, Spencer (2009) Functional Data Analysis
    with R and Matlab (Springer). The package includes data sets and script files working
    many examples including all but one of the 76 figures in this latter book.  Matlab
    versions of the code and sample analyses are no longer distributed through CRAN,
```

```
    as they were when the book was published.  For those, ftp from http://www.psych.mcgill.ca/misc/fd
    There you find a set of .zip files containing the functions and sample analyses,
    as well as two .txt files giving instructions for installation and some additional
    information. The changes from Version 2.4.1 are fixes of bugs in density.fd and
    removal of functions create.polynomial.basis, polynompen, and  polynomial. These
    were deleted because the monomial basis does the same thing and because there were
    errors in the code.'


# The original CRAN metadata for this package was:

# Package: fda
# Version: 2.4.4
# Date: 2014.05.03
# Title: Functional Data Analysis
# Author: J. O. Ramsay <ramsay@psych.mcgill.ca>, Hadley Wickham <h.wickham@gmail.com>, Spencer Graves
# Maintainer: J. O. Ramsay <ramsay@psych.mcgill.ca>
# Depends: R (>= 2.10.0), splines, Matrix, graphics
# Suggests: deSolve, R.matlab, quadprog, nlme, lattice, RCurl, zoo
# Description: These functions were developed to support functional data analysis as described in Ram
# License: GPL (>= 2)
# URL: http://www.functionaldata.org
# LazyData: true
# Repository: CRAN
# Repository/R-Forge/Project: fda
# Repository/R-Forge/Revision: 761
# Repository/R-Forge/DateTimeStamp: 2014-12-10 23:04:14
# Date/Publication: 2014-12-16 17:59:38
# Packaged: 2014-12-10 23:25:10 UTC; rforge
# NeedsCompilation: no

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 373

r-flowr

373.1 Summary

This framework allows you to design and implement complex pipelines, and deploy them on your institution's computing cluster. This has been built keeping in mind the needs of bioinformatics workflows. However, it is easily extendable to any field where a series of steps (shell commands) are to be executed in a (work)flow.

373.2 Home

https://github.com/sahilseth/flowr

373.3 Versions

- 0.9.9.5

373.4 License

MIT + file LICENSE

373.5 Meta

```
package:
  name: r-flowr
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.9.9.5"

source:
  fn: flowr_0.9.9.5.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/flowr_0.9.9.5.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/flowr/flowr_0.9.9.5.tar.gz
```

```
  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: reshape2, knitr, ggplot2, openxlsx, testthat, funr
requirements:
  build:
    - r
    - r-diagram
    - r-params >=0.3
    - r-whisker

  run:
    - r
    - r-diagram
    - r-params >=0.3
    - r-whisker

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('flowr')" # [not win]
    - "\"%R%\" -e \"library('flowr')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: https://github.com/sahilseth/flowr
  license: MIT + file LICENSE
  summary: This framework allows you to design and implement complex pipelines, and deploy them
    on your institution's computing cluster. This has been built keeping in mind the
    needs of bioinformatics workflows. However, it is easily extendable to any field
    where a series of steps (shell commands) are to be executed in a (work)flow.

# The original CRAN metadata for this package was:

# Package: flowr
# Type: Package
# Title: Streamlining Design and Deployment of Complex Workflows
# Description: This framework allows you to design and implement complex pipelines, and deploy them
# Version: 0.9.9.5
```

```
# Depends: R (>= 3.0.2), methods, params (>= 0.3), utils
# Imports: diagram, whisker, tools
# Suggests: reshape2, knitr, ggplot2, openxlsx, testthat, funr
# VignetteBuilder: knitr
# URL: https://github.com/sahilseth/flowr
# BugReports: https://github.com/sahilseth/flowr/issues
# Authors@R: c(person("Sahil", "Seth", role = c("aut", "cre"), email = "me@sahilseth.com"))
# License: MIT + file LICENSE
# RoxygenNote: 5.0.1.9000
# NeedsCompilation: no
# Packaged: 2015-12-03 16:30:57 UTC; sahilseth
# Author: Sahil Seth [aut, cre]
# Maintainer: Sahil Seth <me@sahilseth.com>
# Repository: CRAN
# Date/Publication: 2015-12-03 17:54:26

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 374

r-funr

374.1 Summary

A small utility which wraps Rscript and provides access to all R functions from the shell.

374.2 Home

https://github.com/sahilseth/funr

374.3 Versions

- 0.2.0

374.4 License

MIT + file LICENSE

374.5 Meta

```
package:
  name: r-funr
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.2.0"

source:
  fn: funr_0.2.0.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/funr_0.2.0.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/funr/funr_0.2.0.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
```

```
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/


requirements:
  build:
    - r

  run:
    - r

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('funr')" # [not win]
    - "\"%R%\" -e \"library('funr')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: https://github.com/sahilseth/funr
  license: MIT + file LICENSE
  summary: A small utility which wraps Rscript and provides access to all R functions from the
    shell.

# The original CRAN metadata for this package was:

# Package: funr
# Title: Simple Utility Providing Terminal Access to all R Functions
# Description: A small utility which wraps Rscript and provides access to all R functions from the sh
# Version: 0.2.0
# Authors@R: person("Sahil", "Seth", email = "me@sahilseth.com", role = c("aut", "cre"))
# License: MIT + file LICENSE
# LazyData: true
# Imports: utils
# URL: https://github.com/sahilseth/funr
# BugReports: https://github.com/sahilseth/funr/issues
# RoxygenNote: 5.0.1.9000
# NeedsCompilation: no
# Packaged: 2015-12-01 22:08:27 UTC; sahilseth
# Author: Sahil Seth [aut, cre]
# Maintainer: Sahil Seth <me@sahilseth.com>
```

```
# Repository: CRAN
# Date/Publication: 2015-12-02 00:03:25

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 375

r-futile.logger

375.1 Summary

Provides a simple yet powerful logging utility. Based loosely on log4j, futile.logger takes advantage of R idioms to make logging a convenient and easy to use replacement for cat and print statements.

375.2 Home

375.3 Versions

- 1.4.1

375.4 License

LGPL-3

375.5 Meta

```
package:
  name: r-futile.logger
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "1.4.1"

source:
  fn: futile.logger_1.4.1.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/futile.logger_1.4.1.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/futile.logger/futile.logger_1.4.1.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
```

```
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: testthat, jsonlite
requirements:
  build:
    - r
    - r-futile.options
    - r-lambda.r >=1.1.0

  run:
    - r
    - r-futile.options
    - r-lambda.r >=1.1.0

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('futile.logger')" # [not win]
    - "\"%R%\" -e \"library('futile.logger')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  #home:
  license: LGPL-3
  summary: !!python/unicode 'Provides a simple yet powerful logging utility. Based loosely on
    log4j, futile.logger takes advantage of R idioms to make logging a convenient and
    easy to use replacement for cat and print statements.'


# The original CRAN metadata for this package was:

# Package: futile.logger
# Type: Package
# Title: A Logging Utility for R
# Version: 1.4.1
# Date: 2015-04-18
# Author: Brian Lee Yung Rowe
# Maintainer: Brian Lee Yung Rowe <r@zatonovo.com>
# Depends: R (>= 3.0.0)
# Imports: lambda.r (>= 1.1.0), futile.options
# Suggests: testthat, jsonlite
# Description: Provides a simple yet powerful logging utility. Based loosely on log4j, futile.logger
```

```
# License: LGPL-3
# LazyLoad: yes
# Collate: 'options.R' 'appender.R' 'constants.R' 'layout.R' 'logger.R' 'scat.R' 'futile.logger-packa
# Packaged: 2015-04-19 18:43:51 UTC; brian
# NeedsCompilation: no
# Repository: CRAN
# Date/Publication: 2015-04-20 11:48:19

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 376

r-futile.options

376.1 Summary

A scoped options management framework

376.2 Home

376.3 Versions

- 1.0.0

376.4 License

LGPL-3

376.5 Meta

```
package:
  name: r-futile.options
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "1.0.0"

source:
  fn: futile.options_1.0.0.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/futile.options_1.0.0.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/futile.options/futile.options_1.0.0.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
```

```
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/


requirements:
  build:
    - r

  run:
    - r

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('futile.options')" # [not win]
    - "\"%R%\" -e \"library('futile.options')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  #home:
  license: LGPL-3
  summary: !!python/unicode 'A scoped options management framework'


# The original CRAN metadata for this package was:

# Package: futile.options
# Type: Package
# Title: Futile options management
# Version: 1.0.0
# Date: 2010-04-05
# Author: Brian Lee Yung Rowe
# Maintainer: Brian Lee Yung Rowe <r@nurometic.com>
# Depends: R (>= 2.8.0)
# Description: A scoped options management framework
# License: LGPL-3
# LazyLoad: yes
# Packaged: Mon Apr 5 21:09:07 2010; brian
# Repository: CRAN
# Date/Publication: 2010-04-06 08:57:40
# NeedsCompilation: no

# See
# http://docs.continuum.io/conda/build.html for
```

```
# more information about meta.yaml
```

CHAPTER 377

r-future

377.1 Summary

A Future API for R is provided. In programming, a future is an abstraction for a value that may be available at some point in the future. The state of a future can either be unresolved or resolved. As soon as it is resolved, the value is available. Futures are useful constructs in for instance concurrent evaluation, e.g. multicore parallel processing and distributed processing on compute clusters. The purpose of this package is to provide a lightweight interface for using futures in R. Functions 'future()' and 'value()' exist for creating futures and requesting their values. An infix assignment operator '%<=%' exists for creating futures whose values are accessible by the assigned variables (as promises). This package implements the synchronous "lazy" and "eager" futures, and the asynchronous "multicore" future (not on Windows). Additional types of futures are provided by other packages enhancing this package.

377.2 Home

https://github.com/HenrikBengtsson/future

377.3 Versions

- 0.9.0

377.4 License

LGPL (>= 2.1)

377.5 Meta

```
package:
  name: r-future
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.9.0"

source:
```

```
  fn: future_0.9.0.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/future_0.9.0.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/future/future_0.9.0.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: parallel, R.rsp
requirements:
  build:
    - r
    - r-globals >=0.5.0
    - r-listenv

  run:
    - r
    - r-globals >=0.5.0
    - r-listenv

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('future')" # [not win]
    - "\"%R%\" -e \"library('future')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: !!python/unicode 'https://github.com/HenrikBengtsson/future'

  license: LGPL (>= 2.1)
  summary: !!python/unicode 'A Future API for R is provided. In programming, a future is an abstracti
    for a value that may be available at some point in the future. The state of a future
    can either be unresolved or resolved. As soon as it is resolved, the value is available.
    Futures are useful constructs in for instance concurrent evaluation, e.g. multicore
    parallel processing and distributed processing on compute clusters. The purpose
    of this package is to provide a lightweight interface for using futures in R. Functions
    ''future()'' and ''value()'' exist for creating futures and requesting their values.
```

```
    An infix assignment operator ''%<=%'' exists for creating futures whose values are
    accessible by the assigned variables (as promises). This package implements the
    synchronous "lazy" and "eager" futures, and the asynchronous "multicore" future
    (not on Windows). Additional types of futures are provided by other packages enhancing
    this package.'


# The original CRAN metadata for this package was:

# Package: future
# Version: 0.9.0
# Title: A Future API for R
# Imports: listenv, globals (>= 0.5.0)
# Suggests: parallel, R.rsp
# VignetteBuilder: R.rsp
# Authors@R: c(person("Henrik", "Bengtsson", role=c("aut", "cre", "cph"), email = "henrikb@braju.com
# Description: A Future API for R is provided. In programming, a future is an abstraction for a value
# License: LGPL (>= 2.1)
# LazyLoad: TRUE
# URL: https://github.com/HenrikBengtsson/future
# BugReports: https://github.com/HenrikBengtsson/future/issues
# RoxygenNote: 5.0.1
# NeedsCompilation: no
# Packaged: 2015-12-12 01:37:50 UTC; hb
# Author: Henrik Bengtsson [aut, cre, cph]
# Maintainer: Henrik Bengtsson <henrikb@braju.com>
# Repository: CRAN
# Date/Publication: 2015-12-12 09:13:56

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 378

r-getopt

378.1 Summary

Package designed to be used with Rscript to write ‘‘#!” shebang scripts that accept short and long flags/options. Many users will prefer using instead the packages optparse or argparse which add extra features like automatically generated help option and usage, support for default values, positional argument support, etc.

378.2 Home

https://github.com/trevorld/getopt

378.3 Versions

- 1.20.0

378.4 License

GPL (>= 2)

378.5 Meta

```
package:
  name: r-getopt
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "1.20.0"

source:
  fn: getopt_1.20.0.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/getopt_1.20.0.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/getopt/getopt_1.20.0.tar.gz
```

```
  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: testthat
requirements:
  build:
    - r

  run:
    - r

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('getopt')" # [not win]
    - "\"%R%\" -e \"library('getopt')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: https://github.com/trevorld/getopt
  license: GPL (>= 2)
  summary: Package designed to be used with Rscript to write ``#!'' shebang scripts that accept
    short and long flags/options. Many users will prefer using instead the packages
    optparse or argparse which add extra features like automatically generated help
    option and usage, support for default values, positional argument support, etc.

# The original CRAN metadata for this package was:

# Package: getopt
# Type: Package
# Title: C-like getopt behavior.
# Version: 1.20.0
# Author: Allen Day. Contributions from Trevor L Davis.
# Maintainer: Trevor L Davis <trevor.l.davis@stanford.edu>
# URL: https://github.com/trevorld/getopt
# BugReports: https://github.com/trevorld/getopt/issues
# Description: Package designed to be used with Rscript to write ``#!'' shebang scripts that accept s
# License: GPL (>= 2)
# Suggests: testthat
```

```
# Collate: 'getopt.R' 'utils.R'
# Packaged: 2013-08-30 07:02:26 UTC; trevorld
# NeedsCompilation: no
# Repository: CRAN
# Date/Publication: 2013-08-30 10:36:29

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 379

r-getoptlong

379.1 Summary

This is yet another command-line argument parser which wraps the powerful Perl module Getopt::Long and with some adaptation for easier use in R. It also provides a simple way for variable interpolation in R.

379.2 Home

https://github.com/jokergoo/GetoptLong

379.3 Versions

- 0.1.0

379.4 License

GPL (>= 2)

379.5 Meta

```
package:
  name: r-getoptlong
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.1.0"

source:
  fn: GetoptLong_0.1.0.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/GetoptLong_0.1.0.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/GetoptLong/GetoptLong_0.1.0.tar.gz


  # You can add a hash for the file here, like md5 or sha1
```

```
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: testthat (>= 0.3), knitr
requirements:
  build:
    - r
    - r-globaloptions >=0.0.6
    - r-rjson

  run:
    - r
    - r-globaloptions >=0.0.6
    - r-rjson

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('GetoptLong')" # [not win]
    - "\"%R%\" -e \"library('GetoptLong')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: https://github.com/jokergoo/GetoptLong
  license: GPL (>= 2)
  summary: This is yet another command-line argument parser which wraps the  powerful Perl module
    Getopt::Long and with some adaptation for easier use in R. It also provides a simple
    way for variable interpolation in R.

# The original CRAN metadata for this package was:

# Package: GetoptLong
# Type: Package
# Title: Parsing Command-Line Arguments and Variable Interpolation
# Version: 0.1.0
# Date: 2015-3-8
# Author: Zuguang Gu
# Maintainer: Zuguang Gu <z.gu@dkfz.de>
# Depends: R (>= 2.10.0)
# Suggests: testthat (>= 0.3), knitr
```

```
# VignetteBuilder: knitr
# Imports: rjson, methods, GlobalOptions (>= 0.0.6)
# Description: This is yet another command-line argument parser which wraps the  powerful Perl module
# URL: https://github.com/jokergoo/GetoptLong
# SystemRequirements: Perl, Getopt::Long
# License: GPL (>= 2)
# Packaged: 2015-03-09 09:55:20 UTC; IBM
# Repository: CRAN
# Date/Publication: 2015-03-09 12:47:36
# NeedsCompilation: no

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 380

r-ggally

380.1 Summary

GGally is designed to be a helper to ggplot2. It contains templates for different plots to be combined into a plot matrix, a parallel coordinate plot function, as well as a function for making a network plot.

380.2 Home

380.3 Versions

- 0.5.0

380.4 License

GPL (>= 2.0)

380.5 Meta

```
package:
  name: r-ggally
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.5.0"

source:
  fn: GGally_0.5.0.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/GGally_0.5.0.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/GGally/GGally_0.5.0.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
```

```
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: arm (>= 1.7), intergraph (>= 2.0-0), network (>= 1.7.2), RColorBrewer (>= 1.0-5), scales
requirements:
  build:
    - r
    - r-ggplot2 >=1.0.0
    - r-gtable >=0.1.2
    - r-plyr >=1.8
    - r-reshape >=0.8.4
    - r-stringr >=0.6.2

  run:
    - r
    - r-ggplot2 >=1.0.0
    - r-gtable >=0.1.2
    - r-plyr >=1.8
    - r-reshape >=0.8.4
    - r-stringr >=0.6.2

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('GGally')" # [not win]
    - "\"%R%\" -e \"library('GGally')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  #home:
  license: GPL (>= 2.0)
  summary: !!python/unicode 'GGally is designed to be a helper to ggplot2. It contains templates
    for different plots to be combined into a plot matrix, a parallel coordinate plot
    function, as well as a function for making a network plot.'


# The original CRAN metadata for this package was:

# Package: GGally
# Version: 0.5.0
# Date: 2014-12-01
# Maintainer: Barret Schloerke <schloerke@gmail.com>
# License: GPL (>= 2.0)
```

```
# Title: Extension to ggplot2.
# Type: Package
# LazyLoad: yes
# LazyData: true
# Author: Barret Schloerke <schloerke@gmail.com>, Jason Crowley <crowley.jason.s@gmail.com>, Di Cook
# Description: GGally is designed to be a helper to ggplot2. It contains templates for different plo
# Depends: R (>= 2.14)
# Imports: ggplot2 (>= 1.0.0), grid (>= 3.0.0), gtable (>= 0.1.2), plyr (>= 1.8), reshape (>= 0.8.4),
# Suggests: arm (>= 1.7), intergraph (>= 2.0-0), network (>= 1.7.2), RColorBrewer (>= 1.0-5), scales
# Packaged: 2014-12-01 21:52:05 UTC; barret
# NeedsCompilation: no
# Repository: CRAN
# Date/Publication: 2014-12-02 00:32:53

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 381

r-ggdendro

381.1 Summary

This is a set of tools for dendrograms and tree plots using 'ggplot2'. The 'ggplot2' philosophy is to clearly separate data from the presentation. Unfortunately the plot method for dendrograms plots directly to a plot device without exposing the data. The 'ggdendro' package resolves this by making available functions that extract the dendrogram plot data. The package provides implementations for tree, rpart, as well as diana and agnes cluster diagrams.

381.2 Home

https://github.com/andrie/ggdendro

381.3 Versions

- 0.1_17

381.4 License

GPL-2 | GPL-3

381.5 Meta

```
package:
  name: r-ggdendro
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.1_17"

source:
  fn: ggdendro_0.1-17.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/ggdendro_0.1-17.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/ggdendro/ggdendro_0.1-17.tar.gz
```

```
  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: rpart(>= 4.0-0), tree, testthat, knitr, cluster
requirements:
  build:
    - r
    - r-mass # [not win]
    - r-ggplot2 >=0.9.2

  run:
    - r
    - r-mass # [not win]
    - r-ggplot2 >=0.9.2

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('ggdendro')" # [not win]
    - "\"%R%\" -e \"library('ggdendro')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: !!python/unicode 'https://github.com/andrie/ggdendro'

  license: GPL-2 | GPL-3
  summary: !!python/unicode 'This is a set of tools for dendrograms and tree plots using ''ggplot2''
    ''ggplot2'' philosophy is to clearly separate data from the presentation. Unfortunately
    the plot method for dendrograms plots directly to a plot device without exposing
    the data. The ''ggdendro'' package resolves this by making available functions that
    extract the dendrogram plot data. The package  provides implementations for tree,
    rpart, as well as diana and agnes cluster diagrams.'


# The original CRAN metadata for this package was:

# Package: ggdendro
# Authors@R: c(person("Andrie", "de Vries", role=c("aut", "cre"), email="apdevries@gmail.com"), perso
```

```
# License: GPL-2 | GPL-3
# Title: Create Dendrograms and Tree Diagrams Using 'ggplot2'
# LazyData: true
# LazyLoad: true
# ByteCompile: true
# Description: This is a set of tools for dendrograms and tree plots using 'ggplot2'.  The 'ggplot2'
# Version: 0.1-17
# URL: https://github.com/andrie/ggdendro
# BugReports: https://github.com/andrie/ggdendro/issues
# Date: 2015-09-06
# Imports: MASS, ggplot2(>= 0.9.2)
# Suggests: rpart(>= 4.0-0), tree, testthat, knitr, cluster
# VignetteBuilder: knitr
# Packaged: 2015-09-08 05:40:23 UTC; adevries
# Author: Andrie de Vries [aut, cre], Brian D. Ripley [aut] (author of package tree)
# Maintainer: Andrie de Vries <apdevries@gmail.com>
# NeedsCompilation: no
# Repository: CRAN
# Date/Publication: 2015-09-08 08:17:05

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 382

r-globaloptions

382.1 Summary

It provides more controls on the option values such as validation and filtering on the values, making options invisible or private.

382.2 Home

https://github.com/jokergoo/GlobalOptions

382.3 Versions

- 0.0.8

382.4 License

GPL (>= 2)

382.5 Meta

```
package:
  name: r-globaloptions
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.0.8"

source:
  fn: GlobalOptions_0.0.8.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/GlobalOptions_0.0.8.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/GlobalOptions/GlobalOptions_0.0.8.tar.gz


  # You can add a hash for the file here, like md5 or sha1
```

```
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: testthat (>= 0.3), knitr
requirements:
  build:
    - r

  run:
    - r

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('GlobalOptions')" # [not win]
    - "\"%R%\" -e \"library('GlobalOptions')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: https://github.com/jokergoo/GlobalOptions
  license: GPL (>= 2)
  summary: It provides more controls on the option values such as validation and filtering on
    the values, making options invisible or private.

# The original CRAN metadata for this package was:

# Package: GlobalOptions
# Type: Package
# Title: Generate Functions to Get or Set Global Options
# Version: 0.0.8
# Date: 2015-8-14
# Author: Zuguang Gu
# Maintainer: Zuguang Gu <z.gu@dkfz.de>
# Depends: R (>= 2.10.0), methods
# Suggests: testthat (>= 0.3), knitr
# VignetteBuilder: knitr
# Description: It provides more controls on the option values such as validation and filtering on the
# URL: https://github.com/jokergoo/GlobalOptions
# License: GPL (>= 2)
# Packaged: 2015-08-18 15:49:10 UTC; jokergoo
```

```
# Repository: CRAN
# Date/Publication: 2015-08-18 20:20:53
# NeedsCompilation: no

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 383

r-globals

383.1 Summary

Identifies global ("unknown") objects in R expressions by code inspection using various strategies, e.g. conservative or liberal. The objective of this package is to make it as simple as possible to identify global objects for the purpose of exporting them in distributed compute environments.

383.2 Home

https://github.com/HenrikBengtsson/globals

383.3 Versions

- 0.6.0

383.4 License

LGPL (>= 2.1)

383.5 Meta

```
package:
  name: r-globals
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.6.0"

source:
  fn: globals_0.6.0.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/globals_0.6.0.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/globals/globals_0.6.0.tar.gz
```

```
  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/


requirements:
  build:
    - r
    - r-codetools # [not win]

  run:
    - r
    - r-codetools # [not win]

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('globals')" # [not win]
    - "\"%R%\" -e \"library('globals')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: !!python/unicode 'https://github.com/HenrikBengtsson/globals'

  license: LGPL (>= 2.1)
  summary: !!python/unicode 'Identifies global ("unknown") objects in R expressions by code inspectio
    using various strategies, e.g. conservative or liberal. The objective of this package
    is to make it as simple as possible to identify global objects for the purpose of
    exporting them in distributed compute environments.'


# The original CRAN metadata for this package was:

# Package: globals
# Version: 0.6.0
# Depends: R (>= 3.1.2)
# Imports: codetools
# Title: Identify Global Objects in R Expressions
# Authors@R: c( person("Henrik", "Bengtsson", role=c("aut", "cre", "cph"), email="henrikb@braju.com",
# Description: Identifies global ("unknown") objects in R expressions by code inspection using variou
```

```
# License: LGPL (>= 2.1)
# LazyLoad: TRUE
# ByteCompile: TRUE
# URL: https://github.com/HenrikBengtsson/globals
# BugReports: https://github.com/HenrikBengtsson/globals/issues
# RoxygenNote: 5.0.1
# NeedsCompilation: no
# Packaged: 2015-12-12 15:03:09 UTC; hb
# Author: Henrik Bengtsson [aut, cre, cph]
# Maintainer: Henrik Bengtsson <henrikb@braju.com>
# Repository: CRAN
# Date/Publication: 2015-12-12 18:49:07

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 384

r-gmd

384.1 Summary

GMD is a package for non-parametric distance measurement between two discrete frequency distributions.

384.2 Home

http://CRAN.R-project.org/package=GMD

384.3 Versions

- 0.3.3

384.4 License

GPL (>= 2)

384.5 Meta

```
package:
  name: r-gmd
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.3.3"

source:
  fn: GMD_0.3.3.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/GMD_0.3.3.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/GMD/GMD_0.3.3.tar.gz

build:
  number: 0
```

```
  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: datasets, MASS, cluster
requirements:
  build:
    - r
    - r-gplots

  run:
    - r
    - r-gplots

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('GMD')" # [not win]
    - "\"%R%\" -e \"library('GMD')\"" # [win]

about:
  home: http://CRAN.R-project.org/package=GMD
  license: GPL (>= 2)
  summary: GMD is a package for non-parametric distance measurement between two discrete frequency di

# The original CRAN metadata for this package was:

# Package: GMD
# Type: Package
# Version: 0.3.3
# Date: 2014-08-26 15:46:45 EDT
# Title: Generalized Minimum Distance of distributions
# Description: GMD is a package for non-parametric distance measurement between two discrete frequenc
# License: GPL (>= 2)
# LazyLoad: TRUE
# NeedsCompilation: no
# URL: http://CRAN.R-project.org/package=GMD
# Repository: CRAN
# Depends: R (>= 3.1.0)
# Imports: stats, grDevices, gplots
# Suggests: datasets, MASS, cluster
# Collate: 'GMD-package.R' 'imports.R' 'util.R' 'GMD-internal.R' 'GMD-data.R' 'ghist.R' 'gdist.R' 'cs
# Authors@R: c( person("Xiaobei", "Zhao", email="xiaobei@binf.ku.dk", role=c("aut", "cre", "cph")), p
# Maintainer: Xiaobei Zhao <xiaobei@binf.ku.dk>
# Packaged: 2014-08-27 12:02:34 UTC; xiaobei
# Author: Xiaobei Zhao [aut, cre, cph], Albin Sandelin [aut]
# Date/Publication: 2014-08-27 14:29:53

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 385

r-gsalib

385.1 Summary

This package contains utility functions used by the Genome Analysis Toolkit (GATK) to load tables and plot data. The GATK is a toolkit for variant discovery in high-throughput sequencing data.

385.2 Home

385.3 Versions

- 2.1

385.4 License

MIT + file LICENSE

385.5 Meta

```
package:
  name: r-gsalib
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "2.1"

source:
  fn: gsalib_2.1.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/gsalib_2.1.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/gsalib/gsalib_2.1.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
```

```
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/


requirements:
  build:
    - r

  run:
    - r

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('gsalib')" # [not win]
    - "\"%R%\" -e \"library('gsalib')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  #home:
  license: MIT + file LICENSE
  summary: !!python/unicode 'This package contains utility functions used by the Genome Analysis
    Toolkit (GATK) to load tables and plot data. The GATK is a toolkit for variant discovery
    in high-throughput sequencing data.'


# The original CRAN metadata for this package was:

# Package: gsalib
# Type: Package
# Title: Utility Functions For GATK
# Version: 2.1
# Date: 2014-12-09
# Author: Kiran Garimella
# Maintainer: Geraldine Van der Auwera <vdauwera@broadinstitute.org>
# Description: This package contains utility functions used by the Genome Analysis Toolkit (GATK) to
# License: MIT + file LICENSE
# LazyLoad: yes
# Packaged: 2014-12-09 21:51:34 UTC; vdauwera
# NeedsCompilation: no
# Repository: CRAN
# Date/Publication: 2014-12-10 08:09:01
```

```
# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 386

r-hdrcde

386.1 Summary

Computation of highest density regions in one and two dimensions, kernel estimation of univariate density functions conditional on one covariate, and multimodal regression.

386.2 Home

http://www.robjhyndman.com/software/hdrcde

386.3 Versions

- 3.1

386.4 License

GPL (>= 2)

386.5 Meta

```
package:
  name: r-hdrcde
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "3.1"

source:
  fn: hdrcde_3.1.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/hdrcde_3.1.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/hdrcde/hdrcde_3.1.tar.gz


  # You can add a hash for the file here, like md5 or sha1
```

```
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/


requirements:
  build:
    - r
    - r-kernsmooth # [not win]
    - r-ash
    - r-ks
    - r-locfit
    - r-mvtnorm

  run:
    - r
    - r-kernsmooth # [not win]
    - r-ash
    - r-ks
    - r-locfit
    - r-mvtnorm

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('hdrcde')" # [not win]
    - "\"%R%\" -e \"library('hdrcde')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: !!python/unicode 'http://www.robjhyndman.com/software/hdrcde'

  license: GPL (>= 2)
  summary: !!python/unicode 'Computation of highest density regions in one and two dimensions,
    kernel estimation of univariate density functions conditional on one covariate,
    and multimodal regression.'


# The original CRAN metadata for this package was:

# Package: hdrcde
```

```
# Type: Package
# Title: Highest density regions and conditional density estimation
# Version: 3.1
# Date: 2013-10-19
# Author: Rob J Hyndman <Rob.Hyndman@monash.edu> with contributions from Jochen Einbeck and Matt Wand
# Maintainer: Rob J Hyndman <Rob.Hyndman@monash.edu>
# Depends: R (>= 2.15), mvtnorm
# Imports: locfit, ash, ks, KernSmooth
# LazyData: yes
# LazyLoad: yes
# Description: Computation of highest density regions in one and two dimensions, kernel estimation of
# License: GPL (>= 2)
# URL: http://www.robjhyndman.com/software/hdrcde
# Packaged: 2013-10-19 12:01:16 UTC; hyndman
# NeedsCompilation: yes
# Repository: CRAN
# Date/Publication: 2013-10-19 15:53:16

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 387

r-hwriter

387.1 Summary

Easy-to-use and versatile functions to output R objects in HTML format

387.2 Home

387.3 Versions

- 1.3.2

387.4 License

LGPL-2.1

387.5 Meta

```
package:
  name: r-hwriter
  version: "1.3.2"

source:
  fn: hwriter_1.3.2.tar.gz
  url: http://cran.r-project.org/src/contrib/hwriter_1.3.2.tar.gz

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  number: 0

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/
```

```
requirements:
  build:
    - r

  run:
    - r

test:
  commands:
    - $R -e "library('hwriter')" # [not win]


about:
  license: LGPL-2.1
  summary: 'Easy-to-use and versatile functions to output R objects in HTML format'
```

CHAPTER 388

r-ks

388.1 Summary

Kernel smoothers for univariate and multivariate data.

388.2 Home

http://www.mvstat.net/tduong

388.3 Versions

- 1.10.0

388.4 License

GPL-2 | GPL-3

388.5 Meta

```
package:
  name: r-ks
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "1.10.0"

source:
  fn: ks_1.10.0.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/ks_1.10.0.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/ks/ks_1.10.0.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
```

```
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: MASS
requirements:
  build:
    - r
    - r-kernsmooth >=2.22 # [not win]
    - r-misc3d >=0.4_0
    - r-multicool
    - r-mvtnorm >=1.0_0
    - r-rgl >=0.66

  run:
    - r
    - r-kernsmooth >=2.22 # [not win]
    - r-misc3d >=0.4_0
    - r-multicool
    - r-mvtnorm >=1.0_0
    - r-rgl >=0.66

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('ks')" # [not win]
    - "\"%R%\" -e \"library('ks')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: !!python/unicode 'http://www.mvstat.net/tduong'

  license: GPL-2 | GPL-3
  summary: !!python/unicode 'Kernel smoothers for univariate and multivariate data.'


# The original CRAN metadata for this package was:

# Package: ks
# Version: 1.10.0
# Date: 2015-10-22
# Title: Kernel Smoothing
```

```
# Author: Tarn Duong <tarn.duong@gmail.com>
# Maintainer: Tarn Duong <tarn.duong@gmail.com>
# Depends: R (>= 1.4.0), KernSmooth (>= 2.22), misc3d (>= 0.4-0), mvtnorm (>= 1.0-0), rgl (>= 0.66)
# Imports: grDevices, graphics, multicool, stats, utils
# Suggests: MASS
# Description: Kernel smoothers for univariate and multivariate data.
# License: GPL-2 | GPL-3
# URL: http://www.mvstat.net/tduong
# NeedsCompilation: yes
# Packaged: 2015-10-22 20:15:26 UTC; duongt
# Repository: CRAN
# Date/Publication: 2015-10-23 01:29:22

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 389

r-lambda.r

389.1 Summary

A language extension to efficiently write functional programs in R. Syntax extensions include multi-part function definitions, pattern matching, guard statements, built-in (optional) type safety.

389.2 Home

389.3 Versions

- 1.1.7

389.4 License

LGPL-3

389.5 Meta

```
package:
  name: r-lambda.r
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "1.1.7"

source:
  fn: lambda.r_1.1.7.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/lambda.r_1.1.7.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/lambda.r/lambda.r_1.1.7.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
```

```
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: RUnit
requirements:
  build:
    - r

  run:
    - r

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('lambda.r')" # [not win]
    - "\"%R%\" -e \"library('lambda.r')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  #home:
  license: LGPL-3
  summary: !!python/unicode 'A language extension to efficiently write functional programs in
    R. Syntax extensions include multi-part function definitions, pattern matching,
    guard statements, built-in (optional) type safety.'


# The original CRAN metadata for this package was:

# Package: lambda.r
# Type: Package
# Title: Modeling Data with Functional Programming
# Version: 1.1.7
# Date: 2015-03-19
# Depends: R (>= 3.0.0)
# Suggests: RUnit
# Author: Brian Lee Yung Rowe
# Maintainer: Brian Lee Yung Rowe <r@zatonovo.com>
# Description: A language extension to efficiently write functional programs in R. Syntax extensions
# License: LGPL-3
# LazyLoad: yes
# Packaged: 2015-03-20 00:09:00 UTC; brian
# NeedsCompilation: no
# Repository: CRAN
```

```
# Date/Publication: 2015-03-20 07:03:24

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 390

r-listenv

390.1 Summary

List environments are environments that can be indexed similarly to lists, e.g. 'x <- listenv(); x[[2]] <- "b"; names(x)[2] <- "B"; print(x$B)'.

390.2 Home

https://github.com/HenrikBengtsson/listenv

390.3 Versions

- 0.5.0

390.4 License

LGPL (>= 2.1)

390.5 Meta

```
package:
  name: r-listenv
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.5.0"

source:
  fn: listenv_0.5.0.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/listenv_0.5.0.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/listenv/listenv_0.5.0.tar.gz


  # You can add a hash for the file here, like md5 or sha1
```

```
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: R.rsp
requirements:
  build:
    - r

  run:
    - r

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('listenv')" # [not win]
    - "\"%R%\" -e \"library('listenv')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: !!python/unicode 'https://github.com/HenrikBengtsson/listenv'

  license: LGPL (>= 2.1)
  summary: !!python/unicode 'List environments are environments that can be indexed similarly
    to lists, e.g. ''x <- listenv(); x[[2]] <- "b"; names(x)[2] <- "B"; print(x$B)''.'


# The original CRAN metadata for this package was:

# Package: listenv
# Version: 0.5.0
# Depends: R (>= 3.1.2)
# Suggests: R.rsp
# VignetteBuilder: R.rsp
# Title: Environments Behaving (Almost) as Lists
# Authors@R: c(person("Henrik", "Bengtsson", role=c("aut", "cre", "cph"), email = "henrikb@braju.com
# Description: List environments are environments that can be indexed similarly to lists, e.g. 'x <-
# License: LGPL (>= 2.1)
# LazyLoad: TRUE
# URL: https://github.com/HenrikBengtsson/listenv
# BugReports: https://github.com/HenrikBengtsson/listenv/issues
```

```
# NeedsCompilation: no
# Packaged: 2015-10-30 20:05:21 UTC; hb
# Author: Henrik Bengtsson [aut, cre, cph]
# Maintainer: Henrik Bengtsson <henrikb@braju.com>
# Repository: CRAN
# Date/Publication: 2015-10-31 00:16:07

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 391

r-locfit

391.1 Summary

Local regression, likelihood and density estimation.

391.2 Home

391.3 Versions

- 1.5_9.1

391.4 License

GPL (>= 2)

391.5 Meta

```
package:
  name: r-locfit
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "1.5_9.1"

source:
  fn: locfit_1.5-9.1.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/locfit_1.5-9.1.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/locfit/locfit_1.5-9.1.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
```

```
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: akima, gam
requirements:
  build:
    - r
    - r-lattice # [not win]
    - gcc # [not win]

  run:
    - r
    - r-lattice # [not win]
    - libgcc # [not win]

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('locfit')" # [not win]
    - "\"%R%\" -e \"library('locfit')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  #home:
  license: GPL (>= 2)
  summary: !!python/unicode 'Local regression, likelihood and density estimation.'


# The original CRAN metadata for this package was:

# Package: locfit
# Version: 1.5-9.1
# Title: Local Regression, Likelihood and Density Estimation.
# Date: 2013-03-22
# Author: Catherine Loader
# Maintainer: Andy Liaw <andy_liaw@merck.com>
# Description: Local regression, likelihood and density estimation.
# Depends: R (>= 2.0.1)
# Imports: lattice
# Suggests: akima, gam
# License: GPL (>= 2)
# Packaged: 2013-04-20 06:56:26 UTC; ripley
# Repository: CRAN
# Date/Publication: 2013-04-20 09:01:16
```

```
# NeedsCompilation: yes

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 392

r-lsd

392.1 Summary

Create lots of colorful plots in a plethora of variations (try the LSD demotour())

392.2 Home

392.3 Versions

- 3.0

392.4 License

Unlimited

392.5 Meta

```
package:
  name: r-lsd
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "3.0"

source:
  fn: LSD_3.0.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/LSD_3.0.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/LSD/LSD_3.0.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
```

```
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/


requirements:
  build:
    - r

  run:
    - r

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('LSD')" # [not win]
    - "\"%R%\" -e \"library('LSD')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  #home:
  license: Unlimited
  summary: !!python/unicode 'Create lots of colorful plots in a plethora of variations (try the
    LSD demotour() )'


# The original CRAN metadata for this package was:

# Package: LSD
# Type: Package
# Title: Lots of Superior Depictions
# Version: 3.0
# Date: 2015-01-02
# Author: Bjoern Schwalb, Achim Tresch, Phillipp Torkler, Sebastian Duemcke, Carina Demel
# Maintainer: Bjoern Schwalb <schwalb.bjoern@gmail.com>
# Description: Create lots of colorful plots in a plethora of variations (try the LSD demotour() )
# License: Unlimited
# LazyLoad: yes
# Packaged: 2015-01-08 14:03:59 UTC; bschwal
# NeedsCompilation: no
# Repository: CRAN
# Date/Publication: 2015-01-09 07:58:48

# See
# http://docs.continuum.io/conda/build.html for
```

```
# more information about meta.yaml
```

CHAPTER 393

r-matrixstats

393.1 Summary

High-performing functions operating on rows and columns of matrices, e.g. col / rowMedians(), col / rowRanks(), and col / rowSds(). Functions optimized per data type and for subsetted calculations such that both memory usage and processing time is minimized. There are also optimized vector-based methods, e.g. binMeans(), madDiff() and weightedMedians().

393.2 Home

https://github.com/HenrikBengtsson/matrixStats

393.3 Versions

- 0.50.1

393.4 License

Artistic-2.0

393.5 Meta

```
package:
  name: r-matrixstats
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.50.1"

source:
  fn: matrixStats_0.50.1.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/matrixStats_0.50.1.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/matrixStats/matrixStats_0.50.1.tar.gz
```

```
  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: base64enc, ggplot2, knitr, microbenchmark, R.devices, R.rsp
requirements:
  build:
    - r

  run:
    - r

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('matrixStats')" # [not win]
    - "\"%R%\" -e \"library('matrixStats')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: !!python/unicode 'https://github.com/HenrikBengtsson/matrixStats'

  license: Artistic-2.0
  summary: !!python/unicode 'High-performing functions operating on rows and columns of matrices,
    e.g. col / rowMedians(), col / rowRanks(), and col / rowSds().  Functions optimized
    per data type and for subsetted calculations such that both memory usage and processing
    time is minimized.  There are also optimized vector-based methods, e.g. binMeans(),
    madDiff() and weightedMedians().'


# The original CRAN metadata for this package was:

# Package: matrixStats
# Version: 0.50.1
# Depends: R (>= 2.12.0)
# Imports: methods
# Suggests: base64enc, ggplot2, knitr, microbenchmark, R.devices, R.rsp
# VignetteBuilder: R.rsp
# Date: 2015-12-14
```

```
# Title: Functions that Apply to Rows and Columns of Matrices (and to Vectors)
# Authors@R: c( person("Henrik", "Bengtsson", role=c("aut", "cre", "cph"), email="henrikb@braju.com",
# Author: Henrik Bengtsson [aut, cre, cph], Hector Corrada Bravo [ctb], Robert Gentleman [ctb], Ola B
# Maintainer: Henrik Bengtsson <henrikb@braju.com>
# Description: High-performing functions operating on rows and columns of matrices, e.g. col / rowMed
# License: Artistic-2.0
# LazyLoad: TRUE
# NeedsCompilation: yes
# ByteCompile: TRUE
# biocViews: Infrastructure, Statistics
# URL: https://github.com/HenrikBengtsson/matrixStats
# BugReports: https://github.com/HenrikBengtsson/matrixStats/issues
# Packaged: 2015-12-15 02:56:11 UTC; hb
# Repository: CRAN
# Date/Publication: 2015-12-15 09:27:16

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 394

r-mclust

394.1 Summary

Normal Mixture Modelling fitted via EM algorithm for Model-Based Clustering, Classification, and Density Estimation, including Bayesian regularization.

394.2 Home

http://www.stat.washington.edu/mclust/

394.3 Versions

- 5.1

394.4 License

GPL (>= 2)

394.5 Meta

```
package:
  name: r-mclust
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "5.1"

source:
  fn: mclust_5.1.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/mclust_5.1.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/mclust/mclust_5.1.tar.gz


  # You can add a hash for the file here, like md5 or sha1
```

```
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  number: 0

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: knitr (>= 1.8), rmarkdown (>= 0.6), mix
requirements:
  build:
    - r
    - gcc # [not win]

  run:
    - r
    - libgcc # [not win]

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('mclust')" # [not win]
    - "\"%R%\" -e \"library('mclust')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: http://www.stat.washington.edu/mclust/
  license: GPL (>= 2)
  summary: Normal Mixture Modelling fitted via EM algorithm for Model-Based Clustering, Classificatio
    and Density Estimation, including Bayesian regularization.

# The original CRAN metadata for this package was:

# Package: mclust
# Version: 5.1
# Date: 2015-10-24
# Authors@R: c(person("Chris", "Fraley", role = "aut"), person("Adrian E.", "Raftery", role = "aut"),
# Title: Normal Mixture Modelling for Model-Based Clustering, Classification, and Density Estimation
# Description: Normal Mixture Modelling fitted via EM algorithm for Model-Based Clustering, Classific
# Depends: R (>= 3.0)
# Imports: stats, utils, graphics, grDevices
# Suggests: knitr (>= 1.8), rmarkdown (>= 0.6), mix
# License: GPL (>= 2)
# URL: http://www.stat.washington.edu/mclust/
# VignetteBuilder: knitr
```

```
# Repository: CRAN
# ByteCompile: true
# LazyLoad: yes
# NeedsCompilation: yes
# Packaged: 2015-10-26 17:30:30 UTC; luca
# Author: Chris Fraley [aut], Adrian E. Raftery [aut], Luca Scrucca [aut, cre], Thomas Brendan Murphy
# Maintainer: Luca Scrucca <luca@stat.unipg.it>
# Date/Publication: 2015-10-27 08:10:04

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 395

r-misc3d

395.1 Summary

A collection of miscellaneous 3d plots, including isosurfaces.

395.2 Home

395.3 Versions

- 0.8_4

395.4 License

GPL

395.5 Meta

```
package:
  name: r-misc3d
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.8_4"

source:
  fn: misc3d_0.8-4.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/misc3d_0.8-4.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/misc3d/misc3d_0.8-4.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
```

```
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: rgl, tkrplot, MASS
requirements:
  build:
    - r

  run:
    - r

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('misc3d')" # [not win]
    - "\"%R%\" -e \"library('misc3d')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  #home:
  license: GPL
  summary: !!python/unicode 'A collection of miscellaneous 3d plots, including isosurfaces.'


# The original CRAN metadata for this package was:

# Package: misc3d
# Title: Miscellaneous 3D Plots
# Version: 0.8-4
# Author: Dai Feng and Luke Tierney
# Maintainer: Luke Tierney <luke-tierney@uiowa.edu>
# Suggests: rgl, tkrplot, MASS
# Description: A collection of miscellaneous 3d plots, including isosurfaces.
# License: GPL
# Packaged: 2013-01-25 14:23:34 UTC; luke
# Repository: CRAN
# Date/Publication: 2013-01-25 15:57:56
# NeedsCompilation: no

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 396

r-multicool

396.1 Summary

A set of tools to permute multisets without loops or hash tables and to generate integer partitions. The permutation functions are based on C code from Aaron Williams. Cool-lex order is similar to colexicographical order. The algorithm is described in Williams, A. Loopless Generation of Multiset Permutations by Prefix Shifts. SODA 2009, Symposium on Discrete Algorithms, New York, United States. The permutation code is distributed without restrictions. The code for stable and efficient computation of multinomial coefficients comes from Dave Barber. The code can be download from http://home.comcast.net/~tamivox/dave/multinomial/index.html and is distributed without conditions. The package also generates the integer partitions of a positive, non-zero integer n. The C++ code for this is based on Python code from Jerome Kelleher which can be found here http://jeromekelleher.net/partitions.php. The C++ code and Python code are distributed without conditions.

396.2 Home

396.3 Versions

- 0.1_9

396.4 License

GPL-2

396.5 Meta

```
package:
  name: r-multicool
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.1_9"

source:
  fn: multicool_0.1-9.tar.gz
  url:
```

```
    - http://cran.r-project.org/src/contrib/multicool_0.1-9.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/multicool/multicool_0.1-9.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/


requirements:
  build:
    - r
    - r-rcpp >=0.11.2

  run:
    - r
    - r-rcpp >=0.11.2

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('multicool')" # [not win]
    - "\"%R%\" -e \"library('multicool')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  #home:
  license: GPL-2
  summary: !!python/unicode 'A set of tools to permute multisets without loops or hash tables
    and to generate integer partitions. The permutation functions are based on C code
    from Aaron Williams. Cool-lex order is similar to colexicographical order. The algorithm
    is described in Williams, A. Loopless Generation of Multiset Permutations by Prefix
    Shifts. SODA 2009, Symposium on Discrete Algorithms, New York, United States. The
    permutation code is distributed without restrictions. The code for stable and efficient
    computation of multinomial coefficients comes from Dave Barber. The code can be
    download from http://home.comcast.net/~tamivox/dave/multinomial/index.html and is
    distributed without conditions. The package also generates the integer partitions
    of a positive, non-zero integer n. The C++ code for this is based on Python code
    from Jerome Kelleher which can be found here http://jeromekelleher.net/partitions.php.
    The C++ code and Python code are distributed without conditions.'
```

```
# The original CRAN metadata for this package was:

# Package: multicool
# Type: Package
# Title: Permutations of Multisets in Cool-Lex Order
# Version: 0.1-9
# Date: 2015-10-28
# Author: James Curran, Aaron Williams, Jerome Kelleher, Dave Barber
# Maintainer: James Curran <j.curran@auckland.ac.nz>
# Description: A set of tools to permute multisets without loops or hash tables and to generate integ
# License: GPL-2
# Depends: methods, Rcpp (>= 0.11.2)
# LinkingTo: Rcpp
# RcppModules: Multicool
# NeedsCompilation: yes
# Packaged: 2015-10-28 08:46:16 UTC; jcur002
# Repository: CRAN
# Date/Publication: 2015-10-28 18:39:18

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 397

r-nozzle.r1

397.1 Summary

The Nozzle package provides an API to generate HTML reports with dynamic user interface elements based on JavaScript and CSS (Cascading Style Sheets). Nozzle was designed to facilitate summarization and rapid browsing of complex results in data analysis pipelines where multiple analyses are performed frequently on big data sets. The package can be applied to any project where user-friendly reports need to be created.

397.2 Home

http://github.com/parklab/nozzle, http://gdac.broadinstitute.org/nozzle

397.3 Versions

- 1.1_1

397.4 License

LGPL-2

397.5 Meta

```
package:
  name: r-nozzle.r1
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "1.1_1"

source:
  fn: Nozzle.R1_1.1-1.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/Nozzle.R1_1.1-1.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/Nozzle.R1/Nozzle.R1_1.1-1.tar.gz
```

```
  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/


requirements:
  build:
    - r

  run:
    - r

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('Nozzle.R1')" # [not win]
    - "\"%R%\" -e \"library('Nozzle.R1')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: !!python/unicode 'http://github.com/parklab/nozzle, http://gdac.broadinstitute.org/nozzle'

  license: LGPL-2
  summary: !!python/unicode 'The Nozzle package provides an API to generate HTML reports with
    dynamic user interface elements based on JavaScript and CSS (Cascading Style Sheets).
    Nozzle was designed to facilitate summarization and rapid browsing of complex results
    in data analysis pipelines where multiple analyses are performed frequently on big
    data sets. The package can be applied to any project where user-friendly reports
    need to be created.'


# The original CRAN metadata for this package was:

# Package: Nozzle.R1
# Type: Package
# Title: Nozzle Reports
# Version: 1.1-1
# Date: 2012-05-15
# Author: Nils Gehlenborg <nils@hms.harvard.edu>
```

```
# Maintainer: Nils Gehlenborg <nils@hms.harvard.edu>
# Description: The Nozzle package provides an API to generate HTML reports with dynamic user interfac
# License: LGPL-2
# URL: http://github.com/parklab/nozzle, http://gdac.broadinstitute.org/nozzle
# BugReports: http://www.github.com/parklab/nozzle/issues
# Copyright: Nozzle is copyright 2013 The Fellows and President of Harvard College and The Broad Insu
# LazyLoad: yes
# Collate: 'nozzle.R'
# Packaged: 2013-05-15 14:05:33 UTC; nils
# NeedsCompilation: no
# Repository: CRAN
# Date/Publication: 2013-05-15 19:25:56

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 398

r-optparse

398.1 Summary

A command line parser inspired by Python's 'optparse' library to be used with Rscript to write "#!" shebang scripts that accept short and long flag/options.

398.2 Home

https://github.com/trevorld/optparse

398.3 Versions

- 1.3.0

398.4 License

GPL (>= 2)

398.5 Meta

```
package:
  name: r-optparse
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "1.3.0"

source:
  fn: optparse_1.3.0.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/optparse_1.3.0.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/optparse/optparse_1.3.0.tar.gz


  # You can add a hash for the file here, like md5 or sha1
```

```
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: knitr, stringr, testthat
requirements:
  build:
    - r
    - r-getopt >=1.19

  run:
    - r
    - r-getopt >=1.19

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('optparse')" # [not win]
    - "\"%R%\" -e \"library('optparse')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: https://github.com/trevorld/optparse
  license: GPL (>= 2)
  summary: A command line parser inspired by Python's 'optparse' library to be used with Rscript
    to write "#!" shebang scripts that accept short and long flag/options.

# The original CRAN metadata for this package was:

# Encoding: UTF-8
# Package: optparse
# Type: Package
# Title: Command line option parser.
# Version: 1.3.0
# Author: Trevor L Davis. Some documentation and examples ported from Allen Day's getopt package. Son
# Maintainer: Trevor L Davis <trevor.l.davis@stanford.edu>
# Description: A command line parser inspired by Python's 'optparse' library to be used with Rscript
# License: GPL (>= 2)
# Copyright: See file (inst/)COPYRIGHTS.
# URL: https://github.com/trevorld/optparse
# BugReports: https://github.com/trevorld/optparse/issues
```

```
# LazyLoad: yes
# Depends: R (>= 2.9.0)
# Imports: methods, getopt (>= 1.19)
# Suggests: knitr, stringr, testthat
# VignetteBuilder: knitr
# Packaged: 2014-12-10 23:10:02 UTC; trevorld
# NeedsCompilation: no
# Repository: CRAN
# Date/Publication: 2014-12-11 08:02:20

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 399

r-params

399.1 Summary

An interface to simplify organizing parameters used in a package, using external configuration files. This attempts to provide a cleaner alternative to options().

399.2 Home

https://github.com/sahilseth/params

399.3 Versions

- 0.4

399.4 License

GPL-2

399.5 Meta

```
package:
  name: r-params
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.4"

source:
  fn: params_0.4.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/params_0.4.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/params/params_0.4.tar.gz


  # You can add a hash for the file here, like md5 or sha1
```

```
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: openxlsx, testthat
requirements:
  build:
    - r
    - r-whisker

  run:
    - r
    - r-whisker

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('params')" # [not win]
    - "\"%R%\" -e \"library('params')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: https://github.com/sahilseth/params
  license: GPL-2
  summary: An interface to simplify organizing parameters used in a package, using external configura
    files. This attempts to provide a cleaner alternative to options().

# The original CRAN metadata for this package was:

# Package: params
# Type: Package
# Title: Simplify Parameters
# Description: An interface to simplify organizing parameters used in a package, using external confi
# Version: 0.4
# Depends: R (>= 3.0.2), whisker
# Imports: utils
# Suggests: openxlsx, testthat
# License: GPL-2
# Authors@R: c( person("Sahil", "Seth", role = c("aut", "cre"), email = "me@sahilseth.com"), person(
# URL: https://github.com/sahilseth/params
# BugReports: https://github.com/sahilseth/params/issues
```

```
# RoxygenNote: 5.0.1.9000
# NeedsCompilation: no
# Packaged: 2015-12-01 21:01:18 UTC; sahilseth
# Author: Sahil Seth [aut, cre], Yihui Xie [ctb] (kable from knitr R/table.R)
# Maintainer: Sahil Seth <me@sahilseth.com>
# Repository: CRAN
# Date/Publication: 2015-12-02 00:01:53

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 400

r-pcapp

400.1 Summary

Robust PCA by Projection Pursuit

400.2 Home

400.3 Versions

- 1.9_60

400.4 License

GPL (>= 3)

400.5 Meta

```
package:
  name: r-pcapp
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "1.9_60"

source:
  fn: pcaPP_1.9-60.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/pcaPP_1.9-60.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/pcaPP/pcaPP_1.9-60.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
```

```
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/


requirements:
  build:
    - r
    - r-mvtnorm

  run:
    - r
    - r-mvtnorm

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('pcaPP')" # [not win]
    - "\"%R%\" -e \"library('pcaPP')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  #home:
  license: GPL (>= 3)
  summary: !!python/unicode 'Robust PCA by Projection Pursuit'


# The original CRAN metadata for this package was:

# Package: pcaPP
# Version: 1.9-60
# Date: 2014-10-20
# Title: Robust PCA by Projection Pursuit
# Author: Peter Filzmoser, Heinrich Fritz, Klaudius Kalcher
# Maintainer: Valentin Todorov <valentin.todorov@chello.at>
# Imports: mvtnorm
# Description: Robust PCA by Projection Pursuit
# License: GPL (>= 3)
# Packaged: 2014-10-21 19:51:01 UTC; Share
# NeedsCompilation: yes
# Repository: CRAN
# Date/Publication: 2014-10-22 00:46:26

# See
# http://docs.continuum.io/conda/build.html for
```

```
# more information about meta.yaml
```

CHAPTER 401

r-permute

401.1 Summary

A set of restricted permutation designs for freely exchangeable, line transects (time series), and spatial grid designs plus permutation of blocks (groups of samples) is provided.

401.2 Home

https://github.com/gavinsimpson/permute

401.3 Versions

- 0.8_4

401.4 License

GPL-2

401.5 Meta

```
package:
  name: r-permute
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.8_4"

source:
  fn: permute_0.8-4.tar.gz
  url:
    - https://cran.r-project.org/src/contrib/permute_0.8-4.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/mclust/permute_0.8-4.tar.gz
  md5: f16b9bd0a87d2db06e0667e0ca787699
```

```
  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  number: 0

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: knitr (>= 1.8), rmarkdown (>= 0.6), mix
requirements:
  build:
    - r

  run:
    - r

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('permute')" # [not win]
    - "\"%R%\" -e \"library('permute')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: https://github.com/gavinsimpson/permute
  license: GPL-2
  summary: A set of restricted permutation designs for freely exchangeable, line transects (time ser
```

CHAPTER 402

r-pheatmap

402.1 Summary

Implementation of heatmaps that offers more control over dimensions and appearance.

402.2 Home

402.3 Versions

- 1.0.8

402.4 License

GPL-2

402.5 Meta

```
package:
  name: r-pheatmap
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "1.0.8"

source:
  fn: pheatmap_1.0.8.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/pheatmap_1.0.8.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/pheatmap/pheatmap_1.0.8.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
```

```
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/


requirements:
  build:
    - r
    - r-rcolorbrewer
    - r-gtable
    - r-scales

  run:
    - r
    - r-rcolorbrewer
    - r-gtable
    - r-scales

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('pheatmap')" # [not win]
    - "\"%R%\" -e \"library('pheatmap')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  #home:
  license: GPL-2
  summary: !!python/unicode 'Implementation of heatmaps that offers more control over dimensions
    and appearance.'


# The original CRAN metadata for this package was:

# Package: pheatmap
# Type: Package
# Title: Pretty Heatmaps
# Version: 1.0.8
# Date: 2015-07-02
# Author: Raivo Kolde
# Maintainer: Raivo Kolde <rkolde@gmail.com>
# Depends: R (>= 2.0)
# Description: Implementation of heatmaps that offers more control over dimensions and appearance.
# Imports: grid, RColorBrewer, scales, gtable, stats, grDevices, graphics
# License: GPL-2
```

```
# LazyLoad: yes
# NeedsCompilation: no
# Packaged: 2015-12-11 14:36:08 UTC; kolde
# Repository: CRAN
# Date/Publication: 2015-12-11 16:50:10

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 403

r-pore

403.1 Summary

An R package to enable organisation and visualisation of nanopore sequencing data

403.2 Home

http://sourceforge.net/projects/rpore/

403.3 Versions

- 0.16

403.4 License

BSD

403.5 Meta

```
package:
  name: r-pore
  version: "0.16"

source:
  fn: poRe_0.16.tar.gz
  url: http://downloads.sourceforge.net/project/rpore/0.16/poRe_0.16.tar.gz
#  patches:
#    - header.patch


build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  number: 0
```

```
  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

requirements:
  build:
    - r
    - bioconductor-rhdf5
    - r-bit64
    - r-shiny
    - r-data.table
    - r-svdialogs

  run:
    - r
    - bioconductor-rhdf5
    - r-bit64
    - r-shiny
    - r-data.table
    - r-svdialogs

test:
  commands:
    - $R -e "library('poRe')" # [not win]

about:
  license: BSD
  summary: 'An R package to enable organisation and visualisation of nanopore sequencing data'
  home: http://sourceforge.net/projects/rpore/

# The original package metadata for this package was

# Package: poRe
# Type: Package
# Title: An R package to enable organisation and visualisation of
#         nanopore sequencing data
# Version: 0.16
# Date: 2015-12-014
# Author: Mick Watson
# Maintainer: Mick Watson <mick.watson@roslin.ed.ac.uk>
# Depends: R (>= 3.0.0), rhdf5, bit64, shiny, data.table, svDialogs
# Description: The Oxford Nanopore MinION is a revolutionary sequencer with a unique model of data de
# License: BSD
# Packaged: 2015-12-14 14:41:45 UTC; mwatson9
```

CHAPTER 404

r-pscbs

404.1 Summary

Segmentation of allele-specific DNA copy number data and detection of regions with abnormal copy number within each parental chromosome. Both tumor-normal paired and tumor-only analyses are supported.

404.2 Home

https://github.com/HenrikBengtsson/PSCBS

404.3 Versions

- 0.60.0

404.4 License

GPL (>= 2)

404.5 Meta

```
package:
  name: r-pscbs
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.60.0"

source:
  fn: PSCBS_0.60.0.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/PSCBS_0.60.0.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/PSCBS/PSCBS_0.60.0.tar.gz


  # You can add a hash for the file here, like md5 or sha1
```

```
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: Hmisc (>= 3.16-0), R.rsp (>= 0.20.0), R.devices (>= 2.13.1), ggplot2 (>= 1.0.1), aroma.li
requirements:
  build:
    - r
    - bioconductor-dnacopy
    - r-r.cache >=0.12.0
    - r-r.methodss3 >=1.7.0
    - r-r.oo >=1.19.0
    - r-r.utils >=2.1.0
    - r-future >=0.8.2
    - r-listenv >=0.5.0
    - r-matrixstats >=0.15.0

  run:
    - r
    - bioconductor-dnacopy
    - r-r.cache >=0.12.0
    - r-r.methodss3 >=1.7.0
    - r-r.oo >=1.19.0
    - r-r.utils >=2.1.0
    - r-future >=0.8.2
    - r-listenv >=0.5.0
    - r-matrixstats >=0.15.0

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('PSCBS')" # [not win]
    - "\"%R%\" -e \"library('PSCBS')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: !!python/unicode 'https://github.com/HenrikBengtsson/PSCBS'

  license: GPL (>= 2)
  summary: !!python/unicode 'Segmentation of allele-specific DNA copy number data and detection
    of regions with abnormal copy number within each parental chromosome.  Both tumor-normal
```

```
    paired and tumor-only analyses are supported.'


# The original CRAN metadata for this package was:

# Package: PSCBS
# Version: 0.60.0
# Depends: R (>= 3.1.1), utils
# Imports: R.methodsS3 (>= 1.7.0), R.oo (>= 1.19.0), R.utils (>= 2.1.0), R.cache (>= 0.12.0), matrixS
# Suggests: Hmisc (>= 3.16-0), R.rsp (>= 0.20.0), R.devices (>= 2.13.1), ggplot2 (>= 1.0.1), aroma.li
# SuggestsNote: BioC (>= 3.0), Recommended: Hmisc, aroma.light
# VignetteBuilder: R.rsp
# Date: 2015-11-17
# Title: Analysis of Parent-Specific DNA Copy Numbers
# Authors@R: c( person("Henrik", "Bengtsson", role=c("aut", "cre", "cph"), email="henrikb@braju.com",
# Description: Segmentation of allele-specific DNA copy number data and detection of regions with abn
# License: GPL (>= 2)
# LazyLoad: TRUE
# ByteCompile: TRUE
# biocViews: aCGH, CopyNumberVariants, SNP, Microarray, OneChannel, TwoChannel, Genetics
# URL: https://github.com/HenrikBengtsson/PSCBS
# BugReports: https://github.com/HenrikBengtsson/PSCBS/issues
# NeedsCompilation: no
# Packaged: 2015-11-17 17:52:13 UTC; hb
# Author: Henrik Bengtsson [aut, cre, cph], Pierre Neuvial [aut], Venkatraman E. Seshan [aut], Adam B
# Maintainer: Henrik Bengtsson <henrikb@braju.com>
# Repository: CRAN
# Date/Publication: 2015-11-18 09:31:06

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 405

r-r.cache

405.1 Summary

Memoization can be used to speed up repetitive and computational expensive function calls. The first time a function that implements memoization is called the results are stored in a cache memory. The next time the function is called with the same set of parameters, the results are momentarily retrieved from the cache avoiding repeating the calculations. With this package, any R object can be cached in a key-value storage where the key can be an arbitrary set of R objects. The cache memory is persistent (on the file system).

405.2 Home

https://github.com/HenrikBengtsson/R.cache

405.3 Versions

- 0.12.0

405.4 License

LGPL (>= 2.1)

405.5 Meta

```
package:
  name: r-r.cache
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.12.0"

source:
  fn: R.cache_0.12.0.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/R.cache_0.12.0.tar.gz
```

```
    - http://cran.r-project.org/src/contrib/Archive/R.cache/R.cache_0.12.0.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/


requirements:
  build:
    - r
    - r-r.methodss3 >=1.7.0
    - r-r.oo >=1.19.0
    - r-r.utils >=2.1.0
    - r-digest >=0.6.8

  run:
    - r
    - r-r.methodss3 >=1.7.0
    - r-r.oo >=1.19.0
    - r-r.utils >=2.1.0
    - r-digest >=0.6.8

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('R.cache')" # [not win]
    - "\"%R%\" -e \"library('R.cache')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: !!python/unicode 'https://github.com/HenrikBengtsson/R.cache'

  license: LGPL (>= 2.1)
  summary: !!python/unicode 'Memoization can be used to speed up repetitive and computational
    expensive function calls.  The first time a function that implements memoization
    is called the results are stored in a cache memory.  The next time the function
    is called with the same set of parameters, the results are momentarily retrieved
    from the cache avoiding repeating the calculations.  With this package, any R object
    can be cached in a key-value storage where the key can be an arbitrary set of R
```

```
    objects.  The cache memory is persistent (on the file system).'


# The original CRAN metadata for this package was:

# Package: R.cache
# Version: 0.12.0
# Depends: R (>= 2.5.0)
# Imports: utils, R.methodsS3 (>= 1.7.0), R.oo (>= 1.19.0), R.utils (>= 2.1.0), digest (>= 0.6.8)
# Date: 2015-11-12
# Title: Fast and Light-Weight Caching (Memoization) of Objects and Results to Speed Up Computations
# Authors@R: c(person("Henrik", "Bengtsson", role=c("aut", "cre", "cph"), email = "henrikb@braju.com
# Author: Henrik Bengtsson [aut, cre, cph]
# Maintainer: Henrik Bengtsson <henrikb@braju.com>
# Description: Memoization can be used to speed up repetitive and computational expensive function ca
# License: LGPL (>= 2.1)
# LazyLoad: TRUE
# URL: https://github.com/HenrikBengtsson/R.cache
# BugReports: https://github.com/HenrikBengtsson/R.cache/issues
# NeedsCompilation: no
# Packaged: 2015-11-12 16:06:08 UTC; hb
# Repository: CRAN
# Date/Publication: 2015-11-12 19:00:04

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 406

r-r.methodss3

406.1 Summary

Methods that simplify the setup of S3 generic functions and S3 methods. Major effort has been made in making definition of methods as simple as possible with a minimum of maintenance for package developers. For example, generic functions are created automatically, if missing, and naming conflict are automatically solved, if possible. The method setMethodS3() is a good start for those who in the future may want to migrate to S4. This is a cross-platform package implemented in pure R that generates standard S3 methods.

406.2 Home

406.3 Versions

- 1.7.0

406.4 License

LGPL (>= 2.1)

406.5 Meta

```
package:
  name: r-r.methodss3
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "1.7.0"

source:
  fn: R.methodsS3_1.7.0.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/R.methodsS3_1.7.0.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/R.methodsS3/R.methodsS3_1.7.0.tar.gz
```

```
  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/


requirements:
  build:
    - r

  run:
    - r

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('R.methodsS3')" # [not win]
    - "\"%R%\" -e \"library('R.methodsS3')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  #home:
  license: LGPL (>= 2.1)
  summary: !!python/unicode 'Methods that simplify the setup of S3 generic functions and S3 methods.
    effort has been made in making definition of methods as simple as possible with
    a minimum of maintenance for package developers.  For example, generic functions
    are created automatically, if missing, and naming conflict are automatically solved,
    if possible.  The method setMethodS3() is a good start for those who in the future
    may want to migrate to S4.  This is a cross-platform package implemented in pure
    R that generates standard S3 methods.'


# The original CRAN metadata for this package was:

# Package: R.methodsS3
# Version: 1.7.0
# Depends: R (>= 2.2.0)
# Imports: utils
# Date: 2015-02-19
# Title: S3 Methods Simplified
# Authors@R: c(person("Henrik", "Bengtsson", role=c("aut", "cre", "cph"), email = "henrikb@braju.com
```

```
# Author: Henrik Bengtsson [aut, cre, cph]
# Maintainer: Henrik Bengtsson <henrikb@braju.com>
# Description: Methods that simplify the setup of S3 generic functions and S3 methods.  Major effort
# License: LGPL (>= 2.1)
# LazyLoad: TRUE
# NeedsCompilation: no
# Packaged: 2015-02-20 03:15:35 UTC; hb
# Repository: CRAN
# Date/Publication: 2015-02-20 09:16:51

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 407

r-r.oo

407.1 Summary

Methods and classes for object-oriented programming in R with or without references. Large effort has been made on making definition of methods as simple as possible with a minimum of maintenance for package developers. The package has been developed since 2001 and is now considered very stable. This is a cross-platform package implemented in pure R that defines standard S3 classes without any tricks.

407.2 Home

https://github.com/HenrikBengtsson/R.oo

407.3 Versions

- 1.19.0

407.4 License

LGPL (>= 2.1)

407.5 Meta

```
package:
  name: r-r.oo
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "1.19.0"

source:
  fn: R.oo_1.19.0.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/R.oo_1.19.0.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/R.oo/R.oo_1.19.0.tar.gz
```

```
  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: tools
requirements:
  build:
    - r
    - r-r.methodss3 >=1.7.0

  run:
    - r
    - r-r.methodss3 >=1.7.0

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('R.oo')" # [not win]
    - "\"%R%\" -e \"library('R.oo')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: !!python/unicode 'https://github.com/HenrikBengtsson/R.oo'

  license: LGPL (>= 2.1)
  summary: !!python/unicode 'Methods and classes for object-oriented programming in R with or
    without references.  Large effort has been made on making definition of methods
    as simple as possible with a minimum of maintenance for package developers.  The
    package has been developed since 2001 and is now considered very stable.  This is
    a cross-platform package implemented in pure R that defines standard S3 classes
    without any tricks.'


# The original CRAN metadata for this package was:

# Package: R.oo
# Version: 1.19.0
# Depends: R (>= 2.4.0), R.methodsS3 (>= 1.7.0)
# Imports: methods, utils
```

```
# Suggests: tools
# Date: 2015-02-27
# Title: R Object-Oriented Programming with or without References
# Authors@R: c(person("Henrik", "Bengtsson", role=c("aut", "cre", "cph"), email = "henrikb@braju.com
# Author: Henrik Bengtsson [aut, cre, cph]
# Maintainer: Henrik Bengtsson <henrikb@braju.com>
# Description: Methods and classes for object-oriented programming in R with or without references.
# License: LGPL (>= 2.1)
# LazyLoad: TRUE
# URL: https://github.com/HenrikBengtsson/R.oo
# BugReports: https://github.com/HenrikBengtsson/R.oo/issues
# NeedsCompilation: no
# Packaged: 2015-02-27 19:06:32 UTC; hb
# Repository: CRAN
# Date/Publication: 2015-02-28 01:28:49

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 408

r-r.utils

408.1 Summary

Utility functions useful when programming and developing R packages.

408.2 Home

https://github.com/HenrikBengtsson/R.utils

408.3 Versions

- 2.2.0

408.4 License

LGPL (>= 2.1)

408.5 Meta

```
package:
  name: r-r.utils
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "2.2.0"

source:
  fn: R.utils_2.2.0.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/R.utils_2.2.0.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/R.utils/R.utils_2.2.0.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
```

```
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: digest (>= 0.6.8)
requirements:
  build:
    - r
    - r-r.methodss3 >=1.7.0
    - r-r.oo >=1.19.0

  run:
    - r
    - r-r.methodss3 >=1.7.0
    - r-r.oo >=1.19.0

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('R.utils')" # [not win]
    - "\"%R%\" -e \"library('R.utils')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: !!python/unicode 'https://github.com/HenrikBengtsson/R.utils'

  license: LGPL (>= 2.1)
  summary: !!python/unicode 'Utility functions useful when programming and developing R packages.'


# The original CRAN metadata for this package was:

# Package: R.utils
# Version: 2.2.0
# Depends: R (>= 2.5.0), R.oo (>= 1.19.0)
# Imports: methods, utils, tools, R.methodsS3 (>= 1.7.0)
# Suggests: digest (>= 0.6.8)
# Date: 2015-12-09
# Title: Various Programming Utilities
# Authors@R: c(person("Henrik", "Bengtsson", role=c("aut", "cre", "cph"), email = "henrikb@braju.com
# Author: Henrik Bengtsson [aut, cre, cph]
# Maintainer: Henrik Bengtsson <henrikb@braju.com>
```

```
# Description: Utility functions useful when programming and developing R packages.
# License: LGPL (>= 2.1)
# LazyLoad: TRUE
# URL: https://github.com/HenrikBengtsson/R.utils
# BugReports: https://github.com/HenrikBengtsson/R.utils/issues
# NeedsCompilation: no
# Packaged: 2015-12-09 22:41:20 UTC; hb
# Repository: CRAN
# Date/Publication: 2015-12-11 13:30:47

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 409

r-rainbow

409.1 Summary

Functions and data sets for functional data display and outlier detection.

409.2 Home

https://sites.google.com/site/hanlinshangswebsite/

409.3 Versions

- 3.3

409.4 License

GPL (>= 2)

409.5 Meta

```
package:
  name: r-rainbow
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "3.3"

source:
  fn: rainbow_3.3.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/rainbow_3.3.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/rainbow/rainbow_3.3.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
```

```
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: forecast
requirements:
  build:
    - r
    - r-mass # [not win]
    - r-cluster # [not win]
    - r-colorspace
    - r-hdrcde
    - r-ks
    - r-pcapp

  run:
    - r
    - r-mass # [not win]
    - r-cluster # [not win]
    - r-colorspace
    - r-hdrcde
    - r-ks
    - r-pcapp

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('rainbow')" # [not win]
    - "\"%R%\" -e \"library('rainbow')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: !!python/unicode 'https://sites.google.com/site/hanlinshangswebsite/'

  license: GPL (>= 2)
  summary: !!python/unicode 'Functions and data sets for functional data display and outlier
    detection.'


# The original CRAN metadata for this package was:

# Package: rainbow
```

```
# Type: Package
# Title: Rainbow Plots, Bagplots and Boxplots for Functional Data
# Version: 3.3
# Date: 2015-04-15
# Depends: R (>= 2.10.0), MASS, pcaPP
# Suggests: forecast
# Imports: hdrcde, cluster, colorspace, ks
# Author: Han Lin Shang and Rob J Hyndman
# Maintainer: Han Lin Shang <hanlin.shang@anu.edu.au>
# Description: Functions and data sets for functional data display and outlier detection.
# License: GPL (>= 2)
# LazyData: yes
# LazyLoad: yes
# LazyDataCompression: xz
# URL: https://sites.google.com/site/hanlinshangswebsite/
# Packaged: 2015-04-15 12:14:46 UTC; hanlinshang
# NeedsCompilation: no
# Repository: CRAN
# Date/Publication: 2015-04-15 21:41:07

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 410

r-rappdirs

410.1 Summary

An easy way to determine which directories on the users computer you should use to save data, caches and logs. A port of Python's Appdirs (url{https://github.com/ActiveState/appdirs}) to R.

410.2 Home

https://github.com/hadley/rappdirs https://github.com/ActiveState/appdirs

410.3 Versions

- 0.3

410.4 License

MIT + file LICENSE

410.5 Meta

```
package:
  name: r-rappdirs
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.3"

source:
  fn: rappdirs_0.3.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/rappdirs_0.3.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/rappdirs/rappdirs_0.3.tar.gz


  # You can add a hash for the file here, like md5 or sha1
```

```
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: testthat, roxygen2
requirements:
  build:
    - r
    - gcc # [not win]

  run:
    - r
    - libgcc # [not win]

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('rappdirs')" # [not win]
    - "\"%R%\" -e \"library('rappdirs')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: https://github.com/hadley/rappdirs https://github.com/ActiveState/appdirs
  license: MIT + file LICENSE
  summary: An easy way to determine which directories on the users computer you should use to
    save data, caches and logs. A port of Python's Appdirs (\url{https://github.com/ActiveState/appdi
    to R.

# The original CRAN metadata for this package was:

# Package: rappdirs
# Type: Package
# Title: Application directories: determine where to save data, caches and logs.
# Version: 0.3
# Authors@R: c( person("Hadley", "Wickham", email = "h.wickham@gmail.com", role = c("trl", "cre", "cp
# Depends: R (>= 2.14), methods
# Suggests: testthat, roxygen2
# Description: An easy way to determine which directories on the users computer you should use to sav
# BugReports: https://github.com/hadley/rappdirs/issues
# URL: https://github.com/hadley/rappdirs https://github.com/ActiveState/appdirs
# License: MIT + file LICENSE
```

```
# Copyright: Original python appdirs module copyright (c) 2010 ActiveState Software Inc. R port copyr
# Packaged: 2014-09-02 15:34:08 UTC; hadley
# Author: Hadley Wickham [trl, cre, cph], RStudio [cph], Sridhar Ratnakumar [aut], Trent Mick [aut],
# Maintainer: Hadley Wickham <h.wickham@gmail.com>
# NeedsCompilation: yes
# Repository: CRAN
# Date/Publication: 2014-09-02 19:44:02

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 411

r-rcircos

411.1 Summary

A simple and flexible way to generate Circos 2D track plot images for genomic data visualization is implemented in this package. The types of plots include: heatmap, histogram, lines, scatterplot, tiles and plot items for further decorations include connector, link (lines and ribbons), and text (gene) label. All functions require only R graphics package that comes with R base installation.

411.2 Home

http://bitbucket.org/henryhzhang/rcircos

411.3 Versions

- 1.1.3

411.4 License

GPL (>= 2)

411.5 Meta

```
package:
  name: r-rcircos
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "1.1.3"

source:
  fn: RCircos_1.1.3.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/RCircos_1.1.3.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/RCircos/RCircos_1.1.3.tar.gz
```

```
  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/


requirements:
  build:
    - r

  run:
    - r

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('RCircos')" # [not win]
    - "\"%R%\" -e \"library('RCircos')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: http://bitbucket.org/henryhzhang/rcircos
  license: GPL (>= 2)
  summary: 'A simple and flexible way to generate Circos 2D track plot images for genomic data
    visualization is implemented in this package. The types of plots include: heatmap,
    histogram, lines, scatterplot, tiles and plot items for further decorations include
    connector, link (lines and ribbons), and text (gene) label. All functions require
    only R graphics package that comes with R base installation.  '


# The original CRAN metadata for this package was:

# Package: RCircos
# Type: Package
# Title: Circos 2D Track Plot
# Version: 1.1.3
# Date: 2015-12-20
# Author: Hongen Zhang
# Maintainer: Hongen Zhang <hzhang@mail.nih.gov>
# Description: A simple and flexible way to generate Circos 2D track plot images for genomic data vis
```

```
# License: GPL (>= 2)
# Depends: R (>= 2.10)
# URL: http://bitbucket.org/henryhzhang/rcircos
# NeedsCompilation: no
# Packaged: 2015-12-11 22:17:24 UTC; hzhang
# Repository: CRAN
# Date/Publication: 2015-12-14 17:29:13

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 412

r-rjson

412.1 Summary

Converts R object into JSON objects and vice-versa

412.2 Home

https://cran.r-project.org/web/packages/rjson/index.html

412.3 Versions

- 0.2.15

412.4 License

GPL-2

412.5 Meta

```
package:
  name: r-rjson
  version: 0.2.15
source:
  fn: rjson_0.2.15.tar.gz
  url: https://cran.r-project.org/src/contrib/rjson_0.2.15.tar.gz
  md5: 87d0e29bc179c6aeaf312b138089f8e9
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
    - r
```

```
  run:
    - r
test:
  commands:
    - '$R -e "library(''rjson'')"'
about:
  home: https://cran.r-project.org/web/packages/rjson/index.html
  license: GPL-2
  summary: 'Converts R object into JSON objects and vice-versa'
```

CHAPTER 413

r-sendmailr

413.1 Summary

Package contains a simple SMTP client which provides a portable solution for sending email, including attachment, from within R.

413.2 Home

413.3 Versions

- 1.2_1

413.4 License

GPL-2

413.5 Meta

```
package:
  name: r-sendmailr
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "1.2_1"

source:
  fn: sendmailR_1.2-1.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/sendmailR_1.2-1.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/sendmailR/sendmailR_1.2-1.tar.gz

build:
  number: 0

  # This is required to make R link correctly on Linux.
  rpaths:
```

```
    - lib/R/lib/
    - lib/

requirements:
  build:
    - r
    - r-base64enc

  run:
    - r
    - r-base64enc

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('sendmailR')" # [not win]
    - "\"%R%\" -e \"library('sendmailR')\"" # [win]

about:
  license: GPL-2
  summary: Package contains a simple SMTP client which provides a portable solution for sending
    email, including attachment, from within R.

# The original CRAN metadata for this package was:

# Package: sendmailR
# Version: 1.2-1
# Title: send email using R
# Description: Package contains a simple SMTP client which provides a portable solution for sending e
# Authors@R: c(person("Olaf", "Mersmann", role=c("aut", "cre"), email="olafm@p-value.net"), person("Q
# Depends: R (>= 3.0.0)
# Imports: base64enc
# License: GPL-2
# LazyData: yes
# Packaged: 2014-09-21 11:16:23 UTC; olafm
# Author: Olaf Mersmann [aut, cre], Quinn Weber [ctb]
# Maintainer: Olaf Mersmann <olafm@p-value.net>
# NeedsCompilation: no
# Repository: CRAN
# Date/Publication: 2014-09-21 13:32:55

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 414

r-seqinr

414.1 Summary

Exploratory data analysis and data visualization for biological sequence (DNA and protein) data. Includes also utilities for sequence data management under the ACNUC system.

414.2 Home

http://seqinr.r-forge.r-project.org/, Mailing list: http://r-forge.r-project.org/mail/?group_id=220

414.3 Versions

- 3.1_3

414.4 License

GPL (>= 2)

414.5 Meta

```
package:
  name: r-seqinr
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "3.1_3"

source:
  fn: seqinr_3.1-3.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/seqinr_3.1-3.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/seqinr/seqinr_3.1-3.tar.gz


  # You can add a hash for the file here, like md5 or sha1
```

```
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: segmented
requirements:
  build:
    - r
    - r-ade4

  run:
    - r
    - r-ade4

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('seqinr')" # [not win]
    - "\"%R%\" -e \"library('seqinr')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: 'http://seqinr.r-forge.r-project.org/, Mailing list: http://r-forge.r-project.org/mail/?group

  license: GPL (>= 2)
  summary: Exploratory data analysis and data visualization for biological sequence (DNA and
    protein) data.  Includes also utilities for sequence data management under the ACNUC
    system.

# The original CRAN metadata for this package was:

# Package: seqinr
# Version: 3.1-3
# Date: 2014-12-04
# Title: Biological Sequences Retrieval and Analysis
# Author: Delphine Charif and Jean R. Lobry and Anamaria Necsulea and Leonor Palmeira and Simon Pene
# Maintainer: Simon Penel <simon.penel@univ-lyon1.fr>
# Depends: ade4, R (>= 2.10.0)
# Suggests: segmented
# Description: Exploratory data analysis and data visualization for biological sequence (DNA and pro
# License: GPL (>= 2)
```

```
# SystemRequirements: zlib headers and library.
# URL: http://seqinr.r-forge.r-project.org/, Mailing list: http://r-forge.r-project.org/mail/?group_
# ZipData: no
# LazyData: no
# Packaged: 2014-12-04 17:05:10 UTC; rforge
# NeedsCompilation: yes
# Repository: CRAN
# Date/Publication: 2014-12-17 18:03:07
# Repository/R-Forge/Project: seqinr
# Repository/R-Forge/Revision: 1835
# Repository/R-Forge/DateTimeStamp: 2014-12-04 17:02:49

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 415

r-shape

415.1 Summary

Functions for plotting graphical shapes such as ellipses, circles, cylinders, arrows, ...

415.2 Home

415.3 Versions

- 1.4.2

415.4 License

GPL (>= 3)

415.5 Meta

```
package:
  name: r-shape
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "1.4.2"

source:
  fn: shape_1.4.2.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/shape_1.4.2.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/shape/shape_1.4.2.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
```

```
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/


requirements:
  build:
    - r

  run:
    - r

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('shape')" # [not win]
    - "\"%R%\" -e \"library('shape')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  #home:
  license: GPL (>= 3)
  summary: Functions for plotting graphical shapes such as ellipses, circles, cylinders, arrows,
    ...

# The original CRAN metadata for this package was:

# Package: shape
# Version: 1.4.2
# Date: 2014-06-01
# Title: Functions for plotting graphical shapes, colors
# Author: Karline Soetaert <karline.soetaert@nioz.nl>
# Maintainer: Karline Soetaert <karline.soetaert@nioz.nl>
# Depends: R (>= 2.01), stats
# Description: Functions for plotting graphical shapes such as ellipses, circles, cylinders, arrows,
# License: GPL (>= 3)
# LazyData: yes
# Packaged: 2014-11-01 08:24:56 UTC; rforge
# Repository: CRAN
# Repository/R-Forge/Project: diagram
# Repository/R-Forge/Revision: 68
# Repository/R-Forge/DateTimeStamp: 2014-11-01 08:20:54
# Date/Publication: 2014-11-05 14:14:32
# NeedsCompilation: no
```

```
# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 416

r-signal

416.1 Summary

A set of signal processing functions originally written for 'Matlab' and 'Octave'. Includes filter generation utilities, filtering functions, resampling routines, and visualization of filter models. It also includes interpolation functions.

416.2 Home

416.3 Versions

- 0.7_6

416.4 License

GPL-2

416.5 Meta

```
package:
  name: r-signal
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.7_6"

source:
  fn: signal_0.7-6.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/signal_0.7-6.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/signal/signal_0.7-6.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
```

```
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  number: 0

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: pracma
requirements:
  build:
    - r
    - r-mass # [not win]
    - gcc # [not win]

  run:
    - r
    - r-mass # [not win]
    - libgcc # [not win]

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('signal')" # [not win]
    - "\"%R%\" -e \"library('signal')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  #home:
  license: GPL-2
  summary: A set of signal processing functions originally written for 'Matlab' and 'Octave'.
    Includes filter generation utilities, filtering functions, resampling routines,
    and visualization of filter models. It also includes interpolation functions.

# The original CRAN metadata for this package was:

# Package: signal
# Title: Signal Processing
# Version: 0.7-6
# Date: 2015-07-29
# Authors@R: c(person("Uwe", "Ligges", role = c("aut", "cre"), email="ligges@statistik.tu-dortmund.de
# Depends: R (>= 2.14.0)
# Imports: MASS, graphics, grDevices, stats, utils
# Suggests: pracma
# Description: A set of signal processing functions originally written for 'Matlab' and 'Octave'. Inc
# License: GPL-2
# NeedsCompilation: yes
# Packaged: 2015-07-29 17:06:27 UTC; ligges
```

```
# Author: Uwe Ligges [aut, cre] (new maintainer), Tom Short [aut] (port to R), Paul Kienzle [aut] (ma
# Maintainer: Uwe Ligges <ligges@statistik.tu-dortmund.de>
# Repository: CRAN
# Date/Publication: 2015-07-30 00:17:37

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 417

r-sleuth

417.1 Summary

Sleuth is an R library for analysis of RNA-Seq experiments for which transcript abundances have been quantified with kallisto.

417.2 Home

http://pachterlab.github.io/sleuth

417.3 Versions

- 0.28.0

417.4 License

GPLv3

417.5 Meta

```
package:
  name: r-sleuth
  version: 0.28.0
source:
  git_url: https://github.com/pachterlab/sleuth.git
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
    - r
    - bioconductor-rhdf5
```

```
    - r-ggplot2
    - r-dplyr
    - r-tidyr
    - r-shiny
    - r-data.table
  run:
    - r
    - bioconductor-rhdf5
    - r-ggplot2
    - r-dplyr
    - r-tidyr
    - r-shiny
    - r-data.table
test:
  commands:
    - '$R -e "library(''sleuth'')"'
about:
  home: http://pachterlab.github.io/sleuth
  license: GPLv3
  summary: "Sleuth is an R library for analysis of RNA-Seq experiments for which transcript abundance
```

CHAPTER 418

r-snow

418.1 Summary

Support for simple parallel computing in R.

418.2 Home

418.3 Versions

- 0.4_1

418.4 License

GPL

418.5 Meta

```
package:
  name: r-snow
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.4_1"

source:
  fn: snow_0.4-1.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/snow_0.4-1.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/snow/snow_0.4-1.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
```

```
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: Rmpi,rlecuyer,nws
requirements:
  build:
    - r

  run:
    - r

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('snow')" # [not win]
    - "\"%R%\" -e \"library('snow')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  #home:
  license: GPL
  summary: Support for simple parallel computing in R.

# The original CRAN metadata for this package was:

# Package: snow
# Title: Simple Network of Workstations
# Version: 0.4-1
# Author: Luke Tierney, A. J. Rossini, Na Li, H. Sevcikova
# Description: Support for simple parallel computing in R.
# Maintainer: Luke Tierney <luke-tierney@uiowa.edu>
# Suggests: Rmpi,rlecuyer,nws
# License: GPL
# Depends: R (>= 2.13.1), utils
# NeedsCompilation: no
# Packaged: 2015-10-29 19:50:26 UTC; luke
# Repository: CRAN
# Date/Publication: 2015-10-31 11:10:46

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 419

r-spp

419.1 Summary

ChIP-seq peak caller

419.2 Home

419.3 Versions

- 1.11

419.4 License

GPL

419.5 Meta

```
package:
  name: r-spp
  version: "1.11"

source:
  fn: spp_1.11.tar.gz
  url: http://compbio.med.harvard.edu/Supplements/ChIP-seq/spp_1.11.tar.gz
  patches:
    - header.patch


build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  number: 0

  # This is required to make R link correctly on Linux.
  rpaths:
```

```
    - lib/R/lib/
    - lib/

requirements:
  build:
    - r
    - boost
    - r-catools

  run:
    - r
    - boost
    - r-catools

test:
  commands:
    - $R -e "library('spp')" # [not win]


about:
  license: GPL
  summary: 'ChIP-seq peak caller'
```

CHAPTER 420

r-statmod

420.1 Summary

A collection of algorithms and functions to aid statistical modeling. Includes growth curve comparisons, limiting dilution analysis (aka ELDA), mixed linear models, heteroscedastic regression, inverse-Gaussian probability calculations, Gauss quadrature and a secure convergence algorithm for nonlinear models. Includes advanced generalized linear model functions that implement secure convergence, dispersion modeling and Tweedie power-law families.

420.2 Home

420.3 Versions

- 1.4.22

420.4 License

GPL-2 | GPL-3

420.5 Meta

```
package:
  name: r-statmod
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "1.4.22"

source:
  fn: statmod_1.4.22.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/statmod_1.4.22.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/statmod/statmod_1.4.22.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
```

```
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: MASS, tweedie
requirements:
  build:
    - r

  run:
    - r

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('statmod')" # [not win]
    - "\"%R%\" -e \"library('statmod')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  #home:
  license: GPL-2 | GPL-3
  summary: !!python/unicode 'A collection of algorithms and functions to aid statistical modeling.
    Includes growth curve comparisons, limiting dilution analysis (aka ELDA), mixed
    linear models, heteroscedastic regression, inverse-Gaussian probability calculations,
    Gauss quadrature and a secure convergence algorithm for nonlinear models.  Includes
    advanced generalized linear model functions that implement secure convergence, dispersion
    modeling and Tweedie power-law families. '


# The original CRAN metadata for this package was:

# Package: statmod
# Version: 1.4.22
# Date: 2015-10-27
# Title: Statistical Modeling
# Author: Gordon Smyth [cre, aut], Yifang Hu [ctb], Peter Dunn [ctb], Belinda Phipson [ctb], Yunshun
# Maintainer: Gordon Smyth <smyth@wehi.edu.au>
# Depends: R (>= 1.6.1)
# Imports: stats, graphics
# Suggests: MASS, tweedie
# Description: A collection of algorithms and functions to aid statistical modeling. Includes growth
```

```
# License: GPL-2 | GPL-3
# NeedsCompilation: yes
# Packaged: 2015-10-27 07:23:26 UTC; smyth
# Repository: CRAN
# Date/Publication: 2015-10-27 09:52:46

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 421

r-svdialogs

421.1 Summary

Rapidly construct dialog boxes for your GUI, including an automatic function assistant

421.2 Home

http://www.sciviews.org/SciViews-R

421.3 Versions

- 0.9_57

421.4 License

GPL-2

421.5 Meta

```
package:
  name: r-svdialogs
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.9_57"

source:
  fn: svDialogs_0.9-57.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/svDialogs_0.9-57.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/svDialogs/svDialogs_0.9-57.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
```

```
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/


requirements:
  build:
    - r
    - r-svgui >=0.9_52

  run:
    - r
    - r-svgui >=0.9_52

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('svDialogs')" # [not win]
    - "\"%R%\" -e \"library('svDialogs')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: http://www.sciviews.org/SciViews-R
  license: GPL-2
  summary: Rapidly construct dialog boxes for your GUI, including an automatic function assistant

# The original CRAN metadata for this package was:

# Package: svDialogs
# Type: Package
# Version: 0.9-57
# Date: 2014-12-19
# Title: SciViews GUI API - Dialog boxes
# Author: Philippe Grosjean [aut, cre]
# Authors@R: c(person("Philippe", "Grosjean", role = c("aut", "cre"), email = "phgrosjean@sciviews.o
# Maintainer: Philippe Grosjean <phgrosjean@sciviews.org>
# Depends: R (>= 2.6.0), svGUI (>= 0.9-52)
# SystemRequirements: zenity
# Description: Rapidly construct dialog boxes for your GUI, including an automatic function assistan
# License: GPL-2
# URL: http://www.sciviews.org/SciViews-R
# BugReports: https://r-forge.r-project.org/tracker/?group_id=194
```

```
# Packaged: 2014-12-19 16:33:09 UTC; phgrosjean
# NeedsCompilation: no
# Repository: CRAN
# Date/Publication: 2014-12-20 10:35:02

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 422

r-svgui

422.1 Summary

Functions to manage GUIs from R

422.2 Home

http://www.sciviews.org/SciViews-R

422.3 Versions

- 0.9_55

422.4 License

GPL-2

422.5 Meta

```
package:
  name: r-svgui
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "0.9_55"

source:
  fn: svGUI_0.9-55.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/svGUI_0.9-55.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/svGUI/svGUI_0.9-55.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
```

```
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/


requirements:
  build:
    - r

  run:
    - r

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('svGUI')" # [not win]
    - "\"%R%\" -e \"library('svGUI')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: http://www.sciviews.org/SciViews-R
  license: GPL-2
  summary: Functions to manage GUIs from R

# The original CRAN metadata for this package was:

# Package: svGUI
# Type: Package
# Version: 0.9-55
# Date: 2014-03-02
# Title: SciViews GUI API - Functions to manage GUIs
# Author: Philippe Grosjean [aut, cre]
# Authors@R: c(person("Philippe", "Grosjean", role = c("aut", "cre"), email = "phgrosjean@sciviews.o
# Maintainer: Philippe Grosjean <phgrosjean@sciviews.org>
# Depends: R (>= 2.6.0)
# Description: Functions to manage GUIs from R
# License: GPL-2
# URL: http://www.sciviews.org/SciViews-R
# BugReports: https://r-forge.r-project.org/tracker/?group_id=194
# Packaged: 2014-03-02 09:34:53 UTC; phgrosjean
# NeedsCompilation: no
# Repository: CRAN
```

```
# Date/Publication: 2014-03-02 12:40:45

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 423

r-tximport

423.1 Summary

Import and summarize transcript-level estimates for gene-level analysis

423.2 Home

https://github.com/mikelove/tximport/

423.3 Versions

- 0.0.15

423.4 License

GPL

423.5 Meta

```
package:
  name: r-tximport
  version: 0.0.15
source:
  git_url: https://github.com/mikelove/tximport/
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
    - r
  run:
    - r
```

```
test:
  commands:
    - '$R -e "library(''tximport'')"'
about:
  home: https://github.com/mikelove/tximport/
  license: GPL
  summary: Import and summarize transcript-level estimates for gene-level analysis
```

CHAPTER 424

r-venndiagram

424.1 Summary

A set of functions to generate high-resolution Venn and Euler plots. Includes handling for several special cases, including two-case scaling, and extensive customization of plot shape and structure.

424.2 Home

424.3 Versions

- 1.6.16

424.4 License

GPL-2

424.5 Meta

```
package:
  name: r-venndiagram
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "1.6.16"

source:
  fn: VennDiagram_1.6.16.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/VennDiagram_1.6.16.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/VennDiagram/VennDiagram_1.6.16.tar.gz


  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
```

```
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: testthat
requirements:
  build:
    - r
    - r-futile.logger

  run:
    - r
    - r-futile.logger

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('VennDiagram')" # [not win]
    - "\"%R%\" -e \"library('VennDiagram')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  #home:
  license: GPL-2
  summary: A set of functions to generate high-resolution Venn and Euler plots. Includes handling
    for several special cases, including two-case scaling, and extensive customization
    of plot shape and structure.

# The original CRAN metadata for this package was:

# Package: VennDiagram
# Version: 1.6.16
# Type: Package
# Title: Generate High-Resolution Venn and Euler Plots
# Date: 2015-08-28
# Author: Hanbo Chen
# Maintainer: Paul Boutros <Paul.Boutros@oicr.on.ca>
# Depends: R (>= 2.14.1), grid (>= 2.14.1), futile.logger
# Description: A set of functions to generate high-resolution Venn and Euler plots. Includes handling
# License: GPL-2
# LazyLoad: yes
# Suggests: testthat
# NeedsCompilation: no
# Packaged: 2015-09-10 20:59:45 UTC; clalansingh
```

```
# Repository: CRAN
# Date/Publication: 2015-09-17 07:51:02

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 425

r-viridis

425.1 Summary

Port of the new 'matplotlib' color maps ('viridis' - the default -, 'magma', 'plasma' and 'inferno') to 'R'. 'matplotlib' <http://matplotlib.org/> is a popular plotting library for 'python'. These color maps are designed in such a way that they will analytically be perfectly perceptually-uniform, both in regular form and also when converted to black-and-white. They are also designed to be perceived by readers with the most common form of color blindness.

425.2 Home

https://github.com/sjmgarnier/viridis

425.3 Versions

- 0.3.1

425.4 License

MIT + file LICENSE

425.5 Meta

```
package:
  name: r-viridis
  version: "0.3.1"

source:
  fn: viridis_0.3.1.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/viridis_0.3.1.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/viridis/viridis_0.3.1.tar.gz

build:
```

```
  rpaths:
    - lib/R/lib/
    - lib/

# Suggests: hexbin (>= 1.27.0), scales, MASS, knitr, dichromat, colorspace, rasterVis, httr, mapproj
requirements:
  build:
    - r
    - r-ggplot2 >=1.0.1
    - r-gridextra

  run:
    - r
    - r-ggplot2 >=1.0.1
    - r-gridextra

test:
  commands:
    - $R -e "library('viridis')" # [not win]
    - "\"%R%\" -e \"library('viridis')\"" # [win]

about:
  home: https://github.com/sjmgarnier/viridis
  license: MIT + file LICENSE
  summary: Port of the new 'matplotlib' color maps ('viridis' - the default -, 'magma', 'plasma'
    and 'inferno') to 'R'. 'matplotlib' <http://matplotlib.org/> is a popular plotting
    library for 'python'. These color maps are designed in such a way that they will
    analytically be perfectly perceptually-uniform, both in regular form and also when
    converted to black-and-white. They are also designed to be perceived by readers
    with the most common form of color blindness.

# The original CRAN metadata for this package was:

# Package: viridis
# Type: Package
# Title: Matplotlib Default Color Map
# Version: 0.3.1
# Date: 2015-10-11
# Authors@R: c( person("Simon", "Garnier", email = "garnier@njit.edu", role = c("aut", "cre")), perso
# Maintainer: Simon Garnier <garnier@njit.edu>
# Description: Port of the new 'matplotlib' color maps ('viridis' - the default -, 'magma', 'plasma'
# License: MIT + file LICENSE
# LazyData: TRUE
# Encoding: UTF-8
# Depends: R (>= 2.10)
# Imports: stats, grDevices, ggplot2 (>= 1.0.1), gridExtra
# Suggests: hexbin (>= 1.27.0), scales, MASS, knitr, dichromat, colorspace, rasterVis, httr, mapproj
# VignetteBuilder: knitr
# URL: https://github.com/sjmgarnier/viridis
# BugReports: https://github.com/sjmgarnier/viridis/issues
# NeedsCompilation: no
# Packaged: 2015-10-11 15:58:02 UTC; simon
# Author: Simon Garnier [aut, cre], Noam Ross [ctb, cph] (Continuous scale), Bob Rudis [ctb, cph] (Co
# Repository: CRAN
# Date/Publication: 2015-10-11 18:45:43

# See
# http://docs.continuum.io/conda/build.html for
```

```
# more information about meta.yaml
```

CHAPTER 426

r-wasabi

426.1 Summary

Prepare Sailfish and Salmon output for downstream analysis

426.2 Home

https://github.com/COMBINE-lab/wasabi

426.3 Versions

- 0.0.1

426.4 License

BSD-3-clause

426.5 Meta

```
package:
  name: r-wasabi
  version: 0.0.1
source:
  git_url: https://github.com/COMBINE-lab/wasabi
build:
  number: 0
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
    - r
    - bioconductor-rhdf5
    - r-data.table
```

```
    - r-rjson
  run:
    - r
    - bioconductor-rhdf5
    - r-data.table
    - r-rjson
test:
  commands:
    - '$R -e "library(''wasabi'')"'
about:
  home: https://github.com/COMBINE-lab/wasabi
  license: BSD-3-clause
  summary: "Prepare Sailfish and Salmon output for downstream analysis"
```

CHAPTER 427

r-writexls

427.1 Summary

Cross-platform Perl based R function to create Excel 2003 (XLS) and Excel 2007 (XLSX) files from one or more data frames. Each data frame will be written to a separate named worksheet in the Excel spreadsheet. The worksheet name will be the name of the data frame it contains or can be specified by the user.

427.2 Home

https://github.com/marcschwartz/WriteXLS

427.3 Versions

- 4.0.0

427.4 License

GPL (>= 2)

427.5 Meta

```
package:
  name: r-writexls
  # Note that conda versions cannot contain -, so any -'s in the version have
  # been replaced with _'s.
  version: "4.0.0"

source:
  fn: WriteXLS_4.0.0.tar.gz
  url:
    - http://cran.r-project.org/src/contrib/WriteXLS_4.0.0.tar.gz
    - http://cran.r-project.org/src/contrib/Archive/WriteXLS/WriteXLS_4.0.0.tar.gz
```

```
  # You can add a hash for the file here, like md5 or sha1
  # md5: 49448ba4863157652311cc5ea4fea3ea
  # sha1: 3bcfbee008276084cbb37a2b453963c61176a322
  # patches:
   # List any patch files here
   # - fix.patch

build:
  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

  # This is required to make R link correctly on Linux.
  rpaths:
    - lib/R/lib/
    - lib/


requirements:
  build:
    - r

  run:
    - r

test:
  commands:
    # You can put additional test commands to be run here.
    - $R -e "library('WriteXLS')" # [not win]
    - "\"%R%\" -e \"library('WriteXLS')\"" # [win]

  # You can also put a file called run_test.py, run_test.sh, or run_test.bat
  # in the recipe that will be run at test time.

  # requires:
    # Put any additional test requirements here.

about:
  home: !!python/unicode 'https://github.com/marcschwartz/WriteXLS'

  license: GPL (>= 2)
  summary: !!python/unicode 'Cross-platform Perl based R function to create Excel 2003 (XLS)
    and Excel 2007 (XLSX) files from one or more data frames. Each data frame will be
    written to a separate named worksheet in the Excel spreadsheet. The worksheet name
    will be the name of the data frame it contains or can be specified by the user. '


# The original CRAN metadata for this package was:

# Package: WriteXLS
# Version: 4.0.0
# Date: 2015-11-07
# Title: Cross-Platform Perl Based R Function to Create Excel 2003 (XLS) and Excel 2007 (XLSX) Files
# Description: Cross-platform Perl based R function to create Excel 2003 (XLS) and Excel 2007 (XLSX)
# Author: Marc Schwartz <marc_schwartz@me.com> and various authors for Perl modules listed in each .p
# Copyright: The copyright holders of the Perl files are listed in each .pm file under the Perl direc
# Maintainer: Marc Schwartz <marc_schwartz@me.com>
# License: GPL (>= 2)
```

```
# SystemRequirements: Perl
# Imports: utils
# URL: https://github.com/marcschwartz/WriteXLS
# BugReports: https://github.com/marcschwartz/WriteXLS/issues
# NeedsCompilation: no
# Packaged: 2015-12-07 12:45:32 UTC; marcschwartz
# Repository: CRAN
# Date/Publication: 2015-12-07 16:17:00

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 428

raxml

428.1 Summary

Phylogenetics - Randomized Axelerated Maximum Likelihood.

428.2 Home

http://sco.h-its.org/exelixis/web/software/raxml/index.html

428.3 Versions

- 8.2.4

428.4 License

GPL

428.5 Meta

```
package:
  name: raxml
  version: "8.2.4"
build:
  number: 0
source:
  fn: v8.2.4.tar.gz
  url: https://github.com/stamatak/standard-RAxML/archive/v8.2.4.tar.gz
requirements:
  build:
  run:
test:
  commands:
    - raxmlHPC-PTHREADS -h > /dev/null
about:
```

```
  home: http://sco.h-its.org/exelixis/web/software/raxml/index.html
  license: GPL
  summary: Phylogenetics - Randomized Axelerated Maximum Likelihood.
```

CHAPTER 429

razers3

429.1 Summary

a tool for mapping millions of short genomic reads onto a reference genome

429.2 Home

http://www.seqan.de/projects/razers/

429.3 Versions

- 3.5.0

429.4 License

GPLv3

429.5 Meta

```
package:
  name: razers3
  version: '3.5.0'

source:
  fn: seqan-src-2.0.1.tar.gz
  url: http://packages.seqan.de/seqan-src/seqan-src-2.0.1.tar.gz

build:
  number: 0

requirements:
  build:
    - cmake
  run:
```

```
test:
  commands:
    - razers3 --help

about:
  home: http://www.seqan.de/projects/razers/
  license: GPLv3
  summary: a tool for mapping millions of short genomic reads onto a reference genome
```

CHAPTER 430

requests-toolbelt

430.1 Summary

A toolbelt of useful classes and functions to be used with python-requests

430.2 Home

https://github.com/sigmavirus24/requests-toolbelt

430.3 Versions

- 0.5.0

430.4 License

Apache License 2.0

430.5 Meta

```
package:
  name: requests-toolbelt
  version: '0.5.0'

source:
  fn: requests-toolbelt-0.5.0.tar.gz
  url: https://pypi.python.org/packages/source/r/requests-toolbelt/requests-toolbelt-0.5.0.tar.gz
  md5: 317a788caa4eec4e3b8f2433c646eaa8

build:
  number: 0

requirements:
  build:
    - python
```

```
    - setuptools
    - requests

  run:
    - python
    - requests

test:
  imports:
    - requests_toolbelt.multipart
    - requests_toolbelt.downloadutils

about:
  home: https://github.com/sigmavirus24/requests-toolbelt
  license: Apache License 2.0
  summary: A toolbelt of useful classes and functions to be used with python-requests
```

CHAPTER 431

retrying

431.1 Summary

Retrying is a general-purpose retrying library, written in Python, to simplify the task of adding retry behavior to just about anything.

431.2 Home

https://github.com/rholder/retrying

431.3 Versions

- 1.3.3

431.4 License

Apache Software License

431.5 Meta

```
package:
  name: retrying
  version: "1.3.3"

source:
  fn: retrying-1.3.3.tar.gz
  url: https://pypi.python.org/packages/source/r/retrying/retrying-1.3.3.tar.gz
  md5: 2a126aeef8b21324ecdeac15ff46ef17

build:
  noarch_python: True
  number: 1

requirements:
```

```
  build:
    - python
    - six >=1.7.0
  run:
    - python
    - six >=1.7.0

test:
  imports:
    - retrying

about:
  home: https://github.com/rholder/retrying
  license: Apache Software License
  summary: 'Retrying is a general-purpose retrying library, written in Python, to simplify the task o
```

CHAPTER 432

rnacode

432.1 Summary

RNAcode - Analyze the protein coding potential in multiple sequence alignments RNAcode relies on evolutionary signatures including synonymous/conservative mutations and conservation of the reading frame. It does not use any species specific sequence characteristics whatsoever and does not use any machine learning techniques.

432.2 Home

http://wash.github.io/rnacode/

432.3 Versions

- 0.3

432.4 License

432.5 Meta

```
about:
  home: http://wash.github.io/rnacode/
  license: ''
  summary: 'RNAcode - Analyze the protein coding potential in multiple sequence alignments
    RNAcode relies on evolutionary signatures including synonymous/conservative mutations
    and conservation of the reading frame. It does not use any species specific sequence
    characteristics whatsoever and does not use any machine learning techniques.'
build:
  number: 0
package:
  name: rnacode
  version: '0.3'
requirements:
  build: []
  run: []
source:
```

```
  fn: RNAcode-0.3.tar.gz
  sha256: 86c600a07ecd04d243fd6eb3c6cc5b20fd6159f34f69423e7391c0ce8f311048
  url: http://github.com/downloads/wash/rnacode/RNAcode-0.3.tar.gz
test:
  commands:
  - RNAcode --help &> /dev/null
```

CHAPTER 433

rnashapes

433.1 Summary

RNAshape abstraction maps structures to a tree-like domain of shapes, retaining adjacency and nesting of structural features, but disregarding helix lengths. Shape abstraction integrates well with dynamic programming algorithms, and hence it can be applied during structure prediction rather than afterwards. This avoids exponential explosion and can still give us a non-heuristic and complete account of properties of the molecule's folding space.

433.2 Home

http://bibiserv.techfak.uni-bielefeld.de/rnashapes

433.3 Versions

- 2.1.6

433.4 License

433.5 Meta

```
about:
  home: http://bibiserv.techfak.uni-bielefeld.de/rnashapes
  license: ''
  summary: 'RNAshape abstraction maps structures to a tree-like domain of shapes,
    retaining adjacency and nesting of structural features, but disregarding helix
    lengths. Shape abstraction integrates well with dynamic programming algorithms,
    and hence it can be applied during structure prediction rather than afterwards.
    This avoids exponential explosion and can still give us a non-heuristic and complete
    account of properties of the molecule''s folding space.'
build:
  number: 0
package:
  name: rnashapes
  version: 2.1.6
requirements:
```

```
  build: []
  run: []
source:
  fn: RNAshapes-2.1.6.tar.gz
  sha256: 6923af49f931efa4f3ad2a05f87a8e5222b6f865d0347e5598de3661e73bb81b
  url: https://github.com/bgruening/download_store/raw/master/RNAshapes/RNAshapes-2.1.6.tar.gz
test:
  commands:
  - RNAshapes  -h &> /dev/null
```

CHAPTER 434

rnastructure

434.1 Summary

RNAstructure is a complete package for RNA and DNA secondary structure prediction and analysis. It includes algorithms for secondary structure prediction, including facility to predict base pairing probabilities. It also can be used to predict bimolecular structures and can predict the equilibrium binding affinity of an oligonucleotide to a structured RNA target. This is useful for siRNA design. It can also predict secondary structures common to two, unaligned sequences, which is much more accurate than single sequence secondary structure prediction. Finally, RNAstructure can take a number of different types of experiment mapping data to constrain or restrain structure prediction. These include chemical mapping, enzymatic mapping, NMR, and SHAPE data.

434.2 Home

http://rna.urmc.rochester.edu/RNAstructure.html

434.3 Versions

- 5.7

434.4 License

434.5 Meta

```
about:
  home: http://rna.urmc.rochester.edu/RNAstructure.html
  license: ''
  summary: 'RNAstructure is a complete package for RNA and DNA secondary structure  prediction
    and analysis. It includes algorithms for   secondary structure  prediction, including
    facility to predict base pairing probabilities. It  also can be used to predict
    bimolecular structures and can predict the  equilibrium binding affinity of an
    oligonucleotide to a structured RNA  target. This is useful for siRNA design.
    It can also predict secondary  structures common to two, unaligned sequences,
    which is much more accurate  than single sequence secondary structure prediction.
    Finally, RNAstructure  can take a number of different types of experiment mapping
```

```
    data to constrain  or restrain structure prediction. These include chemical mapping,
    enzymatic  mapping, NMR, and SHAPE data.'
build:
  number: 0
package:
  name: rnastructure
  version: '5.7'
requirements:
  build: []
  run: []
source:
  fn: RNAstructure-5.7.tgz
  sha256: 7d7060c2180b95e0d0e0a840499df48de3571e37ca6bef51325377fe7ca28ae6
  url: http://depot.galaxyproject.org/package/source/RNAstructure-5.7.tgz
test:
  commands:
    - refold -h
    - ProbKnot -h
    - dot2ct -h
```

CHAPTER 435

rpy2

435.1 Summary

Python interface to the R language (embedded R)

435.2 Home

http://rpy.sourceforge.net

435.3 Versions

- 2.7.6

435.4 License

GNU General Public License v2 or later (GPLv2+)

435.5 Meta

```
package:
  name: rpy2
  version: "2.7.6"

source:
  fn: rpy2-2.7.6.tar.gz
  url: https://pypi.python.org/packages/source/r/rpy2/rpy2-2.7.6.tar.gz
  md5: e2fdcbc5bbd3803256c39568c423dcd9
#  patches:
   # List any patch files here
   # - fix.patch

build:
  rpaths:
    - lib/R/lib/
```

```
    - lib/

requirements:
  build:
    - python
    - r
    - setuptools
    - argparse # [py26]
    - singledispatch # [not (py34 or py35)]
    - six
    - readline

  run:
    - python
    - r
    - argparse # [py26]
    - singledispatch # [not (py34 or py35)]
    - six
    - readline

test:
  # Python imports
  imports:
    - rpy2
    - rpy2.interactive
    - rpy2.interactive.tests
    - rpy2.ipython
    - rpy2.ipython.tests
    - rpy2.rinterface
    - rpy2.rinterface.tests
    - rpy2.rlike
    - rpy2.rlike.tests
    - rpy2.robjects
    - rpy2.robjects.lib
    - rpy2.robjects.lib.tests
    - rpy2.robjects.tests

  commands:
    - echo
    # - python -m rpy2.tests

  requires:
    - ipython
    - r-survival
    - r-ggplot2
    - numpy
    - pandas

about:
  home: http://rpy.sourceforge.net
  license: GNU General Public License v2 or later (GPLv2+)
  summary: 'Python interface to the R language (embedded R)'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 436

rsa

436.1 Summary

Pure-Python RSA implementation

436.2 Home

http://stuvel.eu/rsa

436.3 Versions

- 3.1.4

436.4 License

Apache Software License

436.5 Meta

```
# Migrated from https://anaconda.org/jakirkham/rsa/

package:
  name: rsa
  version: "3.1.4"

source:
  fn: rsa-3.1.4.tar.gz
  url: https://pypi.python.org/packages/source/r/rsa/rsa-3.1.4.tar.gz
  md5: b6b1c80e1931d4eba8538fd5d4de1355
#  patches:
   # List any patch files here
   # - fix.patch

build:
```

```
  # preserve_egg_dir: True
  entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - rsa = rsa:main
    #
    # Would create an entry point called rsa that calls rsa.main()

    - pyrsa-priv2pub = rsa.util:private_to_public
    - pyrsa-keygen = rsa.cli:keygen
    - pyrsa-encrypt = rsa.cli:encrypt
    - pyrsa-decrypt = rsa.cli:decrypt
    - pyrsa-sign = rsa.cli:sign
    - pyrsa-verify = rsa.cli:verify
    - pyrsa-encrypt-bigfile = rsa.cli:encrypt_bigfile
    - pyrsa-decrypt-bigfile = rsa.cli:decrypt_bigfile

  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools
    - pyasn1 >=0.1.3

  run:
    - python
    - pyasn1 >=0.1.3

test:
  # Python imports
  imports:
    - rsa

  commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.

    - pyrsa-priv2pub --help
    - pyrsa-keygen --help
    - pyrsa-encrypt --help
    - pyrsa-decrypt --help
    - pyrsa-sign --help
    - pyrsa-verify --help
    - pyrsa-encrypt-bigfile --help
    - pyrsa-decrypt-bigfile --help

  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
```

```
  home: http://stuvel.eu/rsa
  license: Apache Software License
  summary: 'Pure-Python RSA implementation'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 437

rseg

437.1 Summary

The RSEG software package is used to analyze ChIP-Seq data, especially for identifying genomic regions and their boundaries marked by diffusive histone modification markers, such as H3K36me3 and H3K27me3.

437.2 Home

http://smithlabresearch.org/software/rseg

437.3 Versions

- 0.4.9

437.4 License

GPLv3

437.5 Meta

```
package:
  name: rseg
  version: "0.4.9"

source:
  fn: rseg-0.4.9.tar.gz
  url: https://github.com/smithlabcode/rseg/archive/rseg-0.4.9.tar.gz
  md5: 890d9d3b364270ab62da012cd87a79ee
  patches:
    - makefile.patch

build:
  number: 0
```

```
requirements:
  build:
  - zlib
  - gcc

  run:
  - zlib
  - libgcc

test:
  commands:
    - rseg -about > /dev/null 2>&1
    - rseg-diff -about > /dev/null 2>&1
    - deadzones -about > /dev/null 2>&1

about:
  home: http://smithlabresearch.org/software/rseg
  license: GPLv3
  summary: The RSEG software package is used to analyze ChIP-Seq data, especially for identifying ger
```

CHAPTER 438

rsem

438.1 Summary

RSEM (RNA-Seq by Expectation-Maximization)

438.2 Home

http://deweylab.biostat.wisc.edu/rsem/

438.3 Versions

- 1.2.22

438.4 License

GPLv3

438.5 Meta

```
about:
  home: http://deweylab.biostat.wisc.edu/rsem/
  license: GPLv3
  summary: RSEM (RNA-Seq by Expectation-Maximization)
package:
  name: rsem
  version: 1.2.22
build:
  rpaths:
    - lib/R/lib/
    - lib/
requirements:
  build:
    - r >=3.1.0
  run:
```

```
    - r >=3.1.0
test:
  commands:
    - rsem-prepare-reference 2>&1 | grep rsem-prepare-reference > /dev/null
    - rsem-for-ebseq-find-DE 2>&1 | grep Usage > /dev/null
source:
  fn: v1.2.22.tar.gz
  url: https://github.com/deweylab/RSEM/archive/v1.2.22.tar.gz
  md5: 7a8373711ca0da79d9e4c9b314955cb3
```

CHAPTER 439

rseqc

439.1 Summary

RSEQC - An RNA-seq Quality Control Package

439.2 Home

http://rseqc.sourceforge.net/

439.3 Versions

- 2.6.2

439.4 License

GPLv3

439.5 Meta

```
about:
  home: http://rseqc.sourceforge.net/
  license: GPLv3
  summary: RSEQC - An RNA-seq Quality Control Package
package:
  name: rseqc
  version: 2.6.2
requirements:
  build:
    - python >=2.7,<3
    - numpy
  run:
    - python >=2.7,<3
    - numpy
test:
```

```
  requires:
    - python >=2.7,<3
    - numpy
  commands:
    - read_distribution.py 2>&1 | grep Usage > /dev/null
source:
  fn: RSeQC-2.6.2.tar.gz
  url: http://downloads.sourceforge.net/project/rseqc/RSeQC-2.6.2.tar.gz
  md5: 4e7fcfed2f4f7cff63ff852e150d80d9
```

CHAPTER 440

rtg-tools

440.1 Summary

RealTimeGenomics Tools – Utilities for accurate VCF comparison and manipulation

440.2 Home

https://github.com/RealTimeGenomics/rtg-tools

440.3 Versions

- 3.6

440.4 License

BSD

440.5 Meta

```
package:
  name: rtg-tools
  version: "3.6"

source:
  fn: rtg-tools-3.6-nojre.zip
  url: https://github.com/RealTimeGenomics/rtg-tools/releases/download/3.6/rtg-tools-3.6-nojre.zip

build:
  number: 0

test:
  commands:
    - "rtg vcfeval --help 2>&1 | grep 'Usage: rtg'"
  requires:
```

```
    - java-jdk

about:
  home: https://github.com/RealTimeGenomics/rtg-tools
  license: BSD
  summary: RealTimeGenomics Tools -- Utilities for accurate VCF comparison and manipulation
```

CHAPTER 441

ruby

441.1 Summary

441.2 Home

https://www.ruby-lang.org/

441.3 Versions

- 2.2.2
- 2.1.7
- 2.0
- 1.9

441.4 License

BSD

441.5 Meta

```
# Based on channel tswicegood
package:
  name: ruby
  version: 2.2.2

build:
  number: 1

source:
  fn: ruby-2.2.2.tar.gz
  url: http://cache.ruby-lang.org/pub/ruby/2.2/ruby-2.2.2.tar.gz
  #md5: e57fdbb8ed56e70c43f39c79da1654b2
```

```
test:
  commands:
    - ruby --version
    - ruby -e 'puts "Hi, from Ruby!"'
    - ruby -e 'require "rubygems"'
    - gem --version
    - ruby -ropenssl -e "puts :OK"

requirements:
  build:
    - python
    - yaml
    - openssl 1.0.1g
    - zlib
  run:
    - python
    - zlib

about:
  home: https://www.ruby-lang.org/
  license: BSD
```

CHAPTER 442

rust

442.1 Summary

Rust is a systems programming language that runs blazingly fast, prevents segfaults, and guarantees thread safety.

442.2 Home

https://www.rust-lang.org

442.3 Versions

- 1.6.0

442.4 License

MIT

442.5 Meta

```
package:
  name: rust
  version: "1.6.0"

build:
  number: 0

source:
  fn: rust-1.6.0-x86_64-unknown-linux-gnu.tar.gz # [linux64]
  url: https://static.rust-lang.org/dist/rust-1.6.0-x86_64-unknown-linux-gnu.tar.gz # [linux64]
  fn: rust-1.6.0-x86_64-apple-darwin.tar.gz
  url: http://static.rust-lang.org/dist/rust-1.6.0-x86_64-apple-darwin.tar.gz # [osx]

test:
  commands:
```

```
    - rustc --help
    - cargo --help

about:
  home: https://www.rust-lang.org
  license: MIT
  summary: Rust is a systems programming language that runs blazingly fast, prevents segfaults, and g
```

CHAPTER 443

s3gof3r

443.1 Summary

Fast, concurrent, streaming access to Amazon S3, including gof3r, a CLI

443.2 Home

https://github.com/rlmcpherson/s3gof3r

443.3 Versions

- 0.5.0

443.4 License

MIT

443.5 Meta

```
package:
  name: s3gof3r
  version: '0.5.0'

source:
  fn: gof3r_0.5.0_linux_amd64.tar.gz # [linux]
  url: https://github.com/rlmcpherson/s3gof3r/releases/download/v0.5.0/gof3r_0.5.0_linux_amd64.tar.gz
  fn: gof3r_0.5.0_darwin_amd64.zip # [osx]
  url: https://github.com/rlmcpherson/s3gof3r/releases/download/v0.5.0/gof3r_0.5.0_darwin_amd64.zip #

build:
  number: 0

requirements:
  build:
```

```
  run:

test:
  commands:
    - "gof3r cp -h 2>&1 | grep 'gof3r'"

about:
  home: https://github.com/rlmcpherson/s3gof3r
  license: MIT
  summary: Fast, concurrent, streaming access to Amazon S3, including gof3r, a CLI
```

CHAPTER 444

sailfish

444.1 Summary

Rapid Mapping-based Isoform Quantification from RNA-Seq Reads

444.2 Home

http://www.cs.cmu.edu/~ckingsf/software/sailfish/

444.3 Versions

- 0.9.0

444.4 License

GPLv3

444.5 Meta

```
about:
    home: http://www.cs.cmu.edu/~ckingsf/software/sailfish/
    license: GPLv3
    summary: Rapid Mapping-based Isoform Quantification from RNA-Seq Reads
package:
    name: sailfish
    version: 0.9.0
source:
    fn: sailfish-0.9.0.tar.gz
    url: https://github.com/kingsfordgroup/sailfish/archive/v0.9.0.tar.gz
requirements:
  build:
    - boost
    - cmake
    - tbb
```

```
  run:
    - boost
    - tbb
test:
    commands:
      - sailfish --help
```

CHAPTER 445

salmon

445.1 Summary

Highly-accurate & wicked fast transcript-level quantification from RNA-seq reads using lightweight alignments

445.2 Home

https://github.com/COMBINE-lab/salmon

445.3 Versions

- 0.6.0

445.4 License

GPLv3

445.5 Meta

```
about:
    home: https://github.com/COMBINE-lab/salmon
    license: GPLv3
    summary: Highly-accurate & wicked fast transcript-level quantification from RNA-seq reads using l
package:
    name: salmon
    version: 0.6.0
source:
    fn: v0.6.0.tar.gz
    url: https://github.com/COMBINE-lab/salmon/archive/v0.6.0.tar.gz
requirements:
  build:
    - boost
    - cmake
    - tbb
```

```
  run:
    - boost
    - tbb
test:
    commands:
      - salmon --help
```

CHAPTER 446

sambamba

446.1 Summary

Tools for working with SAM/BAM data

446.2 Home

https://github.com/lomereiter/sambamba

446.3 Versions

- 0.5.9

446.4 License

GPLv2

446.5 Meta

```
package:
  name: sambamba
  version: '0.5.9'
source:
  fn: sambamba_v0.5.9.tar.bz2
  url: https://github.com/lomereiter/sambamba/releases/download/v0.5.9/sambamba_v0.5.9_linux.tar.bz2
  url: https://github.com/lomereiter/sambamba/releases/download/v0.5.9/sambamba_v0.5.9_osx.tar.bz2 #
build:
  number: 0
requirements:
  build:
  run:
test:
  commands:
    - sambamba view
```

```
about:
  home: https://github.com/lomereiter/sambamba
  license: GPLv2
  summary: Tools for working with SAM/BAM data
```

CHAPTER 447

samblaster

447.1 Summary

A tool to mark duplicates and extract discordant and split reads from sam files.

447.2 Home

https://github.com/GregoryFaust/samblaster

447.3 Versions

- 0.1.22

447.4 License

MIT

447.5 Meta

```
# Started based on: https://anaconda.org/Judowill/samblaster

package:
  name: samblaster
  version: '0.1.22'
source:
  fn: samblaster-v.0.1.22.tar.gz
  url: https://github.com/GregoryFaust/samblaster/releases/download/v.0.1.22/samblaster-v.0.1.22.tar

requirements:
  build:
  run:

test:
    commands:
```

```
        - samblaster -h

about:
  home: https://github.com/GregoryFaust/samblaster
  license: MIT
  summary: A tool to mark duplicates and extract discordant and split reads from sam files.
```

CHAPTER 448

samtools

448.1 Summary

Tools for dealing with SAM, BAM and CRAM files

448.2 Home

https://github.com/samtools/samtools

448.3 Versions

- 1.3
- 1.1
- 1.0
- 0.1.19
- 0.1.18
- 0.1.16

448.4 License

MIT

448.5 Meta

```
package:
  name: samtools
  version: "1.3"
build:
  number: 1
source:
  fn: samtools-1.3.tar.bz2
```

```
  url: https://github.com/samtools/samtools/releases/download/1.3/samtools-1.3.tar.bz2
requirements:
  build:
  - ncurses
  - zlib
  run:
  - ncurses
  - zlib
about:
  home: https://github.com/samtools/samtools
  license: MIT
  summary: Tools for dealing with SAM, BAM and CRAM files
test:
  commands:
    - samtools --help
```

CHAPTER 449

scalpel

449.1 Summary

Sensitive detection of INDELs (INsertions and DELetions)

449.2 Home

http://scalpel.sourceforge.net/

449.3 Versions

- 0.5.1

449.4 License

MIT

449.5 Meta

```
package:
  name: scalpel
  version: '0.5.1'

source:
  fn: scalpel-0.5.1.tar.gz
  url: http://downloads.sourceforge.net/project/scalpel/scalpel-0.5.1.tar.gz

build:
  number: 2

requirements:
  build:
    - cmake
    - bamtools
```

```
  run:
    - bamtools
    - samtools
    - bcftools

test:
  commands:
    - scalpel-discovery --help

about:
  home: http://scalpel.sourceforge.net/
  license: MIT
  summary: Sensitive detection of INDELs (INsertions and DELetions)
```

CHAPTER 450

scikit-bio

450.1 Summary

Data structures, algorithms and educational resources for bioinformatics.

450.2 Home

http://scikit-bio.org

450.3 Versions

- 0.2.3

450.4 License

BSD License

450.5 Meta

```
package:
  name: scikit-bio
  version: "0.2.3"

source:
  fn: scikit-bio-0.2.3.tar.gz
  url: https://pypi.python.org/packages/source/s/scikit-bio/scikit-bio-0.2.3.tar.gz
  md5: 2bb1148468d3e5129fa8ff5b29cbeaa3

build:
  number: 0

requirements:
  build:
    - python
```

```
    - setuptools
    - numpy
    - matplotlib >=1.1.0
    - scipy >=0.13.0
    - pandas
    - future
    - six
    - natsort
    - ipython

  run:
    - python
    - numpy
    - matplotlib >=1.1.0
    - scipy >=0.13.0
    - pandas
    - future
    - six
    - natsort
    - ipython

test:
  # Python imports
  imports:
    - skbio
    - skbio.alignment
    - skbio.alignment._lib
    - skbio.alignment.tests
    - skbio.diversity
    - skbio.diversity.alpha
    - skbio.diversity.alpha.tests
    - skbio.diversity.beta
    - skbio.diversity.beta.tests
    - skbio.draw
    - skbio.draw.tests
    - skbio.format
    - skbio.format.sequences
    - skbio.format.sequences.tests
    - skbio.io
    - skbio.io.tests
    - skbio.parse
    - skbio.parse.sequences
    - skbio.parse.sequences.tests
    - skbio.parse.tests
    - skbio.sequence
    - skbio.sequence.tests
    - skbio.stats
    - skbio.stats.distance
    - skbio.stats.distance.tests
    - skbio.stats.ordination
    - skbio.stats.ordination.tests
    - skbio.stats.tests
    - skbio.tests
    - skbio.tree
    - skbio.tree.tests
    - skbio.util
    - skbio.util.tests
```

```
about:
  home: http://scikit-bio.org
  license: BSD License
  summary: 'Data structures, algorithms and educational resources for bioinformatics.'
  license_file: COPYING.txt
```

CHAPTER 451

screed

451.1 Summary

a simple read-only sequence database, designed for short reads

451.2 Home

https://github.com/dib-lab/screed

451.3 Versions

- 0.9

451.4 License

BSD

451.5 Meta

```
about:
  home: https://github.com/dib-lab/screed
  license: BSD
  summary: a simple read-only sequence database, designed for short reads
build:
  number: 0
package:
  name: screed
  version: '0.9'
requirements:
  build:
  - python
  - bz2file ==0.98
  run:
  - python
```

```
  - bz2file ==0.98
source:
  fn: screed-0.9.tar.gz
  md5: 611dd11105489e4153265e055f13debd
  url: https://pypi.python.org/packages/source/s/screed/screed-0.9.tar.gz
test:
  imports:
    - screed
```

CHAPTER 452

scrm

452.1 Summary

A coalescent simulator for genome-scale sequences

452.2 Home

https://scrm.github.io/

452.3 Versions

- 1.6.1

452.4 License

GNU General Public License v3 or later (GPLv3+)

452.5 Meta

```
package:
  name: scrm
  version: 1.6.1

source:
  fn:  scrm-src.tar.gz
  url: https://github.com/scrm/scrm/releases/download/v1.6.1/scrm-src.tar.gz
  md5: 6692b4db0c150e421a996240a3ea1d4d

test:
  commands:
    - scrm 2 1 -T > /dev/null

about:
  home: https://scrm.github.io/
```

```
  summary: A coalescent simulator for genome-scale sequences
  license: GNU General Public License v3 or later (GPLv3+)
```

CHAPTER 453

semidbm

453.1 Summary

Cross platform (fast) DBM interface in python

453.2 Home

https://github.com/jamesls/semidbm

453.3 Versions

- 0.5.1

453.4 License

BSD License

453.5 Meta

```
package:
  name: semidbm
  version: "0.5.1"

source:
  fn: semidbm-0.5.1.tar.gz
  url: https://pypi.python.org/packages/source/s/semidbm/semidbm-0.5.1.tar.gz
  md5: e0e45cf55fb0cfca1da04368619ff116
#  patches:
   # List any patch files here
   # - fix.patch

# build:
  # noarch_python: True
  # preserve_egg_dir: True
```

```
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - semidbm = semidbm:main
    #
    # Would create an entry point called semidbm that calls semidbm.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools

  run:
    - python

test:
  # Python imports
  imports:
    - semidbm
    - semidbm.loaders

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: https://github.com/jamesls/semidbm
  license: BSD License
  summary: 'Cross platform (fast) DBM interface in python'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 454

seqbuster

454.1 Summary

miRNA and isomiR annotation

454.2 Home

https://github.com/lpantano/seqbuster

454.3 Versions

- 2.3

454.4 License

MIT

454.5 Meta

```
about:
  home: https://github.com/lpantano/seqbuster
  license: MIT
  summary: miRNA and isomiR annotation

package:
  name: seqbuster
  version: '2.3'

source:
  git_url: https://github.com/lpantano/seqbuster
  git_tag: miraligner-2.3

build:
  number: 3
```

```
requirements:
  run:
    - java-jdk >=7,<8

test:
  commands:
    - miraligner -h
```

CHAPTER 455

seqcluster

455.1 Summary

small RNA analysis from NGS data

455.2 Home

https://github.com/lpantano/seqclsuter

455.3 Versions

- 1.1.13

455.4 License

MIT

455.5 Meta

```
about:
  home: https://github.com/lpantano/seqclsuter
  license: MIT
  summary: small RNA analysis from NGS data

package:
  name: seqcluster
  version: '1.1.13'

source:
  git_url: https://github.com/lpantano/seqcluster
  git_rev: 99f2fac
build:
  number: 3
  skip: True # [not py27]
```

```
requirements:
  build:
    - python
    - setuptools
    - gcc
  run:
    - python
    - pyyaml
    - pysam >=0.8.1
    - pandas
    - pybedtools
    - progressbar
    - matplotlib

test:
  commands:
    - seqcluster cluster -h
  imports:
    - seqcluster
```

CHAPTER 456

seqprep

456.1 Summary

456.2 Home

https://github.com/jstjohn/SeqPrep

456.3 Versions

- 1.1

456.4 License

MIT

456.5 Meta

```
package:
  name: seqprep
  version: 1.1

source:
  fn: v1.1.tar.gz
  url: https://github.com/jstjohn/SeqPrep/archive/v1.1.tar.gz
  md5: 42bd8e62e8bf99befb37ed29ce047115

  patches:
    - cflags.patch

requirements:
  build:
    - zlib
  run:
    - zlib
```

```
about:
  home: https://github.com/jstjohn/SeqPrep
  license: MIT
```

CHAPTER 457

seqtk

457.1 Summary

Seqtk is a fast and lightweight tool for processing sequences in the FASTA or FASTQ format

457.2 Home

https://github.com/lh3/seqtk

457.3 Versions

- r82

457.4 License

MIT License

457.5 Meta

```
package:
  name: seqtk
  version: r82
source:
  git_rev: 4feb6e81444ab6bc44139dd3a125068f81ae4ad8
  git_url: https://github.com/lh3/seqtk.git
about:
  home: https://github.com/lh3/seqtk
  license: MIT License
  summary: Seqtk is a fast and lightweight tool for processing sequences in the FASTA or FASTQ format
test:
  commands:
    - seqtk seq
```

CHAPTER 458

setuptools_cython

458.1 Summary

Cython setuptools integration

458.2 Home

http://pypi.python.org/pypi/setuptools_cython/

458.3 Versions

- 0.2.1

458.4 License

http://www.gnu.org/licenses/gpl-2.0.html

458.5 Meta

```
package:
  name: setuptools_cython
  version: "0.2.1"

source:
  fn: setuptools_cython-0.2.1.tar.gz
  url: https://pypi.python.org/packages/source/s/setuptools_cython/setuptools_cython-0.2.1.tar.gz
  md5: c29fc5bf2894e69cbd98e3800cef4707
#  patches:
   # List any patch files here
   # - fix.patch

build:
  # noarch_python: True
  preserve_egg_dir: True
```

```
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - setuptools_cython = setuptools_cython:main
    #
    # Would create an entry point called setuptools_cython that calls setuptools_cython.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools
    - cython

  run:
    - python
    - setuptools
    - cython

# test:
  # Python imports
  # imports:

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: http://pypi.python.org/pypi/setuptools_cython/
  license: http://www.gnu.org/licenses/gpl-2.0.html
  summary: 'Cython setuptools integration'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 459

sga

459.1 Summary

SGA - String Graph Assembler. SGA is a de novo assembler for DNA sequence reads. It is based on Gene Myers string graph formulation of assembly and uses the FM-index/Burrows-Wheeler transform to efficiently find overlaps between sequence reads.

459.2 Home

https://github.com/jts/sga

459.3 Versions

- 0.10.13

459.4 License

GPLv3

459.5 Meta

```
package:
  name: sga
  version: "0.10.13"
source:
  fn: v0.10.13.tar.gz
  url: https://github.com/jts/sga/archive/v0.10.13.tar.gz
  md5: d4f6aefc48c940dba96cc6513649ecdd
requirements:
  build:
    - bamtools
  run:
    - bamtools
about:
```

```
  home: https://github.com/jts/sga
  license: GPLv3
  summary: SGA - String Graph Assembler. SGA is a de novo assembler for DNA sequence reads. It is bas
```

CHAPTER 460

sickle-trim

460.1 Summary

Windowed Adaptive Trimming for fastq files using quality

460.2 Home

https://github.com/najoshi/sickle

460.3 Versions

- 1.33

460.4 License

MIT

460.5 Meta

```
package:
  name: sickle-trim
  version: '1.33'

source:
  fn: sickle-1.33.tar.gz
  url: https://github.com/najoshi/sickle/archive/v1.33.tar.gz

build:
  number: 0

requirements:
  build:
  run:
```

```
test:
  commands:
    - sickle --version

about:
  home: https://github.com/najoshi/sickle
  license: MIT
  summary: Windowed Adaptive Trimming for fastq files using quality
```

CHAPTER 461

sickle

461.1 Summary

A lightweight OAI client library for Python

461.2 Home

http://github.com/mloesch/sickle

461.3 Versions

- 0.5

461.4 License

BSD License

461.5 Meta

```
package:
  name: sickle
  version: "0.5"

source:
  fn: Sickle-0.5.tar.gz
  url: https://pypi.python.org/packages/source/S/Sickle/Sickle-0.5.tar.gz
  md5: 9c93e7f3e0db98ab1a18107dfa096082
#  patches:
   # List any patch files here
   # - fix.patch

# build:
  # noarch_python: True
  # preserve_egg_dir: True
```

```
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - sickle = sickle:main
    #
    # Would create an entry point called sickle that calls sickle.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools
    - requests >=1.1.0
    - lxml >=3.2.3

  run:
    - python
    - requests >=1.1.0
    - lxml >=3.2.3

test:
  # Python imports
  imports:
    - sickle

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  requires:
    - mock >=1.0.1
    - nose >=1.0
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: http://github.com/mloesch/sickle
  license: BSD License
  summary: 'A lightweight OAI client library for Python'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 462

simple_sv_annotation

462.1 Summary

Simplify snpEff annotations for interesting cases

462.2 Home

https://github.com/AstraZeneca-NGS/simple_sv_annotation

462.3 Versions

- 2015.11.24

462.4 License

MIT

462.5 Meta

```
package:
  name: simple_sv_annotation
  version: 2015.11.24

source:

  fn: simple_sv_annotation-dd376c8.tar.gz
  url: https://github.com/AstraZeneca-NGS/simple_sv_annotation/archive/dd376c8.tar.gz

build:
  number: 0

requirements:
  build:
    - python
```

```
  run:
    - python
    - pyvcf

test:
  commands:
    - simple_sv_annotation.py --help

about:
  home: https://github.com/AstraZeneca-NGS/simple_sv_annotation
  license: MIT
  summary:  Simplify snpEff annotations for interesting cases
```

CHAPTER 463

simplejson

463.1 Summary

Simple, fast, extensible JSON encoder/decoder for Python

463.2 Home

http://github.com/simplejson/simplejson

463.3 Versions

- 3.8.1

463.4 License

MIT License or Academic Free License (AFL)

463.5 Meta

```
package:
  name: simplejson
  version: "3.8.1"

source:
  fn: simplejson-3.8.1.tar.gz
  url: https://pypi.python.org/packages/source/s/simplejson/simplejson-3.8.1.tar.gz
  md5: b8441f1053edd9dc335ded8c7f98a974
#  patches:
   # List any patch files here
   # - fix.patch

# build:
  # noarch_python: True
  # preserve_egg_dir: True
```

```
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - simplejson = simplejson:main
    #
    # Would create an entry point called simplejson that calls simplejson.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python

  run:
    - python

test:
  # Python imports
  imports:
    - simplejson
    - simplejson.tests

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: http://github.com/simplejson/simplejson
  license: MIT License or Academic Free License (AFL)
  summary: 'Simple, fast, extensible JSON encoder/decoder for Python'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 464

slang

464.1 Summary

464.2 Home

http://www.jedsoft.org/slang/index.html

464.3 Versions

- 2.3.0

464.4 License

GPL

464.5 Meta

```
package:
  name: slang
  version: 2.3.0

source:
  fn: slang-2.3.0.tar.bz2
  url: http://www.jedsoft.org/releases/slang/slang-2.3.0.tar.bz2
  sha1: 6e26e90307d4569e5feef195648c0858ba27f7ac

requirements:
  build:
    - readline
    - ncurses
    - libpng
    - zlib
  run:
    - readline
    - ncurses
```

```
    - libpng
    - zlib

test:
  commands:
    - "slsh --help 2>&1 | grep 'Usage: '"

about:
  home: http://www.jedsoft.org/slang/index.html
  license: GPL
```

CHAPTER 465

snakemake

465.1 Summary

Snakemake is a workflow management system that aims to reduce the complexity of creating workflows by providing a fast and comfortable execution environment, together with a clean and modern specification language in python style. Snakemake workflows are essentially Python scripts extended by declarative code to define rules. Rules describe how to create output files from input files.

465.2 Home

http://snakemake.bitbucket.org

465.3 Versions

- 3.5.5

465.4 License

MIT License

465.5 Meta

```
package:
  name: snakemake
  version: "3.5.5"
source:
  fn: snakemake-3.5.5.tar.gz
  url: https://pypi.python.org/packages/source/s/snakemake/snakemake-3.5.5.tar.gz
build:
  number: 1
  skip: True # [py27]
  entry_points:
    - snakemake = snakemake:main
```

```
    - snakemake-bash-completion = snakemake:bash_completion
requirements:
  build:
    - python
    - setuptools
  run:
    - python
    - docutils
    - pyyaml
test:
    imports:
      - snakemake
    commands:
      - snakemake --help > /dev/null
about:
  home: http://snakemake.bitbucket.org
  license: MIT License
  summary: 'Snakemake is a workflow management system that aims to reduce the complexity of creating
```

CHAPTER 466

snippy

466.1 Summary

Rapid bacterial SNP calling and core genome alignments

466.2 Home

https://github.com/tseemann/snippy

466.3 Versions

- 2.9

466.4 License

GPL2

466.5 Meta

```
package:
  name: snippy
  version: '2.9'

source:
  fn: v2.9.zip
  md5: a0a0f14510c37b5a1f36be06e2afdf3c
  url: https://github.com/tseemann/snippy/archive/v2.9.zip

build:
  number: 0

requirements:
  build:
    - perl
```

```
    - perl-bioperl
    - perl-app-cpanminus
    - perl-module-build
    - bwa
    - samtools
    - parallel
    - freebayes
    - vcflib
    - vcftools
    - snpeff
  run:
    - perl
    - perl-bioperl
    - bwa
    - samtools
    - parallel
    - freebayes
    - vcflib
    - vcftools
    - snpeff

test:
  commands:
  - snippy --version

about:
  home: https://github.com/tseemann/snippy
  license: GPL2
  summary: Rapid bacterial SNP calling and core genome alignments
```

CHAPTER 467

snpeff

467.1 Summary

Genetic variant annotation and effect prediction toolbox

467.2 Home

http://snpeff.sourceforge.net/

467.3 Versions

- 4.11

467.4 License

LGPLv3

467.5 Meta

```
about:
  home: 'http://snpeff.sourceforge.net/'
  license: "LGPLv3"
  summary: "Genetic variant annotation and effect prediction toolbox"

package:
  name: snpeff
  version: '4.11'

build:
  number: 2

source:
  fn: snpEff_v4_11_core.zip
  md5: 43dd4b41f3223bbb4cc094ec5c5e2aac
```

```
  url: http://downloads.sourceforge.net/project/snpeff/snpEff_v4_11_core.zip

requirements:
  run:
      - java-jdk

test:
    commands:
      - snpEff -version
```

CHAPTER 468

sortmerna [linux64]

468.1 Summary

SortMeRNA is a biological sequence analysis tool for filtering, mapping and OTU-picking NGS reads.

468.2 Home

http://bioinfo.lifl.fr/RNA/sortmerna

468.3 Versions

- 2.0

468.4 License

LGPL

468.5 Meta

```
package:
  name: sortmerna [linux64]
  version: 2.0

source:
  fn: 2.0.tar.gz
  url: https://github.com/biocore/sortmerna/archive/2.0.tar.gz
  md5: f233f7734105c75c14bd4c2fa4e2aefe

build:
  number: 0

test:
  commands:
     - sortmerna --version
```

```
about:
  home: http://bioinfo.lifl.fr/RNA/sortmerna
  license: LGPL
  summary: SortMeRNA is a biological sequence analysis tool for filtering, mapping and OTU-picking NG
```

CHAPTER 469

spades

469.1 Summary

SPAdes – St. Petersburg genome assembler – is intended for both standard isolates and single-cell MDA bacteria assemblies.

469.2 Home

http://bioinf.spbau.ru/en/spades

469.3 Versions

- 3.6.2

469.4 License

GPLv2

469.5 Meta

```
package:
  name: spades
  version: '3.6.2'

source:
  fn: SPAdes-3.6.2-Linux.tar.gz                                          # [linux]
  url: http://spades.bioinf.spbau.ru/release3.6.2/SPAdes-3.6.2-Linux.tar.gz  # [linux]
  fn: SPAdes-3.6.2-Darwin.tar.gz                                         # [osx]
  url: http://spades.bioinf.spbau.ru/release3.6.2/SPAdes-3.6.2-Darwin.tar.gz # [osx]

build:
  number: 0

requirements:
```

```
  build:
  run:

test:
  commands:
    - spades.py --test

about:
  home: http://bioinf.spbau.ru/en/spades
  license: GPLv2
  summary: SPAdes - St. Petersburg genome assembler - is intended for both standard isolates and sing
```

CHAPTER 470

sparsehash

470.1 Summary

An extremely memory-efficient hash_map implementation. 2 bits/entry overhead! The SparseHash library contains several hash-map implementations, including implementations that optimize for space or speed. These hashtable implementations are similar in API to SGI's hash_map class and the tr1 unordered_map class, but with different performance characteristics. It's easy to replace hash_map or unordered_map by sparse_hash_map or dense_hash_map in C++ code. They also contain code to serialize and unserialize from disk.

470.2 Home

https://github.com/sparsehash/sparsehash

470.3 Versions

- 2.0.3
- 2.0.2

470.4 License

470.5 Meta

```
about:
  home: https://github.com/sparsehash/sparsehash
  license: ''
  summary: 'An extremely memory-efficient hash_map implementation. 2 bits/entry overhead!
    The SparseHash library contains several hash-map implementations, including implementations
    that optimize for space or speed.  These hashtable implementations are similar
    in API to SGI''s hash_map class and the tr1 unordered_map class, but with different
    performance characteristics. It''s easy to replace hash_map or unordered_map by
    sparse_hash_map or dense_hash_map in C++ code.  They also contain code to serialize
    and unserialize from disk.'
build:
  number: 0
```

```
package:
  name: sparsehash
  version: 2.0.3
requirements:
  build: []
  run: []
source:
  fn: sparsehash-2.0.3.tar.gz
  sha256: 05e986a5c7327796dad742182b2d10805a8d4f511ad090da0490f146c1ff7a8c
  url: https://github.com/sparsehash/sparsehash/archive/sparsehash-2.0.3.tar.gz
```

CHAPTER 471

sphinxcontrib-programoutput

471.1 Summary

Sphinx extension to include program output

471.2 Home

http://sphinxcontrib-programoutput.readthedocs.org/

471.3 Versions

- 0.8

471.4 License

BSD License

471.5 Meta

```
package:
  name: sphinxcontrib-programoutput
  version: "0.8"

source:
  fn: sphinxcontrib-programoutput-0.8.tar.gz
  url: https://pypi.python.org/packages/source/s/sphinxcontrib-programoutput/sphinxcontrib-programout
  md5: bb0be17ef13f268378b2af51ff413c58
#  patches:
   # List any patch files here
   # - fix.patch

# build:
  # noarch_python: True
  # preserve_egg_dir: True
```

```
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - sphinxcontrib-programoutput = sphinxcontrib-programoutput:main
    #
    # Would create an entry point called sphinxcontrib-programoutput that calls sphinxcontrib-progra


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools
    - sphinx >=1.1

  run:
    - python
    - sphinx >=1.1

test:
  # Python imports
  imports:
    - sphinxcontrib

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: http://sphinxcontrib-programoutput.readthedocs.org/
  license: BSD License
  summary: 'Sphinx extension to include program output'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 472

sqt

472.1 Summary

Command-line tools for the analysis of high-throughput sequencing data

472.2 Home

https://bitbucket.org/marcelm/sqt

472.3 Versions

- 0.6.1

472.4 License

MIT

472.5 Meta

```
about:
  home: https://bitbucket.org/marcelm/sqt
  license: MIT
  summary: 'Command-line tools for the analysis of high-throughput sequencing data'
package:
  name: sqt
  version: "0.6.1"
source:
  fn: sqt-0.6.1.tar.gz
  url: https://pypi.python.org/packages/source/s/sqt/sqt-0.6.1.tar.gz
  md5: 3fed3ab31996520017a73b7ac10f3e61
requirements:
  run:
    - python
    - cutadapt
```

```
    - pysam >=0.8.4
    - matplotlib
    - seaborn
  build:
    - python
    - cutadapt
    - pysam >=0.8.4
    - matplotlib
    - seaborn
test:
  imports:
    - sqt
  commands:
    - sqt --version > /dev/null
build:
  skip: True  # [py27]
  script: python3 setup.py install
```

CHAPTER 473

srprism

473.1 Summary

SRPRISM - Short Read Alignment Tool

473.2 Home

ftp://ftp.ncbi.nlm.nih.gov/pub/agarwala/srprism/

473.3 Versions

- 2.4.24

473.4 License

473.5 Meta

```
package:
  name: srprism
  version: 2.4.24
about:
    home: 'ftp://ftp.ncbi.nlm.nih.gov/pub/agarwala/srprism/'
    summary: "SRPRISM - Short Read Alignment Tool"
build:
  number: 2
source:
  fn: srprism.tar.gz
  md5: 09b43fcf8f2db2376bcb2f27ac3a1f00
  url: ftp://ftp.ncbi.nlm.nih.gov/pub/agarwala/bmtagger/src/srprism.tar.gz
requirements:
  build:
    - autoconf
    - gcc
  run:
    - libgcc
```

```
test:
    commands:
        - srprism help
```

CHAPTER 474

stamp

474.1 Summary

A graphical software package for analyzing taxonomic and functional profiles.

474.2 Home

http://pypi.python.org/pypi/stamp/

474.3 Versions

- 2.1.3

474.4 License

Custom

474.5 Meta

```
package:
  name: stamp
  version: "2.1.3"

source:
  fn: STAMP-2.1.3.tar.gz
  url: https://pypi.python.org/packages/source/S/STAMP/STAMP-2.1.3.tar.gz
  md5: 81a5e0df4094d65007c3c27bf1796ec8
#  patches:
   # List any patch files here
   # - fix.patch

build:
  skip: True # [not py27]
  # noarch_python: True
```

```
  # preserve_egg_dir: True
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - stamp = stamp:main
    #
    # Would create an entry point called stamp that calls stamp.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - numpy >=1.9.1
    - scipy >=0.15.1
    - matplotlib >=1.4.2
    - six >=1.3
    - biom-format >=2.0.1
    - pyqi >=0.3.2

  run:
    - python
    - numpy >=1.9.1
    - scipy >=0.15.1
    - matplotlib >=1.4.2
    - six >=1.3
    - biom-format >=2.0.1
    - pyqi >=0.3.2

test:
  # Python imports
  imports:
    - stamp
    - stamp.GUI
    - stamp.metagenomics
    - stamp.metagenomics.fileIO
    - stamp.metagenomics.simulations
    - stamp.metagenomics.stats
    - stamp.metagenomics.stats.CI
    - stamp.metagenomics.stats.distributions
    - stamp.metagenomics.stats.empiricalTests
    - stamp.metagenomics.stats.tests
    - stamp.plugins
    - stamp.plugins.common
    - stamp.plugins.common.multipleComparisonCorrections
    - stamp.plugins.groups
    - stamp.plugins.groups.effectSizeFilters
    - stamp.plugins.groups.plots
    - stamp.plugins.groups.plots.configGUI
    - stamp.plugins.groups.statisticalTests
    - stamp.plugins.multiGroups
    - stamp.plugins.multiGroups.effectSizeFilters
    - stamp.plugins.multiGroups.plots
    - stamp.plugins.multiGroups.plots.configGUI
```

```
    - stamp.plugins.multiGroups.postHoc
    - stamp.plugins.multiGroups.statisticalTests
    - stamp.plugins.samples
    - stamp.plugins.samples.confidenceIntervalMethods
    - stamp.plugins.samples.effectSizeFilters
    - stamp.plugins.samples.plots
    - stamp.plugins.samples.plots.configGUI
    - stamp.plugins.samples.statisticalTests

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: http://pypi.python.org/pypi/stamp/
  license: Custom
  license_file: LICENSE.txt
  summary: 'A graphical software package for analyzing taxonomic and functional profiles.'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 475

star-fusion

475.1 Summary

A fusion gene caller for STAR. The FusionFilter tools to create needed index data structures are not included.

475.2 Home

https://github.com/STAR-Fusion/STAR-Fusion

475.3 Versions

- 0.5.4

475.4 License

MIT

475.5 Meta

```
package:
  name: star-fusion
  version: "0.5.4"

source:
  fn: STAR-Fusion_v0.5.4.FULL.tar.gz
  url: https://github.com/STAR-Fusion/STAR-Fusion/releases/download/v0.5.4/STAR-Fusion_v0.5.4.FULL.ta

requirements:
  run:
      - blast
      - perl
      - perl-set-intervaltree
      - perl-db-file
      - perl-uri
```

```
test:
  commands:
      - STAR-Fusion --help 2>&1 | grep Optional > /dev/null

about:
  home: https://github.com/STAR-Fusion/STAR-Fusion
  license: MIT
  summary: A fusion gene caller for STAR. The FusionFilter tools to create needed index data structur
```

CHAPTER 476

star

476.1 Summary

An RNA-seq read aligner.

476.2 Home

https://github.com/alexdobin/STAR

476.3 Versions

- 2.5.0c

476.4 License

GPLv3

476.5 Meta

```
package:
  name: star
  version: "2.5.0c"
source:
  fn: 2.5.0c.tar.gz
  url: https://github.com/alexdobin/STAR/archive/2.5.0c.tar.gz
about:
  home: https://github.com/alexdobin/STAR
  license: GPLv3
  summary: An RNA-seq read aligner.
test:
  commands:
    - STAR --version
```

CHAPTER 477

stringtie

477.1 Summary

Transcriptome assembly and quantification for RNA-seq

477.2 Home

http://ccb.jhu.edu/software/stringtie/

477.3 Versions

- 1.2.0
- 1.0.4
- 1.0.3
- 1.0.1
- 0.97

477.4 License

Artistic License 2.0

477.5 Meta

```
package:
  name: stringtie
  version: "1.2.0"
source:
  fn: v1.2.0.tar.gz
  url: https://github.com/gpertea/stringtie/archive/v1.2.0.tar.gz
  sha256: 0e2a9124d578a68f2444703d96bbc755037dfbc4657d4b2d0ee9724c8abc4b37
build:
```

```
  number: 1
about:
  home: http://ccb.jhu.edu/software/stringtie/
  license: Artistic License 2.0
  summary: Transcriptome assembly and quantification for RNA-seq
test:
  commands:
    - stringtie --version
```

CHAPTER 478

subread

478.1 Summary

High-performance read alignment, quantification, and mutation discovery

478.2 Home

http://subread.sourceforge.net/

478.3 Versions

- 1.5.0

478.4 License

GPLv3

478.5 Meta

```
about:
    home: http://subread.sourceforge.net/
    license: GPLv3
    summary: High-performance read alignment, quantification, and mutation discovery
package:
    name: subread
    version: 1.5.0
test:
    commands:
        - featureCounts -v 2>&1 > /dev/null
source:
    fn: subread-1.5.0-Linux-x86_64.tar.gz
    url: http://sourceforge.net/projects/subread/files/subread-1.5.0/subread-1.5.0-Linux-x86_64.tar.g
    md5: e985e16a89e311199add9a47776d78ac
    fn: subread-1.5.0-MacOSX-x86_64.tar.gz
```

```
    url: http://sourceforge.net/projects/subread/files/subread-1.5.0/subread-1.5.0-MacOSX-x86_64.tar.
    md5: 57c2ae0585b1ea721d074f8a9f170fff
```

CHAPTER 479

suma_package [linux64]

479.1 Summary

Fast and exact comparison of sequences

479.2 Home

http://metabarcoding.org/sumatra

479.3 Versions

- 1.0.00

479.4 License

CeCILL FSLA

479.5 Meta

```
package:
  name: suma_package [linux64]
  version: 1.0.00

source:
  fn: suma_package_V_1.0.00.tar.gz
  url: ftp://ftp.microbio.me/pub/QIIME-v1.9.0-dependencies/suma_package_V_1.0.00.tar.gz
  md5: e528493d05225a605adacd0961b8f50c
  patches:
    - ldflags.patch

build:
  number: 0

requirements:
```

```
  build:
    - zlib
  run:
    - zlib

test:
  commands:
     - sumaclust -h > /dev/null
     - sumatra -h > /dev/null

about:
  home: http://metabarcoding.org/sumatra
  license: CeCILL FSLA
  license_file: Licence_CeCILL_V2-en.txt
  summary: Fast and exact comparison of sequences
```

CHAPTER 480

sure

480.1 Summary

utility belt for automated testing in python for python

480.2 Home

http://github.com/gabrielfalcao/sure

480.3 Versions

- 1.2.24

480.4 License

GNU General Public License v3 or later (GPLv3+)

480.5 Meta

```
package:
  name: sure
  version: "1.2.24"

source:
  fn: sure-1.2.24.tar.gz
  url: https://pypi.python.org/packages/source/s/sure/sure-1.2.24.tar.gz
  md5: a396cc3c71d551bfdb9bc45363ca05da
#  patches:
   # List any patch files here
   # - fix.patch

# build:
  # noarch_python: True
  # preserve_egg_dir: True
```

```
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - sure = sure:main
    #
    # Would create an entry point called sure that calls sure.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools
    - mock
    - six

  run:
    - python
    - mock
    - six

test:
  # Python imports
  imports:
    - sure

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  requires:
    - nose
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: http://github.com/gabrielfalcao/sure
  license: GNU General Public License v3 or later (GPLv3+)
  summary: 'utility belt for automated testing in python for python'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 481

svgutils

481.1 Summary

Python SVG editor that allows to automatically create publication ready composite SVG figures.

481.2 Home

http://neuroscience.telenczuk.pl

481.3 Versions

- 0.1.0

481.4 License

MIT License

481.5 Meta

```
package:
  name: svgutils
  version: "0.1.0"

source:
  git_url: https://github.com/btel/svg_utils.git
  git_rev: 145502d680744274dea66ae0d19da4e4c62d77e4

requirements:
  build:
    - python
    - setuptools
    - lxml

  run:
```

```
    - python
    - lxml

test:
  imports:
    - svgutils

about:
  home: http://neuroscience.telenczuk.pl
  license: MIT License
  summary: 'Python SVG editor that allows to automatically create publication ready composite SVG fig
```

CHAPTER 482

svgwrite

482.1 Summary

A Python library to create SVG drawings.

482.2 Home

http://bitbucket.org/mozman/svgwrite

482.3 Versions

- 1.1.6

482.4 License

MIT License

482.5 Meta

```
package:
  name: svgwrite
  version: "1.1.6"

source:
  fn: svgwrite-1.1.6.tar.gz
  url: https://pypi.python.org/packages/source/s/svgwrite/svgwrite-1.1.6.tar.gz
  md5: 0d54ccf5584dd1f98fe22b7ac172bef1
#  patches:
   # List any patch files here
   # - fix.patch

# build:
  # noarch_python: True
  # preserve_egg_dir: True
```

```
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - svgwrite = svgwrite:main
    #
    # Would create an entry point called svgwrite that calls svgwrite.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools
    - pyparsing >=2.0.1

  run:
    - python
    - pyparsing >=2.0.1

test:
  # Python imports
  imports:
    - svgwrite

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: http://bitbucket.org/mozman/svgwrite
  license: MIT License
  summary: 'A Python library to create SVG drawings.'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 483

svtyper

483.1 Summary

Bayesian genotyper for structural variants

483.2 Home

https://github.com/hall-lab/svtyper

483.3 Versions

- 0.0.2

483.4 License

MIT

483.5 Meta

```
package:
  name: svtyper
  version: 0.0.2

source:
  fn: svtyper-faecbc5.tar.gz
  url: https://github.com/hall-lab/svtyper/archive/faecbc5.tar.gz
  #fn: svtyper-0.0.2.tar.gz
  #url: https://github.com/hall-lab/svtyper/archive/v0.0.2.tar.gz

build:
  number: 4
  skip: True # [not py27]

requirements:
```

```
  build:
    - python
    - setuptools
    - pysam

  run:
    - python
    - setuptools
    - pysam

test:
  commands:
    - svtyper -h

about:
  home: https://github.com/hall-lab/svtyper
  license: MIT
  summary: Bayesian genotyper for structural variants
```

CHAPTER 484

swarm [linux64]

484.1 Summary

A robust and fast clustering method for amplicon-based studies.

484.2 Home

https://github.com/torognes/swarm

484.3 Versions

- 2.1.5
- 1.2.19

484.4 License

Affero GPL

484.5 Meta

```
package:
  name: swarm [linux64]
  version: 2.1.5

source:
  fn: v2.1.5.tar.gz
  url: https://github.com/torognes/swarm/archive/v2.1.5.tar.gz
  md5: 0ab87c5c55b28f63daedf406332c4f8d

requirements:
  run:
    - python
    - python-igraph
```

```
build:
  number: 0

test:
  commands:
     - swarm -v 2>&1 | grep 2.1.5
     - graph_plot.py --version

about:
  home: https://github.com/torognes/swarm
  license: Affero GPL
  summary: A robust and fast clustering method for amplicon-based studies.
```

CHAPTER 485

t_coffee

485.1 Summary

A collection of tools for Computing, Evaluating and Manipulating Multiple Alignments of DNA, RNA, Protein Sequences and Structures.

485.2 Home

http://www.tcoffee.org/Projects/tcoffee/

485.3 Versions

- 11.0.8
- t_coffee

485.4 License

GNU

485.5 Meta

```
package:
  name: t_coffee
  version: "11.0.8"

source:
  fn: T-COFFEE_installer_Version_11.00.8cbe486_linux_x64.bin
  url: http://www.tcoffee.org/Packages/Stable/Latest/linux/T-COFFEE_installer_Version_11.00.8cbe486_l
  md5: 2e375405c9ebb977adf87c145ca698bb

build:
  number: 1
  entry_points:
```

```
    - t_coffee = t_coffee.__main__:main

requirements:
  build:
    - python
    - openssl
    - curl
    - zlib
  run:
    - python
    - openssl
    - curl
    - zlib

test:
  imports:
    - t_coffee
  commands:
    - t_coffee
    - t_coffee --help

about:
    home: http://www.tcoffee.org/Projects/tcoffee/
    license: GNU
    summary: A collection of tools for Computing, Evaluating and Manipulating Multiple Alignments of
```

CHAPTER 486

tabulate

486.1 Summary

Pretty-print tabular data

486.2 Home

https://bitbucket.org/astanin/python-tabulate

486.3 Versions

- 0.7.5

486.4 License

MIT

486.5 Meta

```
package:
  name: tabulate
  version: "0.7.5"

source:
  fn: tabulate-0.7.5.tar.gz
  url: https://pypi.python.org/packages/source/t/tabulate/tabulate-0.7.5.tar.gz
  md5: 576e1f063b8e74dbfeda02d978564987

build:
  number: 0

requirements:
  build:
    - python
```

```
    - setuptools
  run:
    - python

test:
  imports:
    - tabulate

about:
  home: https://bitbucket.org/astanin/python-tabulate
  license: MIT
  summary: Pretty-print tabular data
```

CHAPTER 487

tbb

487.1 Summary

487.2 Home

https://www.threadingbuildingblocks.org/

487.3 Versions

- 4.4_20150728

487.4 License

GPLv2

487.5 Meta

```
# Updated tbb recipe from https://github.com/menpo/conda-recipes

package:
  name: tbb
  version: "4.4_20150728"

source:
  fn: tbb44_20150728oss_osx.tgz # [osx]
  url: https://www.threadingbuildingblocks.org/sites/default/files/software_releases/mac/tbb44_20150
  fn: tbb44_20150728oss_src.tgz # [linux]
  url: https://www.threadingbuildingblocks.org/sites/default/files/software_releases/source/tbb44_201

about:
  home: https://www.threadingbuildingblocks.org/
  license: GPLv2
```

CHAPTER 488

tdrmapper

488.1 Summary

tRNA detection and quantification

488.2 Home

https://github.com/sararselitsky/tDRmapper

488.3 Versions

- 1.0

488.4 License

academic

488.5 Meta

```
package:
  name: tdrmapper
  version: '1.0'

source:
    git_url: https://github.com/lpantano/tDRmapper
    git_rev: 3200576

build:
  number: 1

test:
  commands:
    - TdrMappingScripts.pl --help
about:
```

```
  home: https://github.com/sararselitsky/tDRmapper
  license: academic
  summary: tRNA detection and quantification
```

CHAPTER 489

theta2

489.1 Summary

Estimate tumor purity and clonal/subclonal copy number aberrations directly from high-throughput DNA sequencing data

489.2 Home

https://github.com/raphael-group/THetA

489.3 Versions

- 0.7

489.4 License

Modified MIT (no inclusion in commercial tools)

489.5 Meta

```
package:
  name: theta2
  version: '0.7'
build:
  number: 0
  skip: True # [not py27]
source:
  fn: theta-0.7.tar.gz
  url: https://github.com/raphael-group/THetA/archive/v0.7.tar.gz

requirements:
  build:
    - python
    - numpy
```

```
    - scipy
    - matplotlib
    - joblib
    - numexpr
  run:
    - python
    - numpy
    - scipy
    - matplotlib
    - joblib
    - numexpr

test:
  commands:
    - RunTHetA.py -h

about:
  home: https://github.com/raphael-group/THetA
  license: Modified MIT (no inclusion in commercial tools)
  summary: Estimate tumor purity and clonal/subclonal copy number aberrations directly from high-thro
```

CHAPTER 490

tmux

490.1 Summary

tmux is a terminal multiplexer.

490.2 Home

http://tmux.sourceforge.net

490.3 Versions

- 2.1

490.4 License

BSD

490.5 Meta

```
package:
  name: tmux
  version: "2.1"

source:
  fn: tmux-2.1.tar.gz
  url: https://github.com/tmux/tmux/releases/download/2.1/tmux-2.1.tar.gz
  md5: 74a2855695bccb51b6e301383ad4818c

build:
  number: 1

requirements:
  build:
    - ncurses
```

```
    - libevent
  run:
    - ncurses
    - libevent

test:
  commands:
    - tmux -V
    - tmux -c "echo 'hello world'"

about:
  home: http://tmux.sourceforge.net
  license: BSD
  summary: tmux is a terminal multiplexer.
```

CHAPTER 491

tophat

491.1 Summary

A spliced read mapper for RNA-Seq

491.2 Home

http://ccb.jhu.edu/software/tophat/index.shtml

491.3 Versions

- 2.1.0

491.4 License

Boost Software License

491.5 Meta

```
about:
    home: 'http://ccb.jhu.edu/software/tophat/index.shtml'
    license: Boost Software License
    summary: A spliced read mapper for RNA-Seq
package:
    name: tophat
    version: 2.1.0
requirements:
    build:
        - python
    run:
        - python
test:
    commands:
        - (tophat --version 2>&1) > /dev/null
```

```
source:
  fn: tophat-2.1.0.Linux_x86_64.tar.gz
  url: http://ccb.jhu.edu/software/tophat/downloads/tophat-2.1.0.Linux_x86_64.tar.gz
  md5: 0b525e8be75815c5dd745b49c379682c
```

CHAPTER 492

toposort

492.1 Summary

A topological sort algorithm for Python.

492.2 Home

https://bitbucket.org/ericvsmith/toposort

492.3 Versions

- 1.4

492.4 License

Apache Software License

492.5 Meta

```
package:
  name: toposort
  version: "1.4"
source:
  fn: toposort-1.4.tar.gz
  url: https://pypi.python.org/packages/source/t/toposort/toposort-1.4.tar.gz
  md5: 02433c00de9eaecf494245c4bca5e922
requirements:
  build:
    - python
  run:
    - python
test:
  imports:
    - toposort
```

```
about:
  home: https://bitbucket.org/ericvsmith/toposort
  license: Apache Software License
  summary: 'A topological sort algorithm for Python.'
```

CHAPTER 493

trackhub

493.1 Summary

nCreate and manage UCSC track hubs from Pythonn

493.2 Home

http://github.com/daler/trackhub

493.3 Versions

- 0.1.2

493.4 License

BSD 3-clause

493.5 Meta

```
package:
  name: trackhub
  version: "0.1.2"

source:
  fn: trackhub-0.1.3.tar.gz
  url: https://pypi.python.org/packages/source/t/trackhub/trackhub-0.1.3.tar.gz
  md5: bb141a415676e86f8c8f4fa09e64608c
#  patches:
   # List any patch files here
   # - fix.patch

build:
  number: 0
  skip: True  # [py3k]
```

```
  # noarch_python: True
  # preserve_egg_dir: True
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - trackhub = trackhub:main
    #
    # Would create an entry point called trackhub that calls trackhub.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools
    - fabric

  run:
    - python
    - fabric

test:
  # Python imports
  imports:
    - trackhub
    - trackhub.scripts
    - trackhub.test
    - trackhub.test.data

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: http://github.com/daler/trackhub
  license: BSD 3-clause
  summary: '\nCreate and manage UCSC track hubs from Python\n'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 494

trimmomatic

494.1 Summary

A flexible read trimming tool for Illumina NGS data

494.2 Home

http://www.usadellab.org/cms/?page=trimmomatic

494.3 Versions

- 0.35

494.4 License

GPLv3

494.5 Meta

```
about:
  home: 'http://www.usadellab.org/cms/?page=trimmomatic'
  license: "GPLv3"
  summary: "A flexible read trimming tool for Illumina NGS data"

package:
  name: trimmomatic
  version: '0.35'

build:
  number: 2

source:
  fn: Trimmomatic-0.35.zip
  md5: 564e62f4f0f9f56d22762b237d4c69c4
```

```
  url: http://www.usadellab.org/cms/uploads/supplementary/Trimmomatic/Trimmomatic-0.35.zip

requirements:
  run:
      - java-jdk

test:
    commands:
      #- trimmomatic -version # trimmomatic currently lacks a simple argument that gives
      # a zero exit code, so...
      # check if the jar file (as a zip file) is valid instead:
      - "unzip -t $PREFIX/share/$PKG_NAME-$PKG_VERSION-$PKG_BUILDNUM/trimmomatic.jar &> /dev/null"
```

CHAPTER 495

trinity

495.1 Summary

Trinity assembles transcript sequences from Illumina RNA-Seq data

495.2 Home

https://github.com/trinityrnaseq/trinityrnaseq

495.3 Versions

- 2.1.1
- 2011_11_26

495.4 License

https://raw.githubusercontent.com/trinityrnaseq/trinityrnaseq/master/LICENSE.txt

495.5 Meta


```
about:
    home: 'https://github.com/trinityrnaseq/trinityrnaseq'
    license: "https://raw.githubusercontent.com/trinityrnaseq/trinityrnaseq/master/LICENSE.txt"
    summary: "Trinity assembles transcript sequences from Illumina RNA-Seq data"
build:
  number: 2
package:
  name: trinity
  version: '2.1.1'
source:
  fn: v2.1.1.tar.gz
  md5: 45c1ad13c331d6a1976f6a9b5b015daa
  url: https://github.com/trinityrnaseq/trinityrnaseq/archive/v2.1.1.tar.gz
```

```
requirements:
  build:
    - perl-threaded
    - java-jdk
  run:
    - perl-threaded
    - java-jdk
test:
    commands:
        - "Trinity --cite &> /dev/null"
```

CHAPTER 496

ucsc-axttomaf

496.1 Summary

Convert from axt to maf format

496.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

496.3 Versions

- 324

496.4 License

varies; see http://genome.ucsc.edu/license

496.5 Meta

```
package:
    name: "ucsc-axttomaf"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/axtToMaf"                 # [osx
    fn: "axtToMaf"                                                                          # [osx

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp axtToMaf $PREFIX/bin; chmod +x $PREFIX/bin/axtToMaf" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Convert from axt to maf format"
```

CHAPTER 497

ucsc-axttopsl

497.1 Summary

Convert axt to psl format

497.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

497.3 Versions

- 324

497.4 License

varies; see http://genome.ucsc.edu/license

497.5 Meta

```
package:
    name: "ucsc-axttopsl"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/axtToPsl"                # [osx
    fn: "axtToPsl"                                                                         # [osx

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp axtToPsl $PREFIX/bin; chmod +x $PREFIX/bin/axtToPsl" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Convert axt to psl format"
```

CHAPTER 498

ucsc-bedclip

498.1 Summary

Remove lines from bed file that refer to off-chromosome places.

498.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

498.3 Versions

- 324

498.4 License

varies; see http://genome.ucsc.edu/license

498.5 Meta

```
package:
    name: "ucsc-bedclip"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/bedClip"                 # [osx]
    fn: "bedClip"                                                                         # [osx]

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp bedClip $PREFIX/bin; chmod +x $PREFIX/bin/bedClip" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Remove lines from bed file that refer to off-chromosome places."
```

CHAPTER 499

ucsc-bedcommonregions

499.1 Summary

Create a bed file (just bed3) that contains the regions common to all inputs.

499.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

499.3 Versions

- 324

499.4 License

varies; see http://genome.ucsc.edu/license

499.5 Meta

```
package:
    name: "ucsc-bedcommonregions"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/bedCommonRegions"
    fn: "bedCommonRegions"

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp bedCommonRegions $PREFIX/bin; chmod +x $PREFIX/bin/bedCommonReg
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Create a bed file (just bed3) that contains the regions common to all inputs."
```

CHAPTER 500

ucsc-bedcoverage

500.1 Summary

Analyse coverage by bed files - chromosome by

500.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

500.3 Versions

- 324

500.4 License

varies; see http://genome.ucsc.edu/license

500.5 Meta

```
package:
    name: "ucsc-bedcoverage"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/bedCoverage"                # [
    fn: "bedCoverage"                                                                       # [

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp bedCoverage $PREFIX/bin; chmod +x $PREFIX/bin/bedCoverage" # [
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Analyse coverage by bed files - chromosome by "
```

CHAPTER 501

ucsc-bedextendranges

501.1 Summary

extend length of entries in bed 6+ data to be at least the given length,

501.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

501.3 Versions

- 324

501.4 License

varies; see http://genome.ucsc.edu/license

501.5 Meta

```
package:
    name: "ucsc-bedextendranges"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/bedExtendRanges"
    fn: "bedExtendRanges"

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp bedExtendRanges $PREFIX/bin; chmod +x $PREFIX/bin/bedExtendRang
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "extend length of entries in bed 6+ data to be at least the given length,"
```

CHAPTER 502

ucsc-bedgeneparts

502.1 Summary

Given a bed, spit out promoter, first exon, or all introns.

502.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

502.3 Versions

- 324

502.4 License

varies; see http://genome.ucsc.edu/license

502.5 Meta

```
package:
    name: "ucsc-bedgeneparts"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/bedGeneParts"                #
    fn: "bedGeneParts"                                                                        #

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp bedGeneParts $PREFIX/bin; chmod +x $PREFIX/bin/bedGeneParts" #
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Given a bed, spit out promoter, first exon, or all introns."
```

CHAPTER 503

ucsc-bedgraphpack

503.1 Summary

Pack together adjacent records representing same value.

503.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

503.3 Versions

- 324

503.4 License

varies; see http://genome.ucsc.edu/license

503.5 Meta

```
package:
    name: "ucsc-bedgraphpack"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/bedGraphPack"                #
    fn: "bedGraphPack"                                                                        #

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp bedGraphPack $PREFIX/bin; chmod +x $PREFIX/bin/bedGraphPack" #
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Pack together adjacent records representing same value."
```

CHAPTER 504

ucsc-bedgraphtobigwig

504.1 Summary

Convert a bedGraph file to bigWig format.

504.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

504.3 Versions

- 324

504.4 License

varies; see http://genome.ucsc.edu/license

504.5 Meta

```
package:
    name: "ucsc-bedgraphtobigwig"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/bedGraphToBigWig"
    fn: "bedGraphToBigWig"

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp bedGraphToBigWig $PREFIX/bin; chmod +x $PREFIX/bin/bedGraphToBi
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Convert a bedGraph file to bigWig format."
```

CHAPTER 505

ucsc-bedintersect

505.1 Summary

Intersect two bed files

505.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

505.3 Versions

- 324

505.4 License

varies; see http://genome.ucsc.edu/license

505.5 Meta

```
package:
    name: "ucsc-bedintersect"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/bedIntersect"                #
    fn: "bedIntersect"                                                                        #

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp bedIntersect $PREFIX/bin; chmod +x $PREFIX/bin/bedIntersect" #
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Intersect two bed files"
```

CHAPTER 506

ucsc-beditemoverlapcount

506.1 Summary

count number of times a base is overlapped by the

506.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

506.3 Versions

- 324

506.4 License

varies; see http://genome.ucsc.edu/license

506.5 Meta

```
package:
    name: "ucsc-beditemoverlapcount"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/bedItemOverlapCount"
    fn: "bedItemOverlapCount"

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp bedItemOverlapCount $PREFIX/bin; chmod +x $PREFIX/bin/bedItemOv
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "count number of times a base is overlapped by the"
```

CHAPTER 507

ucsc-bedpileups

507.1 Summary

Find (exact) overlaps if any in bed input

507.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

507.3 Versions

- 324

507.4 License

varies; see http://genome.ucsc.edu/license

507.5 Meta

```
package:
    name: "ucsc-bedpileups"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [lin
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [lin
    patches:                                                                              # [linux
        - "include.patch"                                                                   # [lin

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/bedPileUps"                # [os
    fn: "bedPileUps"                                                                        # [os

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp bedPileUps $PREFIX/bin; chmod +x $PREFIX/bin/bedPileUps" # [osx
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Find (exact) overlaps if any in bed input"
```

CHAPTER 508

ucsc-bedremoveoverlap

508.1 Summary

Remove overlapping records from a (sorted) bed file. Gets rid of

508.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

508.3 Versions

- 324

508.4 License

varies; see http://genome.ucsc.edu/license

508.5 Meta

```
package:
    name: "ucsc-bedremoveoverlap"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/bedRemoveOverlap"
    fn: "bedRemoveOverlap"

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp bedRemoveOverlap $PREFIX/bin; chmod +x $PREFIX/bin/bedRemoveOve
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Remove overlapping records from a (sorted) bed file.  Gets rid of"
```

CHAPTER 509

ucsc-bedrestricttopositions

509.1 Summary

Filter bed file, restricting to only ones that match chrom/start/ends specified in restrict.bed file.

509.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

509.3 Versions

- 324

509.4 License

varies; see http://genome.ucsc.edu/license

509.5 Meta

```
package:
    name: "ucsc-bedrestricttopositions"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/bedRestrictToPositions"
    fn: "bedRestrictToPositions"

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp bedRestrictToPositions $PREFIX/bin; chmod +x $PREFIX/bin/bedRes
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Filter bed file, restricting to only ones that match chrom/start/ends specified in rest
```

CHAPTER 510

ucsc-bedsort

510.1 Summary

Sort a .bed file by chrom,chromStart

510.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

510.3 Versions

- 324

510.4 License

varies; see http://genome.ucsc.edu/license

510.5 Meta

```
package:
    name: "ucsc-bedsort"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [lin
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [lin
    patches:                                                                              # [linux
        - "include.patch"                                                                   # [lin

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/bedSort"                # [osx]
    fn: "bedSort"                                                                         # [osx]

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp bedSort $PREFIX/bin; chmod +x $PREFIX/bin/bedSort" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Sort a .bed file by chrom,chromStart"
```

CHAPTER 511

ucsc-bedtobigbed

511.1 Summary

Convert bed file to bigBed. (BigBed version: 4)

511.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

511.3 Versions

- 324

511.4 License

varies; see http://genome.ucsc.edu/license

511.5 Meta

```
package:
    name: "ucsc-bedtobigbed"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [lin
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [lin
    patches:                                                                              # [linux
        - "include.patch"                                                                   # [lin

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/bedToBigBed"                # [
    fn: "bedToBigBed"                                                                         # [

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp bedToBigBed $PREFIX/bin; chmod +x $PREFIX/bin/bedToBigBed" # [
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Convert bed file to bigBed. (BigBed version: 4)"
```

CHAPTER 512

ucsc-bedtogenepred

512.1 Summary

convert bed format files to genePred format

512.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

512.3 Versions

- 324

512.4 License

varies; see http://genome.ucsc.edu/license

512.5 Meta

```
package:
    name: "ucsc-bedtogenepred"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/bedToGenePred"                #
    fn: "bedToGenePred"                                                                        #

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp bedToGenePred $PREFIX/bin; chmod +x $PREFIX/bin/bedToGenePred"
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "convert bed format files to genePred format"
```

CHAPTER 513

ucsc-bedtopsl

513.1 Summary

convert bed format files to psl format

513.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

513.3 Versions

- 324

513.4 License

varies; see http://genome.ucsc.edu/license

513.5 Meta

```
package:
    name: "ucsc-bedtopsl"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/bedToPsl"                # [osx
    fn: "bedToPsl"                                                                         # [osx

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp bedToPsl $PREFIX/bin; chmod +x $PREFIX/bin/bedToPsl" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "convert bed format files to psl format"
```

CHAPTER 514

ucsc-bedweedoverlapping

514.1 Summary

Filter out beds that overlap a 'weed.bed' file.

514.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

514.3 Versions

- 324

514.4 License

varies; see http://genome.ucsc.edu/license

514.5 Meta

```
package:
    name: "ucsc-bedweedoverlapping"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/bedWeedOverlapping"
    fn: "bedWeedOverlapping"

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp bedWeedOverlapping $PREFIX/bin; chmod +x $PREFIX/bin/bedWeedOve
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Filter out beds that overlap a 'weed.bed' file."
```

CHAPTER 515

ucsc-bigbedinfo

515.1 Summary

Show information about a bigBed file.

515.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

515.3 Versions

- 324

515.4 License

varies; see http://genome.ucsc.edu/license

515.5 Meta

```
package:
    name: "ucsc-bigbedinfo"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [lin
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [lin
    patches:                                                                              # [linux
        - "include.patch"                                                                   # [lin

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/bigBedInfo"                # [os
    fn: "bigBedInfo"                                                                        # [os

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp bigBedInfo $PREFIX/bin; chmod +x $PREFIX/bin/bigBedInfo" # [osx
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Show information about a bigBed file."
```

CHAPTER 516

ucsc-bigbednameditems

516.1 Summary

Extract item of given name from bigBed

516.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

516.3 Versions

- 324

516.4 License

varies; see http://genome.ucsc.edu/license

516.5 Meta

```
package:
    name: "ucsc-bigbednameditems"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/bigBedNamedItems"
    fn: "bigBedNamedItems"

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp bigBedNamedItems $PREFIX/bin; chmod +x $PREFIX/bin/bigBedNamedI
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Extract item of given name from bigBed"
```

CHAPTER 517

ucsc-bigbedsummary

517.1 Summary

Extract summary information from a bigBed file.

517.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

517.3 Versions

- 324

517.4 License

varies; see http://genome.ucsc.edu/license

517.5 Meta

```
package:
    name: "ucsc-bigbedsummary"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/bigBedSummary"                #
    fn: "bigBedSummary"                                                                        #

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp bigBedSummary $PREFIX/bin; chmod +x $PREFIX/bin/bigBedSummary"
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Extract summary information from a bigBed file."
```

CHAPTER 518

ucsc-bigbedtobed

518.1 Summary

Convert from bigBed to ascii bed format.

518.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

518.3 Versions

- 324

518.4 License

varies; see http://genome.ucsc.edu/license

518.5 Meta

```
package:
    name: "ucsc-bigbedtobed"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/bigBedToBed"                # [
    fn: "bigBedToBed"                                                                       # [

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp bigBedToBed $PREFIX/bin; chmod +x $PREFIX/bin/bigBedToBed" # [
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Convert from bigBed to ascii bed format."
```

CHAPTER 519

ucsc-bigwigaverageoverbed

519.1 Summary

Compute average score of big wig over each bed, which may have introns.

519.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

519.3 Versions

- 324

519.4 License

varies; see http://genome.ucsc.edu/license

519.5 Meta

```
package:
    name: "ucsc-bigwigaverageoverbed"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/bigWigAverageOverBed"
    fn: "bigWigAverageOverBed"

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp bigWigAverageOverBed $PREFIX/bin; chmod +x $PREFIX/bin/bigWigAv
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Compute average score of big wig over each bed, which may have introns."
```

CHAPTER 520

ucsc-bigwigcat

520.1 Summary

merge non-overlapping bigWig files

520.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

520.3 Versions

- 324

520.4 License

varies; see http://genome.ucsc.edu/license

520.5 Meta

```
package:
    name: "ucsc-bigwigcat"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                # [lin
    md5: "c49c168584c5917081d71df854e3cd9d"                                               # [lin
    patches:                                                                              # [linux
        - "include.patch"                                                                 # [lin

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/bigWigCat"               # [osx
    fn: "bigWigCat"                                                                       # [osx

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp bigWigCat $PREFIX/bin; chmod +x $PREFIX/bin/bigWigCat" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "merge non-overlapping bigWig files"
```

CHAPTER 521

ucsc-bigwigcluster

521.1 Summary

Cluster bigWigs using a hacTree

521.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

521.3 Versions

- 324

521.4 License

varies; see http://genome.ucsc.edu/license

521.5 Meta

```
package:
    name: "ucsc-bigwigcluster"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/bigWigCluster"                #
    fn: "bigWigCluster"                                                                        #

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp bigWigCluster $PREFIX/bin; chmod +x $PREFIX/bin/bigWigCluster"
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Cluster bigWigs using a hacTree"
```

CHAPTER 522

ucsc-bigwigcorrelate

522.1 Summary

Correlate bigWig files, optionally only on target regions.

522.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

522.3 Versions

- 324

522.4 License

varies; see http://genome.ucsc.edu/license

522.5 Meta

```
package:
    name: "ucsc-bigwigcorrelate"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/bigWigCorrelate"
    fn: "bigWigCorrelate"

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp bigWigCorrelate $PREFIX/bin; chmod +x $PREFIX/bin/bigWigCorrela
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Correlate bigWig files, optionally only on target regions."
```

CHAPTER 523

ucsc-bigwiginfo

523.1 Summary

Print out information about bigWig file.

523.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

523.3 Versions

- 324

523.4 License

varies; see http://genome.ucsc.edu/license

523.5 Meta

```
package:
    name: "ucsc-bigwiginfo"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [lin
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [lin
    patches:                                                                              # [linux
        - "include.patch"                                                                   # [lin

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/bigWigInfo"                # [os
    fn: "bigWigInfo"                                                                        # [os

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp bigWigInfo $PREFIX/bin; chmod +x $PREFIX/bin/bigWigInfo" # [osx
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Print out information about bigWig file."
```

CHAPTER 524

ucsc-bigwigmerge

524.1 Summary

Merge together multiple bigWigs into a single output bedGraph.

524.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

524.3 Versions

- 324

524.4 License

varies; see http://genome.ucsc.edu/license

524.5 Meta

```
package:
    name: "ucsc-bigwigmerge"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/bigWigMerge"                # [
    fn: "bigWigMerge"                                                                       # [

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp bigWigMerge $PREFIX/bin; chmod +x $PREFIX/bin/bigWigMerge" # [
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Merge together multiple bigWigs into a single output bedGraph."
```

CHAPTER 525

ucsc-bigwigsummary

525.1 Summary

Extract summary information from a bigWig file.

525.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

525.3 Versions

- 324

525.4 License

varies; see http://genome.ucsc.edu/license

525.5 Meta

```
package:
    name: "ucsc-bigwigsummary"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/bigWigSummary"                #
    fn: "bigWigSummary"                                                                        #

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp bigWigSummary $PREFIX/bin; chmod +x $PREFIX/bin/bigWigSummary"
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Extract summary information from a bigWig file."
```

CHAPTER 526

ucsc-bigwigtobedgraph

526.1 Summary

Convert from bigWig to bedGraph format.

526.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

526.3 Versions

- 324

526.4 License

varies; see http://genome.ucsc.edu/license

526.5 Meta

```
package:
    name: "ucsc-bigwigtobedgraph"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/bigWigToBedGraph"
    fn: "bigWigToBedGraph"

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp bigWigToBedGraph $PREFIX/bin; chmod +x $PREFIX/bin/bigWigToBed
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Convert from bigWig to bedGraph format."
```

CHAPTER 527

ucsc-bigwigtowig

527.1 Summary

Convert bigWig to wig. This will keep more of the same structure of the

527.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

527.3 Versions

- 324

527.4 License

varies; see http://genome.ucsc.edu/license

527.5 Meta

```
package:
    name: "ucsc-bigwigtowig"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/bigWigToWig"                # [
    fn: "bigWigToWig"                                                                       # [

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp bigWigToWig $PREFIX/bin; chmod +x $PREFIX/bin/bigWigToWig" # [
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Convert bigWig to wig.  This will keep more of the same structure of the"
```

CHAPTER 528

ucsc-blasttopsl

528.1 Summary

Convert blast alignments to PSLs.

528.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

528.3 Versions

- 324

528.4 License

varies; see http://genome.ucsc.edu/license

528.5 Meta

```
package:
    name: "ucsc-blasttopsl"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [lin
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [lin
    patches:                                                                              # [linux
        - "include.patch"                                                                   # [lin

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/blastToPsl"                # [os
    fn: "blastToPsl"                                                                        # [os

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp blastToPsl $PREFIX/bin; chmod +x $PREFIX/bin/blastToPsl" # [osx
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Convert blast alignments to PSLs."
```

CHAPTER 529

ucsc-chainantirepeat

529.1 Summary

Get rid of chains that are primarily the results of repeats and degenerate DNA

529.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

529.3 Versions

- 324

529.4 License

varies; see http://genome.ucsc.edu/license

529.5 Meta

```
package:
    name: "ucsc-chainantirepeat"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/chainAntiRepeat"
    fn: "chainAntiRepeat"

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp chainAntiRepeat $PREFIX/bin; chmod +x $PREFIX/bin/chainAntiRepe
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Get rid of chains that are primarily the results of repeats and degenerate DNA"
```

CHAPTER 530

ucsc-chainfilter

530.1 Summary

Filter chain files. Output goes to standard out.

530.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

530.3 Versions

- 324

530.4 License

varies; see http://genome.ucsc.edu/license

530.5 Meta

```
package:
    name: "ucsc-chainfilter"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/chainFilter"                # [
    fn: "chainFilter"                                                                         # [

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp chainFilter $PREFIX/bin; chmod +x $PREFIX/bin/chainFilter" # [
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Filter chain files.  Output goes to standard out."
```

CHAPTER 531

ucsc-chainmergesort

531.1 Summary

Combine sorted files into larger sorted file

531.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

531.3 Versions

- 324

531.4 License

varies; see http://genome.ucsc.edu/license

531.5 Meta

```
package:
    name: "ucsc-chainmergesort"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/chainMergeSort"                 #
    fn: "chainMergeSort"                                                                         #

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp chainMergeSort $PREFIX/bin; chmod +x $PREFIX/bin/chainMergeSort
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Combine sorted files into larger sorted file"
```

CHAPTER 532

ucsc-chainnet

532.1 Summary

Make alignment nets out of chains

532.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

532.3 Versions

- 324

532.4 License

varies; see http://genome.ucsc.edu/license

532.5 Meta

```
package:
    name: "ucsc-chainnet"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/chainNet"                # [osx
    fn: "chainNet"                                                                        # [osx

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp chainNet $PREFIX/bin; chmod +x $PREFIX/bin/chainNet" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Make alignment nets out of chains"
```

CHAPTER 533

ucsc-chainprenet

533.1 Summary

Remove chains that don't have a chance of being netted

533.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

533.3 Versions

- 324

533.4 License

varies; see http://genome.ucsc.edu/license

533.5 Meta

```
package:
    name: "ucsc-chainprenet"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/chainPreNet"                # [
    fn: "chainPreNet"                                                                         # [

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp chainPreNet $PREFIX/bin; chmod +x $PREFIX/bin/chainPreNet" # [
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Remove chains that don't have a chance of being netted"
```

CHAPTER 534

ucsc-chainsort

534.1 Summary

Sort chains. By default sorts by score.

534.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

534.3 Versions

- 324

534.4 License

varies; see http://genome.ucsc.edu/license

534.5 Meta

```
package:
    name: "ucsc-chainsort"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/chainSort"                 # [os
    fn: "chainSort"                                                                         # [os

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp chainSort $PREFIX/bin; chmod +x $PREFIX/bin/chainSort" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Sort chains.  By default sorts by score."
```

CHAPTER 535

ucsc-chainsplit

535.1 Summary

Split chains up by target or query sequence

535.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

535.3 Versions

- 324

535.4 License

varies; see http://genome.ucsc.edu/license

535.5 Meta

```
package:
    name: "ucsc-chainsplit"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                               # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                 # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/chainSplit"              # [o
    fn: "chainSplit"                                                                      # [o

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp chainSplit $PREFIX/bin; chmod +x $PREFIX/bin/chainSplit" # [os
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Split chains up by target or query sequence"
```

CHAPTER 536

ucsc-chainstitchid

536.1 Summary

Join chain fragments with the same chain ID into a single

536.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

536.3 Versions

- 324

536.4 License

varies; see http://genome.ucsc.edu/license

536.5 Meta

```
package:
    name: "ucsc-chainstitchid"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/chainStitchId"                #
    fn: "chainStitchId"                                                                        #

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp chainStitchId $PREFIX/bin; chmod +x $PREFIX/bin/chainStitchId"
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Join chain fragments with the same chain ID into a single"
```

CHAPTER 537

ucsc-chainswap

537.1 Summary

Swap target and query in chain

537.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

537.3 Versions

- 324

537.4 License

varies; see http://genome.ucsc.edu/license

537.5 Meta

```
package:
    name: "ucsc-chainswap"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                 # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                # [li
    patches:                                                                             # [linu
        - "include.patch"                                                                  # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/chainSwap"                # [os
    fn: "chainSwap"                                                                        # [os

build:                                                                                   # [osx]
    script: "mkdir -p $PREFIX/bin; cp chainSwap $PREFIX/bin; chmod +x $PREFIX/bin/chainSwap" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Swap target and query in chain"
```

CHAPTER 538

ucsc-chaintoaxt

538.1 Summary

Convert from chain to axt file

538.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

538.3 Versions

- 324

538.4 License

varies; see http://genome.ucsc.edu/license

538.5 Meta

```
package:
    name: "ucsc-chaintoaxt"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [lin
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [lin
    patches:                                                                              # [linux
        - "include.patch"                                                                   # [lin

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/chainToAxt"                # [os
    fn: "chainToAxt"                                                                        # [os

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp chainToAxt $PREFIX/bin; chmod +x $PREFIX/bin/chainToAxt" # [osx
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Convert from chain to axt file"
```

CHAPTER 539

ucsc-chaintopsl

539.1 Summary

Convert chain file to psl format

539.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

539.3 Versions

- 324

539.4 License

varies; see http://genome.ucsc.edu/license

539.5 Meta

```
package:
    name: "ucsc-chaintopsl"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [lin
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [lin
    patches:                                                                              # [linux
        - "include.patch"                                                                   # [lin

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/chainToPsl"                # [os
    fn: "chainToPsl"                                                                        # [os

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp chainToPsl $PREFIX/bin; chmod +x $PREFIX/bin/chainToPsl" # [osx
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Convert chain file to psl format"
```

CHAPTER 540

ucsc-chaintopslbasic

540.1 Summary

Basic conversion chain file to psl format

540.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

540.3 Versions

- 324

540.4 License

varies; see http://genome.ucsc.edu/license

540.5 Meta

```
package:
    name: "ucsc-chaintopslbasic"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/chainToPslBasic"
    fn: "chainToPslBasic"

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp chainToPslBasic $PREFIX/bin; chmod +x $PREFIX/bin/chainToPslBas
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Basic conversion chain file to psl format"
```

CHAPTER 541

ucsc-crtreeindexbed

541.1 Summary

Create an index for a bed file.

541.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

541.3 Versions

- 324

541.4 License

varies; see http://genome.ucsc.edu/license

541.5 Meta

```
package:
    name: "ucsc-crtreeindexbed"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/crTreeIndexBed"                 #
    fn: "crTreeIndexBed"                                                                         #

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp crTreeIndexBed $PREFIX/bin; chmod +x $PREFIX/bin/crTreeIndexBe
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Create an index for a bed file."
```

CHAPTER 542

ucsc-crtreesearchbed

542.1 Summary

Search a crTree indexed bed file and print all items that overlap query.

542.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

542.3 Versions

- 324

542.4 License

varies; see http://genome.ucsc.edu/license

542.5 Meta

```
package:
    name: "ucsc-crtreesearchbed"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/crTreeSearchBed"
    fn: "crTreeSearchBed"

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp crTreeSearchBed $PREFIX/bin; chmod +x $PREFIX/bin/crTreeSearchB
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Search a crTree indexed bed file and print all items that overlap query."
```

CHAPTER 543

ucsc-fatotwobit

543.1 Summary

Convert DNA from fasta to 2bit format

543.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

543.3 Versions

- 324

543.4 License

varies; see http://genome.ucsc.edu/license

543.5 Meta

```
package:
  name: ucsc-fatotwobit
  version: 324
source:
  url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"  # [linux]
  fn: "userApps.src.tgz"                                                 # [linux]
  md5: "c49c168584c5917081d71df854e3cd9d"                                # [linux]
  patches:                                                               # [linux]
      - "include.patch"                                                  # [linux]
  url: http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/faToTwoBit # [osx]
  fn: faToTwoBit                                                         # [osx]
build:
  number: 0
  script: "mkdir -p $PREFIX/bin; cp faToTwoBit $PREFIX/bin; chmod +x $PREFIX/bin/faToTwoBit" # [osx]
requirements:
```

```
  build:
    - libpng                                                    # [linux]
    - mysql                                                     # [linux]
    - zlib                                                      # [linux]
    - openssl                                                   # [linux]
  run:
    - libpng                                                    # [linux]
    - mysql                                                     # [linux]
    - zlib                                                      # [linux]
    - openssl                                                   # [linux]
test:
  commands:
    - faToTwoBit 2>&1 | grep faToTwoBit
about:
  home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
  license: "varies; see http://genome.ucsc.edu/license"
  summary: Convert DNA from fasta to 2bit format
```

CHAPTER 544

ucsc-fetchchromsizes

544.1 Summary

used to fetch chrom.sizes information from UCSC for the given <db>

544.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

544.3 Versions

- 324

544.4 License

varies; see http://genome.ucsc.edu/license

544.5 Meta

```
package:
    name: "ucsc-fetchchromsizes"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/fetchChromSizes"
    fn: "fetchChromSizes"

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp fetchChromSizes $PREFIX/bin; chmod +x $PREFIX/bin/fetchChromSi
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "
used to fetch chrom.sizes information from UCSC for the given <db>
"
```

CHAPTER 545

ucsc-genepredtobed

545.1 Summary

Convert from genePred to bed format. Does not yet handle genePredExt

545.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

545.3 Versions

- 324

545.4 License

varies; see http://genome.ucsc.edu/license

545.5 Meta

```
package:
    name: "ucsc-genepredtobed"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/genePredToBed"                #
    fn: "genePredToBed"                                                                        #

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp genePredToBed $PREFIX/bin; chmod +x $PREFIX/bin/genePredToBed"
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Convert from genePred to bed format. Does not yet handle genePredExt"
```

CHAPTER 546

ucsc-genepredtofakepsl

546.1 Summary

Create a psl of fake-mRNA aligned to gene-preds from a file or table.

546.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

546.3 Versions

- 324

546.4 License

varies; see http://genome.ucsc.edu/license

546.5 Meta

```
package:
    name: "ucsc-genepredtofakepsl"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/genePredToFakePsl"
    fn: "genePredToFakePsl"

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp genePredToFakePsl $PREFIX/bin; chmod +x $PREFIX/bin/genePredToF
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Create a psl of fake-mRNA aligned to gene-preds from a file or table."
```

CHAPTER 547

ucsc-genepredtomafframes

547.1 Summary

create mafFrames tables from a genePreds

547.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

547.3 Versions

- 324

547.4 License

varies; see http://genome.ucsc.edu/license

547.5 Meta

```
package:
    name: "ucsc-genepredtomafframes"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/genePredToMafFrames"
    fn: "genePredToMafFrames"

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp genePredToMafFrames $PREFIX/bin; chmod +x $PREFIX/bin/genePred
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "create mafFrames tables from a genePreds"
```

CHAPTER 548

ucsc-gff3topsl

548.1 Summary

convert a GFF3 CIGAR file to a PSL file

548.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

548.3 Versions

- 324

548.4 License

varies; see http://genome.ucsc.edu/license

548.5 Meta

```
package:
    name: "ucsc-gff3topsl"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                               # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                 # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/gff3ToPsl"               # [os
    fn: "gff3ToPsl"                                                                       # [os

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp gff3ToPsl $PREFIX/bin; chmod +x $PREFIX/bin/gff3ToPsl" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "convert a GFF3 CIGAR file to a PSL file"
```

CHAPTER 549

ucsc-gtftogenepred

549.1 Summary

convert a GTF file to a genePred

549.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

549.3 Versions

- 324

549.4 License

varies; see http://genome.ucsc.edu/license

549.5 Meta

```
package:
  name: ucsc-gtftogenepred
  version: 324
source:
  url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"            # [linux]
  fn: "userApps.src.tgz"                                                           # [linux]
  md5: "c49c168584c5917081d71df854e3cd9d"                                          # [linux]
  patches:                                                                         # [linux]
      - "include.patch"                                                            # [linux]
  url: http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/gtfToGenePred        # [osx]
  fn: gtfToGenePred                                                                # [osx]
build:
  number: 0
  script: "mkdir -p $PREFIX/bin; cp gtfToGenePred $PREFIX/bin; chmod +x $PREFIX/bin/gtfToGenePred" #
requirements:
```

```
  build:
    - libpng                                                          # [linux]
    - mysql                                                           # [linux]
    - zlib                                                            # [linux]
    - openssl                                                         # [linux]
  run:
    - libpng                                                          # [linux]
    - mysql                                                           # [linux]
    - zlib                                                            # [linux]
    - openssl                                                         # [linux]
test:
  commands:
    - gtfToGenePred 2>&1 | grep gtfToGenePred
about:
  home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
  license: "varies; see http://genome.ucsc.edu/license"
  summary: convert a GTF file to a genePred
```

CHAPTER 550

ucsc-hgloadbed

550.1 Summary

Load a generic bed file into database

550.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

550.3 Versions

- 324

550.4 License

varies; see http://genome.ucsc.edu/license

550.5 Meta

```
package:
    name: "ucsc-hgloadbed"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                               # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                 # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/hgLoadBed"               # [os
    fn: "hgLoadBed"                                                                       # [os

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp hgLoadBed $PREFIX/bin; chmod +x $PREFIX/bin/hgLoadBed" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Load a generic bed file into database"
```

CHAPTER 551

ucsc-hgloadchain

551.1 Summary

Load a generic Chain file into database

551.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

551.3 Versions

- 324

551.4 License

varies; see http://genome.ucsc.edu/license

551.5 Meta

```
package:
    name: "ucsc-hgloadchain"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/hgLoadChain"                # [
    fn: "hgLoadChain"                                                                         # [

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp hgLoadChain $PREFIX/bin; chmod +x $PREFIX/bin/hgLoadChain" # [
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Load a generic Chain file into database"
```

CHAPTER 552

ucsc-hgloadmaf

552.1 Summary

Load a maf file index into the database

552.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

552.3 Versions

- 324

552.4 License

varies; see http://genome.ucsc.edu/license

552.5 Meta

```
package:
    name: "ucsc-hgloadmaf"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [lin
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [lin
    patches:                                                                              # [linux
        - "include.patch"                                                                   # [lin

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/hgLoadMaf"                # [osx
    fn: "hgLoadMaf"                                                                         # [osx

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp hgLoadMaf $PREFIX/bin; chmod +x $PREFIX/bin/hgLoadMaf" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Load a maf file index into the database"
```

CHAPTER 553

ucsc-hgloadwiggle

553.1 Summary

Load a wiggle track definition into database

553.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

553.3 Versions

- 324

553.4 License

varies; see http://genome.ucsc.edu/license

553.5 Meta

```
package:
    name: "ucsc-hgloadwiggle"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/hgLoadWiggle"                #
    fn: "hgLoadWiggle"                                                                        #

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp hgLoadWiggle $PREFIX/bin; chmod +x $PREFIX/bin/hgLoadWiggle" #
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Load a wiggle track definition into database"
```

CHAPTER 554

ucsc-lavtopsl

554.1 Summary

Convert blastz lav to psl format

554.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

554.3 Versions

- 324

554.4 License

varies; see http://genome.ucsc.edu/license

554.5 Meta

```
package:
    name: "ucsc-lavtopsl"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                               # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                 # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/lavToPsl"                # [osx
    fn: "lavToPsl"                                                                        # [osx

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp lavToPsl $PREFIX/bin; chmod +x $PREFIX/bin/lavToPsl" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Convert blastz lav to psl format"
```

CHAPTER 555

ucsc-liftover

555.1 Summary

Move annotations from one assembly to another

555.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

555.3 Versions

- 324

555.4 License

varies; see http://genome.ucsc.edu/license

555.5 Meta

```
package:
    name: "ucsc-liftover"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                 # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                  # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/liftOver"                # [osx
    fn: "liftOver"                                                                         # [osx

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp liftOver $PREFIX/bin; chmod +x $PREFIX/bin/liftOver" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Move annotations from one assembly to another"
```

CHAPTER 556

ucsc-liftup

556.1 Summary

change coordinates of .psl, .agp, .gap, .gl, .out, .align, .gff, .gtf

556.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

556.3 Versions

- 324

556.4 License

varies; see http://genome.ucsc.edu/license

556.5 Meta

```
package:
    name: "ucsc-liftup"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                # [lin
    md5: "c49c168584c5917081d71df854e3cd9d"                                               # [lin
    patches:                                                                              # [linux
        - "include.patch"                                                                 # [lin

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/liftUp"                 # [osx]
    fn: "liftUp"                                                                          # [osx]

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp liftUp $PREFIX/bin; chmod +x $PREFIX/bin/liftUp" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "change coordinates of .psl, .agp, .gap, .gl, .out, .align, .gff, .gtf"
```

CHAPTER 557

ucsc-mafaddirows

557.1 Summary

add 'i' rows to a maf

557.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

557.3 Versions

- 324

557.4 License

varies; see http://genome.ucsc.edu/license

557.5 Meta

```
package:
    name: "ucsc-mafaddirows"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/mafAddIRows"                # [
    fn: "mafAddIRows"                                                                         # [

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp mafAddIRows $PREFIX/bin; chmod +x $PREFIX/bin/mafAddIRows" # [
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "add 'i' rows to a maf"
```

CHAPTER 558

ucsc-mafaddqrows

558.1 Summary

Add quality data to a maf

558.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

558.3 Versions

- 324

558.4 License

varies; see http://genome.ucsc.edu/license

558.5 Meta

```
package:
    name: "ucsc-mafaddqrows"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/mafAddQRows"               # [
    fn: "mafAddQRows"                                                                       # [

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp mafAddQRows $PREFIX/bin; chmod +x $PREFIX/bin/mafAddQRows" # [
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Add quality data to a maf"
```

CHAPTER 559

ucsc-mafcoverage

559.1 Summary

Analyse coverage by maf files - chromosome by

559.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

559.3 Versions

- 324

559.4 License

varies; see http://genome.ucsc.edu/license

559.5 Meta

```
package:
    name: "ucsc-mafcoverage"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/mafCoverage"               # [
    fn: "mafCoverage"                                                                       # [

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp mafCoverage $PREFIX/bin; chmod +x $PREFIX/bin/mafCoverage" # [
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Analyse coverage by maf files - chromosome by "
```

CHAPTER 560

ucsc-maffetch

560.1 Summary

get overlapping records from an MAF using an index table

560.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

560.3 Versions

- 324

560.4 License

varies; see http://genome.ucsc.edu/license

560.5 Meta

```
package:
    name: "ucsc-maffetch"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/mafFetch"                 # [osx
    fn: "mafFetch"                                                                          # [osx

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp mafFetch $PREFIX/bin; chmod +x $PREFIX/bin/mafFetch" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "get overlapping records from an MAF using an index table"
```

CHAPTER 561

ucsc-maffilter

561.1 Summary

Filter out maf files. Output goes to standard out

561.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

561.3 Versions

- 324

561.4 License

varies; see http://genome.ucsc.edu/license

561.5 Meta

```
package:
    name: "ucsc-maffilter"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                # [lin
    md5: "c49c168584c5917081d71df854e3cd9d"                                               # [lin
    patches:                                                                              # [linux
        - "include.patch"                                                                 # [lin

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/mafFilter"               # [osx
    fn: "mafFilter"                                                                       # [osx

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp mafFilter $PREFIX/bin; chmod +x $PREFIX/bin/mafFilter" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Filter out maf files. Output goes to standard out"
```

CHAPTER 562

ucsc-maffrag

562.1 Summary

Extract maf sequences for a region from database

562.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

562.3 Versions

- 324

562.4 License

varies; see http://genome.ucsc.edu/license

562.5 Meta

```
package:
    name: "ucsc-maffrag"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/mafFrag"                # [osx]
    fn: "mafFrag"                                                                         # [osx]

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp mafFrag $PREFIX/bin; chmod +x $PREFIX/bin/mafFrag" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Extract maf sequences for a region from database"
```

CHAPTER 563

ucsc-maffrags

563.1 Summary

Collect MAFs from regions specified in a 6 column bed file

563.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

563.3 Versions

- 324

563.4 License

varies; see http://genome.ucsc.edu/license

563.5 Meta

```
package:
    name: "ucsc-maffrags"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                               # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                 # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/mafFrags"                # [osx
    fn: "mafFrags"                                                                        # [osx

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp mafFrags $PREFIX/bin; chmod +x $PREFIX/bin/mafFrags" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Collect MAFs from regions specified in a 6 column bed file"
```

CHAPTER 564

ucsc-mafgene

564.1 Summary

output protein alignments using maf and genePred

564.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

564.3 Versions

- 324

564.4 License

varies; see http://genome.ucsc.edu/license

564.5 Meta

```
package:
    name: "ucsc-mafgene"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/mafGene"                # [osx]
    fn: "mafGene"                                                                         # [osx]

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp mafGene $PREFIX/bin; chmod +x $PREFIX/bin/mafGene" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "output protein alignments using maf and genePred"
```

CHAPTER 565

ucsc-mafmefirst

565.1 Summary

Move component to top if it is one of the named ones.

565.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

565.3 Versions

- 324

565.4 License

varies; see http://genome.ucsc.edu/license

565.5 Meta

```
package:
    name: "ucsc-mafmefirst"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                # [lin
    md5: "c49c168584c5917081d71df854e3cd9d"                                               # [lin
    patches:                                                                              # [linux
        - "include.patch"                                                                 # [lin

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/mafMeFirst"              # [os
    fn: "mafMeFirst"                                                                      # [os

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp mafMeFirst $PREFIX/bin; chmod +x $PREFIX/bin/mafMeFirst" # [osx
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Move component to top if it is one of the named ones.  "
```

CHAPTER 566

ucsc-maforder

566.1 Summary

order components within a maf file

566.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

566.3 Versions

- 324

566.4 License

varies; see http://genome.ucsc.edu/license

566.5 Meta

```
package:
    name: "ucsc-maforder"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/mafOrder"                 # [osx
    fn: "mafOrder"                                                                          # [osx

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp mafOrder $PREFIX/bin; chmod +x $PREFIX/bin/mafOrder" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "order components within a maf file"
```

CHAPTER 567

ucsc-mafranges

567.1 Summary

Extract ranges of target (or query) coverage from maf and

567.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

567.3 Versions

- 324

567.4 License

varies; see http://genome.ucsc.edu/license

567.5 Meta

```
package:
    name: "ucsc-mafranges"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                               # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                 # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/mafRanges"               # [os
    fn: "mafRanges"                                                                       # [os

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp mafRanges $PREFIX/bin; chmod +x $PREFIX/bin/mafRanges" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Extract ranges of target (or query) coverage from maf and "
```

CHAPTER 568

ucsc-mafsinregion

568.1 Summary

Extract MAFS in a genomic region

568.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

568.3 Versions

- 324

568.4 License

varies; see http://genome.ucsc.edu/license

568.5 Meta

```
package:
    name: "ucsc-mafsinregion"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/mafsInRegion"                #
    fn: "mafsInRegion"                                                                        #

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp mafsInRegion $PREFIX/bin; chmod +x $PREFIX/bin/mafsInRegion" #
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Extract MAFS in a genomic region"
```

CHAPTER 569

ucsc-mafspecieslist

569.1 Summary

Scan maf and output all species used in it.

569.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

569.3 Versions

- 324

569.4 License

varies; see http://genome.ucsc.edu/license

569.5 Meta

```
package:
    name: "ucsc-mafspecieslist"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/mafSpeciesList"                 #
    fn: "mafSpeciesList"                                                                         #

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp mafSpeciesList $PREFIX/bin; chmod +x $PREFIX/bin/mafSpeciesList
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Scan maf and output all species used in it."
```

CHAPTER 570

ucsc-mafspeciessubset

570.1 Summary

Extract a maf that just has a subset of species.

570.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

570.3 Versions

- 324

570.4 License

varies; see http://genome.ucsc.edu/license

570.5 Meta

```
package:
    name: "ucsc-mafspeciessubset"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/mafSpeciesSubset"
    fn: "mafSpeciesSubset"

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp mafSpeciesSubset $PREFIX/bin; chmod +x $PREFIX/bin/mafSpeciesSu
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Extract a maf that just has a subset of species."
```

CHAPTER 571

ucsc-mafsplit

571.1 Summary

Split multiple alignment files

571.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

571.3 Versions

- 324

571.4 License

varies; see http://genome.ucsc.edu/license

571.5 Meta

```
package:
    name: "ucsc-mafsplit"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                               # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                 # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/mafSplit"                # [osx
    fn: "mafSplit"                                                                        # [osx

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp mafSplit $PREFIX/bin; chmod +x $PREFIX/bin/mafSplit" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Split multiple alignment files"
```

CHAPTER 572

ucsc-mafsplitpos

572.1 Summary

Pick positions to split multiple alignment input files

572.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

572.3 Versions

- 324

572.4 License

varies; see http://genome.ucsc.edu/license

572.5 Meta

```
package:
    name: "ucsc-mafsplitpos"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/mafSplitPos"               # [
    fn: "mafSplitPos"                                                                       # [

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp mafSplitPos $PREFIX/bin; chmod +x $PREFIX/bin/mafSplitPos" # [
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Pick positions to split multiple alignment input files"
```

CHAPTER 573

ucsc-maftoaxt

573.1 Summary

Convert from maf to axt format

573.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

573.3 Versions

- 324

573.4 License

varies; see http://genome.ucsc.edu/license

573.5 Meta

```
package:
    name: "ucsc-maftoaxt"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                               # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                 # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/mafToAxt"                # [osx
    fn: "mafToAxt"                                                                        # [osx

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp mafToAxt $PREFIX/bin; chmod +x $PREFIX/bin/mafToAxt" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Convert from maf to axt format"
```

CHAPTER 574

ucsc-maftopsl

574.1 Summary

Convert maf to psl format

574.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

574.3 Versions

- 324

574.4 License

varies; see http://genome.ucsc.edu/license

574.5 Meta

```
package:
    name: "ucsc-maftopsl"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                               # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                 # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/mafToPsl"                # [osx
    fn: "mafToPsl"                                                                        # [osx

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp mafToPsl $PREFIX/bin; chmod +x $PREFIX/bin/mafToPsl" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Convert maf to psl format"
```

CHAPTER 575

ucsc-maftosnpbed

575.1 Summary

finds SNPs in MAF and builds a bed with their functional consequence

575.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

575.3 Versions

- 324

575.4 License

varies; see http://genome.ucsc.edu/license

575.5 Meta

```
package:
    name: "ucsc-maftosnpbed"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/mafToSnpBed"                # [
    fn: "mafToSnpBed"                                                                         # [

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp mafToSnpBed $PREFIX/bin; chmod +x $PREFIX/bin/mafToSnpBed" # [
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "finds SNPs in MAF and builds a bed with their functional consequence"
```

CHAPTER 576

ucsc-netchainsubset

576.1 Summary

Create chain file with subset of chains that appear in the net

576.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

576.3 Versions

- 324

576.4 License

varies; see http://genome.ucsc.edu/license

576.5 Meta

```
package:
    name: "ucsc-netchainsubset"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/netChainSubset"                 #
    fn: "netChainSubset"                                                                         #

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp netChainSubset $PREFIX/bin; chmod +x $PREFIX/bin/netChainSubset
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Create chain file with subset of chains that appear in the net"
```

CHAPTER 577

ucsc-nettobed

577.1 Summary

Convert target coverage of net to a bed file.

577.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

577.3 Versions

- 324

577.4 License

varies; see http://genome.ucsc.edu/license

577.5 Meta

```
package:
    name: "ucsc-nettobed"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/netToBed"                 # [osx
    fn: "netToBed"                                                                          # [osx

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp netToBed $PREFIX/bin; chmod +x $PREFIX/bin/netToBed" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Convert target coverage of net to a bed file."
```

CHAPTER 578

ucsc-pslcat

578.1 Summary

concatenate psl files

578.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

578.3 Versions

- 324

578.4 License

varies; see http://genome.ucsc.edu/license

578.5 Meta

```
package:
    name: "ucsc-pslcat"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/pslCat"                 # [osx]
    fn: "pslCat"                                                                          # [osx]

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp pslCat $PREFIX/bin; chmod +x $PREFIX/bin/pslCat" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "concatenate psl files"
```

CHAPTER 579

ucsc-pslcdnafilter

579.1 Summary

Filter cDNA alignments in psl format. Filtering criteria are comparative, selecting near best in genome alignments for each given cDNA and non-comparative, based only on the quality of an individual alignment.

579.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

579.3 Versions

- 324

579.4 License

varies; see http://genome.ucsc.edu/license

579.5 Meta

```
package:
    name: "ucsc-pslcdnafilter"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                     # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                    # [li
    patches:                                                                                 # [linu
        - "include.patch"                                                                      # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/pslCDnaFilter"                  #
    fn: "pslCDnaFilter"                                                                          #
```

```
build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp pslCDnaFilter $PREFIX/bin; chmod +x $PREFIX/bin/pslCDnaFilter"
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "
Filter cDNA alignments in psl format.  Filtering criteria are
comparative, selecting near best in genome alignments for each given
cDNA and non-comparative, based only on the quality of an individual
alignment.
"
```

CHAPTER 580

ucsc-pslcheck

580.1 Summary

validate PSL files

580.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

580.3 Versions

- 324

580.4 License

varies; see http://genome.ucsc.edu/license

580.5 Meta

```
package:
    name: "ucsc-pslcheck"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/pslCheck"                 # [osx
    fn: "pslCheck"                                                                          # [osx

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp pslCheck $PREFIX/bin; chmod +x $PREFIX/bin/pslCheck" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "validate PSL files"
```

CHAPTER 581

ucsc-psldropoverlap

581.1 Summary

deletes all overlapping self alignments.

581.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

581.3 Versions

- 324

581.4 License

varies; see http://genome.ucsc.edu/license

581.5 Meta

```
package:
    name: "ucsc-psldropoverlap"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/pslDropOverlap"                 #
    fn: "pslDropOverlap"                                                                         #

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp pslDropOverlap $PREFIX/bin; chmod +x $PREFIX/bin/pslDropOverlap
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "deletes all overlapping self alignments. "
```

CHAPTER 582

ucsc-pslfilter

582.1 Summary

filter out psl file

582.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

582.3 Versions

- 324

582.4 License

varies; see http://genome.ucsc.edu/license

582.5 Meta

```
package:
    name: "ucsc-pslfilter"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                               # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                 # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/pslFilter"               # [os
    fn: "pslFilter"                                                                       # [os

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp pslFilter $PREFIX/bin; chmod +x $PREFIX/bin/pslFilter" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "filter out psl file"
```

CHAPTER 583

ucsc-pslhisto

583.1 Summary

Collect counts on PSL alignments for making histograms. These then be analyzed with R, textHistogram, etc.

583.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

583.3 Versions

- 324

583.4 License

varies; see http://genome.ucsc.edu/license

583.5 Meta

```
package:
    name: "ucsc-pslhisto"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                     # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                    # [li
    patches:                                                                                 # [linu
        - "include.patch"                                                                      # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/pslHisto"                   # [osx
    fn: "pslHisto"                                                                           # [osx

build:                                                                                       # [osx]
```

```
    script: "mkdir -p $PREFIX/bin; cp pslHisto $PREFIX/bin; chmod +x $PREFIX/bin/pslHisto" # [osx]
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "
Collect counts on PSL alignments for making histograms. These then be
analyzed with R, textHistogram, etc.
"
```

CHAPTER 584

ucsc-pslliftsubrangeblat

584.1 Summary

lift PSLs from blat subrange alignments

584.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

584.3 Versions

- 324

584.4 License

varies; see http://genome.ucsc.edu/license

584.5 Meta

```
package:
    name: "ucsc-pslliftsubrangeblat"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/pslLiftSubrangeBlat"
    fn: "pslLiftSubrangeBlat"

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp pslLiftSubrangeBlat $PREFIX/bin; chmod +x $PREFIX/bin/pslLiftSu
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "lift PSLs from blat subrange alignments"
```

CHAPTER 585

ucsc-pslmap

585.1 Summary

map PSLs alignments to new targets using alignments of

585.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

585.3 Versions

- 324

585.4 License

varies; see http://genome.ucsc.edu/license

585.5 Meta

```
package:
    name: "ucsc-pslmap"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/pslMap"                 # [osx]
    fn: "pslMap"                                                                          # [osx]

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp pslMap $PREFIX/bin; chmod +x $PREFIX/bin/pslMap" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "map PSLs alignments to new targets using alignments of"
```

CHAPTER 586

ucsc-pslmrnacover

586.1 Summary

Make histogram of coverage percentage of mRNA in psl.

586.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

586.3 Versions

- 324

586.4 License

varies; see http://genome.ucsc.edu/license

586.5 Meta

```
package:
    name: "ucsc-pslmrnacover"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/pslMrnaCover"                #
    fn: "pslMrnaCover"                                                                        #

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp pslMrnaCover $PREFIX/bin; chmod +x $PREFIX/bin/pslMrnaCover" #
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Make histogram of coverage percentage of mRNA in psl."
```

CHAPTER 587

ucsc-pslpairs

587.1 Summary

join paired ends in psl alignments

587.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

587.3 Versions

- 324

587.4 License

varies; see http://genome.ucsc.edu/license

587.5 Meta

```
package:
    name: "ucsc-pslpairs"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                               # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                 # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/pslPairs"                # [osx
    fn: "pslPairs"                                                                        # [osx

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp pslPairs $PREFIX/bin; chmod +x $PREFIX/bin/pslPairs" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "join paired ends in psl alignments"
```

CHAPTER 588

ucsc-pslpartition

588.1 Summary

split PSL files into non-overlapping sets

588.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

588.3 Versions

- 324

588.4 License

varies; see http://genome.ucsc.edu/license

588.5 Meta

```
package:
    name: "ucsc-pslpartition"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/pslPartition"                #
    fn: "pslPartition"                                                                        #

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp pslPartition $PREFIX/bin; chmod +x $PREFIX/bin/pslPartition" #
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "split PSL files into non-overlapping sets"
```

CHAPTER 589

ucsc-pslpostarget

589.1 Summary

flip psl strands so target is positive and implicit

589.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

589.3 Versions

- 324

589.4 License

varies; see http://genome.ucsc.edu/license

589.5 Meta

```
package:
    name: "ucsc-pslpostarget"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/pslPosTarget"                #
    fn: "pslPosTarget"                                                                        #

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp pslPosTarget $PREFIX/bin; chmod +x $PREFIX/bin/pslPosTarget" #
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "flip psl strands so target is positive and implicit"
```

CHAPTER 590

ucsc-pslpretty

590.1 Summary

Convert PSL to human-readable output

590.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

590.3 Versions

- 324

590.4 License

varies; see http://genome.ucsc.edu/license

590.5 Meta

```
package:
    name: "ucsc-pslpretty"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                               # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                 # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/pslPretty"               # [os
    fn: "pslPretty"                                                                       # [os

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp pslPretty $PREFIX/bin; chmod +x $PREFIX/bin/pslPretty" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Convert PSL to human-readable output"
```

CHAPTER 591

ucsc-pslrecalcmatch

591.1 Summary

Recalculate match,mismatch,repMatch columns in psl file.

591.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

591.3 Versions

- 324

591.4 License

varies; see http://genome.ucsc.edu/license

591.5 Meta

```
package:
    name: "ucsc-pslrecalcmatch"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/pslRecalcMatch"                 #
    fn: "pslRecalcMatch"                                                                         #

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp pslRecalcMatch $PREFIX/bin; chmod +x $PREFIX/bin/pslRecalcMatch
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Recalculate match,mismatch,repMatch columns in psl file."
```

CHAPTER 592

ucsc-pslreps

592.1 Summary

Analyze repeats and generate genome-wide best alignments from a

592.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

592.3 Versions

- 324

592.4 License

varies; see http://genome.ucsc.edu/license

592.5 Meta

```
package:
    name: "ucsc-pslreps"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/pslReps"                # [osx]
    fn: "pslReps"                                                                         # [osx]

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp pslReps $PREFIX/bin; chmod +x $PREFIX/bin/pslReps" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Analyze repeats and generate genome-wide best alignments from a"
```

CHAPTER 593

ucsc-pslscore

593.1 Summary

calculate web blat score from psl files

593.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

593.3 Versions

- 324

593.4 License

varies; see http://genome.ucsc.edu/license

593.5 Meta

```
package:
    name: "ucsc-pslscore"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/pslScore"                # [osx
    fn: "pslScore"                                                                        # [osx

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp pslScore $PREFIX/bin; chmod +x $PREFIX/bin/pslScore" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "calculate web blat score from psl files"
```

CHAPTER 594

ucsc-pslselect

594.1 Summary

select records from a PSL file.

594.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

594.3 Versions

- 324

594.4 License

varies; see http://genome.ucsc.edu/license

594.5 Meta

```
package:
    name: "ucsc-pslselect"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                               # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                 # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/pslSelect"               # [os
    fn: "pslSelect"                                                                       # [os

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp pslSelect $PREFIX/bin; chmod +x $PREFIX/bin/pslSelect" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "select records from a PSL file."
```

CHAPTER 595

ucsc-pslsort

595.1 Summary

Merge and sort psCluster .psl output files

595.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

595.3 Versions

- 324

595.4 License

varies; see http://genome.ucsc.edu/license

595.5 Meta

```
package:
    name: "ucsc-pslsort"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/pslSort"                # [osx]
    fn: "pslSort"                                                                         # [osx]

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp pslSort $PREFIX/bin; chmod +x $PREFIX/bin/pslSort" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Merge and sort psCluster .psl output files"
```

CHAPTER 596

ucsc-pslstats

596.1 Summary

collect statistics from a psl file.

596.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

596.3 Versions

- 324

596.4 License

varies; see http://genome.ucsc.edu/license

596.5 Meta

```
package:
    name: "ucsc-pslstats"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/pslStats"                # [osx
    fn: "pslStats"                                                                        # [osx

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp pslStats $PREFIX/bin; chmod +x $PREFIX/bin/pslStats" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "collect statistics from a psl file."
```

CHAPTER 597

ucsc-pslswap

597.1 Summary

Swap target and query in psls

597.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

597.3 Versions

- 324

597.4 License

varies; see http://genome.ucsc.edu/license

597.5 Meta

```
package:
    name: "ucsc-pslswap"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/pslSwap"                # [osx]
    fn: "pslSwap"                                                                         # [osx]

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp pslSwap $PREFIX/bin; chmod +x $PREFIX/bin/pslSwap" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "
Swap target and query in psls
"
```

CHAPTER 598

ucsc-psltobed

598.1 Summary

transform a psl format file to a bed format file.

598.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

598.3 Versions

- 324

598.4 License

varies; see http://genome.ucsc.edu/license

598.5 Meta

```
package:
    name: "ucsc-psltobed"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                               # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                 # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/pslToBed"                # [osx
    fn: "pslToBed"                                                                        # [osx

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp pslToBed $PREFIX/bin; chmod +x $PREFIX/bin/pslToBed" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "
transform a psl format file to a bed format file.
"
```

CHAPTER 599

ucsc-psltochain

599.1 Summary

Convert psl records to chain records

599.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

599.3 Versions

- 324

599.4 License

varies; see http://genome.ucsc.edu/license

599.5 Meta

```
package:
    name: "ucsc-psltochain"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [lin
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [lin
    patches:                                                                              # [linux
        - "include.patch"                                                                   # [lin

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/pslToChain"                # [os
    fn: "pslToChain"                                                                        # [os

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp pslToChain $PREFIX/bin; chmod +x $PREFIX/bin/pslToChain" # [osx
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Convert psl records to chain records "
```

CHAPTER 600

ucsc-psltopslx

600.1 Summary

Convert from psl to pslx format, which includes sequences

600.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

600.3 Versions

- 324

600.4 License

varies; see http://genome.ucsc.edu/license

600.5 Meta

```
package:
    name: "ucsc-psltopslx"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                               # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                 # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/pslToPslx"               # [os
    fn: "pslToPslx"                                                                       # [os

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp pslToPslx $PREFIX/bin; chmod +x $PREFIX/bin/pslToPslx" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Convert from psl to pslx format, which includes sequences"
```

CHAPTER 601

ucsc-pslxtofa

601.1 Summary

convert pslx (with sequence) to fasta file

601.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

601.3 Versions

- 324

601.4 License

varies; see http://genome.ucsc.edu/license

601.5 Meta

```
package:
    name: "ucsc-pslxtofa"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/pslxToFa"                # [osx
    fn: "pslxToFa"                                                                          # [osx

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp pslxToFa $PREFIX/bin; chmod +x $PREFIX/bin/pslxToFa" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "convert pslx (with sequence) to fasta file"
```

CHAPTER 602

ucsc-qactowig

602.1 Summary

convert from compressed quality score format to wiggle format.

602.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

602.3 Versions

- 324

602.4 License

varies; see http://genome.ucsc.edu/license

602.5 Meta

```
package:
    name: "ucsc-qactowig"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                               # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                 # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/qacToWig"                # [osx
    fn: "qacToWig"                                                                        # [osx

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp qacToWig $PREFIX/bin; chmod +x $PREFIX/bin/qacToWig" # [osx]
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "convert from compressed quality score format to wiggle format."
```

CHAPTER 603

ucsc-wigcorrelate

603.1 Summary

Produce a table that correlates all pairs of wigs.

603.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

603.3 Versions

- 324

603.4 License

varies; see http://genome.ucsc.edu/license

603.5 Meta

```
package:
    name: "ucsc-wigcorrelate"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/wigCorrelate"                #
    fn: "wigCorrelate"                                                                        #

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp wigCorrelate $PREFIX/bin; chmod +x $PREFIX/bin/wigCorrelate" #
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Produce a table that correlates all pairs of wigs."
```

CHAPTER 604

ucsc-wigtobigwig

604.1 Summary

Convert ascii format wig file (in fixedStep, variableStep

604.2 Home

http://hgdownload.cse.ucsc.edu/admin/exe/

604.3 Versions

- 324

604.4 License

varies; see http://genome.ucsc.edu/license

604.5 Meta

```
package:
    name: "ucsc-wigtobigwig"
    version: "324"
source:
    url: "http://hgdownload.cse.ucsc.edu/admin/exe/userApps.v324.src.tgz"                # [linux]
    fn: "userApps.src.tgz"                                                                  # [li
    md5: "c49c168584c5917081d71df854e3cd9d"                                                 # [li
    patches:                                                                              # [linu
        - "include.patch"                                                                   # [li

    url: "http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/wigToBigWig"                # [
    fn: "wigToBigWig"                                                                       # [

build:                                                                                    # [osx]
    script: "mkdir -p $PREFIX/bin; cp wigToBigWig $PREFIX/bin; chmod +x $PREFIX/bin/wigToBigWig" # [
```

```
requirements:
    build:
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]

    run:                                                            # [linux]
        - libpng                                                    # [linux]
        - mysql                                                     # [linux]
        - zlib                                                      # [linux]
        - openssl                                                   # [linux]
about:
    home: "http://hgdownload.cse.ucsc.edu/admin/exe/"
    license: "varies; see http://genome.ucsc.edu/license"
    summary: "Convert ascii format wig file (in fixedStep, variableStep"
```

CHAPTER 605

uritemplate

605.1 Summary

Python implementation of RFC6570, URI Template, and can expand templates up to and including Level 4 in that specification.

605.2 Home

https://github.com/uri-templates/uritemplate-py/

605.3 Versions

- 0.6

605.4 License

Apache 2.0

605.5 Meta

```
package:
  name: uritemplate
  version: '0.6'

source:
  fn: uritemplate-0.6.tar.gz
  url: https://pypi.python.org/packages/source/u/uritemplate/uritemplate-0.6.tar.gz
  md5: ecfc1ea8d62c7f2b47aad625afae6173

build:
  number: 0

requirements:
  build:
```

```
    - python
    - setuptools

  run:
    - python

test:
  imports:
    - uritemplate

about:
  home: https://github.com/uri-templates/uritemplate-py/
  license: Apache 2.0
  summary: Python implementation of RFC6570, URI Template, and can expand templates up to and includi
```

CHAPTER 606

urllib3

606.1 Summary

HTTP library with thread-safe connection pooling, file post, and more.

606.2 Home

http://urllib3.readthedocs.org/

606.3 Versions

- 1.12

606.4 License

MIT License

606.5 Meta

```
package:
  name: urllib3
  version: "1.12"

source:
  fn: urllib3-1.12.tar.gz
  url: https://pypi.python.org/packages/source/u/urllib3/urllib3-1.12.tar.gz
  md5: befd9dbb2c373681bd88710ba96abbdb
#  patches:
   # List any patch files here
   # - fix.patch

# build:
  # noarch_python: True
  # preserve_egg_dir: True
```

```
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - urllib3 = urllib3:main
    #
    # Would create an entry point called urllib3 that calls urllib3.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools

  run:
    - python

test:
  # Python imports
  imports:
    - urllib3
    - urllib3.contrib
    - urllib3.packages
    - urllib3.packages.ssl_match_hostname
    - urllib3.util

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  requires:
    - mock
    - nose
    - tornado
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: http://urllib3.readthedocs.org/
  license: MIT License
  summary: 'HTTP library with thread-safe connection pooling, file post, and more.'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 607

validators

607.1 Summary

Python Data Validation for Humans™.

607.2 Home

https://github.com/kvesteri/validators

607.3 Versions

- 0.10

607.4 License

BSD License

607.5 Meta

```
package:
  name: validators
  version: "0.10"

source:
  fn: validators-0.10.tar.gz
  url: https://pypi.python.org/packages/source/v/validators/validators-0.10.tar.gz
  md5: 9ddd9d77aadc047723080da500e0bbf2

requirements:
  build:
    - python
    - setuptools
    - six >=1.4.0
    - decorator >=3.4.0
```

```
  run:
    - python
    - six >=1.4.0
    - decorator >=3.4.0

test:
  imports:
    - validators
    - validators.i18n

about:
  home: https://github.com/kvesteri/validators
  license: BSD License
  summary: 'Python Data Validation for Humans™.'
```

CHAPTER 608

vardict-java

608.1 Summary

Java port of the VarDict variant discovery program

608.2 Home

https://github.com/AstraZeneca-NGS/VarDictJava

608.3 Versions

- 1.4.3

608.4 License

MIT

608.5 Meta

```
package:
  name: vardict-java
  version: '1.4.3'

source:
  fn: VarDict-1.4.3.zip
  url: https://github.com/AstraZeneca-NGS/VarDictJava/releases/download/v1.4.3/VarDict-1.4.3.zip

build:
  number: 1

requirements:
  run:
    - java-jdk
```

```
test:
  commands:
    - vardict-java -h

about:
  home: https://github.com/AstraZeneca-NGS/VarDictJava
  license: MIT
  summary: Java port of the VarDict variant discovery program
```

CHAPTER 609

vardict

609.1 Summary

A sensitive variant caller for both single and paired sample variant calling

609.2 Home

https://github.com/AstraZeneca-NGS/VarDict

609.3 Versions

- 2015.10.30

609.4 License

MIT

609.5 Meta

```
package:
  name: vardict
  version: '2015.10.30'

source:
  fn: VarDict-bac2a39d.tar.gz
  url: https://github.com/AstraZeneca-NGS/VarDict/archive/bac2a39d.tar.gz

build:
  number: 0

requirements:
  build:
  run:
```

```
test:
  commands:
    - vardict -h

about:
  home: https://github.com/AstraZeneca-NGS/VarDict
  license: MIT
  summary: A sensitive variant caller for both single and paired sample variant calling
```

CHAPTER 610

variant-effect-predictor

610.1 Summary

The VEP determines the effect of your variants (SNPs, insertions, deletions, CNVs or structural variants) on genes, transcripts, and protein sequence, as well as regulatory regions.

610.2 Home

http://www.ensembl.org/info/docs/tools/vep/index.html

610.3 Versions

- 83

610.4 License

Apache 2.0

610.5 Meta

```
package:
  name: variant-effect-predictor
  version: '83'

source:
  fn: vep-83.zip
  url: https://github.com/Ensembl/ensembl-tools/archive/release/83.zip

build:
  number: 2

requirements:
  build:
    - perl
```

```
    - perl-archive-extract
    - perl-archive-zip
    - perl-lwp-simple
    - perl-lwp-protocol-https
  run:
    - perl
    - perl-bioperl
    - perl-encode-locale
    - perl-archive-extract
    - perl-archive-zip
    - perl-cgi
    - perl-compress-raw-zlib
    - perl-dbi
    - perl-dbd-mysql
    - perl-file-fetch
    - perl-file-sharedir
    - perl-file-sharedir-install
    - perl-ipc-system-simple
    - perl-lwp-simple
    - perl-lwp-protocol-https
    - perl-statistics-descriptive
    - perl-time-hires

test:
  commands:
     - variant_effect_predictor.pl --help
     - vep_convert_cache.pl --help
     - vep_install.pl --help

about:
  home: http://www.ensembl.org/info/docs/tools/vep/index.html
  license: Apache 2.0
  summary:  The VEP determines the effect of your variants (SNPs, insertions, deletions, CNVs or stru
```

CHAPTER 611

variantbam

611.1 Summary

Filtering and profiling of next-generational sequencing data using region-specific rules

611.2 Home

https://github.com/jwalabroad/VariantBam

611.3 Versions

- 1.2.1_2015.01.08

611.4 License

GPLv3

611.5 Meta

```
package:
  name: variantbam
  version: 1.2.1_2015.01.08

build:
  number: 0

source:
  git_url: https://github.com/jwalabroad/VariantBam.git
  git_rev: 78b9905

requirements:
  build:
    - boost
    - icu
```

```
  run:
    - boost
    - icu

test:
    commands:
      - "variant --help 2>&1 | grep 'Usage: variant'"

about:
    home: https://github.com/jwalabroad/VariantBam
    license: GPLv3
    summary: Filtering and profiling of next-generational sequencing data using region-specific rules
```

CHAPTER 612

varscan

612.1 Summary

variant detection in massively parallel sequencing data

612.2 Home

http://dkoboldt.github.io/varscan/

612.3 Versions

- 2.4.0

612.4 License

The Non-Profit Open Software License version 3.0 (NPOSL-3.0)

612.5 Meta

```
about:
    home: http://dkoboldt.github.io/varscan/
    license: The Non-Profit Open Software License version 3.0 (NPOSL-3.0)
    summary: variant detection in massively parallel sequencing data
package:
    name: varscan
    version: 2.4.0
build:
  number: 1
source:
    fn: VarScan-2.4.0.jar
    url: https://github.com/dkoboldt/varscan/raw/master/VarScan.v2.4.0.jar
requirements:
  build:
  run:
```

```
test:
    commands:
      # skip test on build boxes since it requires java
      #- varscan mpileup2cns --help
```

CHAPTER 613

vawk

613.1 Summary

An awk-like VCF parser

613.2 Home

https://github.com/cc2qe/vawk

613.3 Versions

- 0.0.2

613.4 License

MIT

613.5 Meta

```
package:
  name: vawk
  version: 0.0.2

source:
  fn: vawk-a63b6b2.tar.gz
  url: https://github.com/cc2qe/vawk/archive/a63b6b2.tar.gz

build:
  number: 0
  skip: True # [not py27]

requirements:
  build:
    - python
```

```
  run:
    - python

test:
  commands:
    - vawk --help

about:
  home: https://github.com/cc2qe/vawk
  license: MIT
  summary: An awk-like VCF parser
```

CHAPTER 614

vcflib

614.1 Summary

Command-line tools for manipulating VCF files

614.2 Home

https://github.com/ekg/vcflib

614.3 Versions

- 1.0.0_rc0

614.4 License

MIT

614.5 Meta

```
package:
  name: vcflib
  version: '1.0.0_rc0'

source:
  git_url: https://github.com/ekg/vcflib.git
  git_rev: 8ac9fd517579134ef3b9797714d20c9c99c18ec6

build:
  number: 0

requirements:
  build:
  run:
```

```
test:
  commands:
    - vcfallelicprimitives -h

about:
  home: https://github.com/ekg/vcflib
  license: MIT
  summary: Command-line tools for manipulating VCF files
```

CHAPTER 615

vcftools

615.1 Summary

A set of tools written in Perl and C++ for working with VCF files.

615.2 Home

https://vcftools.github.io/

615.3 Versions

- 0.1.14

615.4 License

LGPL

615.5 Meta

```
package:
  name: vcftools
  version: '0.1.14'

source:
  fn: vcftools-0.1.14.tar.gz
  url: https://github.com/vcftools/vcftools/releases/download/v0.1.14/vcftools-0.1.14.tar.gz

build:
  number: 2

requirements:
  build:
    - perl
    - zlib
```

```
    - perl-vcftools-vcf ==0.953

  run:
    - perl
    - zlib
    - perl-vcftools-vcf ==0.953

test:
  commands:
    - vcftools -h
    #- vcf-isec -h  # outputs to stderr, can't use this as a test.

about:
  home: https://vcftools.github.io/
  license: LGPL
  summary: A set of tools written in Perl and C++ for working with VCF files.
```

CHAPTER 616

viennarna

616.1 Summary

Tools for RNA secondary structure prediction and comparison

616.2 Home

http://www.tbi.univie.ac.at/RNA/

616.3 Versions

- 2.1.9
- 2.1.8
- 2.1.5

616.4 License

MIT-like

616.5 Meta

```
package:
  name: viennarna
  version: "2.1.9"
build:
  number: 1
source:
  fn: ViennaRNA-2.1.9.tar.gz
  url: "http://www.tbi.univie.ac.at/RNA/download.php?id=viennarna-2.1.9"
  sha1: 4916031938404aabe3b7fe725e43b1b75fe9527e
requirements:
  build:
```

```
  run:
about:
  home: http://www.tbi.univie.ac.at/RNA/
  license: MIT-like
  license_file: COPYING
  summary: Tools for RNA secondary structure prediction and comparison
```

CHAPTER 617

vispr

617.1 Summary

VISPR is a visualization framework and analysis workflow for CRISPR/Cas9 knockout screens. VISPR is designed to display results calculated by MAGeCK.

617.2 Home

https://bitbucket.org/liulab/vispr

617.3 Versions

- 0.4.11

617.4 License

MIT License

617.5 Meta

```
package:
  name: vispr
  version: "0.4.11"

source:
  fn: vispr-0.4.11.tar.gz
  url: https://pypi.python.org/packages/source/v/vispr/vispr-0.4.11.tar.gz

build:
  skip: True # [py27]
  entry_points:
    - vispr = vispr.cli:main

requirements:
```

```
  build:
    - python
    - setuptools
    - numpy
    - flask
    - pandas >=0.17.1
    - pyyaml
    - scipy
    - scikit-learn
    - appdirs
  run:
    - python
    - numpy
    - flask
    - pandas >=0.17.1
    - pyyaml
    - scipy
    - scikit-learn
    - appdirs

test:
  commands:
    - vispr --help > /dev/null

about:
  home: https://bitbucket.org/liulab/vispr
  license: MIT License
  summary: VISPR is a visualization framework and analysis workflow for CRISPR/Cas9 knockout screens.
```

CHAPTER 618

voluptuous

618.1 Summary

Python data validation library

618.2 Home

https://github.com/alecthomas/voluptuous

618.3 Versions

- 0.8.8

618.4 License

BSD

618.5 Meta

```
package:
  name: voluptuous
  version: "0.8.8"

source:
  fn: voluptuous-0.8.8.tar.gz
  url: https://pypi.python.org/packages/source/v/voluptuous/voluptuous-0.8.8.tar.gz
  md5: d39128d69dce5395c8a3c5c6474bf740

build:
  number: 0

requirements:
  build:
    - python
```

```
    - setuptools

  run:
    - python

test:
  imports:
    - voluptuous

about:
  home: https://github.com/alecthomas/voluptuous
  license: BSD
  summary: Python data validation library
```

CHAPTER 619

vphaser2

619.1 Summary

V-Phaser 2 is a tool to call variants in genetically heterogeneous populations from ultra-deep sequence data

619.2 Home

https://www.broadinstitute.org/scientific-community/science/projects/viral-genomics/v-phaser-2

619.3 Versions

- 2.0

619.4 License

https://www.broadinstitute.org/node/4962

619.5 Meta

```
about:
    home: 'https://www.broadinstitute.org/scientific-community/science/projects/viral-genomics/v-phas
    license: 'https://www.broadinstitute.org/node/4962'
    summary: 'V-Phaser 2 is a tool to call variants in genetically heterogeneous populations from ult
package:
  name: "vphaser2"
  version: '2.0'
source:
  git_url: https://github.com/broadinstitute/v-phaser2.git #[osx or linux64]
build:
  number: 1
requirements:
  build:
    - bamtools
    - zlib
```

```
  run:
    - bamtools
    - zlib
test:
    commands:
        - 'vphaser2 | grep "BAM file"'
```

CHAPTER 620

vsearch

620.1 Summary

a versatile open source tool for metagenomics (USEARCH alternative)

620.2 Home

https://github.com/torognes/vsearch

620.3 Versions

- 1.9.7

620.4 License

dual-licensed under GPLv3+ or BSD 2-clause

620.5 Meta

```
package:
  name: vsearch
  version: "1.9.7"
source:
  git_url: https://github.com/torognes/vsearch.git
  git_rev: v1.9.7
test:
  commands:
    - vsearch --version > /dev/null
about:
  home: https://github.com/torognes/vsearch
  license: "dual-licensed under GPLv3+ or BSD 2-clause"
  summary: "a versatile open source tool for metagenomics (USEARCH alternative)"
```

CHAPTER 621

vt

621.1 Summary

A tool set for short variant discovery in genetic sequence data

621.2 Home

https://github.com/atks/vt

621.3 Versions

- 2015.11.10

621.4 License

MIT

621.5 Meta

```
package:
  name: vt
  version: '2015.11.10'

source:
  fn: vt-15f90de5.tar.gz
  url: https://github.com/atks/vt/archive/15f90de5.tar.gz

build:
  number: 0

requirements:
  build:
  run:
```

```
test:
  commands:
    - vt

about:
  home: https://github.com/atks/vt
  license: MIT
  summary: A tool set for short variant discovery in genetic sequence data
```

CHAPTER 622

watchdog

622.1 Summary

Filesystem events monitoring

622.2 Home

http://github.com/gorakhargosh/watchdog

622.3 Versions

- 0.8.3

622.4 License

Apache Software License

622.5 Meta

```
package:
  name: watchdog
  version: "0.8.3"

source:
  fn: watchdog-0.8.3.tar.gz
  url: https://pypi.python.org/packages/source/w/watchdog/watchdog-0.8.3.tar.gz
  md5: bb16926bccc98eae2a04535e4512ddf1
#  patches:
   # List any patch files here
   # - fix.patch

build:
  # noarch_python: True
  # preserve_egg_dir: True
```

```
  entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - watchdog = watchdog:main
    #
    # Would create an entry point called watchdog that calls watchdog.main()

    - watchmedo = watchdog.watchmedo:main

  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools
    - pyyaml >=3.10
    - argh >=0.24.1
    - pathtools >=0.1.1

  run:
    - python
    - pyyaml >=3.10
    - argh >=0.24.1
    - pathtools >=0.1.1

test:
  # Python imports
  imports:
    - watchdog
    - watchdog.observers
    - watchdog.tricks
    - watchdog.utils

  commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.

    - watchmedo --help

  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  requires:
    - pytest
    - pytest-cov
    - pytest-timeout >=0.3
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: http://github.com/gorakhargosh/watchdog
  license: Apache Software License
  summary: 'Filesystem events monitoring'

# See
```

```
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 623

weblogo

623.1 Summary

Web based application designed to generate sequence logos

623.2 Home

http://weblogo.berkeley.edu/

623.3 Versions

- 2.8.2

623.4 License

MIT

623.5 Meta

```
about:
  home: http://weblogo.berkeley.edu/
  license: MIT
  summary: Web based application designed to generate sequence logos
package:
  name: weblogo
  version: 2.8.2

source:
  url: http://weblogo.berkeley.edu/release/weblogo.2.8.2.tar.gz
  fn: weblogo.2.8.2.tar.gz
  md5: 12886e0f41757e32ac2823d0f990ce0c

test:
```

```
  commands:
    - seqlogo 2>&1 | grep usage > /dev/null
```

CHAPTER 624

wham

624.1 Summary

Structural variant detection and association testing

624.2 Home

https://github.com/jewmanchue/wham

624.3 Versions

- 1.7.0.162

624.4 License

MIT

624.5 Meta

```
package:
  name: wham
  version: '1.7.0.162'

source:
  git_url: https://github.com/jewmanchue/wham.git
  git_rev: eef6cfa

build:
  number: 0

requirements:
  build:
    - cmake
  run:
```

```
test:
  commands:
    # - WHAM-GRAPHENING  -- returns an error code, no way to call just --help

about:
  home: https://github.com/jewmanchue/wham
  license: MIT
  summary: Structural variant detection and association testing
```

CHAPTER 625

whatshap

625.1 Summary

phase genomic variants using DNA sequencing reads (haplotype assembly)

625.2 Home

https://whatshap.readthedocs.org/

625.3 Versions

- 0.9

625.4 License

MIT License

625.5 Meta

```
package:
  name: whatshap
  version: "0.9"
about:
  home: https://whatshap.readthedocs.org/
  license: MIT License
  summary: 'phase genomic variants using DNA sequencing reads (haplotype assembly)'
source:
  fn: whatshap-0.9.tar.gz
  url: https://pypi.python.org/packages/source/w/whatshap/whatshap-0.9.tar.gz
  md5: 6bee34d05b76e77dc73e956a277092a2
requirements:
  build:
    - python
    - pysam
```

```
    - pyvcf
  run:
    - python
    - pysam
    - pyvcf
build:
  skip: True  # [not py3k]
  script: python3 setup.py install
test:
  imports:
    - whatshap
    - whatshap.scripts
  commands:
    - whatshap --help > /dev/null
```

CHAPTER 626

ws4py

626.1 Summary

WebSocket library for Python

626.2 Home

https://github.com/Lawouach/WebSocket-for-Python

626.3 Versions

- 0.3.2
- 0.2.2

626.4 License

BSD License

626.5 Meta

```
package:
  name: ws4py
  version: "0.3.2"

source:
  fn: ws4py-0.3.2.tar.gz
  url: https://pypi.python.org/packages/source/w/ws4py/ws4py-0.3.2.tar.gz
  md5: 22fc2d79734473aa5cbb489161842354
#  patches:
   # List any patch files here
   # - fix.patch

# build:
```

```
  # noarch_python: True
  # preserve_egg_dir: True
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - ws4py = ws4py:main
    #
    # Would create an entry point called ws4py that calls ws4py.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools

  run:
    - python

test:
  # Python imports
  imports:
    - ws4py
    - ws4py.client
    - ws4py.server

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: https://github.com/Lawouach/WebSocket-for-Python
  license: BSD License
  summary: 'WebSocket library for Python'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 627

wtforms-components

627.1 Summary

Additional fields, validators and widgets for WTForms.

627.2 Home

https://github.com/kvesteri/wtforms-components

627.3 Versions

- 0.10.0

627.4 License

BSD License

627.5 Meta

```
package:
  name: wtforms-components
  version: "0.10.0"

source:
  fn: WTForms-Components-0.10.0.tar.gz
  url: https://pypi.python.org/packages/source/W/WTForms-Components/WTForms-Components-0.10.0.tar.gz
  md5: 2b5a5201e679bceb32aecc2099a276e1
  patches:
    - setup.py.patch

requirements:
  build:
    - python
    - setuptools
```

```
    - wtforms >=1.0.4
    - six >=1.4.1
    - validators >=0.5.0
    - intervals >=0.6.0
    - phonenumbers

  run:
    - python
    - wtforms >=1.0.4
    - six >=1.4.1
    - validators >=0.5.0
    - intervals >=0.6.0
    - phonenumbers

test:
  imports:
    - wtforms_components
    - wtforms_components.fields

about:
  home: https://github.com/kvesteri/wtforms-components
  license: BSD License
  summary: 'Additional fields, validators and widgets for WTForms.'
```

CHAPTER 628

xmltodict

628.1 Summary

Makes working with XML feel like you are working with JSON

628.2 Home

https://github.com/martinblech/xmltodict

628.3 Versions

- 0.9.2

628.4 License

MIT License

628.5 Meta

```
package:
  name: xmltodict
  version: "0.9.2"

source:
  fn: xmltodict-0.9.2.tar.gz
  url: https://pypi.python.org/packages/source/x/xmltodict/xmltodict-0.9.2.tar.gz
  md5: ab17e53214a8613ad87968e9674d75dd
#  patches:
   # List any patch files here
   # - fix.patch

# build:
  # noarch_python: True
  # preserve_egg_dir: True
```

```
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - xmltodict = xmltodict:main
    #
    # Would create an entry point called xmltodict that calls xmltodict.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools

  run:
    - python

# test:
  # Python imports
  # imports:

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  # requires:
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: https://github.com/martinblech/xmltodict
  license: MIT License
  summary: 'Makes working with XML feel like you are working with JSON'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 629

xsv

629.1 Summary

A fast CSV toolkit written in Rust.

629.2 Home

https://github.com/BurntSushi/xsv

629.3 Versions

- 0.9.8

629.4 License

MIT

629.5 Meta

```
package:
  name: xsv
  version: "0.9.8"
source:
  git_url: https://github.com/BurntSushi/xsv.git
  git_rev: 0.9.8
test:
  commands:
    - xsv --help > /dev/null
about:
  home: https://github.com/BurntSushi/xsv
  license: MIT
  summary: A fast CSV toolkit written in Rust.
```

CHAPTER 630

yaggo

630.1 Summary

Yaggo is a tool to generate command line parsers for C++. Yaggo stands for "Yet Another GenGetOpt" and is inspired by GNU Gengetopt.

630.2 Home

https://github.com/gmarcais/yaggo

630.3 Versions

- 1.5.9

630.4 License

GPLv3

630.5 Meta

```
package:
  name: yaggo
  version: "1.5.9"
build:
  number: 0
source:
  fn: yaggo
  url: https://github.com/gmarcais/yaggo/releases/download/v1.5.9/yaggo
requirements:
  build:
  run:
    - ruby
test:
  commands:
```

```
    - yaggo -h 2>&1 | grep Usage > /dev/null
about:
  home: https://github.com/gmarcais/yaggo
  license: GPLv3
  summary: Yaggo is a tool to generate command line parsers for C++. Yaggo stands for "Yet Another Ge
```

CHAPTER 631

yanc

631.1 Summary

Yet another nose colorer

631.2 Home

https://github.com/0compute/yanc

631.3 Versions

- 0.3.3

631.4 License

GNU General Public License v3 (GPLv3)

631.5 Meta

```
package:
  name: yanc
  version: "0.3.3"

source:
  fn: yanc-0.3.3.tar.gz
  url: https://pypi.python.org/packages/source/y/yanc/yanc-0.3.3.tar.gz
  md5: e1c6630d9c7e1210975c8d23ca50700f
#  patches:
   # List any patch files here
   # - fix.patch

build:
  # noarch_python: True
  preserve_egg_dir: True
```

```
  # entry_points:
    # Put any entry points (scripts to be generated automatically) here. The
    # syntax is module:function.  For example
    #
    # - yanc = yanc:main
    #
    # Would create an entry point called yanc that calls yanc.main()


  # If this is a new build for the same version, increment the build
  # number. If you do not include this key, it defaults to 0.
  # number: 1

requirements:
  build:
    - python
    - setuptools

  run:
    - python
    - setuptools

test:
  # Python imports
  imports:
    - yanc

  # commands:
    # You can put test commands to be run here.  Use this to test that the
    # entry points work.


  # You can also put a file called run_test.py in the recipe that will be run
  # at test time.

  requires:
    - nose
    # Put any additional test requirements here.  For example
    # - nose

about:
  home: https://github.com/0compute/yanc
  license: GNU General Public License v3 (GPLv3)
  summary: 'Yet another nose colorer'

# See
# http://docs.continuum.io/conda/build.html for
# more information about meta.yaml
```

CHAPTER 632

Indices and tables

- genindex
- modindex
- search