Planemo Documentation

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Galaxy Project and Community

Jul 02, 2019
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17 Indices and tables
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Command-line utilities to assist in developing Galaxy and Common Workflow Language tools.

- Free software: Academic Free License version 3.0
- Documentation: https://planemo.readthedocs.io.
- Code: https://github.com/galaxyproject/planemo
CHAPTER 1

Quick Start

1.1 Obtaining

For a traditional Python installation of Planemo, first set up a virtualenv for \texttt{planemo} (this example creates a new one in \texttt{.venv}) and then install with \texttt{pip}. Planemo requires \texttt{pip} 7.0 or newer.

\begin{verbatim}
$ virtualenv .venv; . .venv/bin/activate
$ pip install "pip>=7" # Upgrade pip if needed.
$ pip install planemo
\end{verbatim}

For information on updating Planemo, installing the latest development release, or installing Planemo via Bioconda - checkout the installation documentation.

Planemo is also available as a virtual appliance bundled with a preconfigured Galaxy server and set up for Galaxy and Common Workflow Language tool development. You can choose from open virtualization format (OVA, .ova) or Docker appliances.

1.2 Basics - Galaxy

This quick start will assume you have a directory with one or more Galaxy tool XML files. If no such directory is available, one can be quickly created for demonstrating \texttt{planemo} as follows \texttt{project_init --template=demo mytools; cd mytools}.

Planemo can check tool XML files for common problems and best practices using the \texttt{lint} command (also aliased as \texttt{l}).

\begin{verbatim}
$ planemo lint
\end{verbatim}

Like many \texttt{planemo} commands - by default this will search the current directory and use all tool files it finds. It can be explicitly passed a path to tool files or a directory of tool files.
The lint command takes in additional options related to reporting levels, exit code, etc. These options are described in the docs or (like with all commands) can be accessed by passing --help to it.

Once tools are syntactically correct - it is time to test. The test command can be used to test a tool or a directory of tools.

If no --galaxy_root is defined, Planemo will download and configure a disposable Galaxy instance for testing. Planemo will create a HTML output report in the current directory named tool_test_output.html (override with --test_output). See an example of such a report for Tophat.

Once tools have been linted and tested - the tools can be viewed in a Galaxy interface using the serve(s) command.

Like test, serve requires a Galaxy root and one can be explicitly specified with --galaxy_root or installed dynamically with --install_galaxy.

For more information on building Galaxy tools in general please check out Building Galaxy Tools Using Planemo.

1.3 Basics - Common Workflow Language

This quick start will assume you have a directory with one or more Common Workflow Language YAML files. If no such directory is available, one can be quickly created for demonstrating planemo as follows planemo project_init --template=seqtk_complete_cwl mytools; cd mytools.

Planemo can check tools YAML files for common problems and best practices using the lint command (also aliased as l).

Like many planemo commands - by default this will search the current directory and use all tool files it finds. It can be explicitly passed a path to tool files or a directory of tool files.

The lint command takes in additional options related to reporting levels, exit code, etc. These options are described in the docs or (like with all commands) can be accessed by passing --help to it.

Once tools are syntactically correct - it is time to test. The test command can be used to test a CWL tool, workflow, or a directories thereof.
Planemo will create a HTML output report in the current directory named `tool_test_output.html`. Check out the file `seqtk_seq_tests.yml` for an example of Planemo test for a CWL tool. A test consists of any number of jobs (with input descriptions) and corresponding output assertions.

Checkout the Common Workflow User Guide for more information on developing CWL tools in general and Building Common Workflow Language Tools for more information on using Planemo to develop CWL tools.

## 1.4 Tool Shed

Planemo can help you publish tools to the Galaxy Tool Shed. Check out Publishing to the Tool Shed for more information.

## 1.5 Conda

Planemo can help develop tools and Conda packages in unison. Check out the Galaxy or CWL version of the “Dependencies and Conda” tutorial for more information.

## 1.6 Docker and Containers

Planemo can help develop tools that run in “Best Practice” containers for scientific workflows. Check out the Galaxy or CWL version of the “Dependencies and Containers” tutorial for more information.
2.1 pip

For a traditional Python 2 installation of Planemo, first set up a virtualenv for planemo (this example creates a new one in .venv) and then install with pip. Planemo requires pip 7.0 or newer.

```
$ virtualenv .venv; . .venv/bin/activate
$ pip install "pip>=7" # Upgrade pip if needed.
$ pip install planemo
```

When installed this way, planemo can be upgraded as follows:

```
$ . .venv/bin/activate
$ pip install -U planemo
```

To install or update to the latest development branch of planemo with pip, use the following `pip install idiom` instead:

```
$ pip install -U git+git://github.com/galaxyproject/planemo.git
```

If your PATH contains a Python installed through Conda it should likely not be used to run Planemo, consider using the `virtualenv` argument `-p` to point at a non-Conda Python 2 executable installed natively on your system or using a tool such as `pyenv`. `virtualenv` can be installed via Conda, `pyenv`, or a package manager - it should make no difference.

Planemo in theory runs under Python 3 but Galaxy does not, so it is best to use a Python 2 with Planemo for now.

2.2 Conda (Experimental)

Another approach for installing Planemo is to use Conda (most easily obtained via the Miniconda Python distribution). Afterwards run the following commands.
 Galaxy is known to have issues when running with a Conda Python so this approach should be considered experimental for now. If you have problems with it or hacks to make it work better - please report them.
See the --help or the documentation for a detailed list of individual options for each command. Certain options that make sense for multiple commands or tools suites can be declared instead globally by placing them in a .planemo.yml file in your home directory.

Below is an annotated outline of some of the options that can be set in this file.

```yaml
# Specify a default galaxy_root for the `test` and `serve` commands here.
galaxy_root: /home/user/galaxy

# Specify github credentials for publishing gist links (e.g. with the `share_test` command).
github:
  username: <username>
  password: <password>

sheds:
  # For each Tool Shed you wish to target enter the API key or both email and password.
  toolshed:
    key: "<TODO>"
    # email: "<TODO>"
    # password: "<TODO>"
  testtoolshed:
    key: "<TODO>"
    # email: "<TODO>"
    # password: "<TODO>"
  local:
    key: "<TODO>"
    # email: "<TODO>"
    # password: "<TODO>"
  custom_shed:
    key: "<TODO>"
    url: "http://customurl/"
    # email: "<TODO>"
    # password: "<TODO>"
```
You can use Planemo as part of a Galaxy tool development virtual appliance which comes pre-configured with Planemo, Galaxy, Docker, Conda, a local Tool Shed, linuxbrew, Komodo and Atom editors.

4.1 Quick Links

If you already know what to do. Otherwise please read on.

- Planemo OVA image: https://images.galaxyproject.org/planemo/latest.ova
- docker run -p 8010:80 -p 9009:9009 -v `pwd`:/opt/galaxy/tools -i -t planemo/interactive This assumes your tools are in your current working directory (replace ‘pwd’ with a path to your tools if this is not the case).

4.2 The Setup

The Galaxy instance that runs in these appliances has been optimized for tool development - Galaxy will monitor your tool directory for changes and reload the tools as they are modified, the server will directly log you into Galaxy as an admin (no need to worry about user management or configuration), Galaxy is configured to use a PostgreSQL database, and execute jobs via SLURM for robustness. If something goes wrong and Galaxy needs to be restarted manually - run restart_galaxy from the command-line.

The virtual appliance is available in four flavors via open virtualization format (OVA, .ova), Docker, Vagrant, and as a Google Compute Engine cloud image.

The OVA image is a stable way to boot a Planemo virtual machine on any platform and comes with a pre-configured Xubuntu-based windowed operating system with graphical editing tools including Komodo and Atom editors. This approach can be thought of more as a complete environment and may be better for tutorials and workshops where consistent user experience is more important.
The Docker and Vagrant versions make it trivial to mount an external directory in the appliance so that one can use their own development tools (such as editors). These can be used in traditional development environments with existing tools and will probably be the preference of power users whereas.

The Google Compute Engine variant is ideal when local compute resources are unavailable or insufficient.

### 4.3 Launching the Appliance

The following sections will describe how to launch the appliance using various platforms.

#### 4.3.1 Launching the Appliance (VirtualBox - OVA)

The VirtualBox OVA variant of the Planemo appliance comes preconfigured with a full windowed development environment (based on Xubuntu). Encompassing the complete environment means it is easier to setup and provides an identical experience for every developer using it. These make the OVA image ideal for tutorials and workshops.

The latest VirtualBox version of the planemo appliance can be found [here](#).

Please download and install VirtualBox. When VirtualBox has been installed - the planemo machine can be imported by downloading the latest image and double clicking the resulting file. This should result in VirtualBox being opened to an import screen. Just follow the prompt and the machine should become available.
When the import is finished (and before starting the VM), right-click on the new appliance and select “Settings”:

1. in the “General” -> “Advanced” tab, select “Bidirectional” for “Shared Clipboard”
2. in the “Display” -> “Screen” tab, tick “Enable 3D Acceleration”
3. in the “Network” -> “Adapter 1” tab, select “PCnet-FAST III (Am79c973)” as “Adapter Type”
4. Click the “OK” button

Now start the appliance by clicking the “Start” button.

The Firefox browser, Komodo and Atom editors, Galaxy, Planemo and everything else is available right away on the desktop along with useful links.

4.3. Launching the Appliance

Various relevant applications are available under the Xubuntu menu which has the following icon.
4.3.2 Launching the Appliance (Docker)

There are two variants of the Docker appliance - one is specifically designed for Kitematic a GUI application available for Mac OS X and Windows that claims to be “the easiest way to start using Docker” and the other is designed to be used with a command-prompt available under Linux or in Mac OS X and Windows when using boot2docker.

Server Edition (for Kitematic)

To get started with Kitematic, please download it if it hasn’t been previously installed and then launch it. Wait for Kitematic to load and search for planemo/server.

Once Kitematic has downloaded, you can use the search bar at the top to locate planemo/server

There may be several Planemo containers discovered - be sure to pick the planemo/server one with the experience optimized for Kitematic. Choose to create this image and it will download.
After a minute or so, you should see logs for the running container appear in the main window.
Galaxy will now be available by clicking the link in the Web Preview section of the GUI.

Clicking the Exec button in the container’s tool bar (at the top, middle of the screen) will launch a root command-prompt. Planemo is configured for the **ubuntu** user - so the first thing you should do is launch an **ubuntu** login session by entering the command **su - ubuntu**.
Interactive Edition

The interactive edition of the Planemo Docker image is designed for environments where the `docker` command-line tool is available. This can easily be installed via package managers under Linux - but for Windows and Mac OS X - `boot2docker` should be installed and launched in order to run these commands.

The Docker version of the planemo appliance can be launched using the following command (which will pull the appliance down from Docker Hub).

```bash
$ docker run -p 8010:80 -p 9009:9009 -v `pwd`:/opt/galaxy/tools -i -t planemo/interactive
```

This command will start Galaxy and various other services and then open a bash shell with Planemo available. This
assumes your tools are in your current working directory (just replace ‘pwd’ with a path to your tools if this is not the case).

Docker commands such as `ps` and `kill` can be used to manage this Docker container.

This Docker environment will contain your tools and modifications made to them will be made directly to your filesystem - so they are persistent. Data loaded into the Galaxy instance (history data for instance) will be lost when the Docker container is stopped. Check out the `docker-galaxy-stable` project for information on running persistent Galaxy processes in Docker.

### 4.3.3 Launching the Appliance (Vagrant)

*The image for this way of launching the appliance is outdated. Please use a different one.*

The latest Vagrant version of the planemo appliance can be found [here](#). Once you have installed Vagrant (download now), the appliance can be enabled by first creating a `Vagrantfile` in your tool directory - the following demonstrates an example of such file.

```ruby
VAGRANTFILE_API_VERSION = "2"

Vagrant.configure(VAGRANTFILE_API_VERSION) do |config|
  config.vm.box = "planemo"
  config.vm.box_url = "https://images.galaxyproject.org/planemo/latest.box"
  config.ssh.username = "ubuntu"

  # Forward nginx and tool shed.
  config.vm.network "forwarded_port", guest: 80, host: 8010
  config.vm.network "forwarded_port", guest: 9009, host: 9009

  # Disable default mount and mount pwd to /opt/galaxy/tools instead.
  config.vm.synced_folder ".", "/vagrant", disabled: true
  config.vm.synced_folder ".", "/opt/galaxy/tools", owner: "ubuntu"

  # config.vm.provider "virtualbox" do |vb|
  #   # Don't boot with headless mode
  #   vb.gui = true
  #   #
  #   # Use VBoxManage to customize the VM. For example to change memory:
  #   # vb.customize ["modifyvm", :id, "--memory", "1024"]
  # end
end
```

This file must literally be named `Vagrantfile`. Next you will need to startup the appliance. This is as easy as

```
vagrant up
```

Once the virtual server has booted up completely, Galaxy will be available at `http://localhost:8010`, the Codebox IDE will be available `http://localhost:8010/ide/`, and the local Tool Shed at `http://localhost:9009`.

### 4.3.4 Launching the Appliance (Google Compute Engine)

*The image for this way of launching the appliance is outdated. Please use a different one.*

The GCE version of the appliance is different in that it doesn’t run locally on your computer, but on a remote ‘cloud’ machine. Using this variant of the appliance requires a Google Cloud Platform account with an active payment method.
The first thing you’ll want to do is get the gcloud administration utility installed and configured. Once you’ve installed gcloud, you can authenticate and (optionally) set your default project, zone, and region (example below, but you should choose whatever region and zone are appropriate for your location). If you set these defaults, you will not have to supply them to all subsequent commands.

```
$ gcloud auth login
$ gcloud config set project YOUR-PROJECT-NAME
$ gcloud config set compute/region us-central1 (replace us-central1 with another region if desired)
$ gcloud config set compute/zone us-central1-f (same for the zone us-central1-f)
```

Import the image to your account with the following statement. This will only need to be done one time, unless you delete the image from your account.

```
```

To launch the image as a fresh instance, use the following command. This command will, upon completion, display an external IP address that you can navigate to in your web browser.

```
$ gcloud compute instances create planemo --machine-type n1-standard-2 --image planemo-machine --tags http-server
```

If you’d like to SSH in to the instance at this point, it’s easy to do with:

```
$ gcloud compute ssh planemo
```

### 4.4 Building the Appliance

These appliances are built using the planemo-machine project which can be used to build customized recipes of this nature or even appliance for cloud environments such as Amazon Web Services and Google Compute Engine.
The following links are for the same tutorial describing the basics of how to build Galaxy tools. The first variant is tailored to local development environments (e.g. if Planemo has been installed with `brew` or `pip`) and the second is for developers using a dedicated Planemo virtual appliance (available as OVA, Docker, Vagrant, etc.).

5.1 Building Galaxy Tools Using Planemo

This tutorial is a gentle introduction to writing Galaxy tools using Planemo. Please read the installation instructions for Planemo if you have not already installed it.

5.1.1 The Basics

This guide is going to demonstrate building up tools for commands from Heng Li’s Seqtk package - a package for processing sequence data in FASTA and FASTQ files.

To get started let’s install Seqtk. Here we are going to use conda to install Seqtk - but however you obtain it should be fine.

```
$ conda install --force --yes -c conda-forge -c bioconda seqtk=1.2
... seqtk installation ...
$ seqtk seq
```

Usage: seqtk seq [options] <in.fq>|<in.fa>

Options: -q INT  mask bases with quality lower than INT [0]
-X INT  mask bases with quality higher than INT [255]
-n CHAR  masked bases converted to CHAR; 0 for lowercase [0]
-l INT  number of residues per line; 0 for 2^32-1 [0]
-Q INT  quality shift: ASCII-INT gives base quality [33]
-s INT  random seed (effective with -f) [11]
-f FLOAT  sample FLOAT fraction of sequences [1]
-M FILE  mask regions in BED or name list FILE [null]
-L INT  drop sequences with length shorter than INT [0]
-c  mask complement region (effective with -M)

(continues on next page)
Next we will download an example FASTQ file and test out the a simple Seqtk command - seq which converts FASTQ files into FASTA.

```bash
$ wget https://raw.githubusercontent.com/galaxyproject/galaxy-test-data/master/2.fastq
$ seqtk seq -A 2.fastq > 2.fasta
$ cat 2.fasta
>chr1_50392_50392
>chr1_50462_50462
```

For fully featured Seqtk wrappers check out Helena Rasche’s wrappers on GitHub.

Galaxy tool files are just XML files, so at this point one could open a text editor and start writing the tool. Planemo has a command tool_init to quickly generate some of the boilerplate XML, so let’s start by doing that.

```bash
$ planemo tool_init --id 'seqtk_seq' --name 'Convert to FASTA (seqtk)'
```

The tool_init command can take various complex arguments - but the two most basic ones are shown above --id and --name. Every Galaxy tool needs an id (this is a short identifier used by Galaxy itself to identify the tool) and a name (this is displayed to the Galaxy user and should be a short description of the tool). A tool’s name can have whitespace but its id must not.

The above command will generate the file seqtk_seq.xml - which looks like this.

```xml
<tool id="seqtk_seq" name="Convert to FASTA (seqtk)" version="0.1.0">
  <requirements>
  </requirements>
  <command detect_errors="exit_code">
    <![CDATA[
      TODO: Fill in command template.
    ]]></command>
  </inputs>
  <outputs>
    </outputs>
  <help><![CDATA[
    TODO: Fill in help.
  ]]]></help>
</tool>
```

This tool file has the common sections required for a Galaxy tool but you will still need to open up the editor and fill out the command template, describe input parameters, tool outputs, write a help section, etc.

The tool_init command can do a little bit better than this as well. We can use the test command we tried above seqtk seq -a 2.fastq > 2.fasta as an example to generate a command block by specifying the inputs and the outputs as follows.
This will generate the following XML file - which now has correct definitions for the input and output as well as an actual command template.

```xml
<tool id="seqtk_seq" name="Convert to FASTA (seqtk)" version="0.1.0">
    <requirements>
        <requirement type="package" version="1.2">seqtk</requirement>
    </requirements>
    <command detect_errors="exit_code">
        <![CDATA[
            seqtk seq -a '$input1' > '$output1'
        ]]>\n    </command>
    <inputs>
        <param type="data" name="input1" format="fastq"/>
    </inputs>
    <outputs>
        <data name="output1" format="fasta"/>
    </outputs>
    <help><![CDATA[
        TODO: Fill in help.
        ]]>\n</tool>
```

As shown at the beginning of this section, the command `seqtk seq` generates a help message for the `seq` command. `tool_init` can take that help message and stick it right in the generated tool file using the `help_from_command` option.

Generally command help messages aren’t exactly appropriate for tools since they mention argument names and simillar details that are abstracted away by the tool - but they can be an excellent place to start.

The following Planemo’s `tool_init` call has been enhanced to use `--help_from_command`.

```bash
$ planemo tool_init --force \
    --id 'seqtk_seq' \
    --name 'Convert to FASTA (seqtk)' \
    --requirement seqtk@1.2 \
    --example_command 'seqtk seq -a 2.fastq > 2.fasta' \
    --example_input 2.fastq \
    --example_output 2.fasta \
    --help_from_command 'seqtk seq'
```

In addition to demonstrating `--help_from_command`, this demonstrates generating a test case from our example with `--test_case` and adding a citation for the underlying tool. The resulting tool XML file is:

```xml
<tool id="seqtk_seq" name="Convert to FASTA (seqtk)" version="0.1.0">
    <requirements>
        <requirement type="package" version="1.2">seqtk</requirement>
    </requirements>
    <command detect_errors="exit_code">
        <![CDATA[
            seqtk seq -a '$input1' > '$output1'
        ]]>\n    </command>
    <inputs>
        <param type="data" name="input1" format="fastq"/>
    </inputs>
    <outputs>
        <data name="output1" format="fasta"/>
    </outputs>
    <help><![CDATA[
        TODO: Fill in help.
        ]]>\n</tool>
```

(continues on next page)
At this point we have a fairly functional Galaxy tool with test and help. This was a pretty simple example - usually you will need to put more work into the tool to get to this point - `tool_init` is really just designed to get you started.

Now let's lint and test the tool we have developed. The Planemo's `lint` (or just `l`) command will review tool for XML validity, obvious mistakes, and compliance with IUC best practices.
By default `lint` will find all the tools in your current working directory, but we could have specified a particular tool with `planemo lint seqtk_seq.xml`.

Next we can run our tool’s functional test with the `test` (or just `t`) command. This will print a lot of output (as it starts a Galaxy instance) but should ultimately reveal our one test passed.

```bash
$ planemo test ...
All 1 test(s) executed passed.
seqtk_seq[0]: passed
```

In addition to the in console display of test results as red (failing) or green (passing), Planemo also creates an HTML report for the test results by default. Many more test report options are available such as `--test_output_xunit` which is useful in certain continuous integration environments. See `planemo test --help` for more options, as well as the `test_reports` command.

Now we can open Galaxy with the `serve` (or just `s`).

```bash
$ planemo serve ...
serving on http://127.0.0.1:9090
```

Open up [http://127.0.0.1:9090](http://127.0.0.1:9090) in a web browser to view your new tool.

Serve and test can be passed various command line arguments such as `--galaxy_root` to specify a Galaxy instance to use (by default `planemo` will download and manage an instance just for planemo).

### 5.1.2 Simple Parameters

We have built a tool wrapper for the `seqtk seq` command - but this tool actually has additional options that we may wish to expose the Galaxy user.

Let’s take a few of the parameters from the help command and build Galaxy `param` blocks to stick in the tool’s `inputs` block.

- `-V` shift quality by `'(\text{-Q}) - 33'`
In the previous section we saw `param` block of type `data` for input files, but there are many different kinds of parameters one can use. Flag parameters such as the above `-V` parameter are frequently represented by `boolean` parameters in Galaxy tool XML.

```xml
<param name="shift_quality" type="boolean" label="Shift quality"
  truevalue="-V" falsevalue=""
  help="shift quality by '-Q - 33' (-V)" />
```

We can then stick `$shift_quality` in our `command` block and if the user has selected this option it will be expanded as `-V` (since we have defined this as the `truevalue`). If the user hasn’t selected this option `$shift_quality` will just expand as an empty string and not affect the generated command line.

Now consider the following `seqtk seq` parameters:

- `-q INT` mask bases with quality lower than INT [0]
- `-X INT` mask bases with quality higher than INT [255]

These can be translated into Galaxy parameters as:

```xml
<param name="quality_min" type="integer" label="Mask bases with quality lower than"
  value="0" min="0" max="255" help="(-q)" />
<br />
<param name="quality_max" type="integer" label="Mask bases with quality higher than"
  value="255" min="0" max="255" help="(-X)" />
```

These can be add to the command tag as `-q $quality_min -X $quality_max`.

At this point the tool would look like:

```xml
<tool id="seqtk_seq" name="Convert to FASTA (seqtk)" version="0.1.0">
  <requirements>
    <requirement type="package" version="1.2">seqtk</requirement>
  </requirements>
  <command detect_errors="exit_code">
    <![CDATA[
    seqtk seq
    $shift_quality
    -q $quality_min
    -X $quality_max
    -a "'$input1' > '$output1'"
    ]]></command>
  <inputs>
    <param type="data" name="input1" format="fastq" />
    <param name="shift_quality" type="boolean" label="Shift quality"
      truevalue="-V" falsevalue=""
      help="shift quality by '-Q - 33' (-V)" />
    <param name="quality_min" type="integer" label="Mask bases with quality lower than"
      value="0" min="0" max="255" help="(-q)" />
    <param name="quality_max" type="integer" label="Mask bases with quality higher than"
      value="255" min="0" max="255" help="(-X)" />
  </inputs>
  <outputs>
    <data name="output1" format="fasta" />
  </outputs>
  <tests>
    <test>
      <param name="input1" value="2.fastq"/>
      <output name="output1" file="2.fasta"/>
    </test>  
  </tests>
</tool>
```
Usage: seqtk seq [options] <in.fq>|<in.fa>

Options: -q INT mask bases with quality lower than INT [0]
-X INT mask bases with quality higher than INT [255]
-n CHAR masked bases converted to CHAR; 0 for lowercase [0]
-l INT number of residues per line; 0 for 2^32−1 [0]
-Q INT quality shift: ASCII-INT gives base quality [33]
-s INT random seed (effective with -f) [11]
-f FLOAT sample FLOAT fraction of sequences [1]
-M FILE mask regions in BED or name list FILE [null]
-L INT drop sequences with length shorter than INT [0]
-c mask complement region (effective with -M)
-r reverse complement
-A force FASTA output (discard quality)
-C drop comments at the header lines
-N drop sequences containing ambiguous bases
-1 output the 2n-1 reads only
-2 output the 2n reads only
-V shift quality by '(-Q) - 33'
-U convert all bases to uppercases

5.1.3 Conditional Parameters

The previous parameters were simple because they always appeared, now consider.

We can mark this data type param as optional by adding the attribute optional="true".

Then instead of just using $mask_regions directly in the command block, one can wrap it in an if statement (because tool XML files support Cheetah).
Next consider the parameters:

```
-s INT    random seed (effective with -f) [11]
-f FLOAT  sample FLOAT fraction of sequences [1]
```

In this case, the -s random seed parameter should only be seen or used if the sample parameter is set. We can express this using a conditional block.

```
<conditional name="sample">
  <param name="sample_selector" type="boolean" label="Sample fraction of sequences">
  
  <param name="fraction" label="Fraction" type="float" value="1.0" help="(-f)" />
  <param name="seed" label="Random seed" type="integer" value="11" help="(-s)" />
  </when>
  <when value="false">
  </when>
</conditional>
```

In our command block, we can again use an if statement to include these parameters.

```
#if $sample.sample_selector
  -f $sample.fraction -s $sample.seed
#endif
```

Notice we must reference the parameters using the sample. prefix since they are defined within the sample conditional block.

The newest version of this tool is now

```
<tool id="seqtk_seq" name="Convert to FASTA (seqtk)" version="0.1.0">
  <requirements>
    <requirement type="package" version="1.2">seqtk</requirement>
  </requirements>
  <command detect_errors="exit_code">
    <![CDATA[
      seqtk seq
      -s $shift_quality
      -q $quality_min
      -X $quality_max
      #if $mask_regions
        -M '$mask_regions'
      #end if
      #if $sample.sample
        -f $sample.fraction
        -s $sample.seed
      #end if
      -a '$input1' > '$output1'
    ]]>"
  </command>
  <inputs>
    <param type="data" name="input1" format="fastq" />
    <param name="shift_quality" type="boolean" label="Shift quality" />
  </inputs>
</tool>
```
truevalue="-V" falsevalue=""  
help="shift quality by '(-Q) - 33' (-V)" />
<param name="quality_min" type="integer" label="Mask bases with quality lower than"
value="0" min="0" max="255" help="(-q)" />
<param name="quality_max" type="integer" label="Mask bases with quality higher than"
value="255" min="0" max="255" help="(-X)" />
<param name="mask_regions" type="data" label="Mask regions in BED" format="bed" help="(-M)" optional="true" />
<conditional name="sample">
  <param name="sample" type="boolean" label="Sample fraction of sequences" />
  <when value="true">
    <param name="fraction" label="Fraction" type="float" value="1.0" help="(-f)" />
    <param name="seed" label="Random seed" type="integer" value="11" help="(-s)" />
  </when>
  <when value="false">
  </when>
</conditional>
</inputs>
<outputs>
  <data name="output1" format="fasta" />
</outputs>
<tests>
  <test>
    <param name="input1" value="2.fastq" />
    <output name="output1" file="2.fasta" />
  </test>
</tests>
</help>

Usage:  seqtk seq [options] <in.fq>|<in.fa>

Options:  -q INT  mask bases with quality lower than INT [0]
-X INT  mask bases with quality higher than INT [255]
-n CHAR  masked bases converted to CHAR; 0 for lowercase [0]
-l INT  number of residues per line; 0 for 2^32-1 [0]
-Q INT  quality shift: ASCII-INT gives base quality [33]
-s INT  random seed (effective with -f) [11]
-f FLOAT  sample FLOAT fraction of sequences [1]
-M FILE  mask regions in BED or name list FILE [null]
-L INT  drop sequences with length shorter than INT [0]
-c  mask complement region (effective with -M)
-r  reverse complement
-A  force FASTA output (discard quality)
-C  drop comments at the header lines
-N  drop sequences containing ambiguous bases
-1  output the 2n-1 reads only
-2  output the 2n reads only
-V  shift quality by '(-Q) - 33'
-U  convert all bases to uppercases

]]>

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For tools like this where there are many options but in the most uses the defaults are preferred - a common idiom is to break the parameters into simple and advanced sections using a conditional.

Updating this tool to use that idiom might look as follows.

```
<tool id="seqtk_seq" name="Convert to FASTA (seqtk)" version="0.1.0">
  <requirements>
    <requirement type="package" version="1.2">seqtk</requirement>
  </requirements>
  <command detect_errors="exit_code">
    <![CDATA[
      seqtk seq
      #if $settings.advanced == "advanced"
      $settings.shift_quality
      -q $settings.quality_min
      -X $settings.quality_max
      #if $settings.mask_regions
      -M "'$settings.mask_regions'"
      #end if
      #if $settings.sample.sample
      -f $settings.sample.fraction
      -s $settings.sample.seed
      #end if
      #end if
      -a "'$input1'" > "'$output1'"
    ]]></command>
  </command>
  <inputs>
    <param type="data" name="input1" format="fastq" />
    <conditional name="settings">
      <param name="advanced" type="select" label="Specify advanced parameters">
        <option value="simple" selected="true">No, use program defaults.</option>
        <option value="advanced">Yes, see full parameter list.</option>
      </param>
      <when value="simple"> </when>
      <when value="advanced">
        <param name="shift_quality" type="boolean" label="Shift quality">
          <truevalue="-V" falsevalue="" help="shift quality by '(-Q) - 33' (-V)" />
        </param>
        <param name="quality_min" type="integer" label="Mask bases with quality lower than">
          <value min="0" max="255" help="(-q)" />
        </param>
        <param name="quality_max" type="integer" label="Mask bases with quality higher than">
          <value min="0" max="255" help="(-q)" />
        </param>
      </when>
    </conditional>
  </inputs>
</tool>
```
Planemo Documentation, Release 0.61.0.dev0

Usage: seqtk seq [options] <in.fq>|<in.fa>

Options:
- -q INT    mask bases with quality lower than INT [0]
- -X INT    mask bases with quality higher than INT [255]
- -n CHAR   masked bases converted to CHAR; 0 for lowercase [0]
- -l INT    number of residues per line; 0 for 2^32-1 [0]
- -Q INT    quality shift: ASCII-INT gives base quality [33]
- -s INT    random seed (effective with -f) [11]
- -f FLOAT  sample FLOAT fraction of sequences [1]
- -M FILE   mask regions in BED or name list FILE [null]
- -L INT    drop sequences with length shorter than INT [0]
- -c        mask complement region (effective with -M)
- -r        reverse complement
- -A        force FASTA output (discard quality)
- -C        drop comments at the header lines
- -N        drop sequences containing ambiguous bases
- -1        output the 2n-1 reads only
- -2        output the 2n reads only
- -V        shift quality by '(-Q) - 33'
- -U        convert all bases to uppercases

}}></help>

5.1. Building Galaxy Tools Using Planemo
5.1.4 Wrapping a Script

Many common bioinformatics applications are available on the Tool Shed already and so a common development task is to integrate scripts of various complexity into Galaxy.

Consider the following small Perl script.

```perl
#!/usr/bin/perl -w

# usage : perl toolExample.pl <FASTA file> <output file>

open (IN, "<$ARGV[0]");
open (OUT, ">$ARGV[1]");
while (<IN>) {
    chop;
    if (m/^>/) {
        s/^>//;
        if ($_. > 1) {
            print OUT sprintf("%.3f", $gc/$length) . "\n";
        }
        $gc = 0;
        $length = 0;
    } else {
        ++$gc while m/[gc]/ig;
        $length += length $_;
    }
}
print OUT sprintf("%.3f", $gc/$length) . "\n";
close( IN );
close( OUT );
```

One can build a tool for this script as follows and place the script in the same directory as the tool XML file itself. The special value `__tool_directory__` here refers to the directory your tool lives in.

```xml
<tool id="gc_content" name="Compute GC content">
    <command>perl $__tool_directory__/gc_content.pl '$input' output.tsv</command>
    <inputs>
        <param name="input" type="data" format="fasta" label="Source file"/>
    </inputs>
    <outputs>
        <data name="output" format="tabular" from_work_dir="output.tsv" />
    </outputs>
    <help>
    This tool computes GC content from a FASTA file.
    </help>
</tool>
```

(continues on next page)
5.1.5 Macros

If your desire is to write a tool for a single relatively simple application or script - this section should be skipped. If you hope to maintain a collection of related tools - experience suggests you will realize there is a lot of duplicated XML to do this well. Galaxy tool XML macros can help reduce this duplication.

Planemo's `tool_init` command can be used to generate a macro file appropriate for suites of tools by using the `--macros` flag. Consider the following variant of the previous `tool_init` command (the only difference is now we are adding the `--macros` flag).

```bash
$ planemo tool_init --force \
   --macros \
   --id 'seqtk_seq' \
   --name 'Convert to FASTA (seqtk)' \
   --requirement seqtk@1.2 \
   --example_command 'seqtk seq -A 2.fastq > 2.fasta' \
   --example_input 2.fastq \
   --example_output 2.fasta \
   --test_case \
   --help_from_command 'seqtk seq'
```

This will produce the two files in your current directory instead of just one - `seqtk_seq.xml` and `macros.xml`.

```xml
<tool id="seqtk_seq" name="Convert to FASTA (seqtk)" version="0.1.0">
  <macros>
    <import>macros.xml</import>
  </macros>
  <expand macro="requirements" />
  <command detect_errors="exit_code"> <![CDATA[
    seqtk seq -a "$input1" > "$output1"
  ]]></command>
  <inputs>
    <param type="data" name="input1" format="fastq" />
  </inputs>
  <outputs>
    <data name="output1" format="fasta" />
  </outputs>
  <tests>
    <test>
      <param name="input1" value="2.fastq"/>
      <output name="output1" file="2.fasta"/>
    </test>
  </tests>
  <help><![CDATA[
Usage: seqtk seq [options] <in.fq>|<in.fa>

Options: -q INT mask bases with quality lower than INT [0]
-X INT mask bases with quality higher than INT [255]
-n CHAR masked bases converted to CHAR; 0 for lowercase [0]
-l INT number of residues per line; 0 for 2^32-1 [0]
-Q INT quality shift: ASCII-INT gives base quality [33]
]]></CDATA>
```

(continues on next page)
-s INT random seed (effective with -f) [11]
-f FLOAT sample FLOAT fraction of sequences [1]
-M FILE mask regions in BED or name list FILE [null]
-L INT drop sequences with length shorter than INT [0]
-c mask complement region (effective with -M)
-r reverse complement
-A force FASTA output (discard quality)
-C drop comments at the header lines
-N drop sequences containing ambiguous bases
-l output the 2n−1 reads only
-2 output the 2n reads only
-V shift quality by \((-Q) - 33\)
5.2 Building Galaxy Tools (Using the Planemo Appliance)

This tutorial is a gentle introduction to writing Galaxy tools using the Planemo virtual appliance (available as OVA, Docker and Vagrant). Check out these instructions for obtaining the virtual appliance if you have not done so already.

**Note:** Please note that you can leverage the clipboard for sharing text between the virtual image environment and your host system. To copy in the VM terminal use `ctrl + shift + C` and to paste use `ctrl + shift + V`. To copy in the VM Firefox browser use `ctrl + C`. Use the corresponding commands on your host system (e.g. `Command + C` on MacOS).

### 5.2.1 The Basics

This guide is going to demonstrate building up tools for commands from Heng Li’s Seqtk package - a package for processing sequence data in FASTA and FASTQ files.

To get started let’s install Seqtk. Here we are going to use conda to install Seqtk - but however you obtain it should be fine.

```bash
$ conda install --force --yes -c conda-forge -c bioconda seqtk=1.2
... seqtk installation ...
$ seqtk seq
```

#### Usage:
```
seqtk seq [options] <in.fq>|<in.fa>
```

#### Options:
- `-q INT` mask bases with quality lower than INT [0]
- `-X INT` mask bases with quality higher than INT [255]
- `-n CHAR` masked bases converted to CHAR; 0 for lowercase [0]
- `-l INT` number of residues per line; 0 for 2^32-1 [0]
- `-Q INT` quality shift: ASCII-INT gives base quality [33]
- `-s INT` random seed (effective with -f) [11]
- `-f FLOAT` sample FLOAT fraction of sequences [1]
- `-M FILE` mask regions in BED or name list FILE [null]
- `-L INT` drop sequences with length shorter than INT [0]
- `-c` mask complement region (effective with -M)
- `-r` reverse complement
- `-A` force FASTA output (discard quality)
- `-C` drop comments at the header lines
- `-N` drop sequences containing ambiguous bases
- `-1` output the 2n-1 reads only
- `-2` output the 2n reads only
- `-V` shift quality by `(-Q) - 33`

Next we will download an example FASTQ file and test out the a simple Seqtk command - `seq` which converts FASTQ files into FASTA.

```bash
$ wget https://raw.githubusercontent.com/galaxyproject/galaxy-test-data/master/2.fastq
$ seqtk seq -A 2.fastq > 2.fasta
$ cat 2.fasta
>BB9F7_C7L_1_0_111_175
>BB9F7_C1L_1_0_111_175
>BB9F7_C2L_1_0_111_175
>BB9F7_C3L_1_0_111_175
>BB9F7_C4L_1_0_111_175
>BB9F7_C5L_1_0_111_175
```

For fully featured Seqtk wrappers check out Helena Rasche’s wrappers on GitHub.
Galaxy tool files are just XML files, so at this point one could open a text editor and start writing the tool. Planemo has a command `tool_init` to quickly generate some of the boilerplate XML, so let’s start by doing that.

```bash
$ planemo tool_init --id 'seqtk_seq' --name 'Convert to FASTA (seqtk)'
```

The `tool_init` command can take various complex arguments - but the two most basic ones are shown above --id and --name. Every Galaxy tool needs an **id** (this is a short identifier used by Galaxy itself to identify the tool) and a **name** (this is displayed to the Galaxy user and should be a short description of the tool). A tool’s **name** can have whitespace but its **id** must not.

The above command will generate the file `seqtk_seq.xml` - which looks like this.

```
<tool id="seqtk_seq" name="Convert to FASTA (seqtk)" version="0.1.0">
  <requirements>
    <requirement type="package" version="1.2">seqtk</requirement>
  </requirements>
  <command detect_errors="exit_code"> <![CDATA[
    TODO: Fill in command template.
  ]]> </command>
  <inputs>
    <param type="data" name="input1" format="fastq" />
  </inputs>
  <outputs>
    <data name="output1" format="fasta" />
  </outputs>
</tool>
```

This tool file has the common sections required for a Galaxy tool but you will still need to open up the editor and fill out the command template, describe input parameters, tool outputs, write a help section, etc.

The `tool_init` command can do a little bit better than this as well. We can use the test command we tried above `seqtk seq -a 2.fastq > 2.fasta` as an example to generate a command block by specifying the inputs and the outputs as follows.

```bash
$ planemo tool_init --force 
 --id 'seqtk_seq' 
 --name 'Convert to FASTA (seqtk)'
 --requirement seqtk@1.2 
 --example_command 'seqtk seq -a 2.fastq > 2.fasta' 
 --example_input 2.fastq 
 --example_output 2.fasta
```

This will generate the following XML file - which now has correct definitions for the input and output as well as an actual command template.

```
<tool id="seqtk_seq" name="Convert to FASTA (seqtk)" version="0.1.0">
  <requirements>
    <requirement type="package" version="1.2">seqtk</requirement>
  </requirements>
  <command detect_errors="exit_code"> <![CDATA[
    seqtk seq -a '$input1' > '$output1'
  ]]> </command>
  <inputs>
    <param type="data" name="input1" format="fastq" />
  </inputs>
  <outputs>
    <data name="output1" format="fasta" />
  </outputs>
</tool>
```
As shown at the beginning of this section, the command `seqtk seq` generates a help message for the `seq` command. `tool_init` can take that help message and stick it right in the generated tool file using the `help_from_command` option.

Generally command help messages aren’t exactly appropriate for tools since they mention argument names and similar details that are abstracted away by the tool - but they can be an excellent place to start.

The following Planemo’s `tool_init` call has been enhanced to use `--help_from_command`.

```
$ planemo tool_init --force \
  --id 'seqtk_seq' \
  --name 'Convert to FASTA (seqtk)' \
  --requirement seqtk@1.2 \
  --example_command 'seqtk seq -a 2.fastq > 2.fasta' \
  --example_input 2.fastq \
  --example_output 2.fasta \
  --test_case \
  --cite_url 'https://github.com/lh3/seqtk' \
  --help_from_command 'seqtk seq'
```

In addition to demonstrating `--help_from_command`, this demonstrates generating a test case from our example with `--test_case` and adding a citation for the underlying tool. The resulting tool XML file is:

```
<tool id="seqtk_seq" name="Convert to FASTA (seqtk)" version="0.1.0">
  <requirements>
    <requirement type="package" version="1.2">seqtk</requirement>
  </requirements>
  <command detect_errors="exit_code">
    <![CDATA[
      seqtk seq -a '$input1' > '$output1'
    ]]> </command>
  <inputs>
    <param type="data" name="input1" format="fastq" />
  </inputs>
  <outputs>
    <data name="output1" format="fasta" />
  </outputs>
  <tests>
    <test>
      <param name="input1" value="2.fastq"/>
      <output name="output1" file="2.fasta"/>
    </test>
  </tests>
  <help><![CDATA[
    Usage: seqtk seq [options] <in.fq>|<in.fa>
    
    Options: 
    -q INT mask bases with quality lower than INT [0]
    -X INT mask bases with quality higher than INT [255]
    -n CHAR masked bases converted to CHAR; 0 for lowercase [0]
    -1 INT number of residues per line; 0 for 2^32-1 [0]
    -O INT quality shift: ASCII-INT gives base quality [33]
    -s INT random seed (effective with -f) [11]
  ]]></help>
</tool>
```

(continues on next page)
At this point we have a fairly functional Galaxy tool with test and help. This was a pretty simple example - usually you will need to put more work into the tool to get to this point. `tool_init` is really just designed to get you started.

Now let's lint and test the tool we have developed. The Planemo's `lint` (or just `l`) command will review tool for XML validity, obvious mistakes, and compliance with IUC best practices.

```
$ planemo l
Linting tool /opt/galaxy/tools/seqtk_seq.xml
Applying linter tests... CHECK
.. CHECK: 1 test(s) found.
Applying linter output... CHECK
.. INFO: 1 outputs found.
Applying linter inputs... CHECK
.. INFO: Found 1 input parameters.
Applying linter help... CHECK
.. CHECK: Tool contains help section.
.. CHECK: Help contains valid reStructuredText.
Applying linter general... CHECK
.. CHECK: Tool defines a version [0.1.0].
.. CHECK: Tool defines a name [Convert to FASTA (seqtk)].
.. CHECK: Tool defines an id [seqtk_seq].
Applying linter command... CHECK
.. INFO: Tool contains a command.
Applying linter citations... CHECK
.. CHECK: Found 1 likely valid citations.
```

By default `lint` will find all the tools in your current working directory, but we could have specified a particular tool with `planemo lint seqtk_seq.xml`. 

---

```
-f FLOAT sample FLOAT fraction of sequences [1]
-M FILE mask regions in BED or name list FILE [null]
-L INT drop sequences with length shorter than INT [0]
-c mask complement region (effective with -M)
-r reverse complement
-A force FASTA output (discard quality)
-C drop comments at the header lines
-N drop sequences containing ambiguous bases
-I output the 2n-1 reads only
-2 output the 2n reads only
-V shift quality by '(-Q) - 33'
-U convert all bases to uppercases
-S strip of white spaces in sequences
```
Next we can run our tool’s functional test with the `test` (or just `t`) command. This will print a lot of output (as it starts a Galaxy instance) but should ultimately reveal our one test passed.

```
$ planemo t
... Galaxy starts and runs the test ...
All 1 test(s) executed passed.
seqtk_seq[0]: passed
```

You can use the following command to open up the test results in your browser.

```
$ firefox /opt/galaxy/tools/tool_test_output.html
```

Normally `planemo` requires an existing Galaxy instance to point at to run the `t` (or `test`) command - but the virtual appliance has a Galaxy instance preconfigured and registered with `planemo`.

### 5.2.2 Simple Parameters

We have built a tool wrapper for the `seqtk seq` command - but this tool actually has additional options that we may wish to expose the Galaxy user.

Let’s take a few of the parameters from the help command and build Galaxy `param` blocks to stick in the tool’s `inputs` block.

```
-V shift quality by '(-Q) - 33'
```

In the previous section we saw `param` block of type `data` for input files, but there are many different kinds of parameters one can use. Flag parameters such as the above `-V` parameter are frequently represented by `boolean` parameters in Galaxy tool XML.

```
<param name="shift_quality" type="boolean" label="Shift quality"
  truevalue="-V" falsevalue="" help="shift quality by '(-Q) - 33' (-V)" />
```

We can then stick `$shift_quality` in our `command` block and if the user has selected this option it will be expanded as `-V` (since we have defined this as the `truevalue`). If the user hasn’t selected this option `$shift_quality` will just expand as an empty string and not affect the generated command line.

Now consider the following `seqtk` `seq` parameters:

```
-q INT mask bases with quality lower than INT [0]
-X INT mask bases with quality higher than INT [255]
```

These can be translated into Galaxy parameters as:

```
<param name="quality_min" type="integer" label="Mask bases with quality lower than"
  value="0" min="0" max="255" help="(-q)" />
<param name="quality_max" type="integer" label="Mask bases with quality higher than"
  value="255" min="0" max="255" help="(-X)" />
```

These can be add to the command tag as `-q $quality_min -X $quality_max`.

At this point the tool would look like:

```
<tool id="seqtk_seq" name="Convert to FASTA (seqtk)" version="0.1.0">
  <requirements>
    <requirement type="package" version="1.2">seqtk</requirement>
  </requirements>
</tool>
```
<command detect_errors="exit_code"> <![CDATA[
seqtk seq
   $shift_quality
   -q $quality_min
   -X $quality_max
   -a '$input1' > '$output1'
]]> </command>

<inputs>
   <param type="data" name="input1" format="fastq" />
   <param name="shift_quality" type="boolean" label="Shift quality"
      truevalue="-V" falsevalue="" help="shift quality by '(-Q) - 33' (-V)" />
   <param name="quality_min" type="integer" label="Mask bases with quality lower than"
      value="0" min="0" max="255" help="(-q)" />
   <param name="quality_max" type="integer" label="Mask bases with quality higher than"
      value="255" min="0" max="255" help="(-X)" />
</inputs>

<outputs>
   <data name="output1" format="fasta" />
</outputs>

<tests>
   <test>
      <param name="input1" value="2.fastq" />
      <output name="output1" file="2.fasta" />
   </test>
</tests>

<help> <![CDATA[
Usage:  seqtk seq [options] <in.fq>|<in.fa>

Options:  -q INT  mask bases with quality lower than INT [0]
          -X INT  mask bases with quality higher than INT [255]
          -n CHAR masked bases converted to CHAR; 0 for lowercase [0]
          -l INT  number of residues per line; 0 for 2^32-1 [0]
          -Q INT  quality shift: ASCII-INT gives base quality [33]
          -s INT  random seed (effective with -f) [11]
          -f FLOAT sample FLOAT fraction of sequences [1]
          -M FILE mask regions in BED or name list FILE [null]
          -L INT  drop sequences with length shorter than INT [0]
          -c mask complement region (effective with -M)
          -r reverse complement
          -A force FASTA output (discard quality)
          -C drop comments at the header lines
          -N drop sequences containing ambiguous bases
          -1 output the 2n-1 reads only
          -2 output the 2n reads only
          -V shift quality by '(-Q) - 33'
          -U convert all bases to uppercases

]]> </help>

<citations>
   <citation type="bibtex">
      @misc{githubseqtk,
         author = {LastTODO, FirstTODO},
   </citation>
</citations>
5.2.3 Conditional Parameters

The previous parameters were simple because they always appeared, now consider.

-M FILE mask regions in BED or name list FILE [null]

We can mark this data type param as optional by adding the attribute optional="true".

<param name="mask_regions" type="data" label="Mask regions in BED"
     format="bed" help="(-M)" optional="true"/>

Then instead of just using $mask_regions directly in the command block, one can wrap it in an if statement (because tool XML files support Cheetah).

#if $mask_regions
-M '$mask_regions'
#endif

Next consider the parameters:

-s INT random seed (effective with -f) [11]
-f FLOAT sample FLOAT fraction of sequences [1]

In this case, the -s random seed parameter should only be seen or used if the sample parameter is set. We can express this using a conditional block.

<conditional name="sample">
   <param name="sample_selector" type="boolean" label="Sample fraction of sequences"/>
   <when value="true">
      <param name="fraction" label="Fraction" type="float" value="1.0" help="(-f)"/>
      <param name="seed" label="Random seed" type="integer" value="11" help="(-s)"/>
   </when>
   <when value="false">
   </when>
</conditional>

In our command block, we can again use an if statement to include these parameters.

#if $sample.sample_selector
-f $sample.fraction -s $sample.seed
#endif
Notice we must reference the parameters using the sample prefix since they are defined within the sample conditional block.

The newest version of this tool is now

```xml
<tool id="seqtk_seq" name="Convert to FASTA (seqtk)" version="0.1.0">
  <requirements>
    <requirement type="package" version="1.2">seqtk</requirement>
  </requirements>
  <command detect_errors="exit_code">
    <![CDATA[
    seqtk seq
    $shift_quality
    -q $quality_min
    -X $quality_max
    #if $mask_regions
    -M '$mask_regions'
    #end if
    #if $sample.sample
    -f $sample.fraction
    -s $sample.seed
    #end if
    -a '$input1' > '$output1'
    ]]>]]>
  </command>
  <inputs>
    <param type="data" name="input1" format="fastq" />
    <param name="shift_quality" type="boolean" label="Shift quality"
      truevalue="-V" falsevalue="" help="shift quality by '(-Q) - 33' (-V)" />
    <param name="quality_min" type="integer" label="Mask bases with quality lower than"
      value="0" min="0" max="255" help="(-q)" />
    <param name="quality_max" type="integer" label="Mask bases with quality higher than"
      value="255" min="0" max="255" help="(-X)" />
    <param name="mask_regions" type="data" label="Mask regions in BED" format="bed" help="(-M)"
      optional="true" />
    <conditional name="sample">
      <param name="sample" type="boolean" label="Sample fraction of sequences" />
      <when value="true">
        <param name="fraction" label="Fraction" type="float" value="1.0"
          help="(-f)" />
        <param name="seed" label="Random seed" type="integer" value="11"
          help="(-s)" />
      </when>
      <when value="false">
      </when>
    </conditional>
  </inputs>
  <outputs>
    <data name="output1" format="fasta" />
  </outputs>
  <tests>
    <test>
      <param name="input1" value="2.fastq"/>
      <output name="output1" file="2.fasta"/>
    </test>
  </tests>
</tool>
```
Usage:  seqtk seq [options] <in.fq>|<in.fa>

Options:  
-q INT  mask bases with quality lower than INT [0]  
-X INT  mask bases with quality higher than INT [255]  
-n CHAR  masked bases converted to CHAR; 0 for lowercase [0]  
-l INT  number of residues per line; 0 for 2^32-1 [0]  
-o INT  quality shift: ASCII-INT gives base quality [33]  
-s INT  random seed (effective with -f) [11]  
-f FLOAT  sample FLOAT fraction of sequences [1]  
-M FILE  mask regions in BED or name list FILE [null]  
-L INT  drop sequences with length shorter than INT [0]  
-c  mask complement region (effective with -M)  
-r  reverse complement  
-A  force FASTA output (discard quality)  
-C  drop comments at the header lines  
-N  drop sequences containing ambiguous bases  
-1  output the 2n-1 reads only  
-2  output the 2n reads only  
-V  shift quality by '(-Q) - 33'  
-U  convert all bases to uppercases

For tools like this where there are many options but in the most uses the defaults are preferred - a common idiom is to break the parameters into simple and advanced sections using a conditional.

Updating this tool to use that idiom might look as follows.

```xml
<tool id="seqtk_seq" name="Convert to FASTA (seqtk)" version="0.1.0">
    <requirements>
        <requirement type="package" version="1.2">seqtk</requirement>
    </requirements>
    <command detect_errors="exit_code"><!CDATA{
        seqtk seq
        #if $settings.advanced == "advanced"
            $settings.shift_quality
            -q $settings.quality_min
            -X $settings.quality_max
            #if $settings.mask_regions
                -M "$settings.mask_regions"
            #end if
        #end if
        #if $settings.sample.sample
    </command>
</tool>
```
Planemo Documentation, Release 0.61.0.dev0

Usage: seqtk seq [options] <in.fq>|<in.fa>

44 Chapter 5. Building Galaxy Tools
5.2.4 Publishing to the Tool Shed

Now that the tool is working and useful - it is time to publish it to the Tool Shed. The Galaxy Tool Shed (referred to colloquially in Planemo as the “shed”) can store Galaxy tools, dependency definitions, and workflows among other Galaxy artifacts. Shed’s goal is to make it easy for any Galaxy to install these.

Configuring a Tool Shed Account

The planemo appliance comes pre-configured with a local Tool Shed and Planemo is configured to talk to it via ~/.planemo.yml configuration file. Check out the publishing docs for information on setting up this file on your development environment.

Creating a Repository

Planemo can be used to publish “repositories” to the Tool Shed. A single GitHub repository or locally managed directory of tools may correspond to any number of Tool Shed repositories. Planemo maps files to Tool Shed repositories using a special file called .shed.yml.
From a directory containing tools the `shed_init` command can be used to bootstrap a new `.shed.yml` file.

```
$ planemo shed_init --name=seqtk_seq \
    --owner=planemo \
    --description=seqtk_seq \
    --long_description="Tool that converts FASTQ to FASTA files using seqtk" \
    --category="Fastq Manipulation"
```

The resulting `.shed.yml` file will look something like this:

```
categories: [Fastq Manipulation]
description: seqtk_seq
long_description: Tool that converts FASTQ to FASTA files using seqtk
name: seqtk_seq
owner: planemo
```

There is not a lot of magic happening here, this file could easily be created directly with a text editor - but the command has a `--help` to assist you and does some very basic validation. More information on `.shed.yml` can be found as part of the IUC's best practice documentation.

This configuration file and shed artifacts can be quickly linted using the following command.

```
$ planemo shed_lint --tools
```

Once the details in the `.shed.yml` are set and it is time to create the remote repository and upload artifacts to it - the following two commands can be used - the first only needs to be run once and creates the repository based on the metadata in `.shed.yml` and the second uploads your actual artifacts to it.

```
$ planemo shed_create --shed_target local
Repository created
cd '/opt/galaxy/tools' && git rev-parse HEAD
Repository seqtk_seq updated successfully.
```

You can now navigate to the local shed (likely at `http://localhost:9009/`) and see the repository there. Optionally you can login with username `planemo@test.com` and password `planemo` but it is not necessary.

### Updating a Repository

In order to push further changes in your local tool development directory to the shed you would run the `shed_update` command as follows.

```
$ planemo shed_update --shed_target local
```

### Serving a Tool from Shed

Once tools (and possible required dependency files) have been published, the whole thing can be automatically installed and the tool served in local Galaxy using this command.

```
$ planemo shed_serve --shed_target local
```
Note: During this tutorial we did not “teach” Galaxy how to obtain the seqtk software so our tool (and thus Galaxy) just expects the command `seqtk` to be available. The seqtk software here is a so called dependency of our tool and in order for our tool to be fully installable we need to create a “recipe” for Galaxy so it knows how to obtain it. This is covered in other sections of this documentation as well as on the wiki.

Main Tool Shed

Once your artifacts are ready for publication to the Main Tool Shed, the following command creates a repository there and populates it with your contents.

```
$ planemo shed_create --shed_target toolshed
```

The planemo machine isn’t preconfigured to allow publishing to the Main Tool Shed so this command will not work here. See the more complete publishing docs for full details about how to setup Planemo to publish to the Main and Test Tool Shed - the process is very similar.

5.2. Building Galaxy Tools (Using the Planemo Appliance)
5.2.5 Wrapping a Script

Many common bioinformatics applications are available on the Tool Shed already and so a common development task is to integrate scripts of various complexity into Galaxy.

Consider the following small Perl script.

```perl
#!/usr/bin/perl -w
# usage : perl toolExample.pl <FASTA file> <output file>
open (IN, "<$ARGV[0]");
open (OUT, ">$ARGV[1]");
while (<IN>) {
    chop;
    if (m/^>/) {
        s/^>//;
        if ($. > 1) {
            print OUT sprintf("%.3f", $gc/$length) . "\n";
        }
        $gc = 0;
        $length = 0;
    } else {
        ++$gc while m/[gc]\//ig;
        $length += length $_;
    }
}
print OUT sprintf("%.3f", $gc/$length) . "\n";
close( IN );
close( OUT );
```

One can build a tool for this script as follows and place the script in the same directory as the tool XML file itself. The special value $__tool_directory__ here refers to the directory your tool lives in.

```xml
<tool id="gc_content" name="Compute GC content">
    <description>for each sequence in a file</description>
    <command>perl '$__tool_directory__/gc_content.pl' '$input' output.tsv</command>
    <inputs>
        <param name="input" type="data" format="fasta" label="Source file"/>
    </inputs>
    <outputs>
        <data name="output" format="tabular" from_work_dir="output.tsv"/>
    </outputs>
    <help>
        This tool computes GC content from a FASTA file.
    </help>
</tool>
```

5.2.6 Macros

If your desire is to write a tool for a single relatively simple application or script - this section should be skipped. If you hope to maintain a collection of related tools - experience suggests you will realize there is a lot of duplicated XML to do this well. Galaxy tool XML macros can help reduce this duplication.

Planemo's tool_init command can be used to generate a macro file appropriate for suites of tools by using the --macros flag. Consider the following variant of the previous tool_init command (the only difference is now we are adding the --macros flag).

```bash
planemo tool_init gc_content --macros
```

This tool computes GC content from a FASTA file.

```xml
<tool id="gc_content" name="Compute GC content">
    <description>for each sequence in a file</description>
    <command>perl '$__tool_directory__/gc_content.pl' '$input' output.tsv</command>
    <inputs>
        <param name="input" type="data" format="fasta" label="Source file"/>
    </inputs>
    <outputs>
        <data name="output" format="tabular" from_work_dir="output.tsv"/>
    </outputs>
    <help>
        This tool computes GC content from a FASTA file.
    </help>
</tool>
```
This will produce the two files in your current directory instead of just one - seqtk_seq.xml and macros.xml.

```xml
<tool id="seqtk_seq" name="Convert to FASTA (seqtk)" version="0.1.0">
  <macros>
    <import>macros.xml</import>
  </macros>
  <expand macro="requirements"/>
  <command detect_errors="exit_code">
    <![CDATA[
      seqtk seq -a '$input1' > '$output1'
    ]]></command>
  <inputs>
    <param type="data" name="input1" format="fastq"/>
  </inputs>
  <outputs>
    <data name="output1" format="fasta"/>
  </outputs>
  <tests>
    <test>
      <param name="input1" value="2.fastq"/>
      <output name="output1" file="2.fasta"/>
    </test>
  </tests>
  <help><![CDATA[
Usage:
seqtk seq [options] <in.fq>|<in.fa>

Options: 
-q INT  mask bases with quality lower than INT [0]
-X INT  mask bases with quality higher than INT [255]
-n CHAR masked bases converted to CHAR; 0 for lowercase [0]
-l INT  number of residues per line; 0 for 2^32-1 [0]
-Q INT  quality shift: ASCII-INT gives base quality [33]
-s INT  random seed (effective with -f) [11]
-f FLOAT sample FLOAT fraction of sequences [1]
-M FILE mask regions in BED or name list FILE [null]
-L INT  drop sequences with length shorter than INT [0]
-c mask complement region (effective with -M)
-r reverse complement
-A force FASTA output (discard quality)
-C drop comments at the header lines
-N drop sequences containing ambiguous bases
-I output the 2n-1 reads only
-Z output the 2n reads only
-V shift quality by '(-Q) - 33'
]]></CDATA>
]]></help>
(continues on next page)
```
As you can see in the above code macros are reusable chunks of XML that make it easier to avoid duplication and keep your XML concise.

Further reading:

- Macros syntax on the Galaxy Wiki.
- GATK tools (example tools making extensive use of macros)
- gemini tools (example tools making extensive use of macros)
- bedtools tools (example tools making extensive use of macros)
- Macros implementation details - Pull Request #129 and Pull Request #140

5.2.7 More Information

- Galaxy’s Tool XML Syntax
- Big List of Tool Development Resources
- Cheetah templating

Additional tutorials include

5.3 Advanced Tool Development Topics

This tutorial covers some more advanced tool development topics - such as testing and collections. It assumes some basic knowledge about wrapping Galaxy tools and that you have an environment with Planemo available - check out tutorial if you have never developed a Galaxy tool.

5.3.1 Test-Driven Development

An Example Tool - BWA

To get started let’s install BWA. Here we are going to use conda to install BWA - but however you obtain it should be fine.
$ conda install --force -c conda-forge -c bioconda bwa
... bwa installation ...
$ bwa
Program: bwa (alignment via Burrows-Wheeler transformation)
Version: 0.7.13-r1126
Contact: Heng Li <lh3@sanger.ac.uk>

Usage: bwa <command> [options]

Command: index  index sequences in the FASTA format
mem  BWA-MEM algorithm
fastmap  identify super-maximal exact matches
pemerge  merge overlapping paired ends (EXPERIMENTAL)
aln  gapped/ungapped alignment
samse  generate alignment (single ended)
sampe  generate alignment (paired ended)
bwasw  BWA-SW for long queries
shm  manage indices in shared memory
fa2pac  convert FASTA to PAC format
pac2bwt  generate BWT from PAC
pac2bwgen  alternative algorithm for generating BWT
bwtupdate  update .bwt to the new format
bwt2sa  generate SA from BWT and Occ

Note: To use BWA, you need to first index the genome with `bwa index'.
There are three alignment algorithms in BWA: `mem', `bwasw', and `aln/samse/sampe'. If you are not sure which to use, try `bwa mem' first. Please `man ./bwa.1' for the manual.

Alternatively you can use Homebrew/linuxbrew to install it:

$ brew install homebrew/science/bwa

Let's start with a simple wrapper for the BWA application (bwa mem in particular). You can create a new mini-project with a minimal bwa-mem tool using Planemo's project_init command.

$ planemo project_init --template bwa bwa
$ cd bwa

This will create a folder with a bwa-mem.xml as follows:

```xml
<?xml version="1.0"?>
<tool id="bwa_mem_test" name="Map with BWA-MEM" version="0.0.1">
  <description>- map medium and long reads</description>
  <requirements>
    <requirement type="package" version="0.7.15">bwa</requirement>
    <requirement type="package" version="1.3">samtools</requirement>
  </requirements>
  <command detect_errors="exit_code"><![CDATA[
    ## Build reference
    #set $reference_fasta_filename = "localref.fa"
    ln -s "$ref_file" "${$reference_fasta_filename}"
    bwa index -a is "${$reference_fasta_filename}"

    ## Begin BWA-MEM command line
    bwa mem

(continues on next page)```
-t \"\${GALAXY_SLOTS:-4}\"
-v 1  # Verbosity is set to 1 (errors only)

"${reference_fasta_filename}\"
"${fastq_input1}\"

| samtools view -Sb - > temporary_bam_file.bam && samtools sort -o ${bam_output} temporary_bam_file.bam |

<command>

<inputs>
  <param name="ref_file" type="data" format="fasta" label="Use the following dataset as the reference sequence" help="You can upload a FASTA sequence to the history and use it as reference" />
  <param name="fastq_input1" type="data" format="fastqsanger" label="Select fastq dataset" help="Specify dataset with single reads" />
</inputs>

<outputs>
  <data format="bam" name="bam_output" label="${tool.name} on ${on_string} (mapped reads in BAM format)" />
</outputs>

<tests>
  <!-- header describing command-line will always be different - hence lines_diff="2" on output tag. -->
  <test>
    <param name="fastq_input1" value="bwa-mem-fastq1.fq" />
    <param name="ref_file" value="bwa-mem-mt-genome.fa" />
    <output name="bam_output" file="bwa-aln-test1.bam" ftype="bam" lines_diff="2" />
  </test>
</tests>

<help>

**BWA MEM options**

Algorithm options::

- k INT minimum seed length [19]
- w INT band width for banded alignment [100]
- d INT off-diagonal X-dropoff [100]
- r FLOAT look for internal seeds inside a seed longer than {-k} * FLOAT [1.5]
- y INT find MEMs longer than {-k} * {-r} with size less than INT [0]
- c INT skip seeds with more than INT occurrences [500]
- D FLOAT drop chains shorter than FLOAT fraction of the longest overlapping chain [0.50]
- W INT discard a chain if seeded bases shorter than INT [0]
- m INT perform at most INT rounds of mate rescues for each read [50]
- S skip mate rescue
- P skip pairing; mate rescue performed unless -S also in use
- e discard full-length exact matches

Scoring options::

(continues on next page)
-A INT score for a sequence match, which scales options -TdBOELU unless overridden [1]
-B INT penalty for a mismatch [4]
-O INT[,INT] gap open penalties for deletions and insertions [6,6]
-E INT[,INT] gap extension penalty; a gap of size k cost \(-O\) + \({-E}*k\) [1,1]
-L INT[,INT] penalty for 5'- and 3'-end clipping [5,5]
-U INT penalty for an unpaired read pair [17]

Input/output options::

-p first query file consists of interleaved paired-end sequences
-R STR read group header line such as '@RG\tID:foo\tSM:bar' [null]
-v INT verbose level: 1=error, 2=warning, 3=message, 4+=debugging [3]
-T INT minimum score to output [30]
-h INT if there are \(<\) INT hits with score \(\geq\) 80% of the max score, output all in XA [5]
-a output all alignments for SE or unpaired PE
-C append FASTA/FASTQ comment to SAM output
-V output the reference FASTA header in the XR tag
-Y use soft clipping for supplementary alignments
-M mark shorter split hits as secondary
-I FLOAT[,FLOAT[,INT[,INT]]] specify the mean, standard deviation (10% of the mean if absent),
 max (4 sigma from the mean if absent) and min of the insert size,
 distribution. FR orientation only. [inferred]

Highlighted are two features of Galaxy’s tool XML syntax. The detect_errors="exit_code" on the
 command block will cause Galaxy to use the actual process exit code to determine failure - in most cases this is
 superior to the default Galaxy behavior of checking for the presence of standard error output.

The <citations> block at the bottom will cause Galaxy to generate exportable citations in the tool form and history
 UIs.

**Improved Input Handling via Test-Driven Development**

In this form, the tool only accepts a single input. The first thing we will do is to expand the tool to also allow paired
datasets.

**Note:** Two big ideas behind test-driven development are:

* Write a failing test first.
* Run the test before you implement the feature. Seeing the initial test failing ensures that your feature is actually
 being tested.

So let’s start by generating a test output for the two input files (the bootstrapped example includes two fastq input
files to work with `bwa-mem-fastq1.fq` and `bwa-mem-fastq2.fq`). The following commands will create a bwa index on the fly, map two input files against it, and build and sort a bam output from the result - all following the pattern from the command block in the tool.

```
$ cd test-data
$ bwa index -a is bwa-mem-mt-genome.fa
$ bwa mem bwa-mem-mt-genome.fa bwa-mem-fastq1.fq bwa-mem-fastq2.fq | \n  samtools view -Sb - > temporary_bam_file.bam && \
  (samtools sort -f temporary_bam_file.bam bwa-aln-test2.bam || samtools sort -o bwa-
  →aln-test2.bam temporary_bam_file.bam)
```

**Warning:** In many ways this magic is the hardest part of wrapping Galaxy tools and is something this tutorial cannot really teach. The command line magic required for each tool is going to be different. Developing a Galaxy wrapper requires a lot of knowledge of the underlying applications.

**Note:** Sort appears twice in this odd command because two different versions of samtools with conflicting syntaxes may happen to be on your machine when running this command. Galaxy manages versioned dependencies and so the tool itself does not reflect this complexity.

The primary result of this is the file `test-data/bwa-aln-test2.bam`. We will now copy and paste the existing test case to add a new test case that specifies both fastq inputs as a collection and expects this new output.

```
<test>
  <param name="fastq_input">
    <collection type="paired">
      <element name="forward" value="bwa-mem-fastq1.fq" />
      <element name="reverse" value="bwa-mem-fastq2.fq" />
    </collection>
  </param>
  <param name="ref_file" value="bwa-mem-mt-genome.fa" />
  <param name="input_type" value="paired_collection" />
  <output name="bam_output" file="bwa-aln-test2.bam" ftype="bam" lines_diff="2" />
</test>
```

We want to specify the input datasets as a paired collection (see the collections documentation in this document for more information) and we need to have a way to allow the user to specify they are submitting a paired collection instead of a single input. This is where the `fastq_input` and `input_type` variables above came from.

Next run `planemo l` to verify the tool doesn’t have any obvious defects. Once the XML is valid - use `planemo t` to verify the new test is failing.

```
$ planemo t
... bunch of output ...
bwa_mem_test[0]: passed
bwa_mem_test[1]: failed
```

**Note:** You can run `$ firefox tool_test_output.html` to see full details of all executed tests.

Here you can see this second new test is failing - that is good! The fix is to create a conditional allowing the user to specify an input type. When modifying the tool and retesting - try passing the `--failed` flag to `planemo t` - it will speed things up by only rerunning tests that have already failed.
If you are comfortable with Galaxy tool development - try modifying the tool to make the failing test pass.

**Hint:**

- You will need to use the `data_collection` param type. It accepts many of the same attributes as data parameters (e.g. see `input_fastq1`) but you will need to specify a `collection_type` of `paired`.
- To access the `data_collection` parameter parts in the command block - use `$collection_param.forward` and `$collection_param.reverse`.

Once you get the new test case passing with the `--failed` parameter - try running all the tests again to ensure you didn’t break the original test.

```bash
$ planemo t
... bunch of output ...
bwa_mem_test[0]: passed
bwa_mem_test[1]: passed
```

One possible implementation for tests is as follows (sections with changes highlighted).

```xml
<?xml version="1.0"?>
<tool id="bwa_mem_test" name="Map with BWA-MEM" version="0.0.1">
  <description>- map medium and long reads</description>
  <requirements>
    <requirement type="package" version="0.7.15">bwa</requirement>
    <requirement type="package" version="1.3">samtools</requirement>
  </requirements>
  <command detect_errors="exit_code">$collection_param.forward
    ## Build reference
    #set $reference_fasta_filename = "localref.fa"
    ln -s "${ref_file}" "${reference_fasta_filename}" &&
    bwa index -a is "${reference_fasta_filename}" &&
    ## Begin BWA-MEM command line
    bwa mem
    -t "\${GALAXY_SLOTS:-4}"
    -v 1
    - Verbosity is set to 1 (errors only)
    "${reference_fasta_filename}"
    #set $input_type = $input_type_conditional.input_type
    #if $input_type == "single"
    "${input_type_conditional.fastq_input1}"
    #elif $input_type == "paired_collection"
    "${input_type_conditional.fastq_input.forward}" "${input_type_conditional.fastq_input.reverse}"
    #end if
    | samtools view -Sb - > temporary_bam_file.bam &&
    samtools sort -o ${bam_output} temporary_bam_file.bam
  </command>

  <inputs>
    <param name="ref_file" type="data" format="fasta" label="Use the following dataset as the reference sequence" help="You can upload a FASTA sequence to the history and use it as reference" />
  </inputs>
</tool>
```

(continues on next page)
<conditional name="input_type_conditional">
  <param name="input_type" type="select" label="Input Type">
    <option value="single" selected="true">Single Dataset</option>
    <option value="paired_collection">Paired Collection</option>
  </param>
  <when value="single">
    <param name="fastq_input1" type="data" format="fastqsanger" label="Select fastq dataset" help="Specify dataset with single reads"/>
  </when>
  <when value="paired_collection">
    <param name="fastq_input" format="fastqsanger" type="data_collection collection_type="paired" label="Select dataset pair" help="Specify paired dataset collection containing paired reads"/>
  </when>
</conditional>

<outputs>
  <data format="bam" name="bam_output" label="${tool.name} on ${on_string} (mapped reads in BAM format)"/>
</outputs>

<tests>
 <!-- header describing command-line will always be different - hence lines_diff="2" on output tag. -->
  <test>
    <param name="fastq_input1" value="bwa-mem-fastq1.fq"/>
    <param name="ref_file" value="bwa-mem-mt-genome.fa"/>
    <output name="bam_output" file="bwa-aln-test1.bam" ftype="bam" lines_diff="2"/>
  </test>
  <test>
    <param name="fastq_input">
      <collection type="paired">
        <element name="forward" value="bwa-mem-fastq1.fq"/>
        <element name="reverse" value="bwa-mem-fastq2.fq"/>
      </collection>
    </param>
    <param name="ref_file" value="bwa-mem-mt-genome.fa"/>
    <param name="input_type" value="paired_collection"/>
    <output name="bam_output" file="bwa-aln-test2.bam" ftype="bam" lines_diff="2"/>
  </test>
</tests>

<help>
**BWA MEM options**
Algorithm options::

- `-k INT` minimum seed length [19]
- `-w INT` band width for banded alignment [100]
- `-d INT` off-diagonal X-dropoff [100]
- `-r FLOAT` look for internal seeds inside a seed longer than `-k` * FLOAT [1.5]
- `-y INT` find MEMs longer than `-k` * `-r` with size less than INT [0]
- `-c INT` skip seeds with more than INT occurrences [500]

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<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>-D FLOAT</td>
<td>drop chains shorter than FLOAT fraction of the longest overlapping chain [0.50]</td>
</tr>
<tr>
<td>-W INT</td>
<td>discard a chain if seeded bases shorter than INT [0]</td>
</tr>
<tr>
<td>-m INT</td>
<td>perform at most INT rounds of mate rescues for each read [50]</td>
</tr>
<tr>
<td>-S</td>
<td>skip mate rescue</td>
</tr>
<tr>
<td>-P</td>
<td>skip pairing; mate rescue performed unless -S also in use</td>
</tr>
<tr>
<td>-e</td>
<td>discard full-length exact matches</td>
</tr>
</tbody>
</table>

**Scoring options:**

- **-A INT** score for a sequence match, which scales options `-TdBOELU` unless overridden [1]
- **-B INT** penalty for a mismatch [4]
- **-O INT[,INT]** gap open penalties for deletions and insertions [6,6]
- **-E INT[,INT]** gap extension penalty; a gap of size k cost `(-O) + (-E)*k` [1,1]
- **-L INT[,INT]** penalty for 5'- and 3'-end clipping [5,5]
- **-U INT** penalty for an unpaired read pair [17]

**Input/output options:**

- **-p** first query file consists of interleaved paired-end sequences
- **-R STR** read group header line such as `@RG\tID:foo\tSM:bar` [null]
- **-v INT** verbose level: 1=error, 2=warning, 3=message, 4+=debugging [3]
- **-T INT** minimum score to output [30]
- **-h INT** if there are <INT hits with score >80% of the max score, output all in XA [5]
- **-a** output all alignments for SE or unpaired PE
- **-C** append FASTA/FASTQ comment to SAM output
- **-V** output the reference FASTA header in the XR tag
- **-Y** use soft clipping for supplementary alignments
- **-M** mark shorter split hits as secondary

- **-I FLOAT[,FLOAT[,INT[,INT]]]** specify the mean, standard deviation (10% of the mean if absent), max (4 sigma from the mean if absent) and min of the insert size.

**FR orientation only. [inferred]**

</help>

</citations>

<citation type="doi">10.1093/bioinformatics/btp698</citation>

</tool>

**Note:** Exercise: The devteam mappers allow users to specify both a paired collection or individual datasets (i.e. using two data parameters). Extend the above conditional to allow that. Remember to write your test case first and make sure it fails.

**Hint:** You should not require additional inputs or outputs to do this.
Adding More Parameters

Next up, let’s add some of BWA’s optional parameters to our tool - these parameters are outlined in the example tool’s help section. To speed this up and demonstrate another feature of Galaxy - the next test will test the command-line generated by Galaxy instead of the exact outputs. Not requiring a complete set of outputs for each test case is convenient because it can speed development and allows testing more parameter combinations. There are certain tools and certain parameters where exact outputs are impossible to pre-determine though.

Let’s start with \textit{algorithm} parameter ‘`-k INT minimum seed length [19]’‘. Again, let’s do a test first!

\begin{verbatim}
<test>
    <param name="fastq_input1" value="bwa-mem-fastq1.fq"/>
    <param name="ref_file" value="bwa-mem-mt-genome.fa"/>
    <param name="set_algorithm_params" value="true"/>
    <param name="k" value="20"/>
    <assert_command>
        <has_text text="-k 20"/>
    </assert_command>
</test>
\end{verbatim}

Continuing our pattern - let’s ensure this new test fails before implementing the \textit{k} parameter.

\begin{verbatim}
$ planemo t
... bunch of output ...
bwa_mem_test[0]: passed
bwa_mem_test[1]: passed
bwa_mem_test[2]: failed
\end{verbatim}

Reviewing the output - indeed this new test failed as expected \textit{(did not contain expected text `-k 20’)}. Now let’s implement the \textit{k} parameter and use \texttt{planemo t --failed} to ensure our implementation is correct.

An example tool with this test and passing.

\begin{verbatim}
<?xml version="1.0"?>
<tool id="bwa_mem_test" name="Map with BWA-MEM" version="0.0.1">
    <description>- map medium and long reads</description>
    <requirements>
        <requirement type="package" version="0.7.15">bwa</requirement>
        <requirement type="package" version="1.3">samtools</requirement>
    </requirements>
    <command detect_errors="exit_code">
        <!\[CDATA[
            ## Build reference
            #set $reference_fasta_filename = "localref.fa"
            ln -s "$\{ref_file\}" "$\{reference_fasta_filename\}"
            bwa index -a is "$\{reference_fasta_filename\}"
            
            ## Begin BWA-MEM command line
            bwa mem
            -t "\$\{GALAXY_SLOTS:-4\}"
            -v 1
            #if $algorithm.set_algorithm_params
            -k $\{algorithm.k\}
            #end if
            "$\{reference_fasta_filename\}"
            #set $input_type = $input_type_conditional.input_type
        ]]>\n    </command>
</tool>
\end{verbatim}

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### Conditional Input Types

```python
# if $input_type == "single"
"${input_type_conditional.fastq_input1}"
# elif $input_type == "paired_collection"
"${input_type_conditional.fastq_input.forward}" "${input_type_conditional.fastq_input.reverse}"
# end if

| samtools view -Sb -> temporary_bam_file.bam &&
| samtools sort -o ${bam_output} temporary_bam_file.bam
```

```xml
<inputs>
  <param name="ref_file" type="data" format="fasta" label="Use the following dataset as the reference sequence" help="You can upload a FASTA sequence to the history and use it as reference" />
  <conditional name="input_type_conditional">
    <param name="input_type" type="select" label="Input Type">
      <option value="single" selected="true">Single Dataset</option>
      <option value="paired_collection">Paired Collection</option>
    </param>
    <when value="single">
      <param name="fastq_input1" type="data" format="fastqsanger" label="Select fastq dataset" help="Specify dataset with single reads"/>
    </when>
    <when value="paired_collection">
      <param name="fastq_input" format="fastqsanger" type="data_collection" collection_type="paired" label="Select a paired collection" help="Specify paired dataset collection containing paired reads"/>
    </when>
  </conditional>
  <conditional name="algorithm">
    <param name="set_algorithm_params" type="boolean" label="Set Algorithm Parameters">
      <when value="true">
        <param argument="-k" label="minimum seed length" type="integer" value="19" />
      </when>
      <when value="false"/>
    </when>
  </conditional>
</inputs>

<outputs>
  <data format="bam" name="bam_output" label="${tool.name} on ${on_string} (mapped reads in BAM format)"/>
</outputs>

<tests>
  <!-- header describing command-line will always be different -->
  <!-- hence lines_diff="2" on output tag. -->
  <test>
    <param name="fastq_input1" value="bwa-mem-fastq1.fq"/>
    <param name="ref_file" value="bwa-mem-mt-genome.fa"/>
    <output name="bam_output" file="bwa-aln-test1.bam" ftype="bam" lines_diff="2"/>
  </test>
</tests>
```

(continues on next page)
<param name="fastq_input">
  <collection type="paired">
    <element name="forward" value="bwa-mem-fastq1.fq" />
    <element name="reverse" value="bwa-mem-fastq2.fq" />
  </collection>
</param>

<param name="ref_file" value="bwa-mem-mt-genome.fa" />
<param name="input_type" value="paired_collection" />
<output name="bam_output" file="bwa-aln-test2.bam" ftype="bam" lines_diff="2" />
</test>
</test>
</tests>
</help>

**BWA MEM options**

Algorithm options::

- k INT minimum seed length [19]
- w INT band width for banded alignment [100]
- d INT off-diagonal X-dropoff [100]
- r FLOAT look for internal seeds inside a seed longer than \(-k\) * FLOAT [1.5]
- y INT find MEMs longer than \(-k\) * \(-r\) with size less than INT [0]
- c INT skip seeds with more than INT occurrences [500]
- D FLOAT drop chains shorter than FLOAT fraction of the longest overlapping chain [0.50]
- W INT discard a chain if seeded bases shorter than INT [0]
- m INT perform at most INT rounds of mate rescues for each read [50]
- S skip mate rescue
- P skip pairing; mate rescue performed unless -S also in use
- e discard full-length exact matches

Scoring options::

- A INT score for a sequence match, which scales options -TdBOELU unless overridden [1]
- B INT penalty for a mismatch [4]
- O INT[,INT] gap open penalties for deletions and insertions [6,6]
- E INT[,INT] gap extension penalty; a gap of size k cost '-O' + '-E' * k' [1,1]
- L INT[,INT] penalty for 5'- and 3'-end clipping [5,5]
- U INT penalty for an unpaired read pair [17]

Input/output options::

- p first query file consists of interleaved paired-end sequences
- R STR read group header line such as '@RG\tID:foo\tSM:bar' [null]
The tool also demonstrates the new argument option on param tag. These work a lot like specifying a parameter name argument - but Galaxy will describe the underlying application argument in the GUI and API - which may be helpful for power users and external applications.

**Exercise 1:** Implement a few more algorithm parameters and start another Scoring section. Extend the above test case as you go.

**Exercise 2:** Extend the first test case to verify by default none of these parameters are present in the command. Use the not_has_text tag to do this (e.g. `<not_has_text text="-k 20">`).

**Exercise 3:** Publish the bwa-mem to the local Tool Shed following the procedure described in the tutorial. (Don’t forget to alter the commands from the used seqtk example to bwa-mem.)

*Hint:*

```
$ planemo shed_init --name=bwa-bwa \  
  --owner=planemo \  
  --description=bwa-mem \  
  --long_description="BWA MEM: Long and medium read mapper" \  
  --category="Next Gen Mappers"
```

**Note:** A full list of the current assertion elements like these that are allowed can be found on the tool syntax page.

In addition to the assertion-based testing of the command, the jobs standard output and standard error can be checked using assert_stdout and assert_stderr respectively - paralleling the assert_command tag.

See the sample tool job_properties.xml for an example of this.

### 5.3.2 Multiple Output Files

Tools which create more than one output file are common. There are several different methods to accommodate this need. Each one of these has their advantages and weaknesses; careful thought should be employed to determine the best method for a particular tool.
Static Multiple Outputs

Handling cases when tools create a static number of outputs is simple. Simply include an `<output>` tag for each output desired within the tool XML file:

```xml
<tool id="example_tool" name="Multiple output" description="example">
  <command>example_tool.sh '$input1' $tool_option1 '$output1' '$output2'</command>
  <inputs>...
  </inputs>
  <outputs>
    <data format="interval" name="output1" metadata_source="input1" />
    <data format="pdf" name="output2" />
  </outputs>
</tool>
```

Static Outputs Determinable from Inputs

In cases when the number of output files varies, but can be determined based upon a user’s parameter selection, the `<filter>` tag can be used. The text contents of the `<filter>` tag are `eval`ed and if the expression is `True` a dataset will be created as normal. If the expression is `False`, the output dataset will not be created; instead a `NoneDataset` object will be created and made available. When used on the command line the text `None` will appear instead of a file path. The local namespace of the filter has been populated with the tool parameters.

```xml
<tool id="example_tool" name="Multiple output" description="example">
  <command>example_tool.sh '$input1' $tool_option1 '$output1' '$output2'</command>
  <inputs>
    <param name="tool_option1" type="select" label="Type of output">
      <option value="1">Single File</option>
      <option value="2">Two Files</option>
    </param>
  </inputs>
  <outputs>
    <data format="interval" name="output1" metadata_source="input1" />
    <data format="pdf" name="output2">
      <filter>tool_option1 == "2"</filter>
    </data>
    <data format="txt" name="output3">
      <filter>condition1['tool_option2'] == "yes"</filter>
    </data>
  </outputs>
</tool>
```

The command line generated when `tool_option1` is set to Single File is:
example_tool.sh input1_FILE_PATH 1 output1_FILE_PATH None

The command line generated when tool_option1 is set to Two Files is:
example_tool.sh input1_FILE_PATH 2 output1_FILE_PATH output2_FILE_PATH

The datatype of an output can be determined by conditional parameter settings as in tools/filter/pasteWrapper.xml

```xml
<outputs>
  <data format="input" name="out_file1" metadata_source="input1">
    <change_format>
      <when input_dataset="input1" attribute="ext" value="bed" format="interval">
        ...
      </when>
    </change_format>
  </data>
</outputs>
```

**Single HTML Output**

There are times when a single history item is desired, but this history item is composed of multiple files which are only useful when considered together. This is done by having a single (primary) output and storing additional files in a directory (single-level) associated with the primary dataset.

A common usage of this strategy is to have the primary dataset be an HTML file and then store additional content (reports, pdfs, images, etc) in the dataset extra files directory. The content of this directory can be referenced using relative links within the primary (HTML) file, clicking on the eye icon to view the dataset will display the HTML page.

If you want to wrap or create a tool that generates an HTML history item that shows the user links to a number of related output objects (files, images...), you need to know where to write the objects and how to reference them when your tool generates HTML which gets written to the HTML file. Galaxy will not write that HTML for you at present.

The fastqc wrapper is an existing tool example where the Java application generates HTML and image outputs but these need to be massaged to make them Galaxy friendly. In other cases, the application or your wrapper must take care of all the fiddly detailed work of writing valid html to display to the user. In either situation, the html datatype offers a flexible way to display very complex collections of related outputs inside a single history item or to present a complex html page generated by an application. There are some things you need to take care of for this to work:

The following example demonstrates declaring an output of type html.

```xml
<outputs>
  <data format="html" name="html_file" label="myToolOutput_${tool_name}.html">
  </data>
</outputs>
```

The application or script must be set up to write all the output files and/or images to a new special subdirectory passed as a command line parameter from Galaxy every time the tool is run. The paths for images and other files will end up looking something like $GALAXY_ROOT/database/files/000/dataset_56/img1.jpg when you prepend the Galaxy provided path to the filenames you want to use. The command line must pass that path to your script and it is specified using the extra_files_path property of the HTML file output.

For example:

```bash
<command>myscript.pl '$input1' '$html_file' '$html_file.extra_files_path' </command>
```

The application must create and write valid html to setup the page $html_file seen by the user when they view (eye icon) the file. It must create and write that new file at the path passed by Galaxy as the $html_file command line parameter. All application outputs that will be included as links in that html code should be placed in the specific
output directory $html_file.extra_files_path passed on the command line. The external application is responsible for creating that directory before writing images and files into it. When generating the html, The files written by the application to $html_file.extra_files_path are referenced in links directly by their name, without any other path decoration - eg:

```html
<a href="file1.xls">Some special output</a>
<br/>
<img src="image1.jpg" >
```

The (now unmaintained) Galaxy Tool Factory includes code to gather all output files and create a page with links and clickable PDF thumbnail images which may be useful as a starting point (e.g. see rgToolFactory2.py.

galaxy.datatypes.text.Html (the html datatype) is a subclass of composite datasets so new subclasses of composite can be used to implement even more specific structured outputs but this requires adding the new definition to Galaxy - whereas Html files require no extension of the core framework. For more information visit Composite Datatypes.

Dynamic Numbers of Outputs

This section discusses the case where the number of output datasets cannot be determined until the tool run is complete. If the outputs can be broken into groups or collections of similar/homogenous datasets - this is possibly a case for using dataset collections. If instead the outputs should be treated individually and Galaxy’s concept of dataset collections doesn’t map cleanly to the outputs - Galaxy can “discover” individual output datasets dynamically after the job is complete.

Collections

See the Planemo documentation on creating collections for more details on this topic.

A blog post on generating dataset collections from tools can be found here.

Individual Datasets

There are times when the number of output datasets varies entirely based upon the content of an input dataset and the user needs to see all of these outputs as new individual history items rather than as a collection of datasets or a group of related files linked in a single new HTML page in the history. Tools can optionally describe how to “discover” an arbitrary number of files that will be added after the job’s completion to the user’s history as new datasets. Whenever possible, one of the above strategies should be used instead since these discovered datasets cannot be used with workflows and require the user to refresh their history before they are shown.

Discovering datasets (arbitrarily) requires a fixed “parent” output dataset to key on - this dataset will act as the reference for our additional datasets. Sometimes the parent dataset that should be used makes sense from context but in instances where one does not readily make sense tool authors can just create an arbitrary text output (like a report of the dataset generation).

Each discovered dataset requires a unique “designation” (used to describe functional tests, the default output name, etc.) and should be located in the job’s working directory or a sub-directory thereof. Regular expressions are used to describe how to discover the datasets and (though not required) a unique such pattern should be specified for each homogeneous group of such files.
Examples

Consider a tool that creates a bunch of text files or bam files and writes them (with extension that matches the Galaxy datatype - e.g. .txt or .bam) to the `split` sub-directory of the working directory. Such outputs can be discovered by adding the following block of XML to your tool description:

```xml
<outputs>
  <data name="report" format="txt">
    <discover_datasets pattern="__designation_and_ext__" directory="split" visible="true" />
  </data>
</outputs>
```

So for instance, if the tool creates 4 files (in addition to the report) such as `split/samp1.bam`, `split/samp2.bam`, `split/samp3.bam`, and `split/samp4.bam` - then 4 discovered datasets will be created of type `bam` with designations of `samp1`, `samp2`, `samp3`, and `samp4`.

If the tool doesn’t create the files in `split` with extensions or does but with extensions that do not match Galaxy’s datatypes - a slightly different pattern can be used and the extension/format can be statically specified (here either `ext` or `format` may be used as the attribute name):

```xml
<outputs>
  <data name="report" format="txt">
    <discover_datasets pattern="__designation__" format="tabular" directory="tables" visible="true" />
  </data>
</outputs>
```

So in this example, if the tool creates 3 tabular files such as `tables/part1.tsv`, `tables/part2.tsv`, and `tables/part3.tsv` - then 3 discovered datasets will be created of type `tabular` with designations of `part1.tsv`, `part2.tsv`, and `part3.tsv`.

It may not be desirable for the extension/format (.tsv) to appear in the designation this way. These patterns `__designation__` and `__designation_and_ext__` are replaced with regular expressions that capture metadata from the file name using named groups. A tool author can explicitly define these regular expressions instead of using these shortcuts - for instance `__designation__` is just `(\w<designation>)(.*)\.(\w<ext>[^\.\._]+)?`. So the above example can be modified as:

```xml
<outputs>
  <data name="report" format="txt">
    <discover_datasets pattern="(?P<&lt;designation&gt;.+).tsv" format="tabular" directory="tables" visible="true" />
  </data>
</outputs>
```

As a result - three datasets are still be captured - but this time with designations of `part1`, `part2`, and `part3`.

Notice here the `<` and `>` in the tool pattern had to be replaced with `\&lt;` and `\&gt;` to be properly embedded in XML (this is very ugly - apologies).

The metadata elements that can be captured via regular expression named groups this way include `ext`, `designation`, `name`, `dbkey`, and `visible`. Each pattern must declare at least either a `designation` or a `name` - the other metadata parts `ext`, `dbkey`, and `visible` are all optional and may also be declared explicitly in via attributes on the `discover_datasets` element (as shown in the above examples).

For tools which do not define a `profile` version or define one before 16.04, if no `discover_datasets` element is nested with a tool output - Galaxy will still look for datasets using the named pattern `__default__`
which expands to `primary_DATASET_ID_(?P<designation>[^\_]+)(?P<visible>[^\_]+)(?P<ext>[^\_]+)(?P<dbkey>[^\_]+)`? Many tools use this mechanism as it traditionally was the only way to discover datasets and has the nice advantage of not requiring an explicit declaration and encoding everything (including the output to map to) right in the name of the file itself.

For instance consider the following output declaration:

```xml
<outputs>
  <data format="interval" name="output1" metadata_source="input1" />
</outputs>
```

If `$output1.id` (accessible in the tool command block) is 546 and the tool (likely a wrapper) produces the files `primary_546_output2_visible_bed` and `primary_546_output3_visible_pdf` in the job’s working directory - then after execution is complete these two additional datasets (a bed file and a pdf file) are added to the user’s history.

Newer tool profile versions disable this and require the tool author to be more explicit about what files are discovered.

**More information**

- Example tools which demonstrate discovered datasets:
  - multi_output.xml
  - multi_output_assign_primary.xml
  - multi_output_configured.xml

- Original pull request for discovered dataset enhancements with implementation details
- Implementation of output collection code in galaxy

**Legacy information**

In the past, it would be necessary to set the attribute `force_history_refresh` to `True` to force the user’s history to fully refresh after the tool run has completed. This functionality is now broken and `force_history_refresh` is ignored by Galaxy. Users now MUST manually refresh their history to see these files. A Trello card used to track the progress on fixing this and eliminating the need to refresh histories in this manner can be found [here](https://trello.com/c/f5Ddv4CS/1993-history-api-determine-history-state-running-from-join-on-running-jobs). [here]

Discovered datasets are available via post job hooks (a deprecated feature) by using the designation - e.g. `__collected_datasets__['primary'][designation]`. In the past these datasets were typically written to `__new_file_path__` instead of the working directory. This is not very scalable and `__new_file_path__` should generally not be used. If you set the option `collect_outputs_from` in `galaxy.ini` ensure `job_working_directory` is listed as an option (if not the only option).

**5.3.3 Collections**

Galaxy has a concept of dataset collections to group together datasets and operate over them as a single unit.

Galaxy collections are hierarchical and composed from two collection types - `list` and `paired`.

- A `list` is a collection of datasets (or other collections) where each element has an identifier. Unlike Galaxy dataset names which are transformed throughout complex analyses - the identifier is generally preserved
and can be used for concepts such as sample name that one wants to preserve in the earlier mapping steps of a workflow and use it during reduction steps and reporting later.

- The **paired** collection type is much simpler and more specific to sequencing applications. Each paired collection consists of a forward and reverse dataset.

**Note:** Read more about creating and managing collections on the Galaxy Wiki.

Composite types include for instance the list:paired collection type - which represents a list of dataset pairs. In this case, instead of each dataset having a list identifier, each pair of datasets does.

### Consuming Collections

Many Galaxy tools can be used without modification in conjunction with collections. Galaxy users can take a collection and map over any tool that consumes individual datasets. For instance, early in typical bioinformatics workflows you may have steps that filter raw data, convert to standard formats, perform QC on individual files - users can take lists, pairs, or lists of paired datasets and map over such tools that consume individual dataset (files). Galaxy will then run the tool once for each dataset in the collection and for each output of that tool Galaxy will rebuild a new collection.

Collection elements have the concept an identifier and an index when the collection is created. Both of these are preserved during these mapping steps. As Galaxy builds output collections from these mapping steps, the identifier and index for the output entries match those of the supplied input.

If a tool’s functionality can be applied to individual files in isolation, the implicit mapping described above should be sufficient and no knowledge of collections by tools should be needed. However, tools may need to process multiple files at once - in this case explicit collection consumption is required. This document outlines three cases:

- consuming pairs of datasets
- consuming lists
- consuming arbitrary collections.

**Note:** If you find yourself consuming a collection of files and calling the underlying application multiple times within the tool command block, you are likely doing something wrong. Just process a pair or a single dataset and allow the user to map over the collection.

### Processing Pairs

Dataset collections are not extensively used by typical Galaxy users yet - so for tools which process paired datasets the recommended best practice is to allow users to either supply paired collections or two individual datasets. Furthermore, many tools which process pairs of datasets can also process single datasets. The following conditional captures this idiom.

```xml
<conditional name="fastq_input">
  <param name="fastq_input_selector" type="select" label="Single or Paired-end reads" help="Select between paired and single end data">
    <option value="paired">Paired</option>
    <option value="single">Single</option>
    <option value="paired_collection">Paired Collection</option>
    <option value="paired_iv">Paired Interleaved</option>
  </param>
</conditional>
```

(continues on next page)
This introduces a new `param` type - `data_collection`. The optional attribute `collection_type` can specify which kinds of collections are appropriate for this input. Additional `data` attributes such as `format` can further restrict valid collections. Here we defined that both items of the paired collection must be of datatype `fastqsanger`.

In Galaxy’s command block, the individual datasets can be accessed using `$fastq_input1.forward` and `$fastq_input1.reverse`. If processing arbitrary collection types an array syntax can also be used (e.g. `$fastq_input['forward']`).

**Note:** Mirroring the ability of Galaxy users to map tools that consume individual datasets over lists (and other collection types), users may also map lists of pairs over tools which explicitly consume dataset pair.

If the output of the tool is datasets, the output of this mapping operation (sometimes referred to as subcollection mapping) will be lists. The element identifier and index of the top level of the list will be preserved.

Some example tools which consume paired datasets include:

- `collection_paired_test` (minimal test tool in Galaxy test suite)
- Bowtie 2
- BWA MEM
- Tophat

### Processing Lists (Reductions)

The `data_collection` parameter type can specify a `collection_type` or `list` but whenever possible, it is recommended to not explicitly consume lists as a tool author. Parameters of type `data` can include a `multiple="True"` attribute to allow many datasets to be selected simultaneously. While the default UI will then have Galaxy users pick individual datasets, they can choose a collections as the tool can process both. This has the benefit of allowing tools to process either individual datasets or collections. A noteworthy difference is that if a parameter of type `data` with `multiple="true"` is used, the elements of the collection are passed to the tool as a (Python) list, i.e. it is not possible:

- to find out if a collection was passed,
- to access properties of the collection (name,…), or
• to write tests that pass a collection to the parameter (which would allow to name the elements explicitly).

Another drawback is that the $\{on_string\} of the label contains the list of data sets in the collection (which can be confusing, since these data sets are in most cases hidden) and not the name of the collection.

```xml
<param type="data" name="inputs" label="Input BAM(s)" format="bam" multiple="true" />
```

The command tag can use for loops to build command lines using these parameters.

For instance:

```bash
#for $input in $inputs
 --input "$input"
#end for
```

or using the single-line form of this expression:

```bash
#for $input in $inputs\n $input \n#end for#
```

Will produce command strings with an argument for each input (e.g. `--input "/path/to/input1" --input "/path/to/input2"`). Other programs may require all inputs to be supplied in a single parameter. This can be accomplished using the idiom:

```bash
--input "${",".join(map(str, $inputs))}"
```

Some example tools which consume multiple datasets (including lists) include:

- multi_data_param (small test tool in Galaxy test suite)
- cuffmerge
- unionBedGraphs

Also see the tools-devteam repository Pull Request #20 modifying the cufflinks suite of tools for collection compatible reductions.

### Processing Identifiers

Collection elements have identifiers that can be used for various kinds of sample tracking. These identifiers are set when the collection is first created - either explicitly in the UI (or API), through mapping over collections that preserves input identifiers, or as the identifier when dynamically discovering collection outputs described below.

During reduction steps one may likely want to use these - for reporting, comparisons, etc. When using these multiple data parameters the dataset objects expose a field called `element_identifier`. When these parameters are used with individual datasets - this will just default to being the dataset’s name, but when used with collections this parameter will be the `element_identifier` (i.e. the preserved sample name).

For instance, imagine merging a collection of tabular datasets into a single table with a new column indicating the sample name the corresponding rows were derived from using a little fictitious program called `merge_rows`.

```bash
#import re
#for $input in $inputs
 merge_rows --name "${re.sub('^[^\w\-\_]','_', $input.element_identifier)}" --file "--$input" --to $output;
#end for
```
Note: Here we are rewriting the element identifiers to assure everything is safe to put on the command-line. In the future, collections will not be able to contain keys that are potentially harmful and this won’t be necessary.

Some example tools which utilize `element_identifier` include:

- `identifier_multiple`
- `identifier_single`
- `vcftools_merge`
- `jbrowse`
- `kraken-mpa-report`

### More on `data_collection` parameters

The above three cases (users mapping over single tools, consuming pairs, and consuming lists using `multiple data parameters`) are hopefully the most common ways to consume collections for a tool author - but the `data_collection` parameter type allows one to handle more cases than just these.

We have already seen that in command blocks `data_collection` parameters can be accessed as arrays by element identifier (e.g. `$input_collection"left"`). This applies for lists and higher-order structures as well as pairs. The valid element identifiers can be iterated over using the `keys` method.

```bash
#for $key in $input_collection.keys()
    --input_name $key
    --input $input_collection[$key]
#end for

#for $input in $input_collection
    --input $input
#end for
```

Importantly, the `keys` method and direct iteration are both strongly ordered. If you take a list of files, do a bunch of processing on them to produce another list, and then consume both collections in a tools - the elements will match up if iterated over simultaneously.

Finally, if processing arbitrarily nested collections - one can access the `is_collection` attribute to determine if a given element is another collection or just a dataset.

```bash
#for $input in $input_collection
    --nested ${input.is_collection}
#end for
```

Some example tools which consume nested collections include:

- `collection_nested_test` (small test tool demonstrating consumption of nested collections)

### Creating Collections

Whenever possible simpler operations that produce datasets should be implicitly “mapped over” to produce collections as described above - but there are a variety of situations for which this idiom is insufficient.

Progressively more complex syntax elements exist for the increasingly complex scenarios. Broadly speaking - the three scenarios covered are when the tool produces...
1. a collection with a static number of elements (mostly for paired collections, but if a tool has fixed binding it might make sense to create a list this way as well)
2. a list with the same number of elements as an input list (this would be a common pattern for normalization applications for instance).
3. a list where the number of elements is not knowable until the job is complete.

1. Static Element Count

For this first case - the tool can declare standard data elements below an output collection element in the outputs tag of the tool definition.

```xml
<collection name="paired_output" type="paired" label="Split Pair">
  <data name="forward" format="txt" />
  <data name="reverse" format_source="input1" from_work_dir="reverse.txt" />
</collection>
```

Templates (e.g. the command tag) can then reference $forward and $reverse or whatever name the corresponding data elements are given as demonstrated in test/functional/tools/collection_creates_pair.xml.

The tool should describe the collection type via the type attribute on the collection element. Data elements can define format, format_source, metadata_source, from_work_dir, and name.

The above syntax would also work for the corner case of static lists. For paired collections specifically however, the type plugin system now knows how to prototype a pair so the following even easier (though less configurable) syntax works.

```xml
<collection name="paired_output" type="paired" label="Split Pair" format_source="input1">
</collection>
```

In this case the command template could then just reference ${paired_output.forward} and ${paired_output.reverse} as demonstrated in test/functional/tools/collection_creates_pair_from_type.xml.

2. Computable Element Count

For the second case - where the structure of the output is based on the structure of an input - a structured_like attribute can be defined on the collection tag.

```xml
<collection name="list_output" type="list" label="Duplicate List" structured_like="input1" inherit_format="true" />
```

Templates can then loop over input1 or list_output when building up command-line expressions. See test/functional/tools/collection_creates_list.xml for an example.

format, format_source, and metadata_source can be defined for such collections if the format and metadata are fixed or based on a single input dataset. If instead the format or metadata depends on the formats of the collection it is structured like - inherit_format="true" and/or inherit_metadata="true" should be used instead - which will handle corner cases where there are for instance subtle format or metadata differences between the elements of the incoming list.

5.3. Advanced Tool Development Topics
3. Dynamic Element Count

The third and most general case is when the number of elements in a list cannot be determined until runtime. For instance, when splitting up files by various dynamic criteria.

In this case a collection may define one of more discover_dataset elements. As an example of one such tool that splits a tabular file out into multiple tabular files based on the first column see test/functional/tools/collection_split_on_column.xml - which includes the following output definition:

```xml
<collection name="split_output" type="list" label="Table split on first column">
  <discover_datasets pattern="__name_and_ext__" directory="outputs" />
</collection>
```

Nested Collections

Galaxy Pull Request #538 implemented the ability to define nested output collections. See the pull request and included example tools for more details.

Further Reading

- Galaxy Community Conference Talk by John Chilton [Slides][Video].
- Creating and Managing Collections
- Pull Request #386 (the initial implementation)
- Pull Request #634 (implementing ability for tools to explicitly output collections)

5.3.4 Macros - Reusable Elements

Frequently, tools may require the same XML fragments be repeated in a file (for instance similar conditional branches, repeated options, etc…) or between tools in the same repository (for instance, nearly all of the GATK tools contain the same standard options). Galaxy tools have a macroing system to address this problem.

Direct XML Macros

The following examples are taken from Pull Request 129 the initial implementation of macros. Prior to to the inclusion of macros, the tophat2 wrapper defined several outputs each which had the following identical actions block associated with them:

```xml
<actions>
  <conditional name="refGenomeSource.genomeSource">
    <when value="indexed">
      <action type="metadata" name="dbkey">
        <option type="from_data_table" name="tophat2_indexes" column="1" offset="0">
          <filter type="param_value" column="0" value="#" compare="startswith" keep="False"/>
          <filter type="param_value" ref="refGenomeSource.index" column="0"/>
        </option>
      </action>
    </when>
    <when value="history">
      <action type="metadata" name="dbkey">
        ...
      </action>
    </when>
  </conditional>
</actions>
```

(continues on next page)
To reuse this action definition, first a macros section has been defined in the tophat2_wpper.xml file.

```xml
<tool>
  ...
  <macros>
    <xml name="dbKeyActions">
      <action> <!-- Whole big example above. -->
        ....
      </action>
    </xml>
  </macros>
</tool>
```

With this in place, each output data element can include this block using the expand XML element as follows:

```xml
<outputs>
  <data format="bed" name="insertions" label="${tool.name} on ${on_string}: insertions" from_work_dir="tophat_out/insertions.bed">
    <expand macro="dbKeyActions" />
  </data>
  <data format="bed" name="deletions" label="${tool.name} on ${on_string}: deletions" from_work_dir="tophat_out/deletions.bed">
    <expand macro="dbKeyActions" />
  </data>
  <data format="bed" name="junctions" label="${tool.name} on ${on_string}: splice junctions" from_work_dir="tophat_out/junctions.bed">
    <expand macro="dbKeyActions" />
  </data>
  <data format="bam" name="accepted_hits" label="${tool.name} on ${on_string}: accepted_hits" from_work_dir="tophat_out/accepted_hits.bam">
    <expand macro="dbKeyActions" />
  </data>
</outputs>
```

This has reduced the size of the XML file by dozens of lines and reduces the long term maintenance associated with copied and pasted code.

**Imported Macros**

The `macros` element described above, can also contain any number of `import` elements. This allows a directory/repository of tool XML files to contain shared macro definitions that can be used by any number of actual tool files in that directory/repository.

Revisiting the tophat example, all three tophat wrappers (tophat_wrapper.xml, tophat_color_wrapper.xml, and tophat2_wparer.xml) shared some common functionality. To reuse XML elements between these files, a tophat_macros.xml file was added to that directory.

The following block is a simplified version of that macros file’s contents:
Any tool definition in that directory can use the macros contained therein once imported as shown below.
This example also demonstrates that macros may themselves expand macros.

### Parameterizing XML Macros (with yield)

In some cases, tools may contain similar though not exact same definitions. Some parameterization can be performed by declaring expand elements with child elements and expanding them in the macro definition with a yield element.

For instance, previously the tophat wrapper contained the following definition:

```xml
<conditional name="refGenomeSource">
  <param name="genomeSource" type="select" label="Will you select a reference genome from your history or use a built-in index?" help="Built-ins were indexed using default options">
    <option value="indexed">Use a built-in index</option>
    <option value="history">Use one from the history</option>
  </param>
  <when value="indexed">
    <param name="index" type="select" label="Select a reference genome" help="If your genome of interest is not listed, contact the Galaxy team">
      <options from_data_table="tophat_indexes_color">
        <filter type="sort_by" column="2"/>
        <validator type="no_options" message="No indexes are available for the selected input dataset"/>
      </options>
    </param>
  </when>
  <when value="history">
    <param name="ownFile" type="data" format="fasta" metadata_name="dbkey" label="Select the reference genome"/>
  </when>
</conditional> <!-- refGenomeSource -->
```

and the tophat2 wrapper contained the highly analogous definition:

```xml
<conditional name="refGenomeSource">
  <param name="genomeSource" type="select" label="Will you select a reference genome from your history or use a built-in index?" help="Built-ins were indexed using default options">
    <option value="indexed">Use a built-in index</option>
    <option value="history">Use one from the history</option>
  </param>
  <when value="indexed">
    <param name="index" type="select" label="Select a reference genome" help="If your genome of interest is not listed, contact the Galaxy team">
      <options from_data_table="tophat_indexes_color">
        <filter type="sort_by" column="2"/>
        <validator type="no_options" message="No indexes are available for the selected input dataset"/>
      </options>
    </param>
  </when>
  <when value="history">
    <param name="ownFile" type="data" format="fasta" metadata_name="dbkey" label="Select the reference genome"/>
  </when>
</conditional> <!-- refGenomeSource -->
```

(continues on next page)
These blocks differ only in the from_data_table attribute on the options element. To capture this pattern, tophat_macros.xml contains the following macro definition:

```xml
<xml name="refGenomeSourceConditional">
  <conditional name="refGenomeSource">
    <param name="genomeSource" type="select" label="Use a built in reference genome or own from your history" help="Built-ins genomes were created using default options">
      <option value="indexed" selected="True">Use a built-in genome</option>
      <option value="history">Use a genome from history</option>
    </param>
    <when value="indexed">
      <param name="index" type="select" label="Select a reference genome" help="If your genome of interest is not listed, contact the Galaxy team">
        <yield />
      </param>
    </when>
    <when value="history">
      <param name="ownFile" type="data" format="fasta" metadata_name="dbkey" label="Select the reference genome" />
    </when>
  </conditional>
</xml>
```

Notice the yield statement in lieu of an options declaration. This allows the nested options element to be declared when expanding the macro:

The following expand declarations have replaced the original conditional elements.

```xml
<expand macro="refGenomeSourceConditional">
  <options from_data_table="tophat_indexes">
    <filter type="sort_by" column="2"/>
    <validator type="no_options" message="No genomes are available for the selected input dataset"/>
  </options>
</expand>

<expand macro="refGenomeSourceConditional">
  <options from_data_table="tophat2_indexes">
    <filter type="sort_by" column="2"/>
    <validator type="no_options" message="No genomes are available for the selected input dataset"/>
  </options>
</expand>
```
Parameterizing XML Macros (with tokens)

In addition to using `yield` blocks, there is another way to parameterize macros through the use of specifying `token_xyz` attributes on the macro definition, and then using `@XYZ@` anywhere within the XML.

```xml
<macros>
  <xml name="color" token_varname="myvar" token_default_color="#00ff00" token_label="Pick a color">
    <param name="@VARNAME@" type="color" label="@LABEL@" value="@DEFAULT_COLOR@" />
  </xml>
</macros>
```

When invoking this macro, you can pass those values and produce varying results.

```xml
<inputs>
  <expand macro="color" default_color="#ff0000" />
  <expand macro="color" default_color="#0000ff" varname="c2" label="Choose a different color" />
</inputs>
```

The attributes passed to the macro definition will be filled in (or defaults used when not provided).

```xml
<inputs>
  <param name="myvar" type="color" label="Pick a color" value="#ff0000" />
  <param name="c2" type="color" label="Choose a different color" value="#0000ff" />
</inputs>
```

Macro Tokens

You can use

```xml
<token name="@IS_PART_OF_VCFLIB@">is a part of VCFlib toolkit developed by Erik Garrison (https://github.com/ekg/vcflib).</token>
```

and then call the token within any element of the file like this:

```xml
Vcfallelicprimitives @IS_PART_OF_VCFLIB@
```

5.3.5 Tool Provided Metadata

This stub of a section provides some initial documentation on tool provided metadata. Galaxy allows datasets to be discovered after a tool has been executed and allows tools to specify metadata for these datasets. Whenever possible, Galaxy’s datatypes and more structured outputs should be used to collect metadata.

If an arbitrary number of outputs is needed but no special metadata must be set, file name patterns can be used to allow Galaxy to discover these datasets. More information on this can be found on the Galaxy wiki.

The file name patterns described in the above link are nice because they don’t need special instrumenting in the tool wrapper to adapt to Galaxy in general and can adapt to many existing application’s output. When more metadata must be supplied or when implementing a custom tool wrapper anyway - it may be beneficial to build a manifest file.

A tool may also produce a file called `galaxy.json` during execution. If upon a job’s completion this file is populated, Galaxy will expect to find metadata about outputs in it.

The format of this file is a bit quirky - each line of this file should be a JSON dictionary. Each such dictionary should contain a `type` attribute - this type may be either `new_primary_dataset` or `dataset`.

5.3. Advanced Tool Development Topics
If the type is `new_primary_dataset`, the dictionary should contain a `filename` entry with a path to a “discovered dataset”. In this case the dictionary may contain any of the following entries `name`, `dbkey`, `info`, `ext`, `metadata`.

- `name` will be used as the output dataset’s name
- `ext` allows specification of the format of the output (e.g. `txt`, `tabular`, `fastqsanger`, etc...)
- `dbkey` allows specifying a genome build for the discovered dataset
- `info` is a short text description for each dataset that appears in the history panel
- `metadata` this should be a dictionary of key-value pairs for metadata registered with the datatype for this output

Examples of tools using `new_primary_dataset` entries:

- `tool_provided_metadata_2.xml` demonstrating using the simpler attributes described here.
- `tool_provided_metadata_3.xml` demonstrates overridding datatype specified metadata.

The type of an entry may also be `dataset`. In this case the metadata descriptions describe an explicit output (one with its own corresponding `output` element definition). In this case, an entry called `dataset` should appear in the dictionary (in lieu of `filename` above) and should be the database id of the output dataset. Such entries may contain all of the other fields described above except `metadata`.

Example tool using a `dataset` entry:

- `tool_provided_metadata_1.xml`

### 5.3.6 Cluster Usage

#### Developing for Clusters - `GALAXY_SLOTS`, `GALAXY_MEMORY_MB`, and `GALAXY_MEMORY_MB_PER_SLOT`

`GALAXY_SLOTS` is a special environment variable that is set in a Galaxy tool’s runtime environment. If the tool you are working on allows configuring the number of processes or threads that should be spawned, this variable should be used.

For example, the StringTie (tool available here) binary `stringtie` can take an argument `-p` that allows specification of the number of threads to be used. The Galaxy tool sets this up as follows

```
stringtie "$input_bam" -o "$output_gtf" -p "\$(GALAXY_SLOTS:-1)" ...
```

Here we use `\$(GALAXY_SLOTS:-Z)` instead of a fixed value (Z being an integer representing a default value in non-Galaxy contexts). The backslash here is because this value is interpreted at runtime as environment variable - not during command building time as a templated value. Now server administrators can configure how many processes the tool should be allowed to use.

For information on how server administrators can configure this value for a particular tool, check out the Galaxy admin documentation.

Analogously `GALAXY_MEMORY_MB` and `GALAXY_MEMORY_MB_PER_SLOT` are special environment variables in a Galaxy tool’s runtime environment that can be used to specify the amount of memory that a tool can use overall and per slot, respectively.

For an example see the samtools sort tool (here) which allows to specify the total memory with the `-m` parameter.
**Test Against Clusters: --job_config_file**

The various commands that start Galaxy servers (serve, test, shed_serve, shed_test, etc...) allow specification of a Galaxy job configuration XML file (e.g. job_conf.xml).

For instance, Slurm is a popular distributed resource manager (DRM) in the Galaxy community. The following job_conf.xml tells Galaxy to run all jobs using Slurm and allocate 2 cores for each job.

```xml
<?xml version="1.0"?>
<job_conf>
  <plugins>
    <plugin id="drmaa" type="runner" load="galaxy.jobs.runners.drmaa:DRMAAJobRunner"/>
  </plugins>
  <handlers>
    <handler id="main"/>
  </handlers>
  <destinations default="drmaa">
    <destination id="drmaa" runner="drmaa">
      <param id="nativeSpecification">
        --time=00:05:00 --nodes=1 --ntasks=2
      </param>
    </destination>
  </destinations>
</job_conf>
```

If this file is named planemo_job_conf.xml and resides in one’s home directory (~), Planemo can test or serve using this configuration with the following commands.

```bash
$ planemo test --job_config_file ~/planemo_job_conf.xml .
$ planemo serve --job_config_file ~/planemo_job_conf.xml .
```

For general information on configuring Galaxy to communicate with clusters check out this page on the Galaxy wiki and for information regarding configuring job configuration XML files in particular check out the example distributed with Galaxy.

### 5.3.7 Dependencies and Conda

**Specifying and Using Tool Requirements**

**Note:** This document discusses using Conda to satisfy tool dependencies from a tool developer perspective. An in depth discussion of using Conda to satisfy dependencies from an administrator’s perspective can be found [here](#). That document also serves as good background for this discussion.

**Note:** Planemo requires a Conda installation to target with its various Conda related commands. A properly configured Conda installation can be initialized with the `conda_init` command. This should only need to be executed once per development machine.

```bash
$ planemo conda_init
```

(continues on next page)
installing: python-3.6.3-h47c878a_7 ...
Python 3.6.3 :: Anaconda, Inc.
installing: ca-certificates-2017.08.26-hae5d58_0 ...
installing: conda-env-2.6.0-h36134e3_0 ...
installing: libcxabi-4.0.1-hebd6815_0 ...
installing: tk-8.6.7-h35a86e2_3 ...
installing: xz-5.2.3-h0278029_2 ...
installing: yaml-0.1.7-hc338f04_2 ...
installing: zlib-1.2.11-hf3cb39b_2 ...
installing: libcx-x-4.0.1-h579ed51_0 ...
installing: openssl1-1.0.2n-hd6c3d79_0 ...
installing: libffi-3.2.1-h475c297_4 ...
installing: ncs-6.0-hd04f020_2 ...
installing: libedit-3.1-hb4e282d_0 ...
installing: readline-7.0-hc338f04_4 ...
installing: sqlite-3.20.1-h7e4c145_2 ...
installing: asn1crypto-0.23.0-py36h782d450_0 ...
installing: certifi-2017.11.5-py36ha569be9_0 ...
installing: charget-3.0.4-py36h96c241c_1 ...
installing: idn-2.6-py36hc628d0a_1 ...
installing: pyscetxt-0.6.3-py36hee92d8f_0 ...
installing: pyopenssl-17.5.0-py36h51e4350_0 ...
installing: requests-2.18.4-py36h724b2fc_1 ...
installing: pysocks-1.6.7-py36hfa33cece_1 ...
installing: python-app-2-py36h54569d5_7 ...
installing: ruamel_yaml-0.11.14-py36h9d7ade0_2 ...
installing: six-1.11.0-py36h0e22d5e_1 ...
installing: cffi-1.11.2-py36hd3e6348_0 ...
installing: setuptools-36.5.0-py36h2134326_0 ...
installing: cryptography-2.1.4-py36h842514c_0 ...
installing: wheel-0.30.0-py36h5eb2c71_1 ...
installing: pip-9.0.1-py36h1555ced_4 ...
installing: pyopenssl-17.5.0-py36h9d7ade0_2 ...
installing: urllib3-1.22-py36h9d7ade0_2 ...
installing: requests-2.18.4-py36h4516966_1 ...
installing: conda-4.3.31-py36_0 ...
installation finished.
/Users/john/miniconda3/bin/conda install -y --override-channels --channel iuc --channel conda-forge --channel bioconda --channel defaults conda=4.3.33 conda-build=2.1.18
Fetching package metadata ..................
Solving package specifications: .

Package plan for installation in environment /Users/john/miniconda3:

The following NEW packages will be INSTALLED:

- beautifulsoup4: 4.6.0-py36_0 conda-forge
- conda-build: 2.1.18-py36_0 conda-forge
- conda-verify: 2.0.0-py36_0 conda-forge
- filelock: 3.0.4-py36_0 conda-forge
- jinja2: 2.10-py36_0 conda-forge
- markupsafe: 1.0-py36_0 conda-forge
- pkginfo: 1.4.2-py36_0 conda-forge
- pycrypto: 2.6.1-py36_1 conda-forge
- pyyaml: 3.12-py36_1 conda-forge

(continues on next page)
The following packages will be UPDATED:

<table>
<thead>
<tr>
<th>Package</th>
<th>Current Version</th>
<th>New Version</th>
<th>Channel</th>
</tr>
</thead>
<tbody>
<tr>
<td>conda</td>
<td>4.3.31-py36_0</td>
<td>--&gt; 4.3.33-py36_0 conda-forge</td>
<td></td>
</tr>
<tr>
<td>beautifulsoup4</td>
<td>100%</td>
<td>#...................</td>
<td>Time: 0:00:00 782.08 kB/s</td>
</tr>
<tr>
<td>filelock-3.0.4</td>
<td>100%</td>
<td>#...................</td>
<td>Time: 0:00:00 7.95 MB/s</td>
</tr>
<tr>
<td>markupsafe-1.0</td>
<td>100%</td>
<td>#...................</td>
<td>Time: 0:00:00 5.82 MB/s</td>
</tr>
<tr>
<td>pkginfo-1.4.2-</td>
<td>100%</td>
<td>#...................</td>
<td>Time: 0:00:00 1.18 MB/s</td>
</tr>
<tr>
<td>pycrypto-2.6.1</td>
<td>100%</td>
<td>#...................</td>
<td>Time: 0:00:00 1.69 MB/s</td>
</tr>
<tr>
<td>pyyaml-3.12-py</td>
<td>100%</td>
<td>#...................</td>
<td>Time: 0:00:00 3.31 MB/s</td>
</tr>
<tr>
<td>conda-verify-2</td>
<td>100%</td>
<td>#...................</td>
<td>Time: 0:00:00 6.91 MB/s</td>
</tr>
<tr>
<td>jinja2-2.10-py</td>
<td>100%</td>
<td>#...................</td>
<td>Time: 0:00:00 2.81 MB/s</td>
</tr>
<tr>
<td>conda-4.3.33-p</td>
<td>100%</td>
<td>#...................</td>
<td>Time: 0:00:00 621.27 kB/s</td>
</tr>
<tr>
<td>conda-build-2.</td>
<td>100%</td>
<td>#...................</td>
<td>Time: 0:00:00 2.16 MB/s</td>
</tr>
</tbody>
</table>

Conda installation succeeded - Conda is available at ‘/Users/john/miniconda3/bin/conda’

While Galaxy can be configured to resolve dependencies various ways, Planemo is configured with opinionated defaults geared at making building tools that target Conda as easy as possible.

During the introductory tool development tutorial, we called `planemo tool_init` with the argument `--requirement seqtk@1.2` and the resulting tool contained the XML:

```xml
<requirements>
  <requirement type="package" version="1.2">seqtk</requirement>
</requirements>
```

As configured by Planemo, when Galaxy encounters these requirement tags it will attempt to install Conda, check for referenced packages (such as seqtk), and install them as needed for tool testing.

**Note:** Why Conda?

Many different package managers could potentially be targeted here, but we focus on Conda for a few key reasons.

- No compilation at install time - binaries with their dependencies and libraries
- Support for all operating systems
- Easy to manage multiple versions of the same recipe
- HPC-ready: no root privileges needed
- Easy-to-write YAML recipes
- Vibrant communities
Fig. 1: Galaxy’s dependency resolution maps tool requirement tags to concrete applications and libraries setup by the Galaxy deployer (or Planemo). As the above diagram indicates the same requirements may be used by multiple Galaxy tools and a single Galaxy tool may depend on multiple requirements. The document describes working with Conda dependencies from a developer perspective but other dependency resolution techniques are covered in the Galaxy docs.
Conda recipes build packages that are published to channels.

Planemo is setup to target a few channels by default, these include iuc, bioconda, conda_forge, defaults - the whole dependency management scheme outlined here works a lot better if packages can be found in one of these “best practice” channels.

We can check if the requirements on a tool are available in best practice Conda channels using an extended form of the planemo lint command. Passing --conda_requirements flag will ensure all listed requirements are found.

```
$ planemo lint --conda_requirements seqtk_seq.xml
Linting tool /Users/john/workspace/planemo/docs/writing/seqtk_seq.xml
...
Applying linter requirements_in_conda... CHECK
.. INFO: Requirement [seqtk@1.2] matches target in best practice Conda channel... →[bioconda].
```

**Note:** You can download the final version of the seqtk seq wrapper from the Planemo tutorial using the command:

```
$ planemo project_init --template=seqtk_complete seqtk_example
$ cd seqtk_example
```

We can verify these tool requirements install with the conda_install command. With its default parameters conda_install processes tools and creates isolated environments for their declared requirements.

5.3. Advanced Tool Development Topics
$ planemo conda_install seqtk_seq.xml
Install conda target CondaTarget[seqtk,version=1.2]
/home/john/miniconda2/bin/conda create -y --name __seqtk@1.2 seqtk=1.2
Fetching package metadata ............
Solving package specifications: ..........

Package plan for installation in environment /home/john/miniconda2/envs/__seqtk@1.2:
The following packages will be downloaded:

<table>
<thead>
<tr>
<th>package</th>
<th>build</th>
</tr>
</thead>
<tbody>
<tr>
<td>seqtk-1.2</td>
<td>0 29 KB bioconda</td>
</tr>
</tbody>
</table>

The following NEW packages will be INSTALLED:

seqtk: 1.2-0  bioconda
zlib: 1.2.8-3

Fetching packages ...
seqtk-1.2-0.ta 100% |##########################################################| ...
-Time: 0:00:00 444.71 kB/s
Extracting packages ...
[ COMPLETE ]|##########################################################| 100%
Linking packages ...
[ COMPLETE ]|##########################################################| 100%

# To activate this environment, use:
# > source activate __seqtk@1.2

# To deactivate this environment, use:
# > source deactivate __seqtk@1.2

$ which seqtk
seqtk not found
$

The above install worked properly, but seqtk is not on your PATH because this merely created an environment within the Conda directory for the seqtk installation. Planemo will configure Galaxy to exploit this installation. If you wish to interactively explore the resulting enviromnt to explore the installed tool or produce test data the output of the conda_env command can be sourced.

$ . <(planemo conda_env seqtk_seq.xml)
Deactivate environment with conda_env_deactivate
(seqtk_seq) $ which seqtk
/home/planemo/miniconda2/envs/jobdepsiJC1EUFec6d406196737781ff4456ec60975c137e04884e4f4b05dc68192f7cec4656/bin/
(seqtk_seq) $ seqtk seq

Usage: seqtk seq [options] <in.fq>|<in.fa>

Options: -q INT  mask bases with quality lower than INT [0]
          -X INT  mask bases with quality higher than INT [255]
          -n CHAR masked bases converted to CHAR; 0 for lowercase [0]
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(continued from previous page)

-1 INT number of residues per line; 0 for 2^32-1 [0]
-Q INT quality shift: ASCII-INT gives base quality [33]
-s INT random seed (effective with -f) [11]
-f FLOAT sample FLOAT fraction of sequences [1]
-M FILE mask regions in BED or name list FILE [null]
-L INT drop sequences with length shorter than INT [0]
-c mask complement region (effective with -M)
-r reverse complement
-A force FASTA output (discard quality)
-C drop comments at the header lines
-N drop sequences containing ambiguous bases
-1 output the 2n-1 reads only
-2 output the 2n reads only
-V shift quality by ‘(-Q) - 33’
-U convert all bases to uppercases
-S strip of white spaces in sequences

(seqtk_seq) $ conda_env_deactivate

As shown above the conda_env_deactivate will be created in this environment and can be used to restore your initial shell configuration.

Confident the underlying application works, we can now use planemo test or planemo serve and it will reuse this environment and find our dependency (in this case seqtk as needed).

Here is a portion of the output from the testing command planemo test seqtk_seq.xml demonstrating using this tool.

$ planemo test seqtk_seq.xml
...
2017-02-22 10:13:28,902 INFO [galaxy.tools.actions] Handled output named output1 for...
2017-02-22 10:13:28,914 INFO [galaxy.tools.actions] Added output datasets to history...
2017-02-22 10:13:28,935 INFO [galaxy.tools.actions] Verified access to datasets for...
2017-02-22 10:13:28,962 INFO [galaxy.tools.actions] Flushed transaction for job...
2017-02-22 10:13:29,064 INFO [galaxy.jobs.handler] (2) Job dispatched
2017-02-22 10:13:29,281 DEBUG [galaxy.tools.deps] Using dependency seqtk version 1.2...
2017-02-22 10:13:29,282 DEBUG [galaxy.tools.deps] Using dependency seqtk version 1.2...
2017-02-22 10:13:29,317 INFO [galaxy.jobs.command_factory] Built script [/tmp/tmpLvKwta/job_working_directory/000/2/tool_script.sh] for tool command [[ "$CONDA_DEFAULT_ENV" = "/Users/john/miniconda2/envs/__seqtk@1.2" ] || . /Users/john/miniconda2/bin/activate '/Users/john/miniconda2/envs/__seqtk@1.2' >conda_activate.log 2>&1 ; seqtk seq -a '/tmp/tmpLvKwta/files/000/dataset_1.dat' > '/tmp/tmpLvKwta/files/000/dataset_2.dat']
2017-02-22 10:13:29,516 DEBUG [galaxy.tools.deps] Using dependency samtools version...
2017-02-22 10:13:29,516 DEBUG [galaxy.tools.deps] Using dependency samtools version...
ok

5.3. Advanced Tool Development Topics

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In this case the tests passed and the line containing `[galaxy.tools.deps] Using dependency seqtk version 1.2 of type conda` indicates Galaxy dependency resolution was successful and it found the environment we previously installed with `conda_install`.

### Finding Existing Conda Packages

How did we know what software name and software version to use? We found the existing packages available for Conda and referenced them. To do this yourself, you can simply use the planemo command `conda_search`. If we do a search for `seqtk` it will show all the software and all the versions available matching that search term - including `seqtk`.

$ planemo conda_search seqtk
/Users/john/miniconda3/bin/conda search --override-channels --channel iuc --channel conda-forge --channel bioconda --channel defaults '*seqtk*

Loading channels: done

<table>
<thead>
<tr>
<th>#</th>
<th>Name</th>
<th>Version</th>
<th>Build</th>
<th>Channel</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>bioconductor-hseqtools</td>
<td>1.26.0</td>
<td>r3.4.1_0</td>
<td>bioconda</td>
</tr>
<tr>
<td>2</td>
<td>bioconductor-seqtools</td>
<td>1.10.0</td>
<td>r3.3.2_0</td>
<td>bioconda</td>
</tr>
<tr>
<td>3</td>
<td>bioconductor-seqtools</td>
<td>1.10.0</td>
<td>r3.4.1_0</td>
<td>bioconda</td>
</tr>
<tr>
<td>4</td>
<td>bioconductor-seqtools</td>
<td>1.12.0</td>
<td>r3.4.1_0</td>
<td>bioconda</td>
</tr>
<tr>
<td>5</td>
<td>seqtk</td>
<td>r75</td>
<td>0</td>
<td>bioconda</td>
</tr>
<tr>
<td>6</td>
<td>seqtk</td>
<td>r82</td>
<td>0</td>
<td>bioconda</td>
</tr>
<tr>
<td>7</td>
<td>seqtk</td>
<td>r82</td>
<td>1</td>
<td>bioconda</td>
</tr>
<tr>
<td>8</td>
<td>seqtk</td>
<td>r93</td>
<td>0</td>
<td>bioconda</td>
</tr>
<tr>
<td>9</td>
<td>seqtk</td>
<td>1.2</td>
<td>0</td>
<td>bioconda</td>
</tr>
<tr>
<td>10</td>
<td>seqtk</td>
<td>1.2</td>
<td>1</td>
<td>bioconda</td>
</tr>
</tbody>
</table>

**Note:** The Planemo command `conda_search` is a light wrapper around the underlying `conda search` command but configured to use the same channels and other options as Planemo and Galaxy. The following Conda command would also work to search:

$ $HOME/miniconda3/bin/conda -c iuc -c conda-forge -c bioconda '*seqtk*

For Conda versions 4.3.X or less, the search invocation would be something a bit different:
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Alternatively the Anaconda website can be used to search for packages. Typing seqtk into the search form on that page and clicking the top result will bring on to this page with information about the Bioconda package.

When using the website to search though, you need to aware of what channel you are using. By default, Planemo and Galaxy will search a few different Conda channels. While it is possible to configure a local Planemo or Galaxy to target different channels - the current best practice is to add tools to the existing channels.

The existing channels include:

- Bioconda (github | conda) - best practice channel for various bioinformatics packages.
- Conda-Forge (github | conda) - best practice channel for general purpose and widely useful computing packages and libraries.
- iuc (github | conda) - best practice channel for other more Galaxy specific packages.

Exercise - Leveraging Bioconda

Use the project_init command to download this exercise.

```
$ planemo project_init --template conda_exercises conda_exercises
$ cd conda_exercises/exercise_1
$ ls
pear.xml   test-data
```

This project template contains a few exercises. The first uses an adapted version of an IUC tool for PEAR - Paired-End read mergeR. This tool however has no requirement tags and so will not work properly.

1. Run planemo test pear.xml to verify the tool does not function without dependencies defined.
2. Use --conda_requirements flag with planemo lint to verify it does indeed lack requirements.
3. Use planemo conda_search or the Anaconda website to search for the correct package and version in a best practice channel.
4. Update pear.xml with the correct requirement tags.
5. Re-run the lint command from above to verify the tool now has the correct dependency definition.
6. Re-run the test command from above to verify the tool test now works properly.

Building New Conda Packages

Frequently packages your tool will require are not found in Bioconda or conda-forge yet. In these cases, it is likely best to contribute your package to one of these projects. Unless the tool is exceedingly general Bioconda is usually the correct starting point.

Note: Many things that are not strictly or even remotely “bio” have been accepted into Bioconda - including tools for image analysis, natural language processing, and cheminformatics.

To get quickly learn to write Conda recipes for typical Galaxy tools, please read the following pieces of external documentation.

- Contributing to Bioconda in particular focusing on
• One time setup
  • Contributing a recipe (through “Write a Recipe”)

• Building conda packages in particular
  • Building conda packages with conda skeleton (the best approach for common scripting languages such as R and Python)
  • Building conda packages from scratch
  • Building conda packages for general code projects
  • Using conda build

• Then return to the Bioconda documentation and read
  • The rest of “Contributing a recipe” continuing from Testing locally
  • And finally Guidelines for bioconda recipes

These guidelines in particular can be skimmed depending on your recipe type, for instance that document provides specific advice for:

• Python
• R (CRAN)
• R (Bioconductor)
• Perl
• C/C++

To go a little deeper, you may want to read:

• Specification for meta.yaml
• Environment variables
• Custom channels

And finally to debug problems the Bioconda troubleshooting documentation may prove useful.

Exercise - Build a Recipe

If you have just completed the exercise above - this exercise can be found in parent folder. Get there with `cd ../exercise_2`. If not, the exercise can be downloaded with

```
$ planemo project_init --template conda_exercises conda_exercises
$ cd conda_exercises/exercise_2
$ ls
fleeqtk_seq.xml test-data
```

This is the skeleton of a tool wrapping the parody bioinformatics software package fleeqtk. fleeqtk is a fork of the project seqtk that many Planemo tutorials are built around and the example tool should hopefully be fairly familiar. fleeqtk version 1.3 can be downloaded from [here](#) and built using `make`. The result of `make` includes a single executable `fleeqtk`.

1. Clone and branch Bioconda.

2. Build a recipe for fleeqtk version 1.3. You may wish to start from scratch (`conda skeleton` is not available for C programs like fleeqtk), or copy the recipe of seqtk and modify it for fleeqtk.

3. Use `conda build` or Bioconda tooling to build the recipe.
4. Run `planemo test --conda_use_local fleeqtk_seq.xml` to verify the resulting package works as expected.

Congratulations on writing a Conda recipe and building a package! Upon successfully building and testing such a Bioconda package, you would normally push your branch to Github and open a pull request. This step is skipped here as to not pollute Bioconda with unneeded software packages.

### 5.3.8 Dependencies and Containers

For years Galaxy has supported running tools inside containers. The details of how to run Galaxy tools inside of containers varies depending on the Galaxy job runner but details can be found in Galaxy’s `job_conf.xml` sample file.

This document doesn’t describe how to run the containers, it describes how Galaxy figures out which container to run for a given tool. There are currently two strategies for finding containers for a tool - and they are each discussed in detail in this document. The newer approach is a bit more experimental but should be considered the best practice approach - it is to allow Galaxy to find or build a BioContainers container using `requirement` tags that resolve to best-practice Conda channels. The older approach is to explicitly declare a container identifier in the tool XML.

While not as flexible as resolving arbitrary image IDs from URLs, the newer approach has a few key advantages that make them a best practice:

- They provide superior reproducibility across Galaxy instances because the same binary Conda packages will automatically be used for both bare metal dependencies and inside containers.
- They are constructed automatically from existing Conda packages so tool developers shouldn’t need to write `Dockerfiles` or register projects on Docker Hub.
- They are produced using `mulled` which produce very small containers that make deployment easy.
- Annotating `requirement` tags reduces the opaqueness of the Docker process. With this method it is entirely traceable how the container was constructed from what sources were fetched, which exact build of every dependency was used, to how packages in the container were built. Beyond that metadata about the packages can be fetched from Bioconda (e.g. [this](https://bioconda.github.io/)).

Read more about this reproducibility stack in our preprint *Practical computational reproducibility in the life sciences*.

### BioContainers

**Note:** This section is a continuation of *Dependencies and Conda*, please review that section for background information on resolving requirements with Conda.

### Finding BioContainers

If a tool contains requirements in best practice Conda channels, a BioContainers-style container can be found or built for it.

As reminder, `planemo lint --conda_requirements <tool.xml>` can be used to check if a tool contains only best-practice `requirement` tags. The `lint` command can also be fed the `--biocontainers` flag to check if a BioContainers container has been registered that is compatible with that tool.

Below is an example of using this with the completed `seqtk_seq.xml` tool from the introductory tutorial.
$ planemo lint --biocontainers seqtk_seq.xml
Linting tool /home/planemo/workspace/planemo/project_templates/seqtk_complete/seqtk_˓
seq.xml
Applying linter tests... CHECK
  . CHECK: 1 test(s) found.
Applying linter output... CHECK
  . INFO: 1 outputs found.
Applying linter inputs... CHECK
  . INFO: Found 9 input parameters.
Applying linter help... CHECK
  . CHECK: Tool contains help section.
  . CHECK: Help contains valid reStructuredText.
Applying linter general... CHECK
  . CHECK: Tool defines a version [0.1.0].
  . CHECK: Tool defines a name [Convert to FASTA (seqtk)].
  . CHECK: Tool targets 16.01 Galaxy profile.
Applying linter command... CHECK
  . INFO: Tool contains a command.
Applying linter citations... CHECK
  . CHECK: Found 1 likely valid citations.
Applying linter tool_xsd... CHECK
  . INFO: File validates against XML schema.
Applying linter biocontainer_registered... CHECK
  . INFO: BioContainer best-practice container found [quay.io/biocontainers/seqtk:1.2--˓
0].

This last linter indicates that indeed a container has been registered that is compatible with this tool – quay.io/ ˓
biocontainers/seqtk:1.2--1. We didn’t do any extra work to build this container for this tool, all Bioconda ˓
recipes are packaged into containers and registered on quay.io as part of the BioContainers project.

This tool can be tested using planemo test in its BioContainer Docker container using the flag ˓
--biocontainers as shown below.

$ planemo test --biocontainers seqtk_seq.xml
...
2017-03-01 08:18:19,669 INFO [galaxy.tools.actions] Handled output named output1 for ˓
tool seqtk_seq (22.145 ms)
2017-03-01 08:18:19,683 INFO [galaxy.tools.actions] Added output datasets to history ˓
(tool seqtk_seq) (14.604 ms)
2017-03-01 08:18:19,703 INFO [galaxy.tools.actions] Verified access to datasets for ˓
Job[unflushed,tool_id=seqtk_seq] (8.687 ms)
2017-03-01 08:18:19,704 INFO [galaxy.tools.actions] Setup for job Job[unflushed,tool_id=.seqtk_seq] complete, ready to flush (20.380 ms)
2017-03-01 08:18:19,719 INFO [galaxy.tools.actions] Flushed transaction for job ˓
Job[unflushed,tool_id=seqtk_seq] (15.191 ms)
2017-03-01 08:18:20,120 INFO [galaxy.jobs.handler] (2) Job dispatched
2017-03-01 08:18:20,311 DEBUG [galaxy.tools.deps] Using dependency seqtk version 1.2 ˓
of type conda
2017-03-01 08:18:20,312 DEBUG [galaxy.tools.deps] Using dependency seqtk version 1.2 ˓
of type conda
2017-03-01 08:18:20,325 INFO [galaxy.tools.deps.containers] Checking with container ˓
resolver [ExplicitDockerContainerResolver[]] found description [None]
2017-03-01 08:18:20,468 INFO [galaxy.tools.deps.containers] Checking with container ˓
resolver [CachedMulledDockerContainerResolver[namespace=None]] found description ˓
[None]
2017-03-01 08:18:20,881 INFO [galaxy.tools.deps.containers] Checking with container ˓
resolver [MulledDockerContainerResolver[namespace=biocontainers]] found description ˓
[ContainerDescription[identifier=quay.io/biocontainers/seqtk:1.2--0,type=docker]]
A very important line here is:

```plaintext
2017-03-01 08:18:20,881 INFO [galaxy.tools.deps.containers] Checking with container
  --resolver [MulledDockerContainerResolver[namespace=biocontainers]] found description
  ->[ContainerDescription[identifier=quay.io/biocontainers/seqtk:1.2--0,type=docker]]
```

This line indicates that Galaxy was able to find a container for this tool and executed the tool in that container.

For interactive testing, the `planemo serve` command also implements the `--biocontainers` flag.

### Building BioContainers

In this `seqtk` example the relevant BioContainer already existed on quay.io, this won’t always be the case. For tools that contain multiple requirement tags an existing container likely won’t exist. The mulled toolkit (distributed with planemo or available standalone) can be used to build containers for such tools. For such tools, if Galaxy is configured to use BioContainers it will attempt to build these containers on the fly by default (though this behavior can be disabled).

You can try it directly using the `mull` command in Planemo. The `conda_testing` Planemo project template has a toy example tool with two requirements for demonstrating this - `bwa_and_samtools.xml`.

```bash
$ planemo project_init --template=conda_testing conda_testing
$ cd conda_testing/
$ planemo mull bwa_and_samtools.xml
  --python2.7/site-packages/galaxy_lib-17.9.0-py2.7.egg/galaxy/tools/deps/mulled/
  --invfile.lua -set CHANNELS='luc,conda-forge,bioconda,defaults' -set TEST='true' -set
  --TARGETS='samtools=1.3.1,bwa=0.7.15' -set REPO='quay.io/biocontainers/mulled-v2-
  --fe8faa35dbf86dc5a0f75df4eae31a79f75de40:03dc1d2818d9de56938078b8b78b82d967c1f820' -
  --set BINDS='build/dist:/usr/local/' -set PREINSTALL='conda install --quiet --yes
  --conda=4.3' build
```

(continues on next page)
/Users/john/.planemo/involucro -v=3 -f /Users/john/workspace/planemo/.venv/lib/python2.7/site-packages/galaxy_lib-17.9.0-py2.7.egg/galaxy/tools/deps/mulled/invfile.lua -set CHANNELS='iuc,conda-forge,bioconda,defaults' -set TEST='true' -set TARGETS='samtools=1.3.1,bwa=0.7.15' -set REPO='quay.io/biocontainers/mulled-v2-fe8faa35dbf6dc65a0f7f5d4ea12e31a79f73e40:03dc1d281d9de56938078b8b82d967c1f820' -set BINDS='build/dist:/usr/local/' -set PREINSTALL='conda install --quiet --yes conda=4.3'
build


[Jun 19 11:28:35] DEBU Created container [5e4b5f83c455 step-730a02d79e], starting it

[Jun 19 11:28:35] DEBU Container [5e4b5f83c455 step-730a02d79e] started, waiting for completion

[Jun 19 11:28:36] DEBU Container [5e4b5f83c455 step-730a02d79e] completed with exit code [0] as expected

[Jun 19 11:28:36] DEBU Container [5e4b5f83c455 step-730a02d79e] removed


[Jun 19 11:28:37] DEBU Creating container [72b9ca0e56f8 step-e95bf001c8]

[Jun 19 11:28:37] DEBU Container [72b9ca0e56f8 step-e95bf001c8] started, waiting for completion

[Jun 19 11:28:46] SOUT Fetching package metadata ............


[Jun 19 11:28:50] SOUT Package plan for installation in environment /opt/conda:

[Jun 19 11:28:50] SOUT The following packages will be UPDATED:

[Jun 19 11:28:50] SOUT Package plan for installation in environment /usr/local:

[Jun 19 11:29:04] SOUT Fetching package metadata ............


[Jun 19 11:29:56] SOUT Package plan for installation in environment /usr/local:

[Jun 19 11:29:56] SOUT The following NEW packages will be INSTALLED:

[Jun 19 11:29:56] SOUT bwa: 0.7.15-1 bioconda

[Jun 19 11:29:56] SOUT curl: 7.52.1-0

[Jun 19 11:29:56] SOUT libgcc: 5.2.0-0

[Jun 19 11:29:56] SOUT openssl: 1.0.2l-0

[Jun 19 11:29:56] SOUT pip: 9.0.1-py27_1

[Jun 19 11:29:56] SOUT python: 2.7.13-0


[Jun 19 11:29:56] SOUT samtools: 1.3.1-5 bioconda

[Jun 19 11:29:56] SOUT sqlite: 3.13.0-0

[Jun 19 11:29:56] SOUT tk: 8.5.18-0

[Jun 19 11:29:56] SOUT wheel: 0.29.0-py27_0

[Jun 19 11:29:56] SOUT zlib: 1.2.8-3

[Jun 19 11:29:57] DEBU Container [72b9ca0e56f8 step-e95bf001c8] completed with exit code [0] as expected (continues on next page)
As the output indicates, this command built the container named quay.io/biocontainers/mulled-v2-fe8faa35dbf6dc65a0f7f5d4ea12e31a79f73e40:03dc1d2818d9de56938078b8b78b82d967c1f820-0. This is the same namespace / URL that would be used if or when published by the BioContainers project.

**Note:** The first part of this `mulled-v2` hash is a hash of the package names that went into it, the second the packages used and build number. Check out the Multi-package Containers web application to explore best practice channels and build such hashes.

We can see this new container when running the Docker command `images` and explore the new container interactively with `docker run`.

```bash
$ docker images
REPOSITORY TAG IMAGE ID CREATED SIZE
--- --------------- --------------- -------
quay.io/biocontainers/mulled-v2-fe8faa35dbf6dc65a0f7f5d4ea12e31a79f73e40 03dc1d2818d9de56938078b8b78b82d967c1f820-0 a740fe1e6a9e 16 hours ago 104 MB
quay.io/biocontainers/seqtk 1.2--0 10bc359ebd30 2 days ago 7.34 MB
continuumio/miniconda latest 6965a4889098 3 weeks ago 437 MB
bgruening/busybox-bash 0.1 3d974f51245c 9 months ago 6.73 MB

$ docker run -i -t quay.io/biocontainers/mulled-v2-fe8faa35dbf6dc65a0f7f5d4ea12e31a79f73e40:03dc1d2818d9de56938078b8b78b82d967c1f820-0 /bin/bash
bash-4.2# which samtools
/usr/local/bin/samtools
bash-4.2# which bwa
/usr/local/bin/bwa

As before, we can test running the tool inside its container in Galaxy using the `--biocontainers` flag.

```bash
$ planemo test --biocontainers bwa_and_samtools.xml
...
2017-03-01 10:20:58,077 INFO [galaxy.tools.actions] Handled output named output_2 for tool bwa_and_samtools (17.443 ms)
2017-03-01 10:20:58,090 INFO [galaxy.tools.actions] Added output datasets to history (12.935 ms)
2017-03-01 10:20:58,095 INFO [galaxy.tools.actions] Verified access to datasets for Job[unflushed,tool_id=bwa_and_samtools] (0.021 ms)
2017-03-01 10:20:58,096 INFO [galaxy.tools.actions] Setup for job Job[unflushed,tool_id=bwa_and_samtools] complete, ready to flush (5.755 ms)
2017-03-01 10:20:58,869 INFO [galaxy.jobs.handler] (1) Job dispatched
2017-03-01 10:20:59,067 DEBUG [galaxy.tools.deps] Using dependency bwa version 0.7.15 of type conda
2017-03-01 10:20:59,067 DEBUG [galaxy.tools.deps] Using dependency samtools version 1.5.3.1 of type conda
```

(continues on next page)
In particular take note of the line:

```
2017-03-01 10:20:59,142 INFO [galaxy.tools.deps.containers] Checking with container
  --resolver [CachedMulledDockerContainerResolver[namespace=biocontainers]] found description
  [ContainerDescription[identifier=quay.io/biocontainers/mulled-v2-
   fe8faa35dbf6dc65a0f7f5d4ea12e31a79f73e40:03dc1d2818d9de56938078b8b78b82d967c1f820-0,
   --type=docker]]
```

Here we can see the container ID (quay.io/biocontainers/mulled-v2-fe8faa35dbf6dc65a0f7f5d4ea12e31a79f73e40:03dc1d2818d9de56938078b8b78b82d967c1f820-0) from earlier has been cached on our Docker host is picked up by Galaxy. This is used to run the simple tool tests and indeed they pass.

In our initial seqtk example, the container resolver that matched was of type MulledDockerContainerResolver indicating that the Docker image would be downloaded from the BioContainer repository and this time the resolve that matched was of type CachedMulledDockerContainerResolver meaning that Galaxy would just use the locally cached version from the Docker host (i.e. the one we built with planemo mull above).
Planemo Documentation, Release 0.61.0.dev0

**Note:** Planemo doesn’t yet expose options that make it possible to build mulled containers for local packages that have yet to be published to anaconda.org but the mulled toolkit allows this. See mulled documentation for more information. However, once a container for a local package is built with mulled-build-tool the --biocontainers command should work to test it.

---

**Publishing BioContainers**

Building unpublished BioContainers on the fly is great for testing but for production use and to increase reproducibility such containers should ideally be published as well.

**BioContainers** maintains a registry of package combinations to be published using these long mulled hashes. This registry is represented as a Github repository named multi-package-containers. The Planemo command `container_register` will inspect a tool and open a Github pull request to add the tool’s combination of packages to the registry. Once merged, this pull request will result in the corresponding BioContainers image to be published (with the correct mulled has as its name) - these can be subsequently be picked up by Galaxy.

Various Github related settings need to be configured in order for Planemo to be able to open pull requests on your behalf as part of the `container_register` command. To simplify all of this - the Planemo community maintains a list of Github repositories containing Galaxy and/or CWL tools that are scanned daily by Travis. For each such repository, the Travis job will run `container_register` across the repository on all tools resulting in new registry pull requests for all new combinations of tools. This list is maintained in a script named `monitor.sh` in the planemo-monitor repository. The easiest way to ensure new containers are built for your tools is simply to open a pull request to add your tool repositories to this list.

**Explicit Annotation**

This section of documentation needs to be filled out but a detailed example is worked through this documentation from Aaron Petkau (@apetakau) built at the 2014 Galaxy Community Conference Hackathon.

### 5.4 How do I...?

This section contains a number of smaller topics with links and examples meant to provide relatively concrete answers for specific tool development scenarios.

#### 5.4.1 ... deal with index/reference data?

Galaxy’s concept of data tables are meant to provide tools with access reference datasets or index data not tied to particular histories or users. A common example would be FASTA files for various genomes or mapper-specific indices of those files (e.g. a BWA index for the hg19 genome).

Galaxy data managers are specialized tools designed to populate tool data tables.

#### 5.4.2 ... cite tools without an obvious DOI?

In the absence of an obvious DOI, tools may contain embedded BibTeX directly.

Further reading:

- `bibtex.xml` (test tool with a bunch of random examples)
• bwa-mem.xml (BWA-MEM tool by Anton Nekrutenko demonstrating citation of an arXiv article)
• macros.xml (Macros for vcflib tool demonstrating citing a github repository)

5.4.3 . . . declare a Docker container for my tool?

Galaxy tools can be decorated to with container tags indicated Docker container ids that the tools can run inside of.

The longer term plan for the Tool Shed ecosystem is to be able to automatically build Docker containers for tool dependency descriptions and thereby obtain this Docker functionality for free and in a way that is completely backward compatible with non-Docker deployments.

Further reading:
• Complete tutorial on Github by Aaron Petkau. Covers installing Docker, building a Dockerfile, publishing to Docker Hub, annotating tools and configuring Galaxy.
• Another tutorial from the Galaxy User Group Grand Ouest.
• Landing page on the Galaxy Wiki
• Implementation details on Pull Request #401

5.4.4 . . . do extra validation of parameters?

Tool parameters support a validator element (syntax) to perform validation of a single parameter. More complex validation across parameters can be performed using arbitrary Python functions using the code file syntax but this feature should be used sparingly.

Further reading:
• validator XML tag syntax on the Galaxy wiki.
• fastq_filter.xml (a FASTQ filtering tool demonstrating validator constructs)
• gffread.xml (a tool by Jim Johnson demonstrating using regular expressions with validator tags)
• code_file.xml, code_file.py (test files demonstrating defining a simple constraint in Python across two parameters)
• deseq2 tool by Björn Grüning demonstrating advanced code file validation.

5.4.5 . . . check input type in command blocks?

Input data parameters may specify multiple formats. For example

```xml
<param name="input" type="data" format="fastq,fasta" label="Input" />
```

If the command-line under construction doesn’t require changes based on the input type - this may just be referenced as $input. However, if the command-line under construction uses different argument names depending on type for instance - it becomes important to dispatch on the underlying type.

In this example $input.ext - would return the short code for the actual datatype of the input supplied - for instance the string fasta or fastqsanger would be valid responses for inputs to this parameter for the above definition.

While .ext may sometimes be useful - there are many cases where it is inappropriate because of subtypes - checking if .ext is equal to fastq in the above example would not catch fastqsanger inputs for instance. To check if an input matches a type or any subtype thereof - the is_of_type method can be used. For instance
$\text{input.is\_of\_type('fastq')}$

would check if the input is of type fastq or any derivative types such as fastqsanger.

- Pull Request 457

### 5.4.6 ... handle arbitrary output data formats?

If the output format of a tool’s output cannot be known ahead of time, Galaxy can be instructed to “sniff” the output and determine the data type using the same method used for uploads. Adding the `auto\_format="true"` attribute to a tool’s output enables this.

```xml
<output name="out1" auto_format="true" label="Auto Output" />
```

- output\_auto\_format.xml

### 5.4.7 ... determine the user submitting a job?

The variable `$__user\_email` (as well as `$__user\_name` and `$__user\_id`) is available when building up your command in the tool’s `<command>` block. The following tool demonstrates the use of this and a few other special parameters available to all tools.

- special\_params.xml

### 5.4.8 ... test with multiple value inputs?

To write tests that supply multiple values to a `multiple="true" select` or `data` parameter - simply specify the multiple values as a comma separated list.

Here are examples of each:

- multi\_data\_param.xml
- muti\_select.xml

### 5.4.9 ... test dataset collections?

Here are some examples of testing tools that consume collections with `type="data\_collection"` parameters.

- collection\_paired\_test.xml
- collection\_mixed\_param.xml
- collection\_nested\_param.xml

Here are some examples of testing tools that produce collections with `output\_collection` elements.

- collection\_creates\_list.xml
- collection\_creates\_list\_2.xml
- collection\_creates\_pair.xml
- collection\_creates\_pair\_from\_type.xml

5.4. How do I...
5.4.10 ... test discovered datasets?

Tools which dynamically discover datasets after the job is complete, either using the `<discovered_datasets>` element, the older default pattern approach (e.g. finding files with names like `primary_DATASET_ID_sample1_true_bam_hg18`), or the undocumented `galaxy.json` approach can be tested by placing discovered_dataset elements beneath the corresponding output element with the designation corresponding to the file to test.

```xml
<test>
  <param name="input" value="7" />
  <output name="report" file="example_output.html">
    <discovered_dataset designation="world1" file="world1.txt" />
    <discovered_dataset designation="world2">
      <assert_contents>
        <has_line line="World Contents" />
      </assert_contents>
    </discovered_dataset>
  </output>
</test>
```

The test examples distributed with Galaxy demonstrating dynamic discovery and the testing thereof include:

- multi_output.xml
- multi_output_assign_primary.xml
- multi_output_configured.xml

5.4.11 ... test composite dataset contents?

Tools which consume Galaxy composite datatypes can generate test inputs using the `composite_data` element demonstrated by the following tool.

- composite.xml

Tools which produce Galaxy composite datatypes can specify tests for the individual output files using the `extra_files` element demonstrated by the following tool.

- composite_output.xml
- macs_wrapper.xml

5.4.12 ... test index (.loc) data?

There is an idiom to supply test data for index during tests using Planemo.

To create this kind of test, one needs to provide a `tool_data_table_conf.xml.test` beside your tool’s `tool_data_table_conf.xml.sample` file that specifies paths to test .loc files which in turn define paths to the test index data. Both the .loc files and the `tool_data_table_conf.xml.test` can use the value `${__HERE__}` which will be replaced with the path to the directory the file lives in. This allows using relative-like paths in these files which is needed for portable tests.

An example commit demonstrating the application of this approach to a Picard tool can be found here.

These tests can then be run with the Planemo test command.
Warning: This idiom does not work with the Tool Shed test automated framework at this time and so these tests will largely only pass with Planemo.

### 5.4.13 ... test exit codes?

A `test` element can check the exit code of the underlying job using the `check_exit_code="n"` attribute.

- `job_properties.xml`

### 5.4.14 ... test failure states?

Normally, all tool test cases described by a `test` element are expected to pass - but one can assert a job should fail by adding `expect_failure="true"` to the `test` element.

- `job_properties.xml`

### 5.4.15 ... test output filters work?

If your tool contains `filter` elements, you can’t verify properties of outputs that are filtered out and do not exist. The `test` element may contain an `expect_num_outputs` attribute to specify the expected number of outputs, this can be used to verify that outputs not listed are expected to be filtered out during tool execution.

- `output_filter.xml`

### 5.4.16 ... test metadata?

Output metadata can be checked using `metadata` elements in the XML description of the `output`.

- `metadata.xml`

### 5.4.17 ... test tools installed in an existing Galaxy instance?

Do not use planemo, Galaxy should be used to test its tools directly. The following two commands can be used to test Galaxy tools in an existing instance.

```
$ sh run_tests.sh --report_file tool_tests_shed.html --installed
```

This above command specifies the `--installed` flag when calling `run_tests.sh`, this tells the test framework to test Tool Shed installed tools and only those tools.

```
$ GALAXY_TEST_TOOL_CONF=config/tool_conf.xml sh run_tests.sh --report_file tool_tests_shed.html functional.test_toolbox
```

The second command sets `GALAXY_TEST_TOOL_CONF` environment variable, which will restrict the testing framework to considering a single tool conf file (such as the default tools that ship with Galaxy config/tool_conf.xml.sample and which must have their dependencies setup manually). The last argument to `run_tests.sh`, `functional.test_toolbox` tells the test framework to run all the tool tests in the configured tool conf file.

**Note:** *Tip:* To speed up tests you can use a pre-migrated database file the way Planemo does by setting the following environment variable before running `run_tests.sh`.  

5.4. How do I...
$ export GALAXY_TEST_DB_TEMPLATE="https://github.com/jmchilton/galaxy-downloads/raw/master/db_gx_rev_0127.sqlite"
Building Common Workflow Language Tools

The following links are for the same tutorial describing the basics of how to build Common Workflow Language tools. The first variant is tailored to local development environments (e.g. if Planemo has been installed with brew or pip) and the second is for developers using a dedicated Planemo virtual appliance (available for Docker, Vagrant, etc...).

6.1 Building Common Workflow Language Tools Using Planemo

This tutorial is a gentle introduction to writing Common Workflow Language tools using Planemo. Please read the installation instructions for Planemo if you have not already installed it.

6.1.1 The Basics

This guide is going to demonstrate building up tools for commands from Heng Li’s Seqtk package - a package for processing sequence data in FASTA and FASTQ files.

To get started let’s install Seqtk. Here we are going to use conda to install Seqtk - but however you obtain it should be fine.

```bash
$ conda install --force --yes -c conda-forge -c bioconda seqtk=1.2
... seqtk installation ...
$ seqtk seq
Usage: seqtk seq [options] <in.fq>|<in.fa>
Options: -q INT mask bases with quality lower than INT [0]
-X INT mask bases with quality higher than INT [255]
-n CHAR masked bases converted to CHAR; 0 for lowercase [0]
-l INT number of residues per line; 0 for 2^32-1 [0]
-Q INT quality shift: ASCII-INT gives base quality [33]
-s INT random seed (effective with -f) [11]
-f FLOAT sample FLOAT fraction of sequences [1]
-M FILE mask regions in BED or name list FILE [null]
-L INT drop sequences with length shorter than INT [0]
-c mask complement region (effective with -M)
```

(continues on next page)
-r reverse complement
-A force FASTA output (discard quality)
-C drop comments at the header lines
-N drop sequences containing ambiguous bases
-1 output the 2n-1 reads only
-2 output the 2n reads only
-V shift quality by '(-Q) - 33'

Next we will download an example FASTQ file and test out the a simple Seqtk command - seq which converts FASTQ files into FASTA.

```
$ wget https://raw.githubusercontent.com/galaxyproject/galaxy-test-data/master/2.fastq
$ seqtk seq -A 2.fastq > 2.fasta
$ cat 2.fasta
>EAS54_6_R1_2_1_413_324
CCCTTCTTGTCTTCAGCGTTTCTCC
>EAS54_6_R1_2_1_540_792
TTGGCAGGCCAAGGCCGATGGATCA
>EAS54_6_R1_2_1_443_348
GTTGCTTCTGGCGTGGGTGGGGGG
```

Common Workflow Language tool files are just simple YAML files, so at this point one could just open a text editor and start implementing the tool. Planemo has a command tool_init to quickly generate a skeleton to work from, so let’s start by doing that.

```
$ planemo tool_init --cwl --id 'seqtk_seq' --name 'Convert to FASTA (seqtk)'
```

The tool_init command can take various complex arguments - but three two most basic ones are shown above --cwl, --id and --name. The --cwl flag tells Planemo to generate a Common Workflow Language tool. --id is a short identifier for this tool and it should be unique across all tools. --name is a short, human-readable name for the tool - it corresponds to the label attribute in the CWL tool document.

The above command will generate the file seqtk_seq.cwl - which should look like this.

```
#!/usr/bin/env cwl-runner
cwlVersion: 'v1.0'
class: CommandLineTool
id: "seqtk_seq"
label: "Convert to FASTA (seqtk)"
inputs: [] # TODO
outputs: [] # TODO
baseCommand: []
arguments: []
doc: |
    TODO: Fill in description.
```

This tool file has the common fields required for a CWL tool with TODO notes, but you will still need to open up the editor and fill out the command, describe input parameters, tool outputs, writeup usage documentation (doc), etc..

The tool_init command can do a little bit better than this as well. We can use the test command we tried above seqtk seq -A 2.fastq > 2.fasta as an example to generate a command block by specifying the inputs and the outputs as follows.

```
$ planemo tool_init --force \
   --cwl \ 
   --id 'seqtk_seq' \
```

(continues on next page)
This will generate the following CWL tool definition - which now has correct definitions for the input, output, and command specified. These represent a best guess by planemo, and in most cases will need to be tweaked manually after the tool is generated.

```yaml
#!/usr/bin/env cwl-runner
cwlVersion: 'v1.0'
class: CommandLineTool
id: "seqtk_seq"
label: "Convert to FASTA (seqtk)"
inputs:
  input1:
    type: File
doc: |
      TODO
    inputBinding:
      position: 1
      prefix: "-a"
outputs:
  output1:
    type: File
    outputBinding:
      glob: out
baseCommand:
  - "seqtk"
  - "seq"
arguments: []
stdout: out
doc: |
      TODO: Fill in description.
```

As shown at the beginning of this section, the command `seqtk seq` generates a help message for the `seq` command. `tool_init` can take that help message and stick it right in the generated tool file using the `help_from_command` option.

Generally command help messages aren’t exactly appropriate for tools since they mention argument names and simillar details that are abstracted away by the tool - but they can be an excellent place to start.

The following Planemo’s `tool_init` call has been enhanced to use `--help_from_command`.

```
$ planemo tool_init --force \
  --id 'seqtk_seq' \
  --name 'Convert to FASTA (seqtk)' \
  --example_command 'seqtk seq -A 2.fastq > 2.fasta' \
  --example_input 2.fastq \
  --example_output 2.fasta \
  --requirement seqtk@1.2 \
  --container 'quay.io/biocontainers/seqtk:1.2--0' \
  --test_case \
  --help_from_command 'seqtk seq'
```

This command generates the following CWL YAML file.
#!/usr/bin/env cwl-runner

cwlVersion: 'v1.0'
class: CommandLineTool
id: "seqtk_seq"
label: "Convert to FASTA (seqtk)"
hints:
  DockerRequirement:
    dockerPull: quay.io/biocontainers/seqtk:1.2--1
SoftwareRequirement:
  packages:
    - package: seqtk
      version: "1.2"
inputs:
  input1:
    type: File
doc: |
    TODO
    inputBinding:
      position: 1
      prefix: "-a"
outputs:
  output1:
    type: File
    outputBinding:
      glob: out
baseCommand:
  - "seqtk"
  - "seq"
arguments: []
stdout: out
doc: |

Usage: seqtk seq [options] <in.fq>|<in.fa>

Options:
-q INT  mask bases with quality lower than INT [0]
-X INT  mask bases with quality higher than INT [255]
-n CHAR masked bases converted to CHAR; 0 for lowercase [0]
-l INT  number of residues per line; 0 for 2^32-1 [0]
-Q INT  quality shift: ASCII-INT gives base quality [33]
-s INT  random seed (effective with -f) [11]
-f FLOAT sample FLOAT fraction of sequences [1]
-M FILE  mask regions in BED or name list FILE [null]
-L INT  drop sequences with length shorter than INT [0]
-c mask complement region (effective with -M)
-r reverse complement
-A force FASTA output (discard quality)
-C drop comments at the header lines
-N drop sequences containing ambiguous bases
-l output the 2n-1 reads only
-2 output the 2n reads only
-V shift quality by '(-Q) - 33'
-U convert all bases to uppercases
-S strip of white spaces in sequences

In addition to generating a CWL tool adding the --test_case flag generates from more files that are useful including seqtk_seq_job.yml as shown below:
**input1:**

```yaml
class: File
path: test-data/2.fastq
```

This is a CWL job input document and should allow you to run the example command using any CWL implementation. For instance if you have `cwltool` (cwltool) or `Toil` (cwltoil) on your PATH the following examples should work.

```
$ cwltool seqtk_seq.cwl seqtk_seq_job.yml
/Users/john/workspace/planemo/.venv/bin/cwltool 1.0.20180508202931
Resolved 'seqtk_seq.cwl' to 'file:///Users/john/tool_init_exercise/seqtk_seq.cwl'
[job seqtk_seq.cwl] /private/tmp/docker_tmpXgtSlt$ docker \
   run \
   -i \
   --volume=/private/tmp/docker_tmpXgtSlt:/private/var/spool/cwl:rw \
   --volume=/private/var/folders/78/zz5mz4d0jn53xf0106j7ppc0000gp/T/tmpGLthW:/ \
   --tmp:rw \
   --volume=/Users/john/tool_init_exercise/test-data/2.fastq:/private/var/lib/cwl/ \
   --stg7db12d3a-2375-4ed-8a0ef6f8e80/2.fastq:ro \
   --workdir=/private/var/spool/cwl \
   --read-only=true \
   --log-driver=none \
   --user=502:20 \
   --rm \
   --env=TMPDIR=/tmp \
   --env=HOME=/private/var/spool/cwl \
   quay.io/biocontainers/seqtk:1.2--1 \
   seqtk \
   seq \
   -A \
   /private/var/lib/cwl/stg7db12d3a-2375-4ed-8a0ef6f8e80/2.fastq > /private/ \
   /tmp/docker_tmpXgtSlt/out
[job seqtk_seq.cwl] completed success
```

```
$ cwltoil seqtk_seq.cwl seqtk_seq_job.yml
jlaptop17.local 2018-05-21 15:25:30,630 MainThread INFO toil.lib.bioio: Root logger is at level 'INFO', 'toil' logger at level 'INFO'.
   abstractJobStore: The workflow ID is: '55a08d91-1852-4069-97a9-741abd2ea04e'
Resolved 'seqtk_seq.cwl' to 'file:///Users/john/tool_init_exercise/seqtk_seq.cwl'
jlaptop17.local 2018-05-21 15:25:30,650 MainThread INFO cwltool: Resolved 'seqtk_seq.cwl' to 'file:///Users/john/tool_init_exercise/seqtk_seq.cwl'
jlaptop17.local 2018-05-21 15:25:31,793 MainThread INFO toil.common: Using the single machine batch system
   singleMachine: Limiting maxCores to CPU count of system (8).
   singleMachine: Limiting maxMemory to physically available memory (17179869184).
```

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jlaptop17.local 2018-05-21 15:25:31,800 MainThread INFO toil.common: Created the workflow directory at /var/folders/78/zxz5mz4d0jn53xf0106j7ppc0000gp/T/toil-55a08d91-1852-4069-97a9-741abd2ea04e-132281828025877
jlaptop17.local 2018-05-21 15:25:31,808 MainThread INFO toil.common: User script ModuleDescriptor(dirPath='/Users/john/workspace/planemo/.venv/lib/python2.7/site-packages', name='toil.cwl.cwltoil', fromVirtualEnv=True) belongs to Toil. No need to auto-deploy it.
jlaptop17.local 2018-05-21 15:25:31,825 MainThread INFO toil: Running Toil version 3.15.0-0e3a87e73f85f0e7c0f64bfda337d592b2d92704.
jlaptop17.local 2018-05-21 15:25:31,832 MainThread INFO toil.leader: Found 1 jobs to start and 0 jobs with successors to run.
2018-05-21 15:25:31,832 - toil.leader - INFO - Found 1 jobs to start and 0 jobs with successors to run.
jlaptop17.local 2018-05-21 15:25:31,832 MainThread INFO toil.leader: Checked batch system has no running jobs and no updated jobs.
jlaptop17.local 2018-05-21 15:25:33,955 MainThread INFO toil.leader: Finished the main loop: no jobs left to run.
jlaptop17.local 2018-05-21 15:25:33,955 MainThread INFO toil.serviceManager: Waiting for service manager thread to finish ...
2018-05-21 15:25:33,955 - toil.serviceManager - INFO - Waiting for service manager thread to finish ...
jlaptop17.local 2018-05-21 15:25:34,841 MainThread INFO toil.serviceManager: finished shutting down the service manager. Took 0.885795116425 seconds.

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At this point we have a fairly functional CWL tool with test and usage documentation. This was a pretty simple example - usually you will need to put more work into the tool to get to this point - \texttt{tool\_init} is really just designed to get you started.

Now let's lint and test the tool we have developed. The Planemo's \texttt{lint} (or just \texttt{l}) command will review tool for validity, obvious mistakes, and Planemo “best practices”.

```
$ planemo l seqtk_seq.cwl
Linting tool /Users/john/workspace/planemo/docs/writing/seqtk_seq.cwl
Applying linter general... CHECK
  .. CHECK: Tool defines a version [0.0.1].
  .. CHECK: Tool defines a name [Convert to FASTA (seqtk)].
  .. CHECK: Tool defines an id [seqtk_seq_v3].
  .. CHECK: Tool specifies profile version [16.04].
Applying linter cwl_validation... CHECK
  .. INFO: CWL appears to be valid.
Applying linter docker_image... CHECK
  .. INFO: Tool will run in Docker image [quay.io/biocontainers/seqtk:1.2--1].
Applying linter new_draft... CHECK
  .. INFO: Modern CWL version [v1.0]
```

In addition to the actual tool and job files, \texttt{--test\_case} caused a test file to be generated using the example command and provided test data. The file contents are as follows:

```
- doc: test generated from example command
  job: seqtk_seq_job.yml
  outputs:
```

(continues on next page)
Unlike the job file, this file is a Planemo-specific artifact. This file may contain 1 or more tests - each test is an element of the top-level list. `tool_init` will use the example command to build just one test.

Each test consists of a few parts:

- **doc** - this attribute provides a short description for the test.
- **job** - this can be the path to a CWL job description or a job description embedded right in the test (`tool_init` builds the latter).
- **outputs** - this section describes the expected output for a test. Each output ID of the tool or workflow under test can appear as a key. The example above just describes expected specific output file contents exactly but many more expectations can be described.

For more information on the test file format check out the Test Format docs.

The tests described in this file can be run using the `planemo test` command on the original file.

```
$ planemo test --no-container seqtk_seq.cwl
Enable beta testing mode for testing.
cwltool INFO: /Users/john/workspace/planemo/.venv/bin/planemo 1.0.20180508202931
cwltool INFO: Resolved '/Users/john/tool_init_exercise/seqtk_seq.cwl' to 'file://
   /Users/john/tool_init_exercise/seqtk_seq.cwl'
cwltool INFO: [job seqtk_seq.cwl] /private/tmp/docker_tmpvLE9SS$ seqtk \
   seq \n   -A \n   /private/var/folders/78/xxz5mz4d0jn53xf0106j7ppc0000gp/T/tmpGM22d_\n   /Users/john/tool_init_exercise/seqtk_seq.cwl'/stg0c0cad75-\n   7ca0-4f3a-9d77-63e9c49f5353/2.fastq > /private/tmp/docker_tmpvLE9SS/out
cwltool INFO: [job seqtk_seq.cwl] completed success
cwltool INFO: Final process status is success
All 1 test(s) executed passed.
seqtk_seq_0: passed
```

This is a bit a different than running the job. For one thing, we don’t need to specify an input job - instead Planemo will automatically find the test file and run all the jobs described inside that file. Additionally, Planemo will check the outputs to ensure the match the test expectations.

In addition to the in console display of test results as red (failing) or green (passing), Planemo also creates an HTML report for the test results by default. Many more test report options are available such `--test_output_xunit` which is useful in certain continuous integration environments. See `planemo test --help` for more options, as well as the `test_reports` command.

The above test example used `cwltool` to run our test and disabled containerization. By dropping the `--no-container` argument we can run the tool in a Docker container. By passing an engine argument as `--engine toil` we can run our test in Toil, an alternative CWL implementation.

```
$ planemo test seqtk_seq.cwl
Enable beta testing mode for testing.
cwltool INFO: /Users/john/workspace/planemo/.venv/bin/planemo 1.0.20180508202931
cwltool INFO: Resolved '/Users/john/tool_init_exercise/seqtk_seq.cwl' to 'file:///n
   /Users/john/tool_init_exercise/seqtk_seq.cwl'
cwltool INFO: [job seqtk_seq.cwl] /private/tmp/docker_tmpUeIpXJ$ docker \n   run \n   -i \
   --volume=/private/tmp/docker_tmpUeIpXJ:/private/var/spool/cwl:rw \n```
6.2 Building Common Workflow Language Tools (Using the Planemo Appliance)

This tutorial is a gentle introduction to writing Common Workflow Language tools using the Planemo virtual appliance (available for Docker and Vagrant). Check out these instructions for obtaining the virtual appliance if you have not done so already.

6.2.1 The Basics

This guide is going to demonstrate building up tools for commands from Heng Li’s Seqtk package - a package for processing sequence data in FASTA and FASTQ files.

To get started let’s install Seqtk. Here we are going to use conda to install Seqtk - but however you obtain it should be fine.

```bash
$ conda install --force --yes -c conda-forge -c bioconda seqtk=1.2
... seqtk installation ...
$ seqtk seq
Usage: seqtk seq [options] <in.fq>|<in.fa>
Options: -q INT mask bases with quality lower than INT [0]
-X INT mask bases with quality higher than INT [255]
-n CHAR masked bases converted to CHAR; 0 for lowercase [0]
-l INT number of residues per line; 0 for 2^32-1 [0]
-Q INT quality shift: ASCII-INT gives base quality [33]
```

For more information on the Common Workflow Language check out the Draft 3 User Guide and Specification.
Next we will download an example FASTQ file and test out the a simple Seqtk command - seq which converts FASTQ files into FASTA.

Next, we will download an example FASTQ file and test out the a simple Seqtk command - seq which converts FASTQ files into FASTA.

$ wget https://raw.githubusercontent.com/galaxyproject/galaxy-test-data/master/2.fastq
$ seqtk seq -A 2.fastq > 2.fasta
$ cat 2.fasta

>`EAS54_6_R1_2_1_413_324
CCTTCTGTCTCCGCTCCGTCC
`EAS54_6_R1_2_1_540_792
TGGCCAGCTAGCCGATACT
`EAS54_6_R1_2_1_443_348
GTTGCTTCTGGCGTGGGTGGGG

Common Workflow Language tool files are just simple YAML files, so at this point one could just open a text editor and start implementing the tool. Planemo has a command `tool_init` to quickly generate a skeleton to work from, so let’s start by doing that.

$ planemo tool_init --cwl --id 'seqtk_seq' --name 'Convert to FASTA (seqtk)'

The `tool_init` command can do a little bit better than this as well. We can use the test command we tried above `seqtk seq -A 2.fastq > 2.fasta` as an example to generate a command block by specifying the inputs and the outputs as follows.

```bash
#!/usr/bin/env cwl-runner
cwlVersion: 'v1.0'
class: CommandLineTool
id: "seqtk_seq"
label: "Convert to FASTA (seqtk)"
inputs: [] # TODO
outputs: [] # TODO
baseCommand: []
arguments: []
doc: |
    TODO: Fill in description.
```

This tool file has the common fields required for a CWL tool with TODO notes, but you will still need to open up the editor and fill out the command, describe input parameters, tool outputs, writeup usage documentation (doc), etc..

The `tool_init` command can do a little bit better than this as well. We can use the test command we tried above `seqtk seq -A 2.fastq > 2.fasta` as an example to generate a command block by specifying the inputs and the outputs as follows.
This will generate the following CWL tool definition - which now has correct definitions for the input, output, and command specified. These represent a best guess by planemo, and in most cases will need to be tweaked manually after the tool is generated.

```bash
#!/usr/bin/env cwl-runner
cwlVersion: 'v1.0'
class: CommandLineTool
id: "seqtk_seq"
label: "Convert to FASTA (seqtk)"
inputs:
  input1:
    type: File
doc: |
    TODO
    inputBinding:
      position: 1
      prefix: "-a"
outputs:
  output1:
    type: File
    outputBinding:
      glob: out
baseCommand:
  - "seqtk"
  - "seq"
arguments: []
stdout: out
doc: |
    TODO: Fill in description.
```

As shown at the beginning of this section, the command `seqtk seq` generates a help message for the `seq` command. `tool_init` can take that help message and stick it right in the generated tool file using the `--help_from_command` option.

Generally command help messages aren’t exactly appropriate for tools since they mention argument names and simillar details that are abstracted away by the tool - but they can be an excellent place to start.

The following Planemo’s `tool_init` call has been enhanced to use `--help_from_command`.

```bash
$ planemo tool_init --force \
  --cwl \  
  --id 'seqtk_seq' \  
  --name 'Convert to FASTA (seqtk)' \  
  --example_command 'seqtk seq -A 2.fastq > 2.fasta' \  
  --example_input 2.fastq \  
  --example_output 2.fasta
```

6.2. Building Common Workflow Language Tools (Using the Planemo Appliance)
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This command generates the following CWL YAML file.

```yaml
#!/usr/bin/env cwl-runner
cwlVersion: 'v1.0'
class: CommandLineTool
id: "seqtk_seq"
label: "Convert to FASTA (seqtk)"
hints:
  DockerRequirement:
    dockerPull: quay.io/biocontainers/seqtk:1.2--1
SoftwareRequirement:
  packages:
    - package: seqtk
      version: "1.2"
inputs:
  input1:
    type: File
doc: |
    TODO
    inputBinding:
      position: 1
      prefix: "-a"
outputs:
  output1:
    type: File
    outputBinding:
      glob: out
baseCommand:
  - "seqtk"
  - "seq"
arguments: []
stdout: out
doc: |
  Usage: seqtk seq [options] <in.fq>|<in.fa>

Options:
  -q INT  mask bases with quality lower than INT [0]
  -X INT  mask bases with quality higher than INT [255]
  -n CHAR  masked bases converted to CHAR; 0 for lowercase [0]
  -l INT  number of residues per line; 0 for 2^32-1 [0]
  -Q INT  quality shift: ASCII-INT gives base quality [33]
  -s INT  random seed (effective with -f) [11]
  -f FLOAT  sample FLOAT fraction of sequences [1]
  -M FILE  mask regions in BED or name list FILE [null]
  -L INT  drop sequences with length shorter than INT [0]
  -c mask complement region (effective with -M)
  -r reverse complement
  -A force FASTA output (discard quality)
  -C drop comments at the header lines
  -N drop sequences containing ambiguous bases
  -1 output the 2n-1 reads only
  -2 output the 2n reads only
  -V shift quality by '(-Q) - 33'
  -U convert all bases to uppercases
  -S strip of white spaces in sequences
```

In addition to generating a CWL tool adding the --test_case flag generates from more files that are useful including seqtk_seq_job.yml as shown below:
This is a CWL job input document and should allow you to run the example command using any CWL implementation. For instance if you have `cwltool` or `Toil` on your PATH the following examples should work.

```bash
$ cwltool seqtk_seq.cwl seqtk_seq_job.yml
Resolved 'seqtk_seq.cwl' to 'file:///Users/john/tool_init_exercise/seqtk_seq.cwl'
[job seqtk_seq.cwl] /private/tmp/docker_tmpXgtSLt$ docker \
   run \
   -i \
   --volume=/private/tmp/docker_tmpXgtSLt:/private/var/spool/cwl:rw \
   --volume=/private/var/folders/78/zxz5mz4d0jn53xf0106j7ppc0000gp/T/tmpGG1thW:/ \
   --tmp:rw \
   --volume=/Users/john/tool_init_exercise/test-data/2.fastq:/private/var/lib/cwl/ \
   --stg7db12d3a-2375-42ed-ba60-8a0ef69ffe80/2.fastq:ro \
   --workdir=/private/var/spool/cwl \
   --read-only=true \
   --log-driver=none \
   --user=502:20 \
   --rm \
   --env=TMPDIR=/tmp \
   --env=HOME=/private/var/spool/cwl \
   quay.io/biocontainers/seqtk:1.2--1 \
   seqtk \
   seq \
   -A \
   /private/var/lib/cwl/stg7db12d3a-2375-42ed-ba60-8a0ef69ffe80/2.fastq > /private/ \
   /tmp/docker_tmpXgtSLt/out
[job seqtk_seq.cwl] completed success
```

```bash
$ cwltoil seqtk_seq.cwl seqtk_seq_job.yml
jlaptop17.local 2018-05-21 15:25:30,630 MainThread INFO toil.lib.bioio: Root logger is at level 'INFO', 'toil' logger at level 'INFO'.
   --abstractJobStore: The workflow ID is: '55a08d91-1852-4069-97a9-741abd2ea04e'
Resolved 'seqtk_seq.cwl' to 'file:///Users/john/tool_init_exercise/seqtk_seq.cwl'
jlaptop17.local 2018-05-21 15:25:30,650 MainThread INFO cwltool: Resolved 'seqtk_seq.cwl' to 'file:///Users/john/tool_init_exercise/seqtk_seq.cwl'
jlaptop17.local 2018-05-21 15:25:31,793 MainThread INFO toil.common: Using the single_machine batch system
   --singleMachine: Limiting maxCores to CPU count of system (8).
   --singleMachine: Limiting maxMemory to physically available memory (17179869184).
```

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```
jlaptop17.local 2018-05-21 15:25:31,800 MainThread INFO toil.common: Created the workflow directory at /var/folders/78/zxx5mz4d0ijn53xf0106j7ppc0000gp/T/toil-55a08d91-1852-4069-97a9-741abd2ea04e-132281828025877
jlaptop17.local 2018-05-21 15:25:31,808 MainThread INFO toil.common: User script ModuleDescriptor(dirPath='/Users/john/workspace/planemo/.venv/lib/python2.7/site-packages', name='toil.cwl.cwltoil', fromVirtualEnv=True) belongs to Toil. No need to auto-deploy it.
jlaptop17.local 2018-05-21 15:25:31,809 MainThread INFO toil.common: Written the environment for the jobs to the environment file
jlaptop17.local 2018-05-21 15:25:31,809 MainThread INFO toil.common: Caching all jobs in job store
jlaptop17.local 2018-05-21 15:25:31,825 MainThread INFO toil.toilState: (Re)building internal scheduler state
2018-05-21 15:25:31,832 MainThread INFO toil.leader: Found 1 jobs to start and 0 jobs with successors to run
2018-05-21 15:25:31,832 - toil.leader - INFO - Found 1 jobs to start and 0 jobs with successors to run
jlaptop17.local 2018-05-21 15:25:31,832 MainThread INFO toil.leader: Checked batch system has no running jobs and no updated jobs
jlaptop17.local 2018-05-21 15:25:31,832 - toil.leader - INFO - Checked batch system has no running jobs and no updated jobs
jlaptop17.local 2018-05-21 15:25:33,953 MainThread INFO toil.leader: Finished the main loop: no jobs left to run
jlaptop17.local 2018-05-21 15:25:33,955 - toil.leader - INFO - Finished the main loop: no jobs left to run
jlaptop17.local 2018-05-21 15:25:33,955 MainThread INFO toil.serviceManager: Waiting for service manager thread to finish ...
jlaptop17.local 2018-05-21 15:25:33,955 - toil.serviceManager - INFO - Waiting for service manager thread to finish ...
jlaptop17.local 2018-05-21 15:25:34,841 MainThread INFO toil.serviceManager: Finished shutting down the service manager. Took 0.885795116425 seconds
```

(continues on next page)
At this point we have a fairly functional CWL tool with test and usage documentation. This was a pretty simple example - usually you will need to put more work into the tool to get to this point - tool_init is really just designed to get you started.

Now lets lint and test the tool we have developed. The Planemo’s `lint` (or just `l`) command will review tool for validity, obvious mistakes, and Planemo “best practices”.

```
$ planemo l seqtk_seq.cwl
Linting tool /Users/john/workspace/planemo/docs/writing/seqtk_seq.cwl
Applying linter general... CHECK
  .. CHECK: Tool defines a version [0.0.1].
  .. CHECK: Tool defines a name [Convert to FASTA (seqtk)].
  .. CHECK: Tool defines an id [seqtk_seq_v3].
  .. CHECK: Tool specifies profile version [16.04].
Applying linter cwl_validation... CHECK
  .. INFO: CWL appears to be valid.
Applying linter docker_image... CHECK
  .. INFO: Tool will run in Docker image [quay.io/biocontainers/seqtk:1.2--1].
Applying linter new_draft... CHECK
  .. INFO: Modern CWL version [v1.0]
```

In addition to the actual tool and job files, `--test_case` caused a test file to be generated using the example command and provided test data. The file contents are as follows:

```
- doc: test generated from example command
  job: seqtk_seq_job.yml
  outputs:
```

(continues on next page)
Unlike the job file, this file is a Planemo-specific artifact. This file may contain 1 or more tests - each test is an element of the top-level list. tool_init will use the example command to build just one test.

Each test consists of a few parts:

- **doc** - this attribute provides a short description for the test.
- **job** - this can be the path to a CWL job description or a job description embedded right in the test (tool_init builds the latter).
- **outputs** - this section describes the expected output for a test. Each output ID of the tool or workflow under test can appear as a key. The example above just describes expected specific output file contents exactly but many more expectations can be described.

For more information on the test file format check out the Test Format docs.

The tests described in this file can be run using the planemo test command on the original file.

```bash
$ planemo test --no-container seqtk_seq.cwl
Enable beta testing mode for testing.
cwltool INFO: /Users/john/workspace/planemo/.venv/bin/cwltool 1.0.20180508202931
cwltool INFO: Resolved '/Users/john/tool_init_exercise/seqtk_seq.cwl' to 'file:///Users/john/tool_init_exercise/seqtk_seq.cwl'
cwltool INFO: [job seqtk_seq.cwl] /private/tmp/docker_tmpvLE9SS$ seqtk seq -A /private/var/folders/78/xxz5mz4d0jn53xf0106j7ppc0000gp/T/tmpGM22d_/stg0c0cad75-7ca0-4f3a-9d77-63e9c49f5353/2.fastq > /private/tmp/docker_tmpvLE9SS/out
cwltool INFO: [job seqtk_seq.cwl] completed success
cwltool INFO: Final process status is success
All 1 test(s) executed passed.
seqtk_seq_0: passed
```

This is a bit a different than running the job. For one thing, we don’t need to specify an input job - instead Planemo will automatically find the test file and run all the jobs described inside that file. Additionally, Planemo will check the outputs to ensure the match the test expectations.

In addition to the in console display of test results as red (failing) or green (passing), Planemo also creates an HTML report for the test results by default. Many more test report options are available such as --test_output_xunit which is useful in certain continuous integration environments. See planemo test --help for more options, as well as the test_reports command.

The above test example used cwltool to run our test and disabled containerization. By dropping the --no-container argument we can run the tool in a Docker container. By passing an engine argument as --engine toil we can run our test in Toil, an alternative CWL implementation.

```bash
$ planemo test seqtk_seq.cwl
Enable beta testing mode for testing.
cwltool INFO: /Users/john/workspace/planemo/.venv/bin/cwltool 1.0.20180508202931
cwltool INFO: Resolved '/Users/john/tool_init_exercise/seqtk_seq.cwl' to 'file:///Users/john/tool_init_exercise/seqtk_seq.cwl'
cwltool INFO: [job seqtk_seq.cwl] /private/tmp/docker_tmpUeIpXJ$ docker \
  run \
  -i \
  --volume=/private/tmp/docker_tmpUeIpXJ:/private/var/spool/cwl:rw \
```

---

output1:
  path: test-data/2.fasta

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Planemo Documentation, Release 0.61.0.dev0

6.3 Advanced Tool Development Topics

This tutorial covers some more advanced tool development topics. It assumes some basic knowledge about developing CWL tools and that you have an environment with Planemo available - check out the CWL User Guide CWL and the Planemo CWL intro tutorial if you have never developed a CWL tool.

6.3.1 Dependencies and Conda

Specifying and Using Software Requirements

Note: Planemo requires a Conda installation to target with its various Conda related commands. A properly configured Conda installation can be initialized with the conda_init command. This should only need to be executed once per development machine.

```
$ planemo conda_init
galaxy.tools.deps.conda_util INFO: Installing conda, this may take several minutes.
wget -q --recursive -O /var/folders/78/zzx5mz4d0jn53xf0106j7ppc0000gp/T/conda_--installLLW5zn1.sh https://repo.continuum.io/miniconda/Miniconda3-4.3.31-MacOSX-x86_64.sh
bash /var/folders/78/zzx5mz4d0jn53xf0106j7ppc0000gp/T/conda_installLLW5zn1.sh -b -p /Users/john/miniconda3
PREFIX=/Users/john/miniconda3
```

(continues on next page)
installing: python-3.6.3-h47c878a_7 ...
Python 3.6.3 :: Anaconda, Inc.
installing: ca-certificates-2017.08.26-ha1e5d58_0 ...
installing: conda-env-2.6.0-h36134e3_0 ...
installing: libgccabi-4.0.1-hebd6815_0 ...
installing: tk-8.6.7-h35a86e2_3 ...
installing: xz-5.2.3-h0278029_2 ...
installing: yam1-0.1.7-hc338f04_2 ...
installing: zlib-1.2.11-hf3cbc9b_b_2 ...
installing: libgcc-4.0.1-h579ed51_0 ...
installing: openssl-1.0.2n-ha569be9_0 ...
installing: ncurses-6.0-hd04f020_2 ...
installing: libedit-3.1-hb4e282d_0 ...
installing: readline-7.0-hc1231fa_4 ...
installing: sqlite-3.20.1-h7e4c145_2 ...
installing: aslncrypto-0.23.0-py36h782d450_0 ...
installing: certifi-2017.11.5-py36ha569be9_0 ...
installing: charmdet-3.0.4-py36h96c241c_1 ...
installing: idna-2.6-py36h63e6348_0 ...
installing: pycosat-0.6.3-py36hee92d8f_0 ...
installing: pycparser-2.18-py36h724b2fc_1 ...
installing: pysocks-1.6.7-py36hfa33ce_1 ...
installing: python-app-2-py36h54569d5_7 ...
installing: ruamel_yaml-0.11.14-py36h9d7ade0_2 ...
installing: six-1.11.0-py36h0e22d5e_1 ...
installing: cffi-1.11.2-py36hd3e6348_0 ...
installing: setuptools-36.5.0-py36h2134326_0 ...
installing: cryptography-2.1.4-py36h842514c_0 ...
installing: wheel-0.30.0-py36h5eb2c71_1 ...
installing: pip-9.0.1-py36h1555ced_4 ...
installing: pyopenssl-17.5.0-py36h51e4350_0 ...
installing: urllib3-1.22-py36h6b9469_0 ...
installing: requests-2.18.4-py36h4516966_1 ...
installing: conda-4.3.33-py36_0 ...
installation finished.
/Users/john/miniconda3/bin/conda install --override-channels --channel iuc --channel conda-forge --channel bioconda --channel defaults conda=4.3.33 conda-
--build=2.1.18
Fetching package metadata .................
Solving package specifications: .

Package plan for installation in environment /Users/john/miniconda3:
The following NEW packages will be INSTALLED:

- beautifulsoup4: 4.6.0-py36_0 conda-forge
- conda-build: 2.1.18-py36_0 conda-forge
- conda-verify: 2.0.0-py36_0 conda-forge
- filelock: 3.0.4-py36_0 conda-forge
- jinja2: 2.10-py36_0 conda-forge
- markupsafe: 1.0-py36_0 conda-forge
- pkginfo: 1.4.2-py36_0 conda-forge
- pycrypto: 2.6.1-py36_1 conda-forge
- pyyaml: 3.12-py36_1 conda-forge

The following packages will be UPDATED:
Note: Why not just use containers?

Containers are great, use containers (be it Docker, Singularity, etc.) whenever possible to increase reproducibility and portability of your tools and workflow. Building ad hoc containers to support CWL tools (e.g. custom Dockerfile definitions) has serious limitations, in the next tutorial on containers we will argue that using Biocontainers built or discovered from your tool’s Software Requirements is a superior approach.

Besides leading to better containers, there are other reasons to describe Software Requirements also - it will allow your tool to be used in environments without container runtimes available and provides valuable and actionable metadata about the computation described by the tool.

Read more about this whole dependency stack in our preprint Practical computational reproducibility in the life sciences

The Common Workflow Language specification loosely describes Software Requirements - a way to map CWL hints to packages, environment modules, or any other mechanism to describe dependencies for running a tool outside of a container. The large and active Galaxy tool development community has built an open source library and set of best practices for describing dependencies for Galaxy that should work just as well for CWL. The library has been integrated with cwltool and Toil to enable CWL tool authors and users to leverage the power and flexibility of the Galaxy dependency management and best practices.

While Software Requirements can be configured to resolve dependencies various ways, Planemo is configured with opinionated defaults geared at making building CWL tools that target Conda as easy as possible and build tools with requirements compatible with cwltool and Toil when running outside containers.

During the tool development introductory tutorial, we called planemo tool_init with the argument --requirement seqtk@1.2 and the resulting tool contained such a SoftwareRequirement in the form the following the YAML fragment:
<table>
<thead>
<tr>
<th>SoftwareRequirement:</th>
</tr>
</thead>
<tbody>
<tr>
<td>packages:</td>
</tr>
<tr>
<td>- package: seqtk</td>
</tr>
<tr>
<td>version:</td>
</tr>
<tr>
<td>- &quot;1.2&quot;</td>
</tr>
</tbody>
</table>

Planemo (and cwltool and Toil) can interpret these `SoftwareRequirement` annotations in various ways including as Conda packages. When interpreting these as Conda packages these runtimes can setup isolated, reproducible Conda environments for tool execution with the correct packages installed (e.g. seqtk in the above example).

**Note:** Why Conda?

Many different package managers could potentially be targeted here, but we focus on Conda for a few key reasons.

- No compilation at install time - binaries with their dependencies and libraries
- Support for all operating systems
- Easy to manage multiple versions of the same recipe
- HPC-ready: no root privileges needed
- Easy-to-write YAML recipes
- Viberant communities

**Note:** Conda Terminology

CONDA®

MINICONDA®

= conda
+ python
+ base packages

= miniconda
+ 150 high quality packages

ANAconda®
Conda recipes build packages that are published to channels.

Planemo is setup to target a few channels by default, these include iuc, bioconda, conda_forge, defaults - the whole dependency management scheme outlined here works a lot better if packages can be found in one of these “best practice” channels.

We can check if the requirements on a tool are available in best practice Conda channels using an extended form of the planemo lint command (planemo lint was introduced in the introductory tutorial). Passing --conda_requirements flag will ensure all listed requirements are found.

```
$ planemo lint --conda_requirements seqtk_seq.cwl
Linting tool /Users/john/workspace/planemo/docs/writing/seqtk_seq.cwl
...
Applying linter requirements_in_conda... CHECK
.. INFO: Requirement [seqtk@1.2] matches target in best practice Conda channel
→[https://conda.anaconda.org/bioconda/osx-64].
```

**Note:** You can download a more complete version of the CWL seqtk seq from the Planemo tutorial using the command:

```
$ planemo project_init --template=seqtk_complete_cwl seqtk_example
$ cd seqtk_example
```

We can verify these tool requirements install with the conda_install command. With its default parameters conda_install processes tools and creates isolated environments for their declared Software Requirements (mirroring what can be done in production with cwltool and Toil).

```
$ planemo conda_install seqtk_seq.cwl
Install conda target CondaTarget[seqtk,version=1.2]
/home/john/miniconda3/bin/conda create -y --name __seqtk@1.2 seqtk=1.2
Fetching package metadata ............... Solving package specifications: .......... Package plan for installation in environment /home/john/miniconda2/envs/__seqtk@1.2:
The following packages will be downloaded:

<table>
<thead>
<tr>
<th>package</th>
<th>build</th>
</tr>
</thead>
<tbody>
<tr>
<td>seqtk-1.2</td>
<td>0</td>
</tr>
</tbody>
</table>

The following NEW packages will be INSTALLED:

seqtk: 1.2-0 bioconda
zlib: 1.2.8-3

Fetching packages ...
seqtk-1.2-0.ta 100% |##########################################|    
→Time: 0:00:00 444.71 kB/s
Extracting packages ...
[ COMPLETE ]|##########################################
...
Linking packages ...
[ COMPLETE ]|########################################## 100%
```
(continues on next page)
# To activate this environment, use:
#   source activate __seqtk@1.2
#
# To deactivate this environment, use:
#   source deactivate __seqtk@1.2
#
$ which seqtk
seqtk not found
$

The above install worked properly, but seqtk is not on your PATH because this merely created an environment within the Conda directory for the seqtk installation. Planemo will configure cwltool during testing to reuse this environment. If you wish to interactively explore the resulting environment to explore the installed tool or produce test data the output of the conda_env command can be sourced.

$ . <(planemo conda_env seqtk_seq.cwl)
Deactivate environment with conda_env_deactivate
(seqtk_seq) $ which seqtk
/home/planemo/miniconda3/envs/…
(seqtk_seq) $ seqtk seq
Usage: seqtk seq [options] <in.fq>|<in.fa>
Options: -q INT mask bases with quality lower than INT [0]
-X INT mask bases with quality higher than INT [255]
-n CHAR masked bases converted to CHAR; 0 for lowercase [0]
-l INT number of residues per line; 0 for 2^32-1 [0]
-Q INT quality shift: ASCII-INT gives base quality [33]
-s INT random seed (effective with -f) [11]
-f FLOAT sample FLOAT fraction of sequences [1]
-M FILE mask regions in BED or name list FILE [null]
-L INT drop sequences with length shorter than INT [0]
-c mask complement region (effective with -M)
-r reverse complement
-A force FASTA output (discard quality)
-C drop comments at the header lines
-N drop sequences containing ambiguous bases
-1 output the 2n-1 reads only
-2 output the 2n reads only
-V shift quality by '(-Q) - 33'
-U convert all bases to uppercases
-S strip of white spaces in sequences

As shown above the conda_env_deactivate will be created in this environment and can be used to restore your initial shell configuration.

Here is a portion of the output from the testing command planemo test seqtk_seq.cwl demonstrating using this tool.

$ planemo test --no-container seqtk_seq.cwl
Enable beta testing mode for testing.

cwltool INFO: /Users/john/workspace/planemo/.venv/bin/planemo 1.0.20170828135420

(continued from previous page)

cwltool INFO: Resolved '/Users/john/workspace/planemo/project_templates/seqtk_complete_cwl/seqtk_seq.cwl' to 'file:///Users/john/workspace/planemo/project_templates/seqtk_complete_cwl/seqtk_seq.cwl'
cwltool INFO: [job seqtk_seq.cwl] /private/var/folders/78/...

Since seqtk isn’t on the path and we did not use a container, we can see the SoftwareRequirement resolution was successful and it found the environment we previously installed with conda_install.

This can be used outside of Planemo testing as well, the following invocation shows running a job with cwltool using an environment like the one created above:

```bash
$ cwltool --no-container --beta-conda-dependencies seqtk_seq.cwl seqtk_seq_job.yml
Resolved 'seqtk_seq.cwl' to 'file:///Users/john/workspace/planemo/project_templates/...

No handlers could be found for logger "rdflib.term"

[job seqtk_seq.cwl] /private/tmp/docker_tmpDQYeqC$ seqtk \
  seq \n  -a \n  /private/var/folders/78/xxz5mz4d0jn53xf0106j7ppc0000gp/T/tmpJtPKCr/stg24cf7e67-...

PREFIX=/Users/john/workspace/planemo/project_templates/seqtk_complete_cwl/cwltool_...
installing: pycparser-2.18-py36h724b2fc_1 ...
installing: pysocks-1.6.7-py36hfa33cec_1 ...
installing: python.app-2-py36h54569d5_7 ...
installing: ruamel_yaml-0.11.14-py36h9d7ade0_2 ...
installing: six-1.11.0-py36h0e22d5e_1 ...
installing: cffi-1.11.2-py36hd3e6348_0 ...
installing: setuptools-36.5.0-py36h2134326_0 ...
installing: cryptography-2.1.4-py36h842514c_0 ...
installing: wheel-0.30.0-py36h5eb2c71_1 ...
installing: pip-9.0.1-py36hfa33cec_1 ...
installing: cffi-1.11.2-py36hd3e6348_0 ...
installing: ruamel_yaml-0.11.14-py36h9d7ade0_2 ...
installing: six-1.11.0-py36h0e22d5e_1 ...
installation finished.
Fetching package metadata .................
Solving package specifications: 

Package plan for installation in environment /Users/john/workspace/planemo/project_ →templates/seqtk_complete_cwl/cwltool_deps/_conda:
The following packages will be UPDATED:
  conda: 4.3.31-py36_0 --> 4.3.33-py36_0 conda-forge
conda-4.3.33-p 100% 1.13 MB/s

Package plan for installation in environment /Users/john/workspace/planemo/project_ →templates/seqtk_complete_cwl/cwltool_deps/_conda/envs/__seqtk@1.2:
The following NEW packages will be INSTALLED:
  seqtk: 1.2.1-1 bioconda
  zlib: 1.2.11-0 conda-forge

[job seqtk_seq.cwl] completed success
{
  "output1": {
    "checksum": "sha1$322e001e5a99f19abdce9f02ad0f02a17b5066c2",
    "basename": "out",
    "location": "file:///Users/john/workspace/planemo/project_templates/seqtk_ →complete_cwl/out",
    "path": "/Users/john/workspace/planemo/project_templates/seqtk_complete_cwl/ →out",
    "class": "File",
    "size": 150
  }
}

Final process status is success

This demonstrates that cwltool will install the packages needed on the first run, if we rerun cwltool it will reuse that previous environment.
$ cwltool --no-container --beta-conda-dependencies seqtk_seq.cwl seqtk_seq_job.yml
/Users/john/workspace/planemo/.venv/bin/cwltool 1.0.20180508202931
Resolved 'seqtk_seq.cwl' to 'file:///Users/john/workspace/planemo/project_templates/→seqtk_complete_cwl/seqtk_seq.cwl'
No handlers could be found for logger "rdflib.term"
[job seqtk_seq.cwl] /private/tmp/docker_tmp4vvE_i$ seqtk \\n  seq \\n  -a \\n/private/var/folders/78/zxz5zm4d0jn53xf0106j7ppc0000gp/T/tmpcvQ3Ph/stg2ef3a21c-→9fb0-4099-88c2-36e24719901d/2.fastq > /private/tmp/docker_tmp4vvE_i/out
[job seqtk_seq.cwl] completed success
  "output1": {
    "checksum": "sha1$322e001e5a99f19abdce9f02ad0f02a17b5066c2",
    "basename": "out",
    "location": "file:///Users/john/workspace/planemo/project_templates/→seqtk_→complete_cwl/out",
    "path": "/Users/john/workspace/planemo/project_templates/seqtk_complete_cwl/
    "class": "File",
    "size": 150
  }
}
Final process status is success

And the same thing is possible with **Toil**.

$ cwltoil --no-container --beta-conda-dependencies seqtk_seq.cwl seqtk_seq_job.yml
jlaptop17.local 2018-05-23 15:27:25,754 MainThread INFO toil.lib.bioio: Root logger is at level 'INFO', 'toil' logger at level 'INFO'.
jlaptop17.local 2018-05-23 15:27:25,785 MainThread INFO toil.jobStores.→abstractJobStore: The workflow ID is: '92328fb2-33b7-44cd-879f-41d8cbbf9455'
Resolved 'seqtk_seq.cwl' to 'file:///Users/john/workspace/planemo/project_templates/→seqtk_complete_cwl/seqtk_seq.cwl'
jlaptop17.local 2018-05-23 15:27:27,002 MainThread INFO toil.common: Using the single→machine batch system
jlaptop17.local 2018-05-23 15:27:29,797 MainThread INFO toil.common: Using the single→machine batch system
jlaptop17.local 2018-05-23 15:27:29,808 MainThread INFO toil.common: Created the→workflow directory at /var/folders/78/zxz5zm4d0jn53xf0106j7ppc0000gp/T/toil-→92328fb2-33b7-44cd-879f-41d8cbbf9455-132281828025877
(continues on next page)


jlaptop17.local 2018-05-23 15:27:29,816 MainThread INFO toil.common: Written the environment for the jobs to the environment file

jlaptop17.local 2018-05-23 15:27:29,816 MainThread INFO toil.common: Caching all jobs in job store


jlaptop17.local 2018-05-23 15:27:29,911 MainThread INFO toil: Running Toil version 3.15.0-0e3a87e738f5e0e7cff64bfdad337d592bd92704.


jlaptop17.local 2018-05-23 15:27:29,937 MainThread INFO toil.toilState: (Re)building internal scheduler state

2018-05-23 15:27:29,938 - toil.toilState - INFO - (Re)building internal scheduler state

jlaptop17.local 2018-05-23 15:27:29,938 MainThread INFO toil.leader: Found 1 jobs to start and 0 jobs with successors to run

2018-05-23 15:27:29,938 - toil.leader - INFO - Found 1 jobs to start and 0 jobs with successors to run

jlaptop17.local 2018-05-23 15:27:29,938 MainThread INFO toil.leader: Checked batch system has no running jobs and no updated jobs

2018-05-23 15:27:29,938 - toil.leader - INFO - Checked batch system has no running jobs and no updated jobs

jlaptop17.local 2018-05-23 15:27:29,938 MainThread INFO toil.leader: Starting the main loop

2018-05-23 15:27:29,938 - toil.leader - INFO - Starting the main loop


jlaptop17.local 2018-05-23 15:27:31,411 MainThread INFO toil.leader: Finished the main loop: no jobs left to run

2018-05-23 15:27:31,411 - toil.leader - INFO - Finished the main loop: no jobs left to run

jlaptop17.local 2018-05-23 15:27:31,411 MainThread INFO toil.serviceManager: Waiting for service manager thread to finish ...

2018-05-23 15:27:31,411 - toil.serviceManager - INFO - Waiting for service manager thread to finish ...

jlaptop17.local 2018-05-23 15:27:31,946 MainThread INFO toil.serviceManager: ... finished shutting down the service manager. Took 0.535056114197 seconds

2018-05-23 15:27:31,946 - toil.serviceManager - INFO - ... finished shutting down the service manager. Took 0.535056114197 seconds
Finding Existing Conda Packages

How did we know what software name and software version to use? We found the existing packages available for Conda and referenced them. To do this yourself, you can simply use the planemo command `conda_search`. If we do a search for `seqtk` it will show all the software and all the versions available matching that search term - including `seqtk`.

```
$ planemo conda_search seqt
/Users/john/miniconda3/bin/conda search --override-channels --channel iuc --channel conda-forge --channel bioconda --channel defaults '*seqtk'
Loading channels: done
  # Name               Version  Build Channel
  biocductor-htseqtools  1.26.0   r3.4.1_0  bioconda
  biocductor-seqtools   1.10.0   r3.3.2_0  bioconda
  biocductor-seqtools   1.10.0   r3.4.1_0  bioconda
  biocductor-seqtools   1.12.0   r3.4.1_0  bioconda
  seqtk                r75      0  bioconda
  seqtk                r82      0  bioconda
  seqtk                r82      1  bioconda
  seqtk                r93      0  bioconda
  seqtk                1.2      0  bioconda
  seqtk                1.2      1  bioconda
```

Note: The Planemo command `conda_search` is a light wrapper around the underlying `conda search` command but configured to use the same channels and other options as Planemo and Galaxy. The following Conda
command would also work to search:

```
$ $HOME/miniconda3/bin/conda -c iuc -c conda-forge -c bioconda '*seqt*'
```

For Conda versions 4.3.X or less, the search invocation would be something a bit different:

```
$ $HOME/miniconda3/bin/conda -c iuc -c conda-forge -c bioconda seqt
```

Alternatively the Anaconda website can be used to search for packages. Typing `seqtk` into the search form on that page and clicking the top result will bring on to this page with information about the Bioconda package.

When using the website to search though, you need to aware of what channel you are using. By default, Planemo and Galaxy will search a few different Conda channels. While it is possible to configure a local Planemo or Galaxy to target different channels - the current best practice is to add tools to the existing channels.

The existing channels include:

- **Bioconda** ([github](https://github.com/bioconda/bioconda-recipes)) - best practice channel for various bioinformatics packages.
- **Conda-Forge** ([github](https://github.com/conda-forge/conda-recipes)) - best practice channel for general purpose and widely useful computing packages and libraries.
- **iuc** ([github](https://github.com/iuc/conda-recipes)) - best practice channel for other more Galaxy specific packages.

### Exercise - Leveraging Bioconda

Use the `project_init` command to download this exercise.

```
$ planemo project_init --template conda_exercises_cwl conda_exercises
$ cd conda_exercises/exercise_1
$ ls
pear.cwl  test-data
```

This project template contains a few exercises. The first uses a CWL tool for PEAR - Paired-End reAd mergeR. This tool however has no `SoftwareRequirement` or container annotations and so will not work properly without modification.

1. Run `planemo test pear.cwl` to verify the tool does not function without dependencies defined.
2. Use `--conda_requirements` flag with `planemo lint` to verify it does indeed lack requirements.
3. Use `planemo conda_search` or the Anaconda website to search for the correct package and version in a best practice channel.
4. Update `pear.cwl` with the correct `SoftwareRequirement` hints.
5. Re-run the `lint` command from above to verify the tool now has the correct dependency definition.
6. Re-run the `test` command from above to verify the tool test now works properly.

### Building New Conda Packages

Frequently packages your tool will require are not found in Bioconda or conda-forge yet. In these cases, it is likely best to contribute your package to one of these projects. Unless the tool is exceedingly general Bioconda is usually the correct starting point.
Note: Many things that are not strictly or even remotely “bio” have been accepted into Bioconda - including tools for image analysis, natural language processing, and cheminformatics.

To get quickly learn to write Conda recipes for typical Galaxy tools, please read the following pieces of external documentation.

- Contributing to Bioconda in particular focusing on
  - One time setup
  - Contributing a recipe (through “Write a Recipe”)
- Building conda packages in particular
  - Building conda packages with conda skeleton (the best approach for common scripting languages such as R and Python)
  - Building conda packages from scratch
  - Building conda packages for general code projects
  - Using conda build
- Then return to the Bioconda documentation and read
  - The rest of “Contributing a recipe” continuing from Testing locally
  - And finally Guidelines for bioconda recipes

These guidelines in particular can be skimmed depending on your recipe type, for instance that document provides specific advice for:

- Python
- R (CRAN)
- R (Bioconductor)
- Perl
- C/C++

To go a little deeper, you may want to read:

- Specification for meta.yaml
- Environment variables
- Custom channels

And finally to debug problems the Bioconda troubleshooting documentation may prove useful.

Exercise - Build a Recipe

If you have just completed the exercise above - this exercise can be found in parent folder. Get there with cd ../exercise_2. If not, the exercise can be downloaded with

```bash
$ planemo project_init --template conda_exercises_cwl conda_exercises
$ cd conda_exercises/exercise_2
$ ls
fleeqtk_seq.cwl  fleeqtk_seq_tests.yml  test-data
```
This is the skeleton of a tool wrapping the parody bioinformatics software package *fleeqtk*. *fleeqtk* is a fork of the project *seqtk* that many Planemo tutorials are built around and the example tool should hopefully be fairly familiar. *fleeqtk* version 1.3 can be downloaded from here and built using *make*. The result of *make* includes a single executable *fleeqtk*.

1. Clone and branch *Bioconda*.
2. Build a recipe for *fleeqtk* version 1.3. You may wish to start from scratch (*conda skeleton* is not available for C programs like *fleeqtk*), or copy the recipe of *seqtk* and modify it for *fleeqtk*.
3. Use *conda build* or *Bioconda* tooling to build the recipe.
4. Run *planemo test --conda_use_local fleeceqtk_seq.cwl* to verify the resulting package works as expected.

Congratulations on writing a *Conda* recipe and building a package! Upon successfully building and testing such a *Bioconda* package, you would normally push your branch to Github and open a pull request. This step is skipped here as to not pollute *Bioconda* with unneeded software packages.

### 6.3.2 Dependencies and Containers

**Note:** This section is a continuation of *Dependencies and Conda*, please review that section for background information on resolving *Software Requirements* with *Conda*.

Common Workflow Language tools can be annotated with arbitrary Docker requirements, see the *CWL User Guide* for a discussion about how to do this in general.

This document will discuss some techniques to find containers automatically from the *SoftwareRequirement* annotations when using *Planemo*, *cwltool*, or *Toil*. You will ultimately want to explicitly annotate your tools with the containers we describe here so that other CWL implementations will be able to find containers for your tool, but there are real advantages to using these containers instead of ad-hoc things you may build with a *Dockerfile*.

- They provide superior reproducibility because the same binary Conda packages will automatically be used for both bare metal dependencies and inside containers.
- They are constructed automatically from existing Conda packages so you as a tool developer won’t need to write *Dockerfiles* or register projects on Docker Hub.
- They are produced using *mulled* which produce very small containers that make deployment easier regardless of the CWL implementation you are using.
- Annotating *Software Requirements* reduces the opaqueness of the Docker process. With this method it is entirely traceable how the container was constructed from what sources were fetched, which exact build of every dependency was used, to how packages in the container were built. Beyond that metadata about the packages can be fetched from *Bioconda* (e.g. this).

Read more about this reproducibility stack in our preprint *Practical computational reproducibility in the life sciences*.

### BioContainers

**Note:** This section is a continuation of *Dependencies and Conda*, please review that section for background information on resolving *Software Requirements* with *Conda*. 

---

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**Finding BioContainers**

If a tool contains Software Requirements in best practice Conda channels, a BioContainers-style container can be found or built for it.

As reminder, `planemo lint --conda_requirements <tool.cwl>` can be used to check if a tool contains only best-practice requirement tags. The lint command can also be fed the `--biocontainers` flag to check if a BioContainers container has been registered that is compatible with that tool.

This last linter indicates that indeed a container has been registered that is compatible with this tool – `quay.io/biocontainers/seqtk:1.2--1`. We didn’t do any extra work to build this container for this tool, all Bioconda recipes are packaged into containers and registered on quay.io as part of the BioContainers project.

This tool can be tested using `planemo test` in its BioContainer Docker container using the flag `--biocontainers` as shown below.

The Conda exercises project template has an example tool (`exercise3`) that we can use to demonstrate `--biocontainers`. If you are continuing from the Conda tutorial, simply move to `../exercise3` otherwise using `planemo project_init` to grab the exercise as show below.

```bash
$ planemo project_init --template conda_exercises_cwl conda_exercises
$ cd conda_exercises/exercise3
$ planemo lint --biocontainers seqtk_seq.cwl
Linting tool /home/planemo/conda_exercises_cwl/exercise_3/seqtk_seq.cwl
Applying linter general... CHECK
.. CHECK: Tool defines a version [0.0.1].
.. CHECK: Tool defines a name [Convert to FASTA (seqtk)].
.. CHECK: Tool defines an id [seqtk_seq].
.. CHECK: Tool specifies profile version [16.04].
Applying linter cwl_validation... CHECK
.. INFO: CWL appears to be valid.
Applying linter docker_image... WARNING
.. WARNING: Tool does not specify a DockerPull source.
Applying linter new_draft... CHECK
.. INFO: Modern CWL version [v1.0]
Applying linter biocontainer_registered... CHECK
.. INFO: BioContainer best-practice container found [quay.io/biocontainers/seqtk:1.2--1].
Failed linting

$ planemo test --biocontainers seqtk_seq.cwl
Enable beta testing mode for testing.
cwltool INFO: /Users/john/workspace/planemo/.venv/bin/planemo 1.0.20180508202931
cwltool INFO: Resolved '/Users/john/workspace/planemo/project_templates/conda__
--exercises_cwl/exercise_3/seqtk_seq.cwl' to 'file:///Users/john/workspace/planemo/
--project_templates/conda_exercises_cwl/exercise_3/seqtk_seq.cwl'
galaxy.tools.deps.containers INFO: Checking with container resolver...
   | [ExplicitContainerResolver[]] found description [None]
galaxy.tools.deps.containers INFO: Checking with container resolver...
   | [CachedMulledDockerContainerResolver[namespace=biocontainers]] found description...
   | [None]
galaxy.tools.deps.containers INFO: Checking with container resolver...
   | [MulledDockerContainerResolver[namespace=biocontainers]] found description...
   | [None]
cwltool INFO: [job seqtk_seq.cwl] /private/tmp/docker_tmpMEipaU$ docker 
   run 
   -i 
   --volume=private/tmp/docker_tmpMEipaU:/private/tmp/docker_tmpMEipaU:rw 
   (continues on next page)
Exercise - Leveraging Bioconda

1. Try the above command without the --biocontainers argument. Verify the tool does not run in a container by default.

2. Add a DockerRequirement based on the lint output above to annotate this tool with a Biocontainers Docker container and rerun test to verify the tool works now.

Building BioContainers

In this seqtk example above the relevant BioContainer already existed on quay.io, this won’t always be the case. For tools that contain multiple Software Requirements tags an existing container likely won’t exist. The mulled toolkit (distributed with planemo or available standalone) can be used to build containers for such tools. For such tools, if cwltool or Toil is configured to use BioContainers it will attempt to build these containers on the fly by default (though this behavior can be disabled).

You can try it directly using the mull command in Planemo. The conda_testing Planemo project template has a toy example tool with two requirements for demonstrating this - bwa_and_samtools.cwl.

```
$ planemo project_init --template=conda_testing_cwl conda_testing
$ cd conda_testing/
$ planemo mull bwa_and_samtools.cwl
```

(continues on next page)
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(continued from previous page)


[Jun 19 11:28:35] DEBU Creating container [step-730a02d79e]

[Jun 19 11:28:35] DEBU Created container [5e4b5f83c455 step-730a02d79e], starting it

[Jun 19 11:28:35] DEBU Container [5e4b5f83c455 step-730a02d79e] started, waiting for completion

[Jun 19 11:28:36] DEBU Container [5e4b5f83c455 step-730a02d79e] completed with exit code [0] as expected

[Jun 19 11:28:36] DEBU Container [5e4b5f83c455 step-730a02d79e] removed

[Jun 19 11:28:36] STEP Run image [continuumio/miniconda:latest] with command [[/bin/sh -c conda install --quiet --yes conda=4.3 && conda install -c iuc -c bioconda -c r -c defaults -c conda-forge samtools=1.3.1 bwa=0.7.15 -p /usr/local --copy --yes --quiet]]

[Jun 19 11:28:36] DEBU Creating container [step-e95bf001c8]

[Jun 19 11:28:36] DEBU Created container [72b9c0e65f8 step-e95bf001c8], starting it

[Jun 19 11:28:37] DEBU Container [72b9c0e65f8 step-e95bf001c8] started, waiting for completion

[Jun 19 11:28:46] SOUT Fetching package metadata ...........


[Jun 19 11:28:50] SOUT

[Jun 19 11:28:50] SOUT Package plan for installation in environment /opt/conda:

[Jun 19 11:28:50] SOUT

[Jun 19 11:28:50] SOUT The following packages will be UPDATED:

[Jun 19 11:28:50] SOUT

[Jun 19 11:28:50] SOUT conda: 4.3.11-py27_0 --> 4.3.22-py27_0

[Jun 19 11:28:50] SOUT

[Jun 19 11:28:50] SOUT

[Jun 19 11:29:04] SOUT Fetching package metadata ...............

[Jun 19 11:29:06] SOUT Solving package specifications: :

[Jun 19 11:29:56] SOUT

[Jun 19 11:29:56] SOUT Package plan for installation in environment /usr/local:

[Jun 19 11:29:56] SOUT

[Jun 19 11:29:56] SOUT The following NEW packages will be INSTALLED:

[Jun 19 11:29:56] SOUT

[Jun 19 11:29:56] SOUT bwa: 0.7.15-1 bioconda

[Jun 19 11:29:56] SOUT curl: 7.52.1-0

[Jun 19 11:29:56] SOUT libgcc: 5.2.0-0

[Jun 19 11:29:56] SOUT openssl: 1.0.2l-0

[Jun 19 11:29:56] SOUT pip: 9.0.1-py27_1

[Jun 19 11:29:56] SOUT python: 2.7.13-0


[Jun 19 11:29:56] SOUT samtools: 1.3.1-5 bioconda

[Jun 19 11:29:56] SOUT sqlite: 3.13.0-0

[Jun 19 11:29:56] SOUT tk: 8.5.18-0

[Jun 19 11:29:56] SOUT wheel: 0.29.0-py27_0

[Jun 19 11:29:56] SOUT zlib: 1.2.8-3

[Jun 19 11:29:56] SOUT

[Jun 19 11:29:56] SOUT

[Jun 19 11:29:57] DEBU Container [72b9c0e65f8 step-e95bf001c8] completed with exit code [0] as expected

[Jun 19 11:29:57] DEBU Container [72b9c0e65f8 step-e95bf001c8] removed

[Jun 19 11:29:57] STEP Wrap [build/dist] as [quay.io/biocontainers/mulled-\(v2-\)\(fe8fa35dbf6dc65a0f7f5d4ea12e31a79f73e40:03dc1d2818d9de569380788b8b7b82d967c1f820-0\)]

[Jun 19 11:29:57] DEBU Creating container [step-6f1c176372]

[Jun 19 11:29:58] DEBU Packing succeeded

6.3. Advanced Tool Development Topics
As the output indicates, this command built the container named `quay.io/biocontainers/mulled-v2-fe8faa35dbf6dc65a0f7f5d4ea12e31a79f73e40:03dc1d2818d9de56938078b8b78b82d967c1f820-0`. This is the same namespace / URL that would be used if or when published by the BioContainers project.

**Note:** The first part of this `mulled-v2` hash is a hash of the package names that went into it, the second the packages used and build number. Check out the Multi-package Containers web application to explore best practice channels and build such hashes.

We can see this new container when running the Docker command `images` and explore the new container interactively with `docker run`.

```
$ docker images
REPOSITORY TAG IMAGE ID CREATED SIZE
--- -------- --------------- --------
quay.io/biocontainers/mulled-v2-fe8faa35dbf6dc65a0f7f5d4ea12e31a79f73e40-03dc1d2818d9de56938078b8b78b82d967c1f820-0 740a1e6a9e 16 hours ago 104 MB
quay.io/biocontainers/seqtk 1.2--0 10bc359e0d30 2 days ago 7.34 MB
continuumio/miniconda latest 6965a4889098 3 weeks ago 437 MB
bgruening/busybox-bash 0.1 3d974f51245c 9 months ago 6.73 MB
```

As before, we can test running the tool inside its container in cwltool using the `--biocontainers` flag.

```
$ docker run -i -t quay.io/biocontainers/mulled-v2-fe8faa35dbf6dc65a0f7f5d4ea12e31a79f73e40:03dc1d2818d9de56938078b8b78b82d967c1f820-0 /bin/bash
bash-4.2# which samtools
/usr/local/bin/samtools
bash-4.2# which bwa
/usr/local/bin/bwa
```

As we can see, this container contains `samtools` and `bwa` as expected. We can test running the tool inside its container in cwltool using the `--biocontainers` flag.

```
$ cwltool INFO: /Users/john/workspace/planemo/.venv/bin/cwltool 1.4.20180509172145
$cwltool INFO: Checking with container resolver
$ [CachedMulledDockerContainerResolver[namespace=biocontainers]] found description
$ [ContainerDescription[identifier=quay.io/biocontainers/mulled-v2-fe8faa35dbf6dc65a0f7f5d4ea12e31a79f73e40:03dc1d2818d9de56938078b8b78b82d967c1f820-0, type=docker]] found description
$cwltool INFO: [job bwa_and_samtools.cwl] /private/tmp/docker_tmpYJnmO4$ docker \
  run \
  -i \
  --volume=/private/tmp/docker_tmpYJnmO4:/private/tmp/docker_tmpYJnmO4:rw \
  --volume=/private/var/folders/78/zxx5mz4d0jn53xf0106j7ppc0000gp/T/tmpVI06me:/tmp:rw \
  --workdir=/private/tmp/docker_tmpYJnmO4 \
  --read-only=true \
  --user=502:20 \
  --rm \
```

(continues on next page)
--env=TMPDIR=/tmp \
--env=HOME=/private/tmp/docker_tmpYJnmO4 \
quay.io/biocontainers/mulled-v2-
fe8faa35dbf6dc65a0f7f5d4ea12e31a79f73e40:03dc1d2818d9d56938078b8b78b82d967c1f820-0
\-
\sh \n-c \n'bwa > bwa_help.txt 2>&1; samtools > samtools_help.txt 2>&1'
cwltool INFO: [job bwa_and_samtools.cwl] completed success
cwltool INFO: Final process status is success
All 1 test(s) executed passed.
bwa_and_samtools_0: passed

In particular take note of the line:

```
2017-03-01 10:20:59,142 INFO [galaxy.tools.deps.containers] Checking with container-
--resolver [CachedMulledDockerContainerResolver[namespace=biocontainers]] found
--description [ContainerDescription[identifier=quay.io/biocontainers/mulled-v2-
--fe8faa35dbf6dc65a0f7f5d4ea12e31a79f73e40:03dc1d2818d9d56938078b8b78b82d967c1f820-0,
--type=docker]]
```

Here we can see the container ID (quay.io/biocontainers/mulled-v2-fe8faa35dbf6dc65a0f7f5d4ea12e31a79f73e40:03dc1d2818d9d56938078b8b78b82d967c1f820-0) from earlier has been cached on our Docker host is picked up by cwltool. This is used to run the simple tool tests and indeed they pass.

In our initial seqtk example, the container resolver that matched was of type MulledDockerContainerResolver indicating that the Docker image would be downloaded from the BioContainers repository and this time the resolve that matched was of type CachedMulledDockerContainerResolver meaning that cwltool would just use the locally cached version from the Docker host (i.e. the one we built with planemo mull above).

**Note:** Planemo doesn’t yet expose options that make it possible to build mulled containers for local packages that have yet to be published to anaconda.org but the mulled toolkit allows this. See mulled documentation for more information. However, once a container for a local package is built with mulled-build-tool the --biocontainers command should work to test it.

### Publishing BioContainers

Building unpublished BioContainers on the fly is great for testing but for production use and to increase reproducibility such containers should ideally be published as well.

BioContainers maintains a registry of package combinations to be published using these long mulled hashes. This registry is represented as a Github repository named multi-package-containers. The Planemo command container_register will inspect a tool and open a Github pull request to add the tool’s combination of packages to the registry. Once merged, this pull request will result in the corresponding BioContainers image to be published (with the correct mulled has as its name) - these can be subsequently be picked up by Galaxy.

Various Github related settings need to be configured in order for Planemo to be able to open pull requests on your behalf as part of the container_register command. To simplify all of this - the Planemo community maintains a list of Github repositories containing Galaxy and/or CWL tools that are scanned daily by Travis. For each such repository, the Travis job will run container_register across the repository on all tools resulting in new registry pull requests for all new combinations of tools. This list is maintained in a script named monitor.sh in the planemo-monitor repository. The easiest way to ensure new containers are built for your tools is simply to open a pull request.
request to add your tool repositories to this list.
The Galaxy Tool Shed (referred to colloquially in Planemo as the “shed”) can store Galaxy tools, dependency definitions, and workflows among other Galaxy artifacts. This guide will assume some basic familiarity with the shed - please review the Tool Shed Wiki for an introduction.

### 7.1 Configuring a Shed Account

Before getting started, it is a good idea to have accounts on the Galaxy test and (optionally) main Tool Sheds. Also, if you haven’t initialized a global Planemo configuration file (~/.planemo.yml) this can be done with.

```
planemo config_init
```

This will populate a template ~/.planemo.yml file and provide locations to fill in shed credentials for the test and main Tool Sheds. For each shed, fill in either an API key or an email and password. Also specify the shed_username created when registering shed accounts. All these options can be specified and/or overridden on each planemo command invocation - but that becomes tedious quickly.

### 7.2 Creating a Repository

Planemo can be used to used to publish “repositories” to the Tool Shed. A single GitHub repository or locally managed directory of tools may correspond to any number of Tool Shed repositories. Planemo maps files to Tool Shed repositories using a special file called .shed.yml.

From a directory containing tools, a package definition, etc... the shed_init command can be used to bootstrap a new .shed.yml file.

```
planemo shed_init --name=<name>
  --owner=<shed_username>
  --description=<short description>
  [--remote_repository_url=<URL to .shed.yml on github>]
```

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There is not a lot of magic happening here, this file could easily be created directly with a text editor - but the command has a `--help` to assist you and does some very basic validation.

**Note:** Periods and hyphens are disallowed in repository names, it is recommended replacing periods in the version number with underscores.

The following naming conventions are recommended and in some cases Planemo will determine the repository type based on adherence to these conventions (for packages and suites specifically).

<table>
<thead>
<tr>
<th>Repository Type</th>
<th>Recommended Name</th>
<th>Examples</th>
</tr>
</thead>
<tbody>
<tr>
<td>Data Managers</td>
<td>data_manager_$name</td>
<td>data_manager_bowtie2</td>
</tr>
<tr>
<td>Packages</td>
<td>package_$name$_$version</td>
<td>package_aragorn_1_2_36</td>
</tr>
<tr>
<td>Tool Suites</td>
<td>suite_$name</td>
<td>suite_samtools</td>
</tr>
<tr>
<td>Tools</td>
<td>$name</td>
<td>stringtie,bedtools</td>
</tr>
</tbody>
</table>

More information on `.shed.yml` can be found as part of the IUC best practice documentation.

After reviewing `.shed.yml`, this configuration file and relevant shed artifacts can be quickly linted using the following command.

```bash
planemo shed_lint --tools
```

Once the details the `.shed.yml` are set and it is time to create the remote repository and upload artifacts to it - the following two commands can be used - the first only needs to be run once and creates the repository based the metadata in `.shed.yml` and the second uploads your actual artifacts to it.

```bash
planemo shed_create --shed_target testtoolshed
```

### 7.3 Updating a Repository

Ensure the Galaxy Test Tool Shed is enabled in Galaxy's `config/tool_sheds_conf.xml` file and install and test the new repository.

If modifications are required these can be reviewed using the `shed_diff` command.

```bash
planemo shed_diff --shed_target testtoolshed
```

**Note:** If you look at tools-iuc you will see it is common practice to leave details such as shed target and change-set revision from `tool_dependencies.xml` and `repository_dependencies.xml` files. These are required by the Tool Shed but it will populate them on upload and leaving them blank allows uploading the same artifacts to the Test and Main sheds. The upshot of this is however is that `shed_diff` will always print diffs on these artifacts.

Modified artifacts can be uploaded using the following command.
planemo shed_update --check_diff --shed_target testtoolshed

The --check_diff option here will ensure there are significant differences before uploading new contents to the tool shed.

Once tools and required dependency files have been published to the tool shed, the actual shed dependencies can be automatically and installed and tool tests ran using the command:

planemo shed_test --shed_target testtoolshed

Once your artifacts are ready for publication to the main Tool Shed, the following commands to create a repository there and populate it with your repository contents.

planemo shed_create

### 7.4 Advanced Usage

The above usage is relatively straightforward - it will map the current directory to a single repository in the Tool Shed.

See Pull Request 143 and linked examples for details on more advanced options such as mapping each tool to its own repository automatically (a best practice) or building entirely custom repository definitions manually.
Planemo has traditionally been used to test Galaxy tools.

```
$ planemo test galaxy_tool.xml
```

This starts a Galaxy instance, runs the tests described in the XML file, prints a nice summary of the test results (pass or fail for each test) in the console and creates an HTML report in the current directory. Additional bells and whistles include the ability to generate XUnit reports, publish test results and get embedded Markdown to link to them for PRs, and test remote artifacts in Git repositories.

Much of this same functionality is now also available for Galaxy Workflows as well as Common Workflow Language (CWL) tools and workflows. The rest of this page describes this testing format and testing options for these artifacts - for information about testing Galaxy tools specifically using the embedded tool XML tests see Test-Driven Development of Galaxy tools tutorial.

Unlike the traditional Galaxy tool approach, these newer types of artifacts should define tests in files located next artifact. For instance, if `planemo test` is called on a Galaxy workflow called `ref-rnaseq.ga` tests should be defined in `ref-rnaseq-tests.yml` or `ref-rnaseq-tests.yaml`. If instead it is called on a CWL tool called `seqtk_seq.cwl`, tests can be defined in `seqtk_seq_tests.yml` for instance.

Below are two examples of such YAML files - the first for a CWL tool and the second for Galaxy workflow. Note the same testing file format is used for both kinds of artifacts.

```yaml
- doc: simple usage test
  job: pear_job.yml
  outputs:
    assembled_pairs:
      path: test-data/pear_assembled_results1.fastq
    unassembled_forward_reads:
      path: test-data/pear_unassembled_forward_results1.fastq
```

```
- doc: Test sample data for Microbial variant calling workflow
  job:
    mutant_R1:
      class: File
```

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The above examples hopefully make it clear that each test file is broken into a list of test cases. Each test case should have a doc describing the test, a job description the describes the inputs for an execution of the target artifact, and an outputs mapping that describes assertions about outputs to test.

8.1 job

The job object can be a mapping embedded right in the file or a reference to a “job” input file. The job input file is a proper CWL job document - which is fairly straight forward as demonstrated in the above examples. Planemo adapts the CWL job document to Galaxy workflows and tools - using input names for Galaxy tools and input node labels for workflows.

Input files can be specified using either path attributes (which should generally be file paths relative to the artifact and test directory) or location (which should be a URI). The examples above demonstrate using both paths relative to the tool file and test data published to Zenodo.

Note: These job objects can be run directly with planemo run.

\$ planemo run --engine=<engine_type> [ENGINE_OPTIONS] [ARTIFACT_PATH] [JOB_PATH]

This should be familiar to CWL developers - and indeed if --engine=cwltool this works as a formal CWL runner. Planemo provides a uniform interface to Galaxy for Galaxy workflows and tools though using the same CLI invocation if --engine=galaxy (for a Planemo managed Galaxy instance), --engine=docker_galaxy (for a Docker instance of Galaxy launched by Planemo), or --engine=external_galaxy (for a running remote Galaxy instance).
8.2 outputs

Galaxy tools and CWL artifacts have obvious output names that much match the mapping in this block on test file. Galaxy workflows require explicit output labels to be used with tests, but the important outputs in your workflows should be labeled anyway to work with Galaxy subworkflows and more cleanly with API calls.

If an output is known, fixed, and small it makes a lot of sense to just include a copy of the output next to your test and set file: `relative/path/to/output` in your output definition block as show in the first example above. For completely reproducible processes this is a great guarantee that results are fixed over time, across CWL engines and engine versions. If the results are fixed but large - it may make sense to just describe the outputs by a SHA1 checksum.

```
- doc: Simple concat workflow test
  job: wfl.gxwf-job.yml
  outputs:
    wf_output_1:
      checksum: "sha1$a0b65939670bc2c010f4d5d6a0b3e4e4590fb92b"
```

One advantage of included an exact file instead of a checksum is that Planemo can produce very nice line by line diffs for incorrect test results by comparing an expected output to an actual output.

There are reasons one may not be able to write such exact test assertions about outputs however, perhaps date or time information is incorporated into the result, unseeded random numbers are used, small numeric differences occur across runtimes of interest, etc.. For these cases, a variety of other assertions can be executed against the execution results to verify outputs. The types and implementation of these test assertions match those available to Galaxy tool outputs in XML but have equivalent YAML formulations that should be used in test descriptions.

Even if one can write exact tests, a really useful technique is to write sanity checks on outputs as one builds up workflows that may be changing rapidly and developing complex tools or workflows via a Test-Driven Development cycle using Planemo. *Tests shouldn’t just be an extra step you have to do after development is done, they should guide development as well.*

The workflow example all the way above demonstrates some assertions one can make about the contents of files. The full list of assertions available is only documented for the Galaxy XML format but it straight forward to adapt to the YAML format above - check out the Galaxy XSD for more information.

Some examples of inexact file comparisons derived from an artificial test case in the Planemo test suite is shown below, these are more options available for checking outputs that may change in small ways over time.

```
- doc: test_shal_pass
  job: cat_tool_job.json
  outputs:
    output_file:
      checksum: sha1$2ef7bde608ce5404e97d5f042f95f89f1c232871
- doc: test_shal_fail
  job: cat_tool_job.json
  outputs:
    output_file:
      checksum: sha1$2ef7bde608ce5404e97d5f042f95f89f1c232872
- doc: test_compare_direct_pass
  job: cat_tool_job.json
  outputs:
    output_file:
      file: hello.txt
- doc: test_compare_sim_size_pass
  job: cat_tool_job.json
  outputs:
```

(continues on next page)
output_file:
    file: not_hello.txt
    compare: sim_size
    delta: 5
- doc: test_compare_sim_size_fail
  job: cat_tool_job.json
outputs:
    output_file:
        file: not_hello.txt
        compare: sim_size
        delta: 3
- doc: test_compare_sim_size_pass
  job: cat_tool_job.json
outputs:
    output_file:
        file: hello_regex.txt
        compare: re_match
- doc: test_compare_re_match_pass
  job: cat_tool_job.json
outputs:
    output_file:
        file: not_hello_regex.txt
        compare: re_match
- doc: test_compare_re_match_fail
  job: cat_tool_job.json
outputs:
    output_file:
        file: hello_regex.txt
        compare: re_match_multiline
- doc: test_compare_re_match_pass
  job: cat_tool_job.json
outputs:
    output_file:
        file: not_hello_regex.txt
        compare: re_match_multiline
- doc: test_compare_re_match_fail
  job: cat_tool_job.json
outputs:
    output_file:
        file: hello_truncated.txt
        compare: contains
- doc: test_compare_contains_pass
  job: cat_tool_job.json
outputs:
    output_file:
        file: not_hello.txt
        compare: contains
- doc: test_compare_contains_fail
  job: cat_tool_job.json
outputs:
    output_file:
        file: not_hello.txt
        compare: diff
        lines_diff: 2
- doc: test_compare_diff_pass
  job: cat_tool_job.json
outputs:
    output_file:
        file: not_hello.txt
        compare: diff
        lines_diff: 2
- doc: test_compare_diff_fail
  job: cat_tool_job.json
outputs:
output_file:
  file: not_hello.txt
  compare: diff
  lines_diff: 1

8.3 Engines for Testing

Below are descriptions of various testing engines that can be used with Planemo (both with the test command and the run command) as well as some command-line options of particular interest for testing. The first two types cwltool and toil can be used to test CWL artifacts (tools and workflows). The remaining engine types are variations on engines that target Galaxy and are useful for testing workflows (and tools with newer style tests or job documents).

8.3.1 cwltool

$ planemo test --engine cwltool [--no-container] [--biocontainers]

This is the most straight forward engine, it can be used to test CWL tools and workflows using the CWL reference implementation cwltool (bundled as a dependency of Planemo). Use the --no-container option to disable Docker and use Conda resolution of SoftwareRequirement’s or applications on the `PATH`. Use the --biocontainers flag to use BioContainers for tools without explicit DockerRequirement hints.

8.3.2 toil

$ planemo test --engine toil [--no-container] [--biocontainers]

This engine largely mirrors the cwltool engine but runs CWL artifacts using Toil. Toil is an optional dependency of Planemo so you will likely have to install it in Planemo’s environment using pip install toil.

8.3.3 galaxy


This is the default engine type, but can be made explicit --engine galaxy. With this engine Planemo will start a Galaxy instance and test against it.

Planemo will automatically detect and load “stock” Galaxy tools used by workflows and install any Tool Shed tools contained in the workflow, if other non-Tool Shed tools are required for a workflow they can be loaded using --extra_tools.

Set --galaxy_root to target an externally cloned Galaxy directory or use --galaxy_branch to target a particular branch of Galaxy other than the latest stable.

Use the --biocontainers flag to enable Docker and use BioContainers for tools or use --docker to use Docker but limited to tools configured with container tags.

By default Galaxy when configured by Planemo will attempt to run with an sqlite database. This configuration is quite buggy and should not be used to test workflows. The --profile option can be used to target a pre-configured Postgres database created with planemo profile_create and use it for testing. In addition to making Galaxy more robust this should speed up testing after the initial setup of the database.
Planemo Documentation, Release 0.61.0.dev0

```
planemo profile_create --database_type [postgres|docker_postgres] my_cool_name
planemo test --profile my_cool_name
```

If `--database_type` is specified as `docker_postgres`, Planemo will attempt to startup a postgres server in a Docker container automatically for testing. If instead `postgres` is specified Planemo will attempt to interact with Postgres using `psql` (assumed to be on the PATH). For a description on more Postgres connection options check out the documentation for the `database_create` command that has similar options.

Profiles may also really help testing local setups by saving previously installed shed repository installations and Conda environments.

### 8.3.4 docker_galaxy

```
$ planemo test --engine docker_galaxy [--extra_tools <path>] [--docker_extra_volume <path>] [--docker_galaxy_image <image>]
```

With this engine Planemo will start a Docker container to run tests against it. See the `docker-galaxy-stable` project spearheaded by Björn Grünig for more information on Docker-ized Galaxy execution. The exact container image to use can be controlled using the `--docker_galaxy_image` option.

Planemo will automatically detect and load "stock" Galaxy tools used by workflows and install any Tool Shed tools contained in the workflow, if other non-Tool Shed tools are required - they can be loaded using `--extra_tools`.

At the time of this writing, there is a bug in Planemo that requires using the `--docker_extra_volume` option to mount test data into the testing container.

### 8.3.5 external_galaxy

```
$ planemo --engine external_galaxy --galaxy_admin_key <admin_key> --galaxy_user_key <user_key> [--no_shed_install] [--polling_backoff <integer>] <url>
```

This is primarily useful for testing workflows against already running Galaxy instances. An admin or master API key should be supplied to install missing tool repositories for the workflow and a user API key should be supplied to run the workflow using. If you wish to skip tool shed repository installation (this requires all the tools be present already), use the `--no_shed_install` option. If you want to reduce the load on the target Galaxy while checking for the status changes use the `--polling_backoff <integer>` option where integer is the incremental increase in seconds for every request.

To run tool tests against a running Galaxy, `galaxy-tool-test` is a script that gets installed with galaxy-lib and so may very well already be on your PATH. Check out the options available with that using `galaxy-tool-test --help`.

### 8.4 Galaxy Testing Template

The following a script that can be used with continuous integration (CI) services such Travis to test Galaxy workflows in a Github repository. This shell script can be configured via various environment variables and shows off some of the modalities Planemo `test` should work in (there may be bugs but we are trying to stablize this functionality).

```
#!/bin/bash

# Usage: http://planemo.readthedocs.io/en/latest/test_format.html#galaxy-testing-template
```

(continues on next page)
Planemo Documentation, Release 0.61.0.dev0

8.4. Galaxy Testing Template 147

(continued from previous page)

```bash
$PLANEMO_TARGET:="planemo==0.52.0"
$PLANEMO_OPTIONS:=""  # e.g. PLANEMO_OPTIONS="--verbose"
$PLANEMO_PROFILE_NAME:="wxflowtest"
$PLANEMO_SERVE_PORT:="9019"
$PLANEMO_GALAXY_BRANCH:="master"
$PLANEMO_TEST_STYLE:="serve_and_test"  # profile_serve_and_test, serve_and_test, ...
docker_serve_and_test, test, docker_test, docker_test_path_paste
$PLANEMO_SERVE_DATABASE_TYPE:="postgres"  # used if not using Docker with PLANEMO_TEST_STYLE
$PLANEMO_DOCKER_GALAXY_IMAGE:="quay.io/bgruening/galaxy:18.01"  # used if used Docker with PLANEMO_TEST_STYLE
$PLANEMO_VIRTUAL_ENV:=".venv"
$GALAXY_URL:="http://localhost:$PLANEMO_SERVE_PORT"

# Ensure Planemo is installed.
if ! [ ! -d "$(PLANEMO_VIRTUAL_ENV)" ]; then
  virtualenv "$(PLANEMO_VIRTUAL_ENV)"
  . "$(PLANEMO_VIRTUAL_ENV)/bin/activate
  pip install -U pip>7
  # Intentionally expand wildcards in PLANEMO_TARGET.
  shopt -s extglob
  pip install $(PLANEMO_TARGET)
fi
. "$(PLANEMO_VIRTUAL_ENV)/bin/activate

# Run test.
# This example shows off a bunch of different ways one could test with Planemo,
# but for actual workflow testing projects - probably best just to take one of the
# last
# two very easy invocations to simplify things.
if [ "$PLANEMO_TEST_STYLE" = "profile_serve_and_test" ]; then
  planemo $PLANEMO_OPTIONS profile_create \
    --database_type "$PLANEMO_SERVE_DATABASE_TYPE" \
    "$PLANEMO_PROFILE_NAME"
  planemo $PLANEMO_OPTIONS serve \
    --daemon \
    --galaxy_branch "$PLANEMO_GALAXY_BRANCH" \
    --profile "$PLANEMO_PROFILE_NAME" \
    --port "$PLANEMO_SERVE_PORT" \
    "$1"
  planemo $PLANEMO_OPTIONS test \
    --galaxy_url "$GALAXY_URL" \
    --engine external_galaxy \
    "$1"
elif [ "$PLANEMO_TEST_STYLE" = "serve_and_test" ]; then
  planemo $PLANEMO_OPTIONS serve \
    --daemon \
    --galaxy_branch "$PLANEMO_GALAXY_BRANCH" \
    --database_type "$PLANEMO_SERVE_DATABASE_TYPE" \
    --port "$PLANEMO_SERVE_PORT" \
    "$1"
  planemo $PLANEMO_OPTIONS test \
    --galaxy_url "$GALAXY_URL" \
    --engine external_galaxy \
    "$1"
elif [ "$PLANEMO_TEST_STYLE" = "docker_serve_and_test" ]; then
```

(continues on next page)
docker pull "$(PLANEMO_DOCKER_GALAXY_IMAGE)"
planemo $PLANEMO_OPTIONS serve
   --daemon
   --engine docker_galaxy
   --docker_galaxy_image "$(PLANEMO_DOCKER_GALAXY_IMAGE)"
   --port "$PLANEMO_SERVE_PORT" "$1"
planemo $PLANEMO_OPTIONS test
   --engine docker_galaxy
   --docker_galaxy_image "$(PLANEMO_DOCKER_GALAXY_IMAGE)"
   "$1"

elif [ "$PLANEMO_TEST_STYLE" = "test" ]; then
   # TODO: this conda_init shouldn't be needed, but this mode is broken without it.
   planemo conda_init || true

planemo $PLANEMO_OPTIONS test
   --database_type "$PLANEMO_SERVE_DATABASE_TYPE"
   --galaxy_branch "$PLANEMO_GALAXY_BRANCH"
   "$1"

elif [ "$PLANEMO_TEST_STYLE" = "docker_test" ]; then
   # TODO: This variant isn't super usable yet because there is too much logging,
   # hence the dev null redirect.
   docker pull "$(PLANEMO_DOCKER_GALAXY_IMAGE)"

planemo $PLANEMO_OPTIONS test
   --engine docker_galaxy
   --docker_extra_volume .
   --paste_test_data_paths
   --docker_galaxy_image "$(PLANEMO_DOCKER_GALAXY_IMAGE)"
   "$1" > /dev/null

elif [ "$PLANEMO_TEST_STYLE" = "docker_test_path_paste" ]; then
   # Same as above but mount the test data and use file:// path pastes when uploading # files (more robust and quick if working with really large files).
   docker pull "$(PLANEMO_DOCKER_GALAXY_IMAGE)"

planemo $PLANEMO_OPTIONS test
   --engine docker_galaxy
   --docker_extra_volume .
   --paste_test_data_paths
   --docker_galaxy_image "$(PLANEMO_DOCKER_GALAXY_IMAGE)"
   "$1" > /dev/null

elif [ "$PLANEMO_TEST_STYLE" = "manual_docker_run_and_test" ]; then
   docker pull "$(PLANEMO_DOCKER_GALAXY_IMAGE)"
   docker run -d -e "NONUSE=nodejs,proftp,reports" -p "$(PLANEMO_SERVE_PORT):80" "$1" > /dev/null
galaxy-wait -g "http://localhost:$(PLANEMO_SERVE_PORT)"
planemo $PLANEMO_OPTIONS test
   --engine external_galaxy
   --galaxy_url "$GALAXY_URL"
   --galaxy_admin_key admin
   --galaxy_user_key admin
   "$1"

elif [ "$PLANEMO_TEST_STYLE" = "external_galaxy" ]; then
   if [[ -n $PLANEMO_INSTALL_TOOLS ]]; then
      INSTALL_TOOLS=""
   else
      INSTALL_TOOLS="--no_shed_install"
   fi
   planemo $PLANEMO_OPTIONS test
      --engine external_galaxy
   else
      INSTALL_TOOLS="--no_shed_install"
   fi

(continues on next page)
A Travis configuration file (.travis.yml) that would test workflows using a Docker Galaxy image might look like:

```yaml
language: python
sudo: true
python: 2.7
env:
  global:
    - PLANEMO_TEST_SCRIPT=https://raw.githubusercontent.com/galaxyproject/planemo/master/scripts/run_galaxy_workflow_tests.sh
    - PLANEMO_TEST_STYLE=docker_serve_and_test
    - PLANEMO_TARGET="planemo==0.52.0"
    - PLANEMO_DOCKER_GALAXY_IMAGE="quay.io/bgruening/galaxy:18.01"
  matrix:
    - WORKFLOW_TEST=example1/ref-rnaseq.ga
    - WORKFLOW_TEST=example2/chipseq.ga
script: bash <(curl -s "$PLANEMO_TEST_SCRIPT") "$WORKFLOW_TEST"
services:
  - docker
```

To skip Docker and instead test with a native Galaxy instance and postgres database one might use the configuration:

```yaml
language: python
python: 2.7
env:
  global:
    - PLANEMO_TEST_SCRIPT=https://raw.githubusercontent.com/galaxyproject/planemo/master/scripts/run_galaxy_workflow_tests.sh
    - PLANEMO_TEST_STYLE=serve_and_test
    - PLANEMO_TARGET="planemo==0.52.0"
    - PLANEMO_GALAXY_BRANCH="release_18.05"
  matrix:
    - WORKFLOW_TEST=example1/ref-rnaseq.ga
    - WORKFLOW_TEST=example2/chipseq.ga
script: bash <(curl -s "$PLANEMO_TEST_SCRIPT") "$WORKFLOW_TEST"
services:
  - postgres
```
Planemo is a set of utilities for developing Galaxy tools. Each utility is implemented as a subcommand of the `planemo` executable. This section of the documentation describes these commands.

### 9.1 bioc_conda_recipe_init command

This section is auto-generated from the help text for the `planemo` command `bioc_conda_recipe_init`. This help message can be generated with `planemo bioc_conda_recipe_init --help`.

**Usage:**
```
planemo bioc_conda_recipe_init [OPTIONS]
```

**Help**

Make a bioconda recipe, given a R or bioconductor package name.

- `package_name = motifbreakR`
- `bioconda_dir = '/Users/nturaga/Documents/workspace'`

**Options:**

- `-u, --update / --no_update` Update an existing bioconda recipe
- `-b, --bioconda_dir_path TEXT` Give the path to folder containing bioconda repository
- `-c, --clone / --no_clone` Clone bioconda repository from github or not?
- `-p, --package_name TEXT` Give the name of a Bioconductor package to create a new bioconda recipe
- `--help` Show this message and exit.
## 9.2 bioc_tool_init command

This section is auto-generated from the help text for the planemo command bioc_tool_init. This help message can be generated with `planemo bioc_tool_init --help`.

### Usage:

```
planemo bioc_tool_init [OPTIONS]
```

### Help

Generate a bioconductor tool outline from supplied arguments. **Options:**

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>-i</code>, <code>--id TEXT</code></td>
<td>Short identifier for new tool (no whitespace)</td>
</tr>
<tr>
<td><code>-f</code>, <code>--force</code></td>
<td>Overwrite existing tool if present.</td>
</tr>
<tr>
<td><code>-t</code>, <code>--tool FILE</code></td>
<td>Output path for new tool (default is <code>&lt;id&gt;.xml</code>)</td>
</tr>
<tr>
<td><code>-n</code>, <code>--name TEXT</code></td>
<td>Name for new R/Bioconductor tool (user facing).</td>
</tr>
<tr>
<td><code>-d</code>, <code>--description TEXT</code></td>
<td>Short description for new tool (user facing)</td>
</tr>
<tr>
<td><code>-c</code>, <code>--command TEXT</code></td>
<td>Command potentially including cheetah variables () (e.g. <code>seqtk seq -a $input &gt; $output</code>)</td>
</tr>
<tr>
<td><code>--rscript PATH</code></td>
<td>Name of an R script from which to create a Tool definition file. Requires use of <code>--input</code> and <code>--output</code> arguments. (e.g. <code>--rscript 'file.R'</code>)</td>
</tr>
<tr>
<td><code>--rversion TEXT</code></td>
<td>R version this tool requires, if not given, the tool defaults to R 3.2.1, (eg: <code>--rversion 'R 3.2.1'</code>). This option adds the R dependency in the tool requirements.</td>
</tr>
<tr>
<td><code>--input TEXT</code></td>
<td>An input description (e.g. <code>input.fasta</code>)</td>
</tr>
<tr>
<td><code>--output TEXT</code></td>
<td>An output location (e.g. <code>output.bam</code>), the Galaxy datatype is inferred from the extension.</td>
</tr>
<tr>
<td><code>--requirement TEXT</code></td>
<td>Name of the R/Bioconductor package. Requirements will be set using Bioconda. (e.g. <code>--requirement 'affy'</code>)</td>
</tr>
<tr>
<td><code>--help_text TEXT</code></td>
<td>Help text (reStructuredText)</td>
</tr>
<tr>
<td><code>--doi TEXT</code></td>
<td>Supply a DOI (<a href="http://www.doi.org/">http://www.doi.org/</a>) easing citation of the tool for Galaxy users (e.g. <code>10.1101/014043</code>).</td>
</tr>
<tr>
<td><code>--cite_url TEXT</code></td>
<td>Supply a URL for citation.</td>
</tr>
<tr>
<td><code>--version TEXT</code></td>
<td>Tool XML version.</td>
</tr>
<tr>
<td><code>--help_from_command TEXT</code></td>
<td>Auto populate help from supplied command.</td>
</tr>
<tr>
<td><code>--test_case</code></td>
<td>For use with <code>--example_command</code>, generate a tool test case from the supplied example.</td>
</tr>
<tr>
<td><code>--macros</code></td>
<td>Generate a macros.xml for reuse across many tools.</td>
</tr>
<tr>
<td><code>--named_output TEXT</code></td>
<td>Create a named output for use with command block for example specify <code>--named_output=output1.bam</code> and then use <code>'-o $output1'</code> in your command block.</td>
</tr>
<tr>
<td><code>--bioconda_path TEXT</code></td>
<td>Path to bioconda repository. If left empty, path will be made in home directory.</td>
</tr>
<tr>
<td><code>--help</code></td>
<td>Show this message and exit.</td>
</tr>
</tbody>
</table>

## 9.3 brew command

This section is auto-generated from the help text for the planemo command brew. This help message can be generated with `planemo brew --help`.

### Usage:

```
planemo brew [OPTIONS]
```

planemo brew [OPTIONS] TOOL_PATH

Help
Install tool requirements using brew.

An experimental approach to versioning brew recipes will be used. See full discussion on the homebrew-science issues page here - https://github.com/Homebrew/homebrew-science/issues/1191. Information on the implementation can be found at https://github.com/jmchilton/platform-brew until a more permanent project home is setup.

Options:

--brew FILE Homebrew 'brew' executable to use.
--help Show this message and exit.

9.4 brew_env command

This section is auto-generated from the help text for the planemo command brew_env. This help message can be generated with planemo brew_env --help.

Usage:

planemo brew_env [OPTIONS] TOOL_PATH

Help
List commands to inject brew dependencies.

Display commands used to modify environment to inject tool’s brew dependencies.

% . <(planemo brew_env bowtie2.xml)
% which bowtie2
/home/john/.linuxbrew/Cellar/bowtie2/2.1.0/bin/bowtie2

By default this will attempt to attempt to install these recipes as needed. This automatic installation can be skipped with the --skip_install flag.

Instead of injecting the environment into your current shell using the above idiom, the --shell flag can be sent to launch a new subshell when sourced.

% . <(planemo brew_env --skip_install --shell bowtie2.xml)
(bowtie2) % which bowtie2
/home/john/.linuxbrew/Cellar/bowtie2/2.1.0/bin/bowtie2

Options:

--brew FILE Homebrew 'brew' executable to use.
--skip_install Skip installation – only source requirements already available.
--shell
--help Show this message and exit.
9.5 brew_init command

This section is auto-generated from the help text for the planemo command `brew_init`. This help message can be generated with `planemo brew_init --help`.

Usage:

```
planemo brew_init [OPTIONS]
```

Help

Download linuxbrew install & run it in ruby.

Linuxbrew is a fork of Homebrew (http://brew.sh/linuxbrew/).

For more information on installing linuxbrew and pre-requisites see https://github.com/Homebrew/linuxbrew#installation.

Homebrew or linuxbrew are required in order to use the other commands `brew` and `brew_shell`.

Options:

```
--help     Show this message and exit.
```

9.6 ci_find_repos command

This section is auto-generated from the help text for the planemo command `ci_find_repos`. This help message can be generated with `planemo ci_find_repos --help`.

Usage:

```
planemo ci_find_repos [OPTIONS] PROJECT
```

Help

Find all shed repositories in one or more directories.

Currently, a shed repository is considered a directory with a `.shed.yml` file.

Options:

```
--exclude PATH      Paths to exclude.
--exclude_from FILE File of paths to exclude.
--changed_in_commit_range TEXT Exclude paths unchanged in git commit range.
--chunk_count INTEGER Split output into chunks of this many item and print --chunk such group.
--chunk INTEGER     When output is split into --chunk_count groups, output the group 0-indexed by this option.
--output TEXT       File to output to, or - for standard output.
--help              Show this message and exit.
```

9.7 ci_find_tools command

This section is auto-generated from the help text for the planemo command `ci_find_tools`. This help message can be generated with `planemo ci_find_tools --help`.

Usage:

planemo ci_find_tools [OPTIONS] PROJECT

Help

Find all tools in one or more directories.

Tools can be chunked up, filtered, etc... to build lists of tools to perform operations over for continuous integration operations.

Options:

--exclude PATH  Paths to exclude.
--exclude_from FILE  File of paths to exclude.
--changed_in_commit_range TEXT  Exclude paths unchanged in git commit range.
--chunk_count INTEGER  Split output into chunks of this many item and print --chunk such group.
--chunk INTEGER  When output is split into --chunk_count groups, output the group 0-indexed by this option.
--output TEXT  File to output to, or - for standard output.
--help  Show this message and exit.

9.8 clone command

This section is auto-generated from the help text for the planemo command clone. This help message can be generated with planemo clone --help.

Usage:

planemo clone [OPTIONS] TARGET PROJECT

Help

Short-cut to quickly clone, fork, and branch a relevant Github repo.

For instance, the following will clone, fork, and branch the tools-iuc repository to allow a subsequent pull request to fix a problem with bwa.

```bash
$ planemo clone --branch bwa-fix tools-iuc
$ cd tools-iuc
$ # Make changes.
$ git add -p # Add desired changes.
$ git commit -m "Fix bwa problem."
$ planemo pull_request -m "Fix bwa problem."
```

These changes do require that a github username and password are specified in ~/.planemo.yml.

Options:

--fork / --skip_fork
--branch TEXT  Create a named branch on result.
--help  Show this message and exit.
9.9 conda_build command

This section is auto-generated from the help text for the planemo command `conda_build`. This help message can be generated with `planemo conda_build --help`.

**Usage:**

```
planemo conda_build [OPTIONS] RECIPE_DIR
```

**Help**

Perform conda build with Planemo’s conda. **Options:**

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>--conda_prefix DIRECTORY</code></td>
<td>Conda prefix to use for conda dependency commands.</td>
</tr>
<tr>
<td><code>--conda_exec FILE</code></td>
<td>Location of conda executable.</td>
</tr>
<tr>
<td><code>--conda_debug</code></td>
<td>Enable more verbose conda logging.</td>
</tr>
<tr>
<td><code>--conda_channels, --conda_ensure_channels TEXT</code></td>
<td>Ensure conda is configured with specified comma separated list of channels.</td>
</tr>
<tr>
<td><code>--conda_use_local</code></td>
<td>Use locally built packages while building Conda environments.</td>
</tr>
<tr>
<td><code>--help</code></td>
<td>Show this message and exit.</td>
</tr>
</tbody>
</table>

9.10 conda_env command

This section is auto-generated from the help text for the planemo command `conda_env`. This help message can be generated with `planemo conda_env --help`.

**Usage:**

```
planemo conda_env [OPTIONS] TOOL_PATH
```

**Help**

Activate a conda environment for tool.

Source the output of this command to activate a conda environment for this tool.

```
$ . <(planemo conda_env seqtk_seq.xml)
Deactivate environment with conda_env_deactivate
(seqtk_seq_v6) $ which seqtk
/home/planemo/miniconda2/envs/˓
→jobdepsDkzcjjfecc6d40619677781ff4456ec60975c137e04884e4f4b05dc68192f7cec4556/bin/ ˓
→seqtk
(seqtk_seq_v6) $ conda_env_deactivate
$
```

**Options:**

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>--conda_prefix DIRECTORY</code></td>
<td>Conda prefix to use for conda dependency commands.</td>
</tr>
<tr>
<td><code>--conda_exec FILE</code></td>
<td>Location of conda executable.</td>
</tr>
<tr>
<td><code>--conda_debug</code></td>
<td>Enable more verbose conda logging.</td>
</tr>
<tr>
<td><code>--conda_channels, --conda_ensure_channels TEXT</code></td>
<td>Ensure conda is configured with specified comma separated list of channels.</td>
</tr>
</tbody>
</table>

(continues on next page)
## 9.11 conda_init command

This section is auto-generated from the help text for the planemo command `conda_init`. This help message can be generated with `planemo conda_init --help`.

**Usage:**

```
planemo conda_init [OPTIONS]
```

**Help**

Download and install conda.

This will download conda for managing dependencies for your platform using the appropriate Miniconda installer.

By running this command, you are agreeing to the terms of the conda license a 3-clause BSD 3 license. Please review full license at http://docs.continuum.io/anaconda/eula.

Planemo will print a warning and terminate with an exit code of 7 if Conda is already installed.

**Options:**

- `--conda_prefix DIRECTORY` Conda prefix to use for conda dependency commands.
- `--conda_exec FILE` Location of conda executable.
- `--conda_debug` Enable more verbose conda logging.
- `--conda_channels, --conda_ensure_channels TEXT` Ensure conda is configured with specified comma separated list of channels.
- `--conda_use_local` Use locally built packages while building Conda environments.
- `--help` Show this message and exit.

## 9.12 conda_install command

This section is auto-generated from the help text for the planemo command `conda_install`. This help message can be generated with `planemo conda_install --help`.

**Usage:**

```
planemo conda_install [OPTIONS] TARGET
```

**Help**

Install conda packages for tool requirements. **Options:**

- `-r, --recursive` Recursively perform command for subdirectories.
- `--conda_prefix DIRECTORY` Conda prefix to use for conda dependency commands.

(continues on next page)
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--conda_exec FILE Location of conda executable.
--conda_debug Enable more verbose conda logging.
--conda_channels, --conda_ensure_channels TEXT
  Ensure conda is configured with specified comma separated list of channels.
--conda_use_local Use locally built packages while building Conda environments.
--global Install Conda dependencies globally instead of in requirement specific environments packaged for tools. If the Conda bin directory is on your PATH, tools may still use binaries but this is more designed for interactive testing and debugging.
--conda_auto_init / --no_conda_auto_init Conda dependency resolution for Galaxy will auto install conda itself using miniconda if not available on conda_prefix.
--help Show this message and exit.

9.13 conda_lint command

This section is auto-generated from the help text for the planemo command conda_lint. This help message can be generated with planemo conda_lint --help.

Usage:

planemo conda_lint [OPTIONS] RECIPE_DIR

Help

Check conda recipe for common issues.

Built in large part on the work from the BSD licensed anaconda-verify project. For more information on anaconda-verify see: https://github.com/ContinuumIO/anaconda-verify.

Options:

--report_level [all|warn|error]  
--fail_level [warn|error]  
-r, --recursive Recursively perform command for nested conda directories.  
--help Show this message and exit.

9.14 conda_search command

This section is auto-generated from the help text for the planemo command conda_search. This help message can be generated with planemo conda_search --help.

Usage:

planemo conda_search [OPTIONS] TERM
Help
Perform conda search with Planemo’s conda.
Implicitly adds channels Planemo is configured with.
Options:

```
--conda_prefix DIRECTORY Conda prefix to use for conda dependency commands.
--conda_exec FILE Location of conda executable.
--conda_debug Enable more verbose conda logging.
--conda_channels, --conda_ensure_channels TEXT
   Ensure conda is configured with specified comma separated list of channels.
--conda_use_local Use locally built packages while building Conda environments.
--help Show this message and exit.
```

9.15 config_init command

This section is auto-generated from the help text for the planemo command config_init. This help message can be generated with planemo config_init --help.

Usage:

```
planemo config_init [OPTIONS] PROJECT
```

Help
Initialise global configuration for Planemo.
Helps initialize global configuration (in home directory) for Planemo.
Options:

```
--template TEXT
--help Show this message and exit.
```

9.16 container_register command

This section is auto-generated from the help text for the planemo command container_register. This help message can be generated with planemo container_register --help.

Usage:

```
planemo container_register [OPTIONS] TOOL_PATH
```

Help
Register multi-requirement containers as needed.
BioContainers publishes all Bioconda packages automatically as individual container images. These however are not enough for tools with multiple best-practice requirements. Such requirements should be recorded and published so that a container can be created and registered for these tools.

Options:
9.17 cwl_script command

This section is auto-generated from the help text for the planemo command cwl_script. This help message can be generated with planemo cwl_script --help.

Usage:

```
planemo cwl_script [OPTIONS] TOOL_PATH JOB_PATH
```

Help

Compile simple CWL workflows to shell script.

Compiles simple common workflow language (CWL) workflows to a shell script.

Options:

```
--no_container
--output_dir PATH
--base_dir PATH
--help Show this message and exit.
```

9.18 database_create command

This section is auto-generated from the help text for the planemo command database_create. This help message can be generated with planemo database_create --help.

Usage:
planemo database_create [OPTIONS] IDENTIFIER

Help
Create a development database.

Currently the only implementation is postgres which will be managed with psql.

Planemo database_ commands make it very easy to create and destroy databases, therefore it should not be used for production data - and it should not even be connected to a production database server. Planemo is intended for development purposes only.

Planemo will assume that it can manage and access postgres databases without specifying a password. This can be accomplished by configuring postgres to not require a password for the planemo user or by specifying a password in a .pgpass file.

Planemo can be configured to not require a password for the planemo user in the postgres configuration file pg_hba.conf (on Ubuntu/Debian linux distros this file is in /etc/postgresql/<postgres_version>/main/ directory). Adding the following lines to that file will allow planemo and Galaxy to access the databases without a password.

```
# "local" is for Unix domain socket connections only
local  all  all  trust
# IPv4 local connections:
host  all  all  127.0.0.1/32  trust
# IPv6 local connections:
host  all  all  ::1/128  trust
```


Information on .pgpass files can be found at the following location: http://www.postgresql.org/docs/9.4/static/libpq-pgpass.html. In Ubuntu and Debian distros - a postgres user likely already exists and its password can be set by setting up a file ~/.pgpass file with the following contents.

```
*:*:*:postgres:<postgres_password>
```

Options:

```
--postgres_psql_path TEXT Name or or path to postgres client binary (psql).
--postgres_database_user TEXT Postgres username for managed development databases.
--postgres_database_host TEXT Postgres host name for managed development databases.
--postgres_database_port TEXT Postgres port for managed development databases.
--help Show this message and exit.
```

9.19 database_delete command

This section is auto-generated from the help text for the planemo command database_delete. This help message can be generated with planemo database_delete --help.

Usage:

planemo database_delete [OPTIONS] IDENTIFIER
Delete a development database.

Currently the only implementation is postgres which will be managed with `psql`.

Planemo database commands make it very easy to create and destroy databases, therefore it should not be used for production data - and it should not even be connected to a production database server. Planemo is intended for development purposes only.

Planemo will assume that it can manage and access postgres databases without specifying a password. This can be accomplished by configuring postgres to not required a password for the planemo user or by specifying a password in a `.pgpass` file.

Planemo can be configured to not require a password for the planemo user in the postgres configuration file `pg_hba.conf` (on Ubuntu/Debian linux distros this file is in `/etc/postgresql/<postgres_version>/main/` directory). Adding the following lines to that file will allow planemo and Galaxy to access the databases without a password.

```plaintext
# "local" is for Unix domain socket connections only
local  all  all          trust
# IPv4 local connections:
host  all  all  127.0.0.1/32  trust
# IPv6 local connections:
host  all  all  ::1/128  trust
```


Information on `.pgpass` files can be found at the following location: http://www.postgresql.org/docs/9.4/static/libpq-pgpass.html. In Ubuntu and Debian distros - a postgres user likely already exists and its password can be set by setting up a file `~/.pgpass` file with the following contents.

```plaintext
*:*:*:*:postgres:<postgres_password>
```

Options:

- `--postgres_psql_path TEXT` Name or path to postgres client binary (`psql`).
- `--postgres_database_user TEXT` Postgres username for managed development databases.
- `--postgres_database_host TEXT` Postgres host name for managed development databases.
- `--postgres_database_port TEXT` Postgres port for managed development databases.
- `--help` Show this message and exit.

## 9.20 database_list command

This section is auto-generated from the help text for the planemo command `database_list`. This help message can be generated with `planemo database_list --help`.

### Usage:

```plaintext
planemo database_list [OPTIONS]
```

### Help

List databases in configured database source.
Currently the only implementation is postgres which will be managed with psql.

Planemo database commands make it very easy to create and destroy databases, therefore it should not be used for production data - and it should not even be connected to a production database server. Planemo is intended for development purposes only.

Planemo will assume that it can manage and access postgres databases without specifying a password. This can be accomplished by configuring postgres to not required a password for the planemo user or by specifying a password in a .pgpass file.

Planemo can be configured to not require a password for the planemo user in the postgres configuration file pg_hba.conf (on Ubuntu/Debian linux distros this file is in /etc/postgresql/<postgres_version>/main/ directory). Adding the following lines to that file will allow planemo and Galaxy to access the databases without a password.

```
# "local" is for Unix domain socket connections only
local  all  all  trust
# IPv4 local connections:
host  all  all  127.0.0.1/32  trust
# IPv6 local connections:
host  all  all  ::1/128  trust
```


Information on .pgpass files can be found at at the following location: http://www.postgresql.org/docs/9.4/static/libpq-pgpass.html. In Ubuntu and Debian distros - a postgres user likely already exists and its password can be set by setting up a file ~/.pgpass file with the following contents.

```
*:*:*:postgres:<postgres_password>
```

Options:

```
--postgres_psql_path TEXT  Name or path to postgres client binary (psql).
--postgres_database_user TEXT  Postgres username for managed development databases.
--postgres_database_host TEXT  Postgres host name for managed development databases.
--postgres_database_port TEXT  Postgres port for managed development databases.
--help  Show this message and exit.
```

**9.21 dependency_script command**

This section is auto-generated from the help text for the planemo command dependency_script. This help message can be generated with planemo dependency_script --help.

**Usage:**

```
planemo dependency_script [OPTIONS] PROJECT
```

**Help**

Compile tool_dependencies.xml to bash script.

An experimental approach parsing tool_dependencies.xml files into bash shell scripts, intended initially for use within Continuous Integration testing setups like TravisCI.
Parses the tool_dependencies.xml files from the specified projects, and converts them into an installation bash script (dep_install.sh), and a shell script (env.sh) defining any new/edited environment variables.

These are intended to be used via bash dep_install.sh (once), and as source env.sh prior to running any of the dependencies to set the environment variable within the current shell session.

Both dep_install.sh and env.sh require $INSTALL_DIR be defined before running them, set to an existing directory with write permissions. Beware than if run on multiple tools, they can over-write each other (for example if you have packages for different versions of the same tool). In this case make separate calls to planemo dependency_script and call the scripts with different installation directories.

This command will download (and cache) any URLs specified via Galaxy download actions. This is in order to decompress them and determine the relevant sub-folder to change into as per the Tool Shed install mechanism, so that this can be recorded as a cd command in the bash script.

The download cache used by planemo dependency_script and the resulting output script dep_install.sh defaults to ./download_cache (under the current working directory), and can be set with $DOWNLOAD_CACHE.

If the tool_dependencies.xml file includes SHA256 checksums for downloads, these will be verified after downloading to the cache (by either planemo dependency_script or bash dep_install.sh).

This is experimental, and is initially intended for use within continuous integration testing setups like TravisCI to both verify the dependency installation recipe works, and to use this to run functional tests.

Options:

```
-r, --recursive             Recursively perform command for nested repository directories.
--fail_fast                If multiple repositories are specified and an error occurs stop immediately instead of processing remaining repositories.
--download_cache DIRECTORY Directory to cache downloaded files, default is $DOWNLOAD_CACHE
--help                    Show this message and exit.
```

### 9.22 docker_build command

This section is auto-generated from the help text for the planemo command docker_build. This help message can be generated with planemo docker_build --help.

**Usage:**

```
planemo docker_build [OPTIONS] TOOL_PATH
```

**Help**

Build (and optionally cache) Docker images.

Loads the tool or tools referenced by TOOL_PATH (by default all tools in current directory), and ensures they all reference the same Docker image and then attempts to find a Dockerfile for these tools (can be explicitly specified with --dockerfile but by default it will check the tool’s directory and the current directory as well).

This command will then build and tag the image so it is ready to be tested and published. The docker_shell command be used to test out the built image.

```
% planemo docker_build bowtie2.xml # assumes Dockerfile in same dir
% planemo docker_shell --from_tag bowtie2.xml
```
This can optionally also cache the images.

**Options:**

```
--dockerfile TEXT
--docker_image_cache TEXT
--docker_cmd TEXT Command used to launch docker (defaults to docker).
--docker_sudo / --no_docker_sudo
--docker_sudo_cmd TEXT sudo command to use when --docker_sudo is enabled (defaults to sudo).
--docker_host TEXT Docker host to target when executing docker commands (defaults to localhost).
--help Show this message and exit.
```

### 9.23 docker_shell command

This section is auto-generated from the help text for the `planemo` command `docker_shell`. This help message can be generated with `planemo docker_shell --help`.

**Usage:**

```
planemo docker_shell [OPTIONS] TOOL_PATH
```

**Help**

Launch shell in Docker container for a tool.

Will launch a shell in the Docker container referenced by the specified tool. Prints a command to do this the way Galaxy would in job files it generates - so be sure to wrap this in $(...) to launch the subshell.

```
$ $(planemo docker_shell bowtie2.xml)
...
root@b8754062f875:/#
```

**Options:**

```
--from_tag Treat the tool's Docker container identifier as a locally cached tag.
--shell TEXT Shell to launch in container (defaults to /bin/bash).
--docker_cmd TEXT Command used to launch docker (defaults to docker).
--docker_sudo / --no_docker_sudo
--docker_sudo_cmd TEXT sudo command to use when --docker_sudo is enabled (defaults to sudo).
--docker_host TEXT Docker host to target when executing docker commands (defaults to localhost).
--help Show this message and exit.
```
9.24 docs command

This section is auto-generated from the help text for the planemo command docs. This help message can be generated with planemo docs --help.

Usage:

planemo docs [OPTIONS]

Help

Open Planemo documentation in web browser. Options:

--help  Show this message and exit.

9.25 lint command

This section is auto-generated from the help text for the planemo command lint. This help message can be generated with planemo lint --help.

Usage:

planemo lint [OPTIONS] TOOL_PATH

Help

Check for common errors and best practices. Options:

--report_level [all|warn|error]  Output an XUnit report, useful for CI testing
--report_xunit PATH
--fail_level [warn|error]  Comma-separated list of lint tests to skip
--skip TEXT  (e.g. passing --skip 'citations,xml_order'
--xsd / --no_xsd  would skip linting of citations and best-practice XML ordering.
--recursive  Include tool XSD validation in linting process.
--urls  Recursively perform command for
--doi  Subdirectories.
--conda_requirements  Check validity of URLs in XML files
--biocontainer, --biocontainers  Check validity of DOIs in XML files
--biocontainer, --biocontainers  Check tool requirements for availability in
--help  best practice Conda channels.
--biocontainer, --biocontainers  Show this message and exit.

9.26 mull command

This section is auto-generated from the help text for the planemo command mull. This help message can be generated with planemo mull --help.
Usage:

```
planemo mull [OPTIONS] TOOL_PATH
```

Help

Build containers for specified tools.

Supplied tools will be inspected for referenced requirement packages. For each combination of requirements a “mulled” container will be built. Galaxy can automatically discover this container and subsequently use it to run or test the tool.

For this to work, the tool’s requirements will need to be present in a known Conda channel such as bioconda (https://github.com/bioconda/bioconda-recipes). This can be verified by running `planemo lint --conda_requirements` on the target tool(s).

Options:

```
-r, --recursive Recursively perform command for subdirectories.
--mulled_conda_version TEXT Install a specific version of Conda before running the command, by default the version that comes with the continuumio miniconda3 image will be used under Linux and under Mac OS X Conda will be upgraded to to work around a bug in 4.2.
--mulled_namespace TEXT Build a mulled image with the specified namespace - defaults to biocontainers. Galaxy currently only recognizes images with the namespace biocontainers.
--mulled_command TEXT Mulled action to perform for targets - this defaults to 'build-and-test'.
--conda_channels, --conda_ensure_channels TEXT Ensure conda is configured with specified comma separated list of channels.
--help Show this message and exit.
```

9.27 mulled_init command

This section is auto-generated from the help text for the planemo command `mulled_init`. This help message can be generated with `planemo mulled_init --help`.

Usage:

```
planemo mulled_init [OPTIONS]
```

Help

Download and install involucro for mull command.

This will happen automatically when using the mull command, but this can be pre-installed in an environment using this command.

Options:

```
--mulled_conda_version TEXT Install a specific version of Conda before running the command, by default the version that comes with the continuumio miniconda3 image will (continues on next page)```
be used under Linux and under Mac OS X Conda will be upgraded to to work around a bug in 4.2.

--mulled_namespace TEXT Build a mulled image with the specified namespace - defaults to biocontainers. Galaxy currently only recognizes images with the namespace biocontainers.

--mulled_command TEXT Mulled action to perform for targets - this defaults to 'build-and-test'.

--help Show this message and exit.

9.28 normalize command

This section is auto-generated from the help text for the planemo command normalize. This help message can be generated with planemo normalize --help.

Usage:

planemo normalize [OPTIONS] TOOL_PATH

Help

Generate normalized tool XML from input.

This will break the formatting of your tool and is currently only intended for viewing macro expansions for for use with XSD validation (see https://github.com/JeanFred/Galaxy-XSD for instance). Please do not use the output as is - it frequently makes tool less readable not more.

The top-level blocks will be reordered and whitespace fixed according to the tool development best practices outlined on the Galaxy wiki.

% # Print normalized version of tool.
% planemo normalize tool.xml
<tool>
  ...
% # Print a variant of tool with all macros expanded out, useful for
% # debugging complex macros.
% planemo normalize --expand_macros tool.xml
<tool>
  ...

Options:

--expand_macros Expand macros while normalizing tool XML - useful to see how macros are evaluated.

--skip_reorder Planemo will reorder top-level tool blocks according to tool development best practices as part of this command, this flag will disable that behavior.

--skip_reindent Planemo will reindent the XML according to tool development best practices as part of this command, this flag will disable that behavior.

--help Show this message and exit.
9.29 open command

This section is auto-generated from the help text for the planemo command open. This help message can be generated with planemo open --help.

Usage:

```
planemo open [OPTIONS] PATH
```

Help

Open latest Planemo test results in a web browser. Options:

```
--help  Show this message and exit.
```

9.30 profile_create command

This section is auto-generated from the help text for the planemo command profile_create. This help message can be generated with planemo profile_create --help.

Usage:

```
planemo profile_create [OPTIONS] PROFILE_NAME
```

Help

Create a profile. Options:

```
--postgres Use postgres database type.
--database_type [postges|postges_docker|sqlite|auto] Type of database to use for profile - 'auto', 'sqlite', 'postges', and 'postges_docker' are available options. Use postgres to use an existing postgres server you can access without a password via the psql command. Use postges_docker to have Planemo manage a docker container running postgres. Data with postges_docker is not yet persisted past when you restart the docker container launched by Planemo so be careful with this option.
--postgres_psql_path TEXT Name or path to postgres client binary (psql).
--postgres_database_user TEXT Postgres username for managed development databases.
--postgres_database_host TEXT Postgres host name for managed development databases.
--postgres_database_port TEXT Postgres port for managed development databases.
--engine [galaxy|docker_galaxy|external_galaxy] Select an engine to serve artifacts such as tools and workflows. Defaults to a local Galaxy, but running Galaxy within a Docker container.
--docker_cmd TEXT Command used to launch docker (defaults to docker).
--docker_sudo / --no_docker_sudo
```

(continues on next page)
Flag to use sudo when running docker.
--docker_host TEXT Docker host to target when executing docker commands (defaults to localhost).
--docker_sudo_cmd TEXT sudo command to use when --docker_sudo is enabled (defaults to sudo).
--help Show this message and exit.

9.31 profile_delete command

This section is auto-generated from the help text for the planemo command `profile_delete`. This help message can be generated with `planemo profile_delete --help`.

Usage:
```
planemo profile_delete [OPTIONS] PROFILE_NAME
```

Help
Delete a profile. Options:

```
--postgres Use postgres database type.
--database_type [postgres|postgres_docker|sqlite|auto] Type of database to use for profile - 'auto', 'sqlite', 'postgres', and 'postgres_docker' are available options. Use postgres to use an existing postgres server you can access without a password via the psql command. Use postgres_docker to have Planemo manage a docker container running postgres. Data with postgres_docker is not yet persisted past when you restart the docker container launched by Planemo so be careful with this option.
--postgres_psql_path TEXT Name or path to postgres client binary (psql).
--postgres_database_user TEXT Postgres username for managed development databases.
--postgres_database_host TEXT Postgres host name for managed development databases.
--postgres_database_port TEXT Postgres port for managed development databases.
--help Show this message and exit.
```

9.32 profile_list command

This section is auto-generated from the help text for the planemo command `profile_list`. This help message can be generated with `planemo profile_list --help`.

Usage:
```
planemo profile_list [OPTIONS]
```

Help
List configured profile names. Options:
9.33 project_init command

This section is auto-generated from the help text for the planemo command `project_init`. This help message can be generated with `planemo project_init --help`.

**Usage:**

```
planemo project_init [OPTIONS] PROJECT
```

**Help**

(Experimental) Initialize a new tool project.

This is only a proof-of-concept demo right now.

**Options:**

```
--template TEXT
--help     Show this message and exit.
```

9.34 pull_request command

This section is auto-generated from the help text for the planemo command `pull_request`. This help message can be generated with `planemo pull_request --help`.

**Usage:**

```
planemo pull_request [OPTIONS] PROJECT
```

**Help**

Short-cut to quickly create a pull request for a relevant Github repo.

For instance, the following will clone, fork, and branch the tools-iuc repository to allow a subsequent pull request to fix a problem with bwa.

```
$ planemo clone --branch bwa-fix tools-iuc
$ cd tools-iuc
$ # Make changes.
$ git add -p # Add desired changes.
$ git commit -m "Fix bwa problem."
$ planemo pull_request -m "Fix bwa problem."
```

These changes do require that a github username and password are specified in ~/.planemo.yml.

**Options:**

```
-m, --message TEXT  Message describing the pull request to create.
--help              Show this message and exit.
```
### 9.35 run command

This section is auto-generated from the help text for the planemo command `run`. This help message can be generated with `planemo run --help`.

**Usage:**

```bash
planemo run [OPTIONS] TOOL_URI JOB_PATH
```

**Help**

Planemo command for running tools and jobs.

```bash
% planemo run cat1-tool.cwl cat-job.json
```

**Options:**

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>--galaxy_root</code> DIRECTORY</td>
<td>Root of development galaxy directory to execute command with.</td>
</tr>
<tr>
<td><code>--galaxy_python_version</code> [2</td>
<td>2.7</td>
</tr>
<tr>
<td><code>--galaxy_database_seed</code> PATH</td>
<td>Preseeded Galaxy sqlite database to target.</td>
</tr>
<tr>
<td><code>--extra_tools</code> PATH</td>
<td>Extra tool sources to include in Galaxy's tool panel (file or directory). These will not be linted/tested/etc... but they will be available to workflows and for interactive use.</td>
</tr>
<tr>
<td><code>--install_galaxy</code></td>
<td>Download and configure a disposable copy of Galaxy from github.</td>
</tr>
<tr>
<td><code>--galaxy_branch</code> TEXT</td>
<td>Branch of Galaxy to target (defaults to master) if a Galaxy root isn't specified.</td>
</tr>
<tr>
<td><code>--galaxy_source</code> TEXT</td>
<td>Git source of Galaxy to target (defaults to the official galaxyproject github source if a Galaxy root isn't specified.</td>
</tr>
<tr>
<td><code>--skip_venv</code></td>
<td>Do not create or source a virtualenv environment for Galaxy, this should be used or instance to preserve an externally configured virtual environment or conda environment.</td>
</tr>
<tr>
<td><code>--no_cache_galaxy</code></td>
<td>Skip caching of Galaxy source and dependencies obtained with --install_galaxy. Not caching this results in faster downloads (no git) - so is better on throw away instances such with TravisCI.</td>
</tr>
<tr>
<td><code>--no_cleanup</code></td>
<td>Do not cleanup temp files created for and by Galaxy.</td>
</tr>
<tr>
<td><code>--galaxy_email</code> TEXT</td>
<td>E-mail address to use when launching single-user Galaxy server.</td>
</tr>
<tr>
<td><code>--docker / --no_docker</code></td>
<td>Run Galaxy tools in Docker if enabled.</td>
</tr>
<tr>
<td><code>--docker_cmd</code> TEXT</td>
<td>Command used to launch docker (defaults to docker).</td>
</tr>
<tr>
<td><code>--docker_sudo / --no_docker_sudo</code></td>
<td>Flag to use sudo when running docker.</td>
</tr>
<tr>
<td><code>--docker_host</code> TEXT</td>
<td>Docker host to target when executing docker commands (defaults to localhost).</td>
</tr>
<tr>
<td><code>--docker_sudo_cmd</code> TEXT</td>
<td>sudo command to use when --docker_sudo is enabled (defaults to sudo).</td>
</tr>
</tbody>
</table>
| `--mulled_containers, --biocontainers` | Test tools against mulled containers (forces (continues on next page)
--job_config_file FILE  Job configuration file for Galaxy to target.
--tool_dependency_dir DIRECTORY  Tool dependency dir for Galaxy to target.
--port INTEGER  Port to serve Galaxy on (default is 9090).
--host TEXT  Host to bind Galaxy to. Default is 127.0.0.1 that is restricted to localhost connections for security reasons set to 0.0.0.0 to bind Galaxy to all ports including potentially publicly accessible ones.
--test_data DIRECTORY  test-data directory to for specified tool(s).
--tool_data_table PATH  tool_data_table_conf.xml file to for specified tool(s).
--dependency_resolvers_config_file FILE  Dependency resolver configuration for Galaxy to target.
--brew_dependency_resolution  Configure Galaxy to use plain brew dependency resolution.
--shed_dependency_resolution  Configure Galaxy to use brewed Tool Shed dependency resolution.
--no_dependency_resolution  Configure Galaxy with no dependency resolvers.
--conda_prefix DIRECTORY  Conda prefix to use for conda dependency commands.
--conda_exec FILE  Location of conda executable.
--conda_debug  Enable more verbose conda logging.
--conda_channels, --conda Ensure_channels TEXT  Ensure conda is configured with specified comma separated list of channels.
--conda_use_local  Use locally built packages while building Conda environments.
--conda_dependency_resolution  Configure Galaxy to use only conda for dependency resolution.
--conda_copy_dependencies  Conda dependency resolution for Galaxy will copy dependencies instead of attempting to link them.
--conda_auto_install / --no_conda_auto_install  Conda dependency resolution for Galaxy will attempt to install requested but missing packages.
--conda_auto_init / --no_conda_auto_init  Conda dependency resolution for Galaxy will auto install conda itself using miniconda if not available on conda_prefix.
--profile TEXT  Name of profile (created with the profile_create command) to use with this command.
--postgres  Use postgres database type.
--database_type [postgres|postgres_docker|sqlite|auto]  Type of database to use for profile - 'auto', 'sqlite', 'postgtes', and 'postgtes_docker' are available options. Use postgres to use an existing postgres server you user can access without a password via the psql command. Use postgres_docker to have Planemo manage a docker container running postgres. Data with postgres_docker is not yet persisted past when you restart the docker container launched by

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```
--postgres_psql_path TEXT Name or path to postgres client binary (psql).
--postgres_database_user TEXT Postgres username for managed development databases.
--postgres_database_host TEXT Postgres host name for managed development databases.
--postgres_database_port TEXT Postgres port for managed development databases.
--file_path DIRECTORY Location for files created by Galaxy (e.g. database/files).
--database_connection TEXT Database connection string to use for Galaxy.
--shed_tool_conf TEXT Location of shed tools conf file for Galaxy.
--shed_tool_path TEXT Location of shed tools directory for Galaxy.
--galaxy_single_user / --no_galaxy_single_user
By default Planemo will configure Galaxy to run in single-user mode where there is just one user and this user is automatically logged in. Use --no_galaxy_single_user to prevent Galaxy from running this way.
--cwl
Configure Galaxy for use with CWL tool. (this option is experimental and will be replaced when and if CWL support is merged into Galaxy).
--cwl_galaxy_root DIRECTORY Root of development galaxy directory to execute command with (must be branch of Galaxy with CWL support, this option is experimental and will be replaced with --galaxy_root when and if CWL support is merged into Galaxy).
--output_directory, --outdir DIRECTORY Where to store outputs of a 'run' task.
--output_json FILE Where to store JSON dictionary describing outputs of a 'run' task.
--engine [galaxy|docker_galaxy|cwltool|toil|external_galaxy]
Select an engine to run or test artifacts such as tools and workflows. Defaults to a local Galaxy, but running Galaxy within a Docker container or the CWL reference implementation 'cwltool' and 'toil' be selected.
--non_strict_cwl
Disable strict validation of CWL.
--no-container, --no_container If cwltool engine is used, disable Docker container usage.
--docker_galaxy_image TEXT Docker image identifier for docker-galaxy-flavor used if engine type is specified as 'docker-galaxy'. Defaults to quay.io/bgruening/galaxy.
--docker_extra_volume PATH Extra path to mount if --engine docker.
--ignore_dependency_problems
When installing shed repositories for workflows, ignore dependency issues. These likely indicate a problem but in some cases may not prevent a workflow from successfully executing.
--shed_install / --no_shed_install
By default Planemo will attempt to install repositories needed for workflow testing. This may not be appropriate for production servers and so this can disabled by calling planemo
```
9.36 serve command

This section is auto-generated from the help text for the planemo command serve. This help message can be generated with planemo serve --help.

Usage:

```
planemo serve [OPTIONS] TOOL_PATH
```

Help

Launch Galaxy instance with specified tools.

The Galaxy tool panel will include just the referenced tool or tools (by default all the tools in the current working directory) and the upload tool.

planemo will search parent directories to see if any is a Galaxy instance - but one can pick the Galaxy instance to use with the --galaxy_root option or force planemo to download a disposable instance with the --install_galaxy flag.

planemo will run the Galaxy instance in an existing virtualenv if one exists in a .venv directory in the specified --galaxy_root. Otherwise, the Galaxy instance will run in a clean virtualenv created in /tmp.

planemo uses temporarily generated config files and environment variables to attempt to shield this execution of Galaxy from manually launched runs against that same Galaxy root - but this may not be bullet proof yet, so please be careful and do not try this against a production Galaxy instance.

Options:

```
--galaxy_root DIRECTORY Root of development galaxy directory to execute command with.
--galaxy_python_version [2|2.7|3|3.3|3.4|3.5|3.6|3.7] Python version to start Galaxy under
--galaxy_database_seed PATH Preseeded Galaxy sqlite database to target.
--extra_tools PATH Extra tool sources to include in Galaxy's tool panel (file or directory). These will not be linted/tested/etc... but they will be available to workflows and for interactive use.
--install_galaxy Download and configure a disposable copy of Galaxy from github.
--galaxy_branch TEXT Branch of Galaxy to target (defaults to master) if a Galaxy root isn't specified.
--galaxy_source TEXT Git source of Galaxy to target (defaults to the official galaxyproject github source if a Galaxy root isn't specified.
--skip_venv Do not create or source a virtualenv environment for Galaxy, this should be used or instance to preserve an externally configured
```
virtual environment or conda environment.

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>--no_cache_galaxy</code></td>
<td>Skip caching of Galaxy source and dependencies obtained with <code>--install_galaxy</code>. Not caching this results in faster downloads (no git) - so is better on throw away instances such with TravisCI.</td>
</tr>
<tr>
<td><code>--no_cleanup</code></td>
<td>Do not cleanup temp files created for and by Galaxy.</td>
</tr>
<tr>
<td><code>--galaxy_email TEXT</code></td>
<td>E-mail address to use when launching single-user Galaxy server.</td>
</tr>
<tr>
<td><code>--docker / --no_docker</code></td>
<td>Run Galaxy tools in Docker if enabled.</td>
</tr>
<tr>
<td><code>--docker_cmd TEXT</code></td>
<td>Command used to launch docker (defaults to docker).</td>
</tr>
<tr>
<td><code>--docker_sudo / --no_docker_sudo</code></td>
<td>Flag to use sudo when running docker.</td>
</tr>
<tr>
<td><code>--docker_host TEXT</code></td>
<td>Docker host to target when executing docker commands (defaults to localhost).</td>
</tr>
<tr>
<td><code>--docker_sudo_cmd TEXT</code></td>
<td>Sudo command to use when <code>--docker_sudo</code> is enabled (defaults to sudo).</td>
</tr>
<tr>
<td><code>--mulled_containers, --biocontainers</code></td>
<td>Test tools against mulled containers (forces <code>--docker</code>).</td>
</tr>
<tr>
<td><code>--job_config_file FILE</code></td>
<td>Job configuration file for Galaxy to target.</td>
</tr>
<tr>
<td><code>--tool_dependency_dir DIRECTORY</code></td>
<td>Tool dependency dir for Galaxy to target.</td>
</tr>
<tr>
<td><code>--port INTEGER</code></td>
<td>Port to serve Galaxy on (default is 9090).</td>
</tr>
<tr>
<td><code>--host TEXT</code></td>
<td>Host to bind Galaxy to. Default is 127.0.0.0.1 that is restricted to localhost connections for security reasons set to 0.0.0.0 to bind Galaxy to all ports including potentially publicly accessible ones.</td>
</tr>
<tr>
<td>`--engine [galaxy</td>
<td>docker_galaxy</td>
</tr>
<tr>
<td><code>--non_strict_cwl</code></td>
<td>Disable strict validation of CWL.</td>
</tr>
<tr>
<td><code>--docker_galaxy_image TEXT</code></td>
<td>Docker image identifier for docker-galaxy-flavor used if engine type is specified as <code>--docker-galaxy</code>. Defaults to quay.io/bgruening/galaxy.</td>
</tr>
<tr>
<td><code>--docker_extra_volume PATH</code></td>
<td>Extra path to mount if <code>--engine docker</code>.</td>
</tr>
<tr>
<td><code>--test_data DIRECTORY</code></td>
<td>test-data directory to for specified tool(s).</td>
</tr>
<tr>
<td><code>--tool_data_table PATH</code></td>
<td>tool_data_table_conf.xml file to for specified tool(s).</td>
</tr>
<tr>
<td><code>--dependency_resolvers_config_file FILE</code></td>
<td>Dependency resolver configuration for Galaxy to target.</td>
</tr>
<tr>
<td><code>--brew_dependency_resolution</code></td>
<td>Configure Galaxy to use plain brew dependency resolution.</td>
</tr>
<tr>
<td><code>--shed_dependency_resolution</code></td>
<td>Configure Galaxy to use brewed Tool Shed dependency resolution.</td>
</tr>
<tr>
<td><code>--no_dependency_resolution</code></td>
<td>Configure Galaxy with no dependency resolvers.</td>
</tr>
<tr>
<td><code>--conda_prefix DIRECTORY</code></td>
<td>Conda prefix to use for conda dependency commands.</td>
</tr>
<tr>
<td><code>--conda_exec FILE</code></td>
<td>Location of conda executable.</td>
</tr>
<tr>
<td><code>--conda_debug</code></td>
<td>Enable more verbose conda logging.</td>
</tr>
</tbody>
</table>
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--conda_channels, --conda_ensure_channels TEXT
Ensure conda is configured with specified comma separated list of channels.

--conda_use_local
Use locally built packages while building Conda environments.

--conda_dependency_resolution
Configure Galaxy to use only conda for dependency resolution.

--conda_copy_dependencies
Conda dependency resolution for Galaxy will copy dependencies instead of attempting to link them.

--conda_auto_install / --no_conda_auto_install
Conda dependency resolution for Galaxy will attempt to install requested but missing packages.

--conda_auto_init / --no_conda_auto_init
Conda dependency resolution for Galaxy will auto install conda itself using miniconda if not available on conda_prefix.

--profile TEXT
Name of profile (created with the profile_create command) to use with this command.

--postgres
Use postgres database type.

--database_type [postgres|postgres_docker|sqlite|auto]
Type of database to use for profile - 'auto', 'sqlite', 'postgres', and 'postgres_docker' are available options. Use postgres to use an existing postgres server you can access without a password via the psql command. Use postgres_docker to have Planemo manage a docker container running postgres. Data with postgres_docker is not yet persisted past when you restart the docker container launched by Planemo so be careful with this option.

--postgres_psql_path TEXT
Name or or path to postgres client binary (psql).

--postgres_database_user TEXT
Postgres username for managed development databases.

--postgres_database_host TEXT
Postgres host name for managed development databases.

--postgres_database_port TEXT
Postgres port for managed development databases.

--file_path DIRECTORY
Location for files created by Galaxy (e.g. database/files).

--database_connection TEXT
Database connection string to use for Galaxy.

--shed_tool_conf TEXT
Location of shed tools conf file for Galaxy.

--shed_tool_path TEXT
Location of shed tools directory for Galaxy.

--galaxy_single_user / --no_galaxy_single_user
By default Planemo will configure Galaxy to run in single-user mode where there is just one user and this user is automatically logged it. Use --no_galaxy_single_user to prevent Galaxy from running this way.

--daemon
Serve Galaxy process as a daemon.

--pid_file FILE
Location of pid file is executed with --daemon.

--ignore_dependency_problems
When installing shed repositories for workflows, ignore dependency issues. These (continues on next page)
likely indicate a problem but in some cases may not prevent a workflow from successfully executing.

--shed_install / --no_shed_install
By default Planemo will attempt to install repositories needed for workflow testing. This may not be appropriate for production servers and so this can disabled by calling planemo with --no_shed_install.

--cwl
Configure Galaxy for use with CWL tool. (this option is experimental and will be replaced when and if CWL support is merged into Galaxy).

--cwl_galaxy_root DIRECTORY Root of development galaxy directory to execute command with (must be branch of Galaxy with CWL support, this option is experimental and will be replaced with --galaxy_root when and if CWL support is merged into Galaxy).

--help
Show this message and exit.

9.37 share_test command

This section is auto-generated from the help text for the planemo command share_test. This help message can be generated with planemo share_test --help.

Usage:

planemo share_test [OPTIONS] FILE_PATH

Help
Publish JSON test results as sharable Gist.
This will upload the JSON test results to Github as a Gist and produce sharable URL.
The sharable URL can be used to share an HTML version of the report that can be easily embedded in pull requests or commit messages.
Requires a ~/.planemo.yml with Github ‘username’ and ‘password’ defined in a ‘github’ section of that configuration file.

Options:

--help  Show this message and exit.

9.38 shed_build command

This section is auto-generated from the help text for the planemo command shed_build. This help message can be generated with planemo shed_build --help.

Usage:

planemo shed_build [OPTIONS] TOOL_PATH
Help
Create a Galaxy tool tarball.
This will use the .shed.yml file to prepare a tarball (which you could upload to the Tool Shed manually).

Options:
--help  Show this message and exit.

9.39 shed_create command

This section is auto-generated from the help text for the planemo command shed_create. This help message can be generated with planemo shed_create --help.

Usage:
planemo shed_create [OPTIONS] PROJECT

Help
Create a repository in a Galaxy Tool Shed.
This will read the settings from the .shed.yml file.

Options:
-r, --recursive  Recursively perform command for nested repository directories.
--fail_fast  If multiple repositories are specified and an error occurs stop immediately instead of processing remaining repositories.
--owner TEXT  Tool Shed repository owner (username).
--name TEXT  Tool Shed repository name (defaults to the inferred tool directory name).
--shed_email TEXT  E-mail for Tool Shed auth (required unless shed_key is specified).
--shed_key TEXT  API key for Tool Shed access. An API key is required unless e-mail and password is specified. This key can be specified with either --shed_key or --shed_key_from_env.
--shed_key_from_env TEXT  Environment variable to read API key for Tool Shed access from.
--shed_password TEXT  Password for Tool Shed auth (required unless shed_key is specified).
-t, --shed_target TEXT  Tool Shed to target (this can be 'toolshed', 'testtoolshed', 'local' (alias for http://localhost:9009/), an arbitrary url or mappings defined ~/.planemo.yml.
-m, --message TEXT  Commit message for tool shed upload.
--skip_upload  Skip upload contents as part of operation, only update metadata.
--help  Show this message and exit.
9.40 shed_diff command

This section is auto-generated from the help text for the planemo command shed_diff. This help message can be generated with planemo shed_diff --help.

Usage:

```bash
planemo shed_diff [OPTIONS] PROJECT
```

Help
diff between local repository and Tool Shed.

By default, this will produce a diff between this repository and what would be uploaded to the Tool Shed with the `shed_upload` command - but this command can be made to compare other combinations of repositories. Here are some examples

```bash
$ # diff for this repository and the main Tool Shed
$ planemo shed_diff
$ # diff for this repository and the test Tool Shed
$ planemo shed_diff --shed_target testtoolshed
$ # diff for the test Tool Shed and main Tool Shed
$ planemo shed_diff --shed_target_source testtoolshed
$ # diff for two an explicitly specified repositories (ignores $ # current project's shed YAML file.)
$ planemo shed_diff --owner peterjc --name blast_rbh --shed_target_source testtoolshed
```

This command will return an exit code of:

- 0 if there are no detected differences.
- 1 if there are differences.
- 2 if the target repository doesn’t exist.
- >200 if there are errors attempting to perform a diff.

Warning: `shed_diff` doesn’t inspect repository metadata, this difference applies only to the file contents of files that would actually be uploaded to the repository.

Options:

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>-r, --recursive</td>
<td>Recursively perform command for nested repository directories.</td>
</tr>
<tr>
<td>--fail_fast</td>
<td>If multiple repositories are specified and an error occurs stop immediately instead of processing remaining repositories.</td>
</tr>
<tr>
<td>--owner TEXT</td>
<td>Tool Shed repository owner (username).</td>
</tr>
<tr>
<td>--name TEXT</td>
<td>Tool Shed repository name (defaults to the inferred tool directory name).</td>
</tr>
<tr>
<td>--shed_email TEXT</td>
<td>E-mail for Tool Shed auth (required unless <code>shed_key</code> is specified).</td>
</tr>
<tr>
<td>--shed_key TEXT</td>
<td>API key for Tool Shed access. An API key is required unless e-mail and password is specified. This key can be specified with either --shed_key or --shed_key_from_env.</td>
</tr>
<tr>
<td>--shed_key_from_env</td>
<td>Environment variable to read API key for Tool Shed access from.</td>
</tr>
<tr>
<td>--shed_password TEXT</td>
<td>Password for Tool Shed auth (required unless</td>
</tr>
</tbody>
</table>
9.41 shed_init command

This section is auto-generated from the help text for the planemo command shed_init. This help message can be generated with planemo shed_init --help.

Usage:
planemo shed_init [OPTIONS] PROJECT

Help
Bootstrap new Tool Shed .shed.yml file.

This Tool Shed configuration file is used by other planemo commands such as shed_lint, shed_create, shed_upload, and shed_diff to manage repositories in a Galaxy Tool Shed.

Options:

- --from_workflow PATH Attempt to generate repository dependencies from specified workflow.
- --description TEXT Specify repository description for .shed.yml.
- --long_description TEXT Specify repository long_description for .shed.yml.
- --remote_repository_url TEXT Specify repository remote_repository_url for .shed.yml.
- --homepage_url TEXT Specify repository homepage_url for .shed.yml.
- --owner TEXT Tool Shed repository owner (username).
- --name TEXT Tool Shed repository name (defaults to the inferred tool directory name).
- -f, --force Overwrite existing files if present.
- --help Show this message and exit.
9.42 shed_lint command

This section is auto-generated from the help text for the planemo command shed_lint. This help message can be generated with planemo shed_lint --help.

Usage:

```
planemo shed_lint [OPTIONS] PROJECT
```

Help

Check Tool Shed repository for common issues.

With the --tools flag, this command lints actual Galaxy tools in addition to tool shed artifacts.

With the --urls flag, this command searches for `<package>$URL</package>` and download actions which specify URLs. Each of those are accessed individually. By default, this tool requests the first hundred or so bytes of each listed URL and validates that a 200 OK was received. In tool XML files, the --urls option checks through the help text for mentioned URLs and checks those.

Options:

```
-r, --recursive          Recursively perform command for nested repository directories.
--fail_fast             If multiple repositories are specified and an error occurs stop immediately instead of processing remaining repositories.
--report_level [all|warn|error]  
--fail_level [warn|error] 
--tools                Lint tools discovered in the process of linting repositories.
--xsd / --no_xsd        Include tool XSD validation in linting process.
--ensure_metadata       Ensure .shed.yml files contain enough metadata for each repository to allow automated creation and/or updates.
--urls                 Check validity of URLs in XML files
--help                 Show this message and exit.
```

9.43 shed_serve command

This section is auto-generated from the help text for the planemo command shed_serve. This help message can be generated with planemo shed_serve --help.

Usage:

```
planemo shed_serve [OPTIONS] PROJECT
```

Help

Launch Galaxy with Tool Shed dependencies.

This command will start a Galaxy instance configured to target the specified shed, find published artifacts (tools and dependencies) corresponding to command-line arguments and `.shed.yml` file(s), install these artifacts, and serve a Galaxy instances that can be logged into and explored interactively.

Options:
```
-r, --recursive
Recursively perform command for nested repository directories.

--fail_fast
If multiple repositories are specified and an error occurs stop immediately instead of processing remaining repositories.

--owner TEXT
Tool Shed repository owner (username).

--name TEXT
Tool Shed repository name (defaults to the inferred tool directory name).

--shed_email TEXT
E-mail for Tool Shed auth (required unless shed_key is specified).

--shed_key TEXT
API key for Tool Shed access. An API key is required unless e-mail and password is specified. This key can be specified with either --shed_key or --shed_key_from_env.

--shed_key_from_env TEXT
Environment variable to read API key for Tool Shed access from.

--shed_password TEXT
Password for Tool Shed auth (required unless shed_key is specified).

-t, --shed_target TEXT
Tool Shed to target (this can be 'toolshed', 'testtoolshed', 'local' (alias for http://localhost:9009/), an arbitrary url or mappings defined ~/.planemo.yml.

--galaxy_root DIRECTORY
Root of development galaxy directory to execute command with.

--galaxy_python_version [2|2.7|3|3.3|3.4|3.5|3.6|3.7]
Python version to start Galaxy under

--galaxy_database_seed PATH
Preseeded Galaxy sqlite database to target.

--extra_tools PATH
Extra tool sources to include in Galaxy's tool panel (file or directory). These will not be linted/tested/etc... but they will be available to workflows and for interactive use.

--install_galaxy
Download and configure a disposable copy of Galaxy from github.

--galaxy_branch TEXT
Branch of Galaxy to target (defaults to master) if a Galaxy root isn't specified.

--galaxy_source TEXT
Git source of Galaxy to target (defaults to the official galaxyproject github source if a Galaxy root isn't specified.

--skip_venv
Do not create or source a virtualenv environment for Galaxy, this should be used or instance to preserve an externally configured virtual environment or conda environment.

--no_cache_galaxy
Skip caching of Galaxy source and dependencies obtained with --install_galaxy. Not caching this results in faster downloads (no git) - so it's better on throw away instances such with TravisCI.

--no_cleanup
Do not cleanup temp files created for and by Galaxy.

--galaxy_email TEXT
E-mail address to use when launching single-user Galaxy server.

--docker / --no_docker
Run Galaxy tools in Docker if enabled.

--docker_cmd TEXT
Command used to launch docker (defaults to docker).

--docker_sudo / --no_docker_sudo
Flag to use sudo when running docker.
```
--docker_host TEXT  Docker host to target when executing docker commands (defaults to localhost).
--docker_sudo_cmd TEXT  sudo command to use when --docker_sudo is enabled (defaults to sudo).
--mulled_containers, --biocontainers  Test tools against mulled containers (forces --docker).
--job_config_file FILE  Job configuration file for Galaxy to target.
--tool_dependency_dir DIRECTORY  Tool dependency dir for Galaxy to target.
--port INTEGER  Port to serve Galaxy on (default is 9090).
--host TEXT  Host to bind Galaxy to. Default is 127.0.0.1 that is restricted to localhost connections for security reasons set to 0.0.0.0 to bind Galaxy to all ports including potentially publicly accessible ones.
--test_data DIRECTORY  test-data directory to for specified tool(s).
--tool_data_table PATH  tool_data_table_conf.xml file to for specified tool(s).
--dependency_resolvers_config_file FILE  Dependency resolver configuration for Galaxy to target.
--brew_dependency_resolution  Configure Galaxy to use plain brew dependency resolution.
--shed_dependency_resolution  Configure Galaxy to use brewed Tool Shed dependency resolution.
--no_dependency_resolution  Configure Galaxy with no dependency resolvers.
--conda_prefix DIRECTORY  Conda prefix to use for conda dependency commands.
--conda_exec FILE  Location of conda executable.
--conda_debug  Enable more verbose conda logging.
--conda_channels, --condaEnsure_channels TEXT  Ensure conda is configured with specified comma separated list of channels.
--conda_use_local  Use locally built packages while building Conda environments.
--conda_dependency_resolution  Configure Galaxy to use only conda for dependency resolution.
--conda_copy_dependencies  Conda dependency resolution for Galaxy will copy dependencies instead of attempting to link them.
--conda_auto_install / --no_conda_auto_install  Conda dependency resolution for Galaxy will attempt to install requested but missing packages.
--conda_auto_init / --no_conda_auto_init  Conda dependency resolution for Galaxy will auto install conda itself using miniconda if not available on conda_prefix.
--profile TEXT  Name of profile (created with the profile_create command) to use with this command.
--postgres  Use postgres database type.
--database_type [postgres|postgres_docker|sqlite|auto]  Type of database to use for profile - 'auto', 'sqlite', 'postgres', and 'postgres_docker' are available options. Use postgres to use an
existing postgres server you can access without a password via the psql command. Use postgres_docker to have Planemo manage a docker container running postgres. Data with postgres_docker is not yet persisted past when you restart the docker container launched by Planemo so be careful with this option.

--postgres_psql_path TEXT
Name or path to postgres client binary (psql).

--postgres_database_user TEXT
Postgres username for managed development databases.

--postgres_database_host TEXT
Postgres host name for managed development databases.

--postgres_database_port TEXT
Postgres port for managed development databases.

--file_path DIRECTORY
Location for files created by Galaxy (e.g. database/files).

--database_connection TEXT
Database connection string to use for Galaxy.

--shed_tool_conf TEXT
Location of shed tools conf file for Galaxy.

--shed_tool_path TEXT
Location of shed tools directory for Galaxy.

--galaxy_single_user / --no_galaxy_single_user
By default Planemo will configure Galaxy to run in single-user mode where there is just one user and this user is automatically logged it. Use --no_galaxy_single_user to prevent Galaxy from running this way.

--pid_file FILE
Location of pid file is executed with --daemon.

--daemon
Serve Galaxy process as a daemon.

--skip_dependencies
Do not install shed dependencies as part of repository installation.

--help
Show this message and exit.

9.44 shed_test command

This section is auto-generated from the help text for the planemo command shed_test. This help message can be generated with planemo shed_test --help.

Usage:

planemo shed_test [OPTIONS] PROJECT

Help

Run tests of published shed artifacts.

This command will start a Galaxy instance configured to target the specified shed, find published artifacts (tools and dependencies) corresponding to command-line arguments and .shed.yml file(s), install these artifacts, and run the tool tests for these commands.

This command requires the target to be version 15.07 or newer.

Options:

-r, --recursive
Recursively perform command for nested repository directories.

9.44. shed_test command
--fail_fast  If multiple repositories are specified and an error occurs stop immediately instead of processing remaining repositories.

--owner TEXT  Tool Shed repository owner (username).
--name TEXT  Tool Shed repository name (defaults to the inferred tool directory name).
--shed_email TEXT  E-mail for Tool Shed auth (required unless shed_key is specified).
--shed_key TEXT  API key for Tool Shed access. An API key is required unless e-mail and password is specified. This key can be specified with either --shed_key or --shed_key_from_env.
--shed_key_from_env TEXT  Environment variable to read API key for Tool Shed access from.
--shed_password TEXT  Password for Tool Shed auth (required unless shed_key is specified).
-t, --shed_target TEXT  Tool Shed to target (this can be 'toolshed', 'testtoolshed', 'local' (alias for http://localhost:9009/), an arbitrary url or mappings defined ~/.planemo.yml.
--galaxy_root DIRECTORY  Root of development galaxy directory to execute command with.
--galaxy_python_version [2|2.7|3|3.3|3.4|3.5|3.6|3.7]  Python version to start Galaxy under.
--galaxy_database_seed PATH  Preseeded Galaxy sqlite database to target.
--extra_tools PATH  Extra tool sources to include in Galaxy's tool panel (file or directory). These will not be linted/tested/etc... but they will be available to workflows and for interactive use.
--install_galaxy  Download and configure a disposable copy of Galaxy from github.
--galaxy_branch TEXT  Branch of Galaxy to target (defaults to master) if a Galaxy root isn't specified.
--galaxy_source TEXT  Git source of Galaxy to target (defaults to the official galaxyproject github source if a Galaxy root isn't specified.
--skip_venv  Do not create or source a virtualenv environment for Galaxy, this should be used or instance to preserve an externally configured virtual environment or conda environment.
--no_cache_galaxy  Skip caching of Galaxy source and dependencies obtained with --install_galaxy. Not caching this results in faster downloads (no git) - so is better on throw away instances such with TravisCI.
--no_cleanup  Do not cleanup temp files created for and by Galaxy.
--galaxy_email TEXT  E-mail address to use when launching single-user Galaxy server.
--docker / --no_docker  Run Galaxy tools in Docker if enabled.
--docker_cmd TEXT  Command used to launch docker (defaults to docker).
--docker_sudo / --no_docker_sudo  Flag to use sudo when running docker.
--docker_host TEXT  Docker host to target when executing docker commands (defaults to localhost).
<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>--docker_sudo_cmd TEXT</td>
<td>sudo command to use when --docker_sudo is enabled (defaults to sudo).</td>
</tr>
<tr>
<td>--mulled_containers, --biocontainers</td>
<td>Test tools against mulled containers (forces --docker).</td>
</tr>
<tr>
<td>--job_config_file FILE</td>
<td>Job configuration file for Galaxy to target.</td>
</tr>
<tr>
<td>--tool_dependency_dir DIRECTORY</td>
<td>Tool dependency dir for Galaxy to target.</td>
</tr>
<tr>
<td>--update_test_data</td>
<td>Update test-data directory with job outputs (normally written to directory if specified.)</td>
</tr>
<tr>
<td>--paste_test_data_paths / --no_paste_test_data_paths</td>
<td>By default Planemo will use or not use Galaxy's path paste option to load test data into a history based on the engine type it is targeting. This can override the logic to explicitly enable or disable path pasting.</td>
</tr>
<tr>
<td>--test_output PATH</td>
<td>Output test report (HTML - for humans) defaults to tool_test_output.html.</td>
</tr>
<tr>
<td>--test_output_text PATH</td>
<td>Output test report (Basic text - for display in CI)</td>
</tr>
<tr>
<td>--test_output_markdown PATH</td>
<td>Output test report (Markdown style - for humans &amp; computers)</td>
</tr>
<tr>
<td>--test_output_xunit PATH</td>
<td>Output test report (xunit style - for CI systems)</td>
</tr>
<tr>
<td>--test_output_junit PATH</td>
<td>Output test report (JUnit style - for CI systems)</td>
</tr>
<tr>
<td>--job_output_files DIRECTORY</td>
<td>Write job outputs to specified directory.</td>
</tr>
<tr>
<td>--summary [none</td>
<td>minimal</td>
</tr>
<tr>
<td>--skip_dependencies</td>
<td>Do not install shed dependencies as part of repository installation.</td>
</tr>
<tr>
<td>--help</td>
<td>Show this message and exit.</td>
</tr>
</tbody>
</table>

### 9.45 shed_update command

This section is auto-generated from the help text for the planemo command `shed_update`. This help message can be generated with `planemo shed_update --help`.

#### Usage:

```
planemo shed_update [OPTIONS] PROJECT
```

#### Help

Update Tool Shed repository.

By default this command will update both repository metadata from `.shed.yml` and upload new contents from the repository directory.

```
planemo shed_update
```
This will update the main tool shed with the repository defined by a `.shed.yml` file in the current working directory. Both the location of the `.shed.yml` and the tool shed to upload to can be easily configured. For instance, the following command can be used if `.shed.yml` is contained in `path/to/repo` and the desire is to update the test tool shed.

```
% planemo shed_update --shed_target testtoolshed path/to/repo
```

Another important option is `--check_diff` - this doesn’t affect the updating of shed metadata but it will check for differences before uploading new contents to the tool shed. This may important because the tool shed will automatically populate certain attributes in tool shed artifact files (such as `tool_dependencies.xml`) and this may cause unwanted installable revisions to be created when there are no important changes.

The lower-level `shed_upload` command should be used instead if the repository doesn’t define complete metadata in a `.shed.yml`.

Options:

```
--report_xunit PATH          Output an XUnit report, useful for CI testing
-r, --recursive             Recursively perform command for nested repository directories.
--fail_fast                  If multiple repositories are specified and an error occurs stop immediately instead of processing remaining repositories.
--owner TEXT                 Tool Shed repository owner (username).
--name TEXT                  Tool Shed repository name (defaults to the inferred tool directory name).
--shed_email TEXT            E-mail for Tool Shed auth (required unless shed_key is specified).
--shed_key TEXT              API key for Tool Shed access. An API key is required unless e-mail and password is specified. This key can be specified with either --shed_key or --shed_key_from_env.
--shed_key_from_env TEXT     Environment variable to read API key for Tool Shed access from.
--shed_password TEXT         Password for Tool Shed auth (required unless shed_key is specified).
-t, --shed_target TEXT       Tool Shed to target (this can be 'toolshed', 'testtoolshed', 'local' (alias for http://localhost:9009/), an arbitrary url or mappings defined ~/.planemo.yml.
-m, --message TEXT           Commit message for tool shed upload.
--force_repository_creation If a repository cannot be found for the specified user/repo name pair, then automatically create the repository in the toolshed.
--check_diff                 Skip uploading if the shed_diff detects there would be no 'difference' (only attributes populated by the shed would be updated.)
--skip_upload                Skip upload contents as part of operation, only update metadata.
--skip_metadata              Skip metadata update as part of operation, only upload new contents.
--help                       Show this message and exit.
```
9.46 sheds_upload command

This section is auto-generated from the help text for the planemo command sheds_upload. This help message can be generated with planemo sheds_upload --help.

Usage:

```
planemo sheds_upload [OPTIONS] PROJECT
```

Help

Low-level command to upload tarballs.

Generally, sheds_update should be used instead since it also updates both tool shed contents (via tar ball generation and upload) as well as metadata (to handle metadata changes in .shed.yml files).

```
% planemo sheds_upload --tar_only ~/
% tar -tzf sheds_upload.tar.gz
test-data/blastdb.loc
...tools/ncbi_blast_plus/tool_dependencies.xml
% tar -tzf sheds_upload.tar.gz | wc -l
117
```

Options:

```
-r, --recursive
    Recursively perform command for nested repository directories.
--fail_fast
    If multiple repositories are specified and an error occurs stop immediately instead of processing remaining repositories.
--owner TEXT
    Tool Shed repository owner (username).
--name TEXT
    Tool Shed repository name (defaults to the inferred tool directory name).
--shed_email TEXT
    E-mail for Tool Shed auth (required unless shed_key is specified).
--shed_key TEXT
    API key for Tool Shed access. An API key is required unless e-mail and password is specified. This key can be specified with either --shed_key or --shed_key_from_env.
--shed_key_from_env TEXT
    Environment variable to read API key for Tool Shed access.
--shed_password TEXT
    Password for Tool Shed auth (required unless shed_key is specified).
-t, --shed_target TEXT
    Tool Shed to target (this can be 'toolshed', 'testtoolshed', 'local' (alias for http://localhost:9009/), an arbitrary url or mappings defined ~/.planemo.yml.
-m, --message TEXT
    Commit message for tool shed upload.
--force_repository_creation
    If a repository cannot be found for the specified user/repo name pair, then automatically create the repository in the toolshed.
--check_diff
    Skip uploading if the shed_diff detects there would be no 'difference' (only attributes populated by the shed would be updated.)
--tar_only
    Produce tar file for upload but do not publish to a tool shed.
--tar FILE
    Specify a pre-existing tar file instead of
```

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9.47 syntax command

This section is auto-generated from the help text for the planemo command syntax. This help message can be generated with planemo syntax --help.

Usage:

```
planemo syntax [OPTIONS]
```

Help

Open tool config syntax page in web browser. Options:

```
--help Show this message and exit.
```

9.48 test command

This section is auto-generated from the help text for the planemo command test. This help message can be generated with planemo test --help.

Usage:

```
planemo test [OPTIONS] TOOL_PATH
```

Help

Run specified tool’s tests within Galaxy.

All referenced tools (by default all the tools in the current working directory) will be tested and the results quickly summarized.

To run these tests planemo needs a Galaxy instance to utilize, planemo will search parent directories to see if any is a Galaxy instance - but one can pick the Galaxy instance to use with the --galaxy_root option or force planemo to download a disposable instance with the --install_galaxy flag.

In addition to the quick summary printed to the console - various detailed output summaries can be configured. tool_test_output.html (settable via --test_output) will contain a human consumable HTML report describing the test run. A JSON file (settable via --test_output_json and defaulting to tool_test_output.json) will also be created. These files can be created by passing in empty arguments or globally by setting the values default_test_output and/or default_test_output_json in ~/.planemo.yml to null. For continuous integration testing a xUnit-style report can be configured using the --test_output_xunit.

planemo uses temporarily generated config files and environment variables to attempt to shield this execution of Galaxy from manually launched runs against that same Galaxy root - but this may not be bullet proof yet so please careful and do not try this against production Galaxy instances.

Options:
<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>--failed</strong></td>
<td>Re-run only failed tests. This command will read tool_test_output.json to determine which tests failed so this file must have been produced with the same set of tool ids previously.</td>
</tr>
<tr>
<td><strong>--polling_backoff</strong> INTEGER</td>
<td>Poll resources with an increasing interval between requests. Useful when testing against remote and/or production instances to limit generated traffic.</td>
</tr>
<tr>
<td><strong>--history_name</strong> TEXT</td>
<td>Name for history (if a history is generated as part of testing.)</td>
</tr>
<tr>
<td><strong>--galaxy_root</strong> DIRECTORY</td>
<td>Root of development galaxy directory to execute command with.</td>
</tr>
<tr>
<td><strong>--galaxy_python_version</strong> [2</td>
<td>2.7</td>
</tr>
<tr>
<td><strong>--galaxy_database_seed</strong> PATH</td>
<td>Preseeded Galaxy sqlite database to target.</td>
</tr>
<tr>
<td><strong>--extra_tools</strong> PATH</td>
<td>Extra tool sources to include in Galaxy's tool panel (file or directory). These will not be linted/tested/etc... but they will be available to workflows and for interactive use.</td>
</tr>
<tr>
<td><strong>--install_galaxy</strong></td>
<td>Download and configure a disposable copy of Galaxy from github.</td>
</tr>
<tr>
<td><strong>--galaxy_branch</strong> TEX</td>
<td>Branch of Galaxy to target (defaults to master) if a Galaxy root isn't specified.</td>
</tr>
<tr>
<td><strong>--galaxy_source</strong> TEXT</td>
<td>Git source of Galaxy to target (defaults to the official galaxyproject github source if a Galaxy root isn't specified.</td>
</tr>
<tr>
<td><strong>--skip_venv</strong></td>
<td>Do not create or source a virtualenv environment for Galaxy, this should be used or instance to preserve an externally configured virtual environment or conda environment.</td>
</tr>
<tr>
<td><strong>--no_cache_galaxy</strong></td>
<td>Skip caching of Galaxy source and dependencies obtained with --install_galaxy. Not caching this results in faster downloads (no git) - so is better on throw away instances such with TravisCI.</td>
</tr>
<tr>
<td><strong>--no_cleanup</strong></td>
<td>Do not cleanup temp files created for and by Galaxy.</td>
</tr>
<tr>
<td><strong>--galaxy_email</strong> TEX</td>
<td>E-mail address to use when launching single-user Galaxy server.</td>
</tr>
<tr>
<td><strong>--docker / --no_docker</strong></td>
<td>Run Galaxy tools in Docker if enabled.</td>
</tr>
<tr>
<td><strong>--docker_cmd</strong> TEXT</td>
<td>Command used to launch docker (defaults to docker).</td>
</tr>
<tr>
<td><strong>--docker_sudo / --no_docker_sudo</strong></td>
<td>Flag to use sudo when running docker.</td>
</tr>
<tr>
<td><strong>--docker_host</strong> TEX</td>
<td>Docker host to target when executing docker commands (defaults to localhost).</td>
</tr>
<tr>
<td><strong>--docker_sudo_cmd</strong> TEX</td>
<td>Sudo command to use when --docker_sudo is enabled (defaults to sudo).</td>
</tr>
<tr>
<td><strong>--mulled_containers, --biocontainers</strong></td>
<td>Test tools against mulled containers (forces --docker).</td>
</tr>
<tr>
<td><strong>--job_config_file</strong> FILE</td>
<td>Job configuration file for Galaxy to target.</td>
</tr>
<tr>
<td><strong>--tool_dependency_dir</strong> DIRECTORY</td>
<td>Tool dependency dir for Galaxy to target.</td>
</tr>
<tr>
<td><strong>--test_data</strong> DIRECTORY</td>
<td>Test-data directory to for specified tool(s).</td>
</tr>
</tbody>
</table>

(continues on next page)
---tool_data_table PATH tool_data_table_conf.xml file to for specified
tool(s).
---dependency_resolvers_config_file FILE
Dependency resolver configuration for Galaxy
to target.
---brew_dependency_resolution Configure Galaxy to use plain brew dependency
resolution.
---shed_dependency_resolution Configure Galaxy to use brewed Tool Shed
dependency resolution.
---no_dependency_resolution Configure Galaxy with no dependency resolvers.
---conda_prefix DIRECTORY Conda prefix to use for conda dependency
commands.
---conda_exec FILE Location of conda executable.
---conda_debug Enable more verbose conda logging.
---conda_channels, --conda_ensure_channels TEXT
Ensure conda is configured with specified
comma separated list of channels.
---conda_use_local Use locally built packages while building
Conda environments.
---conda_dependency_resolution Configure Galaxy to use only conda for
dependency resolution.
---conda_copy_dependencies Conda dependency resolution for Galaxy will
copy dependencies instead of attempting to
link them.
---conda_auto_install / --no_conda_auto_install
Conda dependency resolution for Galaxy will
attempt to install requested but missing
packages.
---conda_auto_init / --no_conda_auto_init
Conda dependency resolution for Galaxy will
auto install conda itself using miniconda if
not available on conda_prefix.
---profile TEXT Name of profile (created with the
profile_create command) to use with this
command.
---postgres Use postgres database type.
---database_type [postgres|postgres_docker|sqlite|auto]
Type of database to use for profile - 'auto',
sqlite', 'postgres', and 'postgres_docker'
are available options. Use postgres to use an
existing postgres server you can access
without a password via the psql command. Use
postgres_docker to have Planemo manage a
docker container running postgres. Data with
postgres_docker is not yet persisted past when
you restart the docker container launched by
Planemo so be careful with this option.
---postgres_psql_path TEXT Name or path to postgres client binary
(psycopg).
---postgres_database_user TEXT Postgres username for managed development
databases.
---postgres_database_host TEXT Postgres host name for managed development
databases.
---postgres_database_port TEXT Postgres port for managed development
databases.
---file_path DIRECTORY Location for files created by Galaxy (e.g.
database/files).
--database_connection TEXT  Database connection string to use for Galaxy.
--shed_tool_conf TEXT   Location of shed tools conf file for Galaxy.
--shed_tool_path TEXT   Location of shed tools directory for Galaxy.
--galaxy_single_user / --no_galaxy_single_user
   By default Planemo will configure Galaxy to run in single-user mode where there is just one user and this user is automatically logged in. Use --no_galaxy_single_user to prevent Galaxy from running this way.

--update_test_data
   Update test-data directory with job outputs (normally written to directory --job_output_files if specified.)

--paste_test_data_paths / --no_paste_test_data_paths
   By default Planemo will use or not use Galaxy's path paste option to load test data into a history based on the engine type it is targeting. This can override the logic to explicitly enable or disable path pasting.

--test_output PATH
   Output test report (HTML - for humans) defaults to tool_test_output.html.
--test_output_text PATH
   Output test report (Basic text - for display in CI)
--test_output_markdown PATH
   Output test report (Markdown style - for humans & computers)
--test_output_xunit PATH
   Output test report (xunit style - for CI systems)
--test_output_junit PATH
   Output test report (JUnit style - for CI systems)
--test_output_json PATH
   Output test report (planemo json) defaults to tool_test_output.json.
--job_output_files DIRECTORY
   Write job outputs to specified directory.
--summary [none|minimal|compact]
   Summary style printed to planemo's standard output (see output reports for more complete summary). Set to 'none' to disable completely.

--engine [galaxy|docker_galaxy|cwltool|toil|external_galaxy]
   Select an engine to run or test artifacts such as tools and workflows. Defaults to a local Galaxy, but running Galaxy within a Docker container or the CWL reference implementation 'cwltool' and 'toil' be selected.

--non_strict_cwl
   Disable strict validation of CWL.
--no-container, --no_container
   If cwltool engine is used, disable Docker container usage.
--docker_galaxy_image TEXT
   Docker image identifier for docker-galaxy-flavor used if engine type is specified as `''docker-galaxy``. Defaults to quay.io/bgruening/galaxy.
--docker_extra_volume PATH
   Extra path to mount if --engine docker.
--ignore_dependency_problems
   When installing shed repositories for workflows, ignore dependency issues. These likely indicate a problem but in some cases may not prevent a workflow from successfully executing.

--shed_install / --no_shed_install
   By default Planemo will attempt to install repositories needed for workflow testing. This

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may not be appropriate for production servers and so this can be disabled by calling planemo with \texttt{--no_shed_install}.

\begin{tabular}{|l|}
\hline
\texttt{--galaxy_url\ TEXT} & Remote Galaxy URL to use with external Galaxy engine. \\
\texttt{--galaxy_admin_key\ TEXT} & Admin key to use with external Galaxy engine. \\
\texttt{--galaxy_user_key\ TEXT} & User key to use with external Galaxy engine. \\
\texttt{--help} & Show this message and exit. \\
\hline
\end{tabular}

\section*{9.49 test_reports command}

This section is auto-generated from the help text for the planemo command \texttt{test_reports}. This help message can be generated with \texttt{planemo test_reports --help}.

\textbf{Usage:}

\begin{verbatim}
planemo test_reports [OPTIONS] FILE_PATH
\end{verbatim}

\textbf{Help}

Generate human readable tool test reports.

Creates reports in various formats (HTML, text, markdown) from the structured test output (tool_test_output.json).

\textbf{Options:}

\begin{tabular}{|l|}
\hline
\texttt{--test_output\ PATH} & Output test report (HTML - \texttt{for} humans) defaults to tool_test_output.html. \\
\texttt{--test_output_text\ PATH} & Output test report (Basic text - \texttt{for} display in CI) \\
\texttt{--test_output_markdown\ PATH} & Output test report (Markdown style - \texttt{for} humans & computers) \\
\texttt{--test_output_xunit\ PATH} & Output test report (xunit style - \texttt{for} CI systems \\
\texttt{--test_output_junit\ PATH} & Output test report (JUnit style - \texttt{for} CI systems \\
\texttt{--help} & Show this message \texttt{and} exit. \\
\hline
\end{tabular}

\section*{9.50 tool_factory command}

This section is auto-generated from the help text for the planemo command \texttt{tool_factory}. This help message can be generated with \texttt{planemo tool_factory --help}.

\textbf{Usage:}

\begin{verbatim}
planemo tool_factory [OPTIONS]
\end{verbatim}

\textbf{Help}

(Experimental) Launch Galaxy with Tool Factory 2.


\textbf{Options:}

<table>
<thead>
<tr>
<th>Command</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>--galaxy_root DIRECTORY</td>
<td>Root of development galaxy directory to execute command with.</td>
</tr>
<tr>
<td>--galaxy_python_version [2</td>
<td>2.7</td>
</tr>
<tr>
<td>--galaxy_database_seed PATH</td>
<td>Preseeded Galaxy sqlite database to target.</td>
</tr>
<tr>
<td>--extra_tools PATH</td>
<td>Extra tool sources to include in Galaxy's tool panel (file or directory). These will not be linted/tested/etc... but they will be available to workflows and for interactive use.</td>
</tr>
<tr>
<td>--install_galaxy</td>
<td>Download and configure a disposable copy of Galaxy from github.</td>
</tr>
<tr>
<td>--galaxy_branch TEXT</td>
<td>Branch of Galaxy to target (defaults to master) if a Galaxy root isn't specified.</td>
</tr>
<tr>
<td>--galaxy_source TEXT</td>
<td>Git source of Galaxy to target (defaults to the official galaxyproject github source if a Galaxy root isn't specified.</td>
</tr>
<tr>
<td>--skip_venv</td>
<td>Do not create or source a virtualenv environment for Galaxy, this should be used or instance to preserve an externally configured virtual environment or conda environment.</td>
</tr>
<tr>
<td>--no_cache_galaxy</td>
<td>Skip caching of Galaxy source and dependencies obtained with --install_galaxy. Not caching this results in faster downloads (no git) - so is better on throw away instances such with TravisCI.</td>
</tr>
<tr>
<td>--no_cleanup</td>
<td>Do not cleanup temp files created for and by Galaxy.</td>
</tr>
<tr>
<td>--galaxy_email TEXT</td>
<td>E-mail address to use when launching single-user Galaxy server.</td>
</tr>
<tr>
<td>--docker / --no_docker</td>
<td>Run Galaxy tools in Docker if enabled.</td>
</tr>
<tr>
<td>--docker_cmd TEXT</td>
<td>Command used to launch docker (defaults to docker).</td>
</tr>
<tr>
<td>--docker_sudo / --no_docker_sudo</td>
<td>Flag to use sudo when running docker.</td>
</tr>
<tr>
<td>--docker_host TEXT</td>
<td>Docker host to target when executing docker commands (defaults to localhost).</td>
</tr>
<tr>
<td>--docker_sudo_cmd TEXT</td>
<td>sudo command to use when --docker_sudo is enabled (defaults to sudo).</td>
</tr>
<tr>
<td>--mulled_containers, --biocontainers</td>
<td>Test tools against mulled containers (forces --docker).</td>
</tr>
<tr>
<td>--job_config_file FILE</td>
<td>Job configuration file for Galaxy to target.</td>
</tr>
<tr>
<td>--tool_dependency_dir DIRECTORY</td>
<td>Tool dependency dir for Galaxy to target.</td>
</tr>
<tr>
<td>--port INTEGER</td>
<td>Port to serve Galaxy on (default is 9090).</td>
</tr>
<tr>
<td>--host TEXT</td>
<td>Host to bind Galaxy to. Default is 127.0.0.1 that is restricted to localhost connections for security reasons set to 0.0.0.0 to bind Galaxy to all ports including potentially publicly accessible ones.</td>
</tr>
<tr>
<td>--engine [galaxy</td>
<td>docker_galaxy</td>
</tr>
<tr>
<td>--non_strict_cwl</td>
<td>Disable strict validation of CWL.</td>
</tr>
</tbody>
</table>
Planemo Documentation, Release 0.61.0.dev0

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<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>--docker_galaxy_image TEXT</td>
<td>Docker image identifier for docker-galaxy-flavor used if engine type is specified as <code>docker-galaxy</code>. Defaults to quay.io/bgruening/galaxy.</td>
</tr>
<tr>
<td>--docker_extra_volume PATH</td>
<td>Extra path to mount if --engine docker.</td>
</tr>
<tr>
<td>--test_data DIRECTORY</td>
<td>Test-data directory to for specified tool(s).</td>
</tr>
<tr>
<td>--tool_data_table PATH</td>
<td>Tool_data_table_conf.xml file to for specified tool(s).</td>
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<tr>
<td>--dependency_resolvers_config_file FILE</td>
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<td>Configure Galaxy with no dependency resolvers.</td>
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<td>--conda_prefix DIRECTORY</td>
<td>Conda prefix to use for conda dependency commands.</td>
</tr>
<tr>
<td>--conda_exec FILE</td>
<td>Location of conda executable.</td>
</tr>
<tr>
<td>--conda_debug</td>
<td>Enable more verbose conda logging.</td>
</tr>
<tr>
<td>--conda_channels, --conda_ensure_channels TEXT</td>
<td>Ensure conda is configured with specified comma separated list of channels.</td>
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<td>Conda dependency resolution for Galaxy will auto install conda itself using miniconda if not available in onda_prefix.</td>
</tr>
<tr>
<td>--profile TEXT</td>
<td>Name of profile (created with the profile_create command) to use with this command.</td>
</tr>
<tr>
<td>--postgres</td>
<td>Use postgres database type.</td>
</tr>
<tr>
<td>--database_type</td>
<td>Type of database to use for profile - 'auto', 'sqlite', 'postgres', and 'postgres_docker' are available options. Use postgres to use an existing postgres server you can access without a password via the psql command. Use postgres_docker to have Planemo manage a docker container running postgres. Data with postgres_docker is not yet persisted past when you restart the docker container launched by Planemo so be careful with this option.</td>
</tr>
<tr>
<td>--postgres_psql_path TEXT</td>
<td>Name or path to postgres client binary (psql).</td>
</tr>
<tr>
<td>--postgres_database_user TEXT</td>
<td>Postgres username for managed development databases.</td>
</tr>
</tbody>
</table>

(continues on next page)
--postgres_database_host TEXT  Postgres host name for managed development databases.
--postgres_database_port TEXT  Postgres port for managed development databases.
--file_path DIRECTORY    Location for files created by Galaxy (e.g. database/files).
--database_connection TEXT  Database connection string to use for Galaxy.
--shed_tool_conf TEXT  Location of shed tools conf file for Galaxy.
--shed_tool_path TEXT  Location of shed tools directory for Galaxy.
--galaxy_single_user / --no_galaxy_single_user
By default Planemo will configure Galaxy to run in single-user mode where there is just one user and this user is automatically logged in. Use --no_galaxy_single_user to prevent Galaxy from running this way.
--daemon
Serve Galaxy process as a daemon.
--pid_file FILE  Location of pid file is executed with --daemon.
--ignore_dependency_problems
When installing shed repositories for workflows, ignore dependency issues. These likely indicate a problem but in some cases may not prevent a workflow from successfully executing.
--shed_install / --no_shed_install
By default Planemo will attempt to install repositories needed for workflow testing. This may not be appropriate for production servers and so this can disabled by calling planemo with --no_shed_install.
--help
Show this message and exit.

9.51 tool_init command

This section is auto-generated from the help text for the planemo command tool_init. This help message can be generated with planemo tool_init --help.

Usage:

planemo tool_init [OPTIONS]

Help
Generate tool outline from given arguments. Options:

-i, --id TEXT  Short identifier for new tool (no whitespace)
-f, --force  Overwrite existing tool if present.
-t, --tool FILE  Output path for new tool (default is <id>.xml)
-n, --name TEXT  Name for new tool (user facing)
--version TEXT  Tool XML version.
-d, --description TEXT  Short description for new tool (user facing)
-c, --command TEXT  Command potentially including cheetah variables
() (e.g. 'seqtk seq -a $input > $output')
--example_command TEXT  Example to command with paths to build Cheetah template from (e.g. 'seqtk seq -a 2.fastq > 2.fasta'). Option cannot be used with --command,
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should be used --example_input and --example_output.

For use with --example_command, replace input file
(e.g. 2.fastq with a data input parameter).

For use with --example_command, replace input file
(e.g. 2.fastq with a tool output).

Create a named output for use with command for
example specify --named_output=output1.bam and then
use '-o $output1' in your command block.

An input description (e.g. input.fasta)

An output location (e.g. output.bam), the Galaxy
datatype is inferred from the extension.

Help text (reStructuredText)

Auto populate help from supplied command.

Supply a DOI (http://www.doi.org/) easing citation
of the tool for Galaxy users (e.g. 10.1101/014043).

Supply a URL for citation.

For use with --example_command, generate a tool
test case from the supplied example.

Generate a macros.xml for reuse across many tools.

Command to print version (e.g. 'seqtk --version')

Add a tool requirement package (e.g. 'seqtk' or
'seqtk@1.68').

Add a Docker image identifier for this tool.

Build a CWL tool instead of a Galaxy tool.

Show this message and exit.

### 9.52 training_fill_data_library command

This section is auto-generated from the help text for the planemo command training_fill_data_library. This help message can be generated with planemo training_fill_data_library --help.

**Usage:**

planemo training_fill_data_library [OPTIONS] TOOL_PATH

**Help**

Build training template from workflow. **Options:**

```plaintext
--topic_name TEXT Name (directory name) of the topic to create or in which
ea tutorial should be created or updates [required]

--tutorial_name TEXT Name (directory name) of the tutorial to modify
[required]

--zenodo_link TEXT Zenodo URL with the input data

--datatypes PATH YAML file with the correspondence between Zenodo
extension and Galaxy datatypes

--help Show this message and exit.
```

### 9.53 training_generate_from_wf command

This section is auto-generated from the help text for the planemo command training_generate_from_wf. This help message can be generated with planemo training_generate_from_wf --help.
Usage:

```
planemo training_generate_from_wf [OPTIONS] TOOL_PATH
```

Help

Create tutorial skeleton from workflow. **Options:**

- `--topic_name TEXT` Name (directory name) of the topic to create or in which a tutorial should be created or updates [required]
- `--tutorial_name TEXT` Name (directory name) of the tutorial to modify [required]
- `--workflow PATH` Workflow of the tutorial (locally)
- `--galaxy_url TEXT` URL of a Galaxy instance with the workflow
- `--galaxy_api_key TEXT` API key on the Galaxy instance with the workflow
- `--workflow_id TEXT` ID of the workflow on the Galaxy instance
- `--galaxy_root DIRECTORY` Root of development galaxy directory to execute command with.
- `--galaxy_python_version [2|2.7|3|3.3|3.4|3.5|3.6|3.7]` Python version to start Galaxy under
- `--galaxy_database_seed PATH` Preseeded Galaxy sqlite database to target.
- `--extra_tools PATH` Extra tool sources to include in Galaxy's tool panel (file or directory). These will not be linted/tested/etc... but they will be available to workflows and for interactive use.
- `--install_galaxy` Download and configure a disposable copy of Galaxy from github.
- `--galaxy_branch TEXT` Branch of Galaxy to target (defaults to master) if a Galaxy root isn't specified.
- `--galaxy_source TEXT` Git source of Galaxy to target (defaults to the official galaxyproject github source if a Galaxy root isn't specified.
- `--skip_venv` Do not create or source a virtualenv environment for Galaxy, this should be used or instance to preserve an externally configured virtual environment or conda environment.
- `--no_cache_galaxy` Skip caching of Galaxy source and dependencies obtained with --install_galaxy. Not caching this results in faster downloads (no git) - so is better on throw away instances such with TravisCI.
- `--no_cleanup` Do not cleanup temp files created for and by Galaxy.
- `--galaxy_email TEXT` E-mail address to use when launching single-user Galaxy server.
- `--docker / --no_docker` Run Galaxy tools in Docker if enabled.
- `--docker_cmd TEXT` Command used to launch docker (defaults to docker).
- `--docker_sudo / --no_docker_sudo` Flag to use sudo when running docker.
- `--docker_host TEXT` Docker host to target when executing docker commands (defaults to localhost).
- `--docker_sudo_cmd TEXT` sudo command to use when --docker_sudo is enabled (defaults to sudo).
- `--mulled_containers, --biocontainers` (continues on next page)
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<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>--job_config_file FILE</td>
<td>Job configuration file for Galaxy to target.</td>
</tr>
<tr>
<td>--tool_dependency_dir DIRECTORY</td>
<td>Tool dependency dir for Galaxy to target.</td>
</tr>
<tr>
<td>--port INTEGER</td>
<td>Port to serve Galaxy on (default is 9090).</td>
</tr>
<tr>
<td>--host TEXT</td>
<td>Host to bind Galaxy to. Default is 127.0.0.1 that is restricted to localhost connections for security reasons set to 0.0.0.0 to bind Galaxy to all ports including potentially publicly accessible ones.</td>
</tr>
<tr>
<td>--engine [galaxy</td>
<td>docker_galaxy</td>
</tr>
<tr>
<td>--non_strict_cwl</td>
<td>Disable strict validation of CWL.</td>
</tr>
<tr>
<td>--docker_galaxy_image TEXT</td>
<td>Docker image identifier for docker-galaxy-flavor used if engine type is specified as <code>docker-galaxy</code>. Defaults to quay.io/bgruening/galaxy.</td>
</tr>
<tr>
<td>--docker_extra_volume PATH</td>
<td>Extra path to mount if --engine docker.</td>
</tr>
<tr>
<td>--test_data DIRECTORY</td>
<td>test-data directory to for specified tool(s).</td>
</tr>
<tr>
<td>--tool_data_table PATH</td>
<td>tool_data_table_conf.xml file to for specified tool(s).</td>
</tr>
<tr>
<td>--dependency_resolvers_config_file FILE</td>
<td>Dependency resolver configuration for Galaxy to target.</td>
</tr>
<tr>
<td>--brew_dependency_resolution</td>
<td>Configure Galaxy to use plain brew dependency resolution.</td>
</tr>
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<td>--shed_dependency_resolution</td>
<td>Configure Galaxy to use brewed Tool Shed dependency resolution.</td>
</tr>
<tr>
<td>--no_dependency_resolution</td>
<td>Configure Galaxy with no dependency resolvers.</td>
</tr>
<tr>
<td>--conda_prefix DIRECTORY</td>
<td>Conda prefix to use for conda dependency commands.</td>
</tr>
<tr>
<td>--conda_exec FILE</td>
<td>Location of conda executable.</td>
</tr>
<tr>
<td>--conda_debug</td>
<td>Enable more verbose conda logging.</td>
</tr>
<tr>
<td>--conda_channels, --conda_ensure_channels TEXT</td>
<td>Ensure conda is configured with specified comma separated list of channels.</td>
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</tr>
<tr>
<td>--profile TEXT</td>
<td>Name of profile (created with the profile_create command) to use with this</td>
</tr>
</tbody>
</table>
command.
--postgres Use postgres database type.
--database_type [postgres|postgres_docker|sqlite|auto]
    Type of database to use for profile - 'auto', 'sqlite', 'postgres', and 'postgres_docker'
    are available options. Use postgres to use an existing postgres server you user can access
    without a password via the psql command. Use postgres_docker to have Planemo manage a
docker container running postgres. Data with postgres_docker is not yet persisted past when
you restart the docker container launched by Planemo so be careful with this option.
--postgres_psql_path TEXT Name or or path to postgres client binary (psql).
--postgres_database_user TEXT Postgres username for managed development
databases.
--postgres_database_host TEXT Postgres host name for managed development
databases.
--postgres_database_port TEXT Postgres port for managed development
databases.
--file_path DIRECTORY Location for files created by Galaxy (e.g. database/files).
--database_connection TEXT Database connection string to use for Galaxy.
--shed_tool_conf TEXT Location of shed tools conf file for Galaxy.
--shed_tool_path TEXT Location of shed tools directory for Galaxy.
--galaxy_single_user / --no_galaxy_single_user
    By default Planemo will configure Galaxy to run in single-user mode where there is just
    one user and this user is automatically logged it. Use --no_galaxy_single_user to prevent
    Galaxy from running this way.
--daemon Serve Galaxy process as a daemon.
--pid_file FILE Location of pid file is executed with --daemon.
--ignore_dependency_problems When installing shed repositories for workflows, ignore dependency issues. These likely indicate a problem but in some cases may not prevent a workflow from successfully executing.
--shed_install / --no_shed_install
    By default Planemo will attempt to install repositories needed for workflow testing. This
    may not be appropriate for production servers and so this can disabled by calling planemo
    with --no_shed_install.
--help Show this message and exit.

9.54 training_init command

This section is auto-generated from the help text for the planemo command training_init. This help message can be generated with planemo training_init --help.

Usage:
planemo training_init [OPTIONS] TOOL_PATH

Help
Build training template from workflow. Options:

--topic_name TEXT  Name (directory name) of the topic to create or in which a tutorial should be created or updates [required]
--topic_title TEXT  Title of the topic to create
--topic_summary TEXT  Summary of the topic
--topic_target [use|admin-dev|instructors]  Target audience for the topic
--tutorial_name TEXT  Name (directory name) of the tutorial to create or to modify
--tutorial_title TEXT  Title of the tutorial
--hands_on  Add hands-on for the new tutorial
--slides  Add slides for the new tutorial
--workflow PATH  Workflow of the tutorial (locally)
--galaxy_url TEXT  URL of a Galaxy instance with the workflow
--galaxy_api_key TEXT  API key on the Galaxy instance with the workflow
--workflow_id TEXT  ID of the workflow on the Galaxy instance
--zenodo_link TEXT  Zenodo URL with the input data
--datatypes PATH  YAML file with the correspondence between Zenodo extension and Galaxy datatypes
--galaxy_root DIRECTORY  Root of development galaxy directory to execute command with.
--galaxy_python_version [2|2.7|3|3.3|3.4|3.5|3.6|3.7]  Python version to start Galaxy under
--galaxy_database_seed PATH  Preseeded Galaxy sqlite database to target.
--extra_tools PATH  Extra tool sources to include in Galaxy's tool panel (file or directory). These will not be linted/tested/etc... but they will be available to workflows and for interactive use.
--install_galaxy  Download and configure a disposable copy of Galaxy from github.
--galaxy_branch TEXT  Branch of Galaxy to target (defaults to master) if a Galaxy root isn't specified.
--galaxy_source TEXT  Git source of Galaxy to target (defaults to the official galaxyproject github source if a Galaxy root isn't specified.
--skip_venv  Do not create or source a virtualenv environment for Galaxy, this should be used or instance to preserve an externally configured virtual environment or conda environment.
--no_cache_galaxy  Skip caching of Galaxy source and dependencies obtained with --install_galaxy. Not caching this results in faster downloads (no git) - so is better on throw away instances such with TravisCI.
--no_cleanup  Do not cleanup temp files created for and by Galaxy.
--galaxy_email TEXT  E-mail address to use when launching single-user Galaxy server.
--docker / --no_docker  Run Galaxy tools in Docker if enabled.
--docker_cmd TEXT  Command used to launch docker (defaults to (continues on next page)
<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>--docker_sudo / --no_docker_sudo</td>
<td>Flag to use sudo when running docker.</td>
</tr>
<tr>
<td>--docker_host TEXT</td>
<td>Docker host to target when executing docker commands (defaults to localhost).</td>
</tr>
<tr>
<td>--docker_sudo_cmd TEXT</td>
<td>Sudo command to use when --docker_sudo is enabled (defaults to sudo).</td>
</tr>
<tr>
<td>--mulled_containers, --biocontainers</td>
<td>Test tools against mulled containers (forces --docker).</td>
</tr>
<tr>
<td>--job_config_file FILE</td>
<td>Job configuration file for Galaxy to target.</td>
</tr>
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<td>--tool_dependency_dir DIRECTORY</td>
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<td>--host TEXT</td>
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</tr>
<tr>
<td>--non_strict_cwl</td>
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</tr>
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<td>--docker_galaxy_image TEXT</td>
<td>Docker image identifier for docker-galaxy-flavor used if engine type is specified as &quot;docker-galaxy&quot;. Defaults to quay.io/bgruening/galaxy.</td>
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<td>--conda_prefix DIRECTORY</td>
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<tr>
<td>--conda_exec FILE</td>
<td>Location of conda executable.</td>
</tr>
<tr>
<td>--conda_debug</td>
<td>Enable more verbose conda logging.</td>
</tr>
<tr>
<td>--conda_channels, --conda_ensure_channels TEXT</td>
<td>Ensure conda is configured with specified comma separated list of channels.</td>
</tr>
<tr>
<td>--conda_use_local</td>
<td>Use locally built packages while building Conda environments.</td>
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<tr>
<td>--conda_dependency_resolution</td>
<td>Configure Galaxy to use only conda for dependency resolution.</td>
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<td>--conda_copy_dependencies</td>
<td>Conda dependency resolution for Galaxy will copy dependencies instead of attempting to link them.</td>
</tr>
<tr>
<td>--conda_auto_install / --no_conda_auto_install</td>
<td>Conda dependency resolution for Galaxy will (continues on next page)</td>
</tr>
</tbody>
</table>
attempt to install requested but missing packages.

--conda_auto_init / --no_conda_auto_init
Conda dependency resolution for Galaxy will auto install conda itself using miniconda if not available on conda_prefix.

--profile TEXT
Name of profile (created with the profile_create command) to use with this command.

--postgres
Use postgres database type.

--database_type [postgres|postgres_docker|sqlite|auto]
Type of database to use for profile - 'auto', 'sqlite', 'postgres', and 'postgres_docker' are available options. Use postgres to use an existing postgres server you user can access without a password via the psql command. Use postgres_docker to have Planemo manage a docker container running postgres. Data with postgres_docker is not yet persisted past when you restart the docker container launched by Planemo so be careful with this option.

--postgres_psql_path TEXT
Name or path to postgres client binary (psql).

--postgres_database_user TEXT
Postgres username for managed development databases.

--postgres_database_host TEXT
Postgres host name for managed development databases.

--postgres_database_port TEXT
Postgres port for managed development databases.

--file_path DIRECTORY
Location for files created by Galaxy (e.g. database/files).

--database_connection TEXT
Database connection string to use for Galaxy.

--shed_tool_conf TEXT
Location of shed tools conf file for Galaxy.

--shed_tool_path TEXT
Location of shed tools directory for Galaxy.

--galaxy_single_user / --no_galaxy_single_user
By default Planemo will configure Galaxy to run in single-user mode where there is just one user and this user is automatically logged it. Use --no_galaxy_single_user to prevent Galaxy from running this way.

--daemon
Serve Galaxy process as a daemon.

--pid_file FILE
Location of pid file is executed with --daemon.

--ignore_dependency_problems
When installing shed repositories for workflows, ignore dependency issues. These likely indicate a problem but in some cases may not prevent a workflow from successfully executing.

--shed_install / --no_shed_install
By default Planemo will attempt to install repositories needed for workflow testing. This may not be appropriate for production servers and so this can disabled by calling planemo with --no_shed_install.

--help
Show this message and exit.
9.55 travis_init command

This section is auto-generated from the help text for the planemo command `travis_init`. This help message can be generated with `planemo travis_init --help`.

Usage:

```
planemo travis_init [OPTIONS] PROJECT
```

Help

Create files to use GitHub/TravisCI testing.

Setup files in a github tool repository to enable continuous integration testing.

```
% planemo travis_init.
% # setup Ubuntu 12.04 w/ dependencies in
% vim .travis/setup_custom_dependencies.bash
% git add .travis.yml .travis
% git commit -m "Add Travis CI testing infrastructure for tools."
% git push # and register repository @ http://travis-ci.org/
```

These tests were inspired by work original done and documented by Peter Cock here http://bit.ly/gxtravisci.

Options:

```
--help     Show this message and exit.
```

9.56 virtualenv command

This section is auto-generated from the help text for the planemo command `virtualenv`. This help message can be generated with `planemo virtualenv --help`.

Usage:

```
planemo virtualenv [OPTIONS] VIRTUALENV_PATH
```

Help

Create a virtualenv.

Use virtualenv as library to create a virtualenv for Galaxy if virtualenv is not available on the PATH.

Options:

```
-p, --python PYTHON_EXE
--help     Show this message and exit.
```

9.57 workflow_convert command

This section is auto-generated from the help text for the planemo command `workflow_convert`. This help message can be generated with `planemo workflow_convert --help`.

Usage:
planemo workflow_convert [OPTIONS] WORKFLOW_PATH

Help
Convert Format 2 workflow to a native Galaxy workflow.

Options:

- **-f, --force**
  Overwrite existing files if present.

- **-o, --output FILE**
  Root of development galaxy directory to execute command with.

- **--galaxy_root DIRECTORY**
  Root of development galaxy directory to execute command with.

- **--galaxy_python_version [2|2.7|3|3.3|3.4|3.5|3.6|3.7]**
  Python version to start Galaxy under

- **--galaxy_database_seed PATH**
  Preseeded Galaxy sqlite database to target.

- **--extra_tools PATH**
  Extra tool sources to include in Galaxy's tool panel (file or directory). These will not be linted/tested/etc... but they will be available to workflows and for interactive use.

- **--install_galaxy**
  Download and configure a disposable copy of Galaxy from github.

- **--galaxy_branch TEXT**
  Branch of Galaxy to target (defaults to master) if a Galaxy root isn't specified.

- **--galaxy_source TEXT**
  Git source of Galaxy to target (defaults to the official galaxyproject github source if a Galaxy root isn't specified).

- **--skip_venv**
  Do not create or source a virtualenv environment for Galaxy, this should be used or instance to preserve an externally configured virtual environment or conda environment.

- **--no_cache_galaxy**
  Skip caching of Galaxy source and dependencies obtained with --install_galaxy. Not caching this results in faster downloads (no git) - so is better on throw away instances such with TravisCI.

- **--no_cleanup**
  Do not cleanup temp files created for and by Galaxy.

- **--galaxy_email TEXT**
  E-mail address to use when launching single-user Galaxy server.

- **--docker / --no_docker**
  Run Galaxy tools in Docker if enabled.

- **--docker_cmd TEXT**
  Command used to launch docker (defaults to docker).

- **--docker_sudo / --no_docker_sudo**
  Flag to use sudo when running docker.

- **--docker_host TEXT**
  Docker host to target when executing docker commands (defaults to localhost).

- **--docker_sudo_cmd TEXT**
  sudo command to use when --docker_sudo is enabled (defaults to sudo).

- **--mulled_containers, --biocontainers**
  Test tools against mulled containers (forces --docker).

- **--job_config_file FILE**
  Job configuration file for Galaxy to target.

- **--tool_dependency_dir DIRECTORY**
  Tool dependency dir for Galaxy to target.

- **--port INTEGER**
  Port to serve Galaxy on (default is 9090).

- **--host TEXT**
  Host to bind Galaxy to. Default is 127.0.0.1 that is restricted to localhost connections.

(continues on next page)
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<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>--engine [galaxy</td>
<td>docker_galaxy</td>
</tr>
<tr>
<td>--non_strict_cwl</td>
<td>Disable strict validation of CWL.</td>
</tr>
<tr>
<td>--docker_galaxy_image TEXT</td>
<td>Docker image identifier for docker-galaxy-flavor used if engine type is specified as <code>docker-galaxy</code>. Defaults to quay.io/bgruening/galaxy.</td>
</tr>
<tr>
<td>--docker_extra_volume PATH</td>
<td>Extra path to mount if --engine docker.</td>
</tr>
<tr>
<td>--test_data DIRECTORY</td>
<td>test-data directory to for specified tool(s).</td>
</tr>
<tr>
<td>--tool_data_table PATH</td>
<td>tool_data_table_conf.xml file to for specified tool(s).</td>
</tr>
<tr>
<td>--dependency_resolvers_config_file FILE</td>
<td>Dependency resolver configuration for Galaxy to target.</td>
</tr>
<tr>
<td>--brew_dependency_resolution</td>
<td>Configure Galaxy to use plain brew dependency resolution.</td>
</tr>
<tr>
<td>--shed_dependency_resolution</td>
<td>Configure Galaxy to use brewed Tool Shed dependency resolution.</td>
</tr>
<tr>
<td>--no_dependency_resolution</td>
<td>Configure Galaxy with no dependency resolvers.</td>
</tr>
<tr>
<td>--conda_prefix DIRECTORY</td>
<td>Conda prefix to use for conda dependency commands.</td>
</tr>
<tr>
<td>--conda_exec FILE</td>
<td>Location of conda executable.</td>
</tr>
<tr>
<td>--conda_debug</td>
<td>Enable more verbose conda logging.</td>
</tr>
<tr>
<td>--conda_channels, --conda_use_local</td>
<td>Ensure conda is configured with specified comma separated list of channels.</td>
</tr>
<tr>
<td>--conda_dependency_resolution</td>
<td>Conda dependency resolution for Galaxy will attempt to install requested but missing packages.</td>
</tr>
<tr>
<td>--conda_auto_install / --no_conda_auto_install</td>
<td>Conda dependency resolution for Galaxy will attempt to auto install conda itself if not available on conda_prefix.</td>
</tr>
<tr>
<td>--conda_auto_init / --no_conda_auto_init</td>
<td>Conda dependency resolution for Galaxy will auto install conda itself using miniconda if not availabe on conda_prefix.</td>
</tr>
<tr>
<td>--profile TEXT</td>
<td>Name of profile (created with the profile_create command) to use with this command.</td>
</tr>
<tr>
<td>--postgres</td>
<td>Use postgres database type.</td>
</tr>
<tr>
<td>--database_type [postgres</td>
<td>postgres_docker</td>
</tr>
</tbody>
</table>
postgres_docker to have Planemo manage a docker container running postgres. Data with postgres_docker is not yet persisted past when you restart the docker container launched by Planemo so be careful with this option.

--postgres_psql_path TEXT Name or or path to postgres client binary (psql).

--postgres_database_user TEXT Postgres username for managed development databases.

--postgres_database_host TEXT Postgres host name for managed development databases.

--postgres_database_port TEXT Postgres port for managed development databases.

--file_path DIRECTORY Location for files created by Galaxy (e.g. database/files).

--database_connection TEXT Database connection string to use for Galaxy.

--shed_tool_conf TEXT Location of shed tools conf file for Galaxy.

--shed_tool_path TEXT Location of shed tools directory for Galaxy.

--galaxy_single_user / --no_galaxy_single_user
By default Planemo will configure Galaxy to run in single-user mode where there is just one user and this user is automatically logged it. Use --no_galaxy_single_user to prevent Galaxy from running this way.

--daemon Serve Galaxy process as a daemon.

--pid_file FILE Location of pid file is executed with --daemon.

--ignore_dependency_problems When installing shed repositories for workflows, ignore dependency issues. These likely indicate a problem but in some cases may not prevent a workflow from successfully executing.

--shed_install / --no_shed_install
By default Planemo will attempt to install repositories needed for workflow testing. This may not be appropriate for production servers and so this can disabled by calling planemo with --no_shed_install.

--help Show this message and exit.

9.58 workflow_edit command

This section is auto-generated from the help text for the planemo command workflow_edit. This help message can be generated with planemo workflow_edit --help.

Usage:

planemo workflow_edit [OPTIONS] WORKFLOW_PATH

Help

Open a synchronized Galaxy workflow editor.

Options:
<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>--galaxy_root DIRECTORY</td>
<td>Root of development galaxy directory to execute command with.</td>
</tr>
<tr>
<td>--galaxy_python_version</td>
<td>Python version to start Galaxy under [2</td>
</tr>
<tr>
<td>--galaxy_database_seed PATH</td>
<td>Preseeded Galaxy sqlite database to target.</td>
</tr>
<tr>
<td>--extra_tools PATH</td>
<td>Extra tool sources to include in Galaxy's tool panel (file or directory). These will not be linted/tested/etc... but they will be available to workflows and for interactive use.</td>
</tr>
<tr>
<td>--install_galaxy</td>
<td>Download and configure a disposable copy of Galaxy from github.</td>
</tr>
<tr>
<td>--galaxy_branch TEXT</td>
<td>Branch of Galaxy to target (defaults to master) if a Galaxy root isn't specified.</td>
</tr>
<tr>
<td>--galaxy_source TEXT</td>
<td>Git source of Galaxy to target (defaults to the official galaxyproject github source if a Galaxy root isn't specified.</td>
</tr>
<tr>
<td>--skip_venv</td>
<td>Do not create or source a virtualenv environment for Galaxy, this should be used or instance to preserve an externally configured virtual environment or conda environment.</td>
</tr>
<tr>
<td>--no_cache_galaxy</td>
<td>Skip caching of Galaxy source and dependencies obtained with --install_galaxy. Not caching this results in faster downloads (no git) - so is better on throw away instances such with TravisCI.</td>
</tr>
<tr>
<td>--no_cleanup</td>
<td>Do not cleanup temp files created for and by Galaxy.</td>
</tr>
<tr>
<td>--galaxy_email TEXT</td>
<td>E-mail address to use when launching single-user Galaxy server.</td>
</tr>
<tr>
<td>--docker / --no_docker</td>
<td>Run Galaxy tools in Docker if enabled.</td>
</tr>
<tr>
<td>--docker_cmd TEXT</td>
<td>Command used to launch docker (defaults to docker).</td>
</tr>
<tr>
<td>--docker_sudo / --no_docker_sudo</td>
<td>Flag to use sudo when running docker.</td>
</tr>
<tr>
<td>--docker_host TEXT</td>
<td>Docker host to target when executing docker commands (defaults to localhost).</td>
</tr>
<tr>
<td>--docker_sudo_cmd TEXT</td>
<td>sudo command to use when --docker_sudo is enabled (defaults to sudo).</td>
</tr>
<tr>
<td>--mulled_containers, --biocontainers</td>
<td>Test tools against mulled containers (forces --docker).</td>
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<td>--job_config_file FILE</td>
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<td>--tool_dependency_dir DIRECTORY</td>
<td>Tool dependency dir for Galaxy to target.</td>
</tr>
<tr>
<td>--port INTEGER</td>
<td>Port to serve Galaxy on (default is 9090).</td>
</tr>
<tr>
<td>--host TEXT</td>
<td>Host to bind Galaxy to. Default is 127.0.0.1 that is restricted to localhost connections for security reasons set to 0.0.0.0 to bind Galaxy to all ports including potentially publicly accessible ones.</td>
</tr>
<tr>
<td>--engine [galaxy</td>
<td>docker_galaxy</td>
</tr>
<tr>
<td>--non_strict_cwl</td>
<td>Disable strict validation of CWL.</td>
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</tbody>
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--docker_galaxy_image TEXT  Docker image identifier for docker-galaxy-flavor used if engine type is specified as `docker-galaxy`. Defaults to quay.io/bgruening/galaxy.
--docker_extra_volume PATH  Extra path to mount if --engine docker.
--test_data DIRECTORY  test-data directory to for specified tool(s).
--tool_data_table PATH  tool_data_table_conf.xml file to for specified tool(s).
--dependency_resolvers_config_file FILE  Dependency resolver configuration for Galaxy to target.
--brew_dependency_resolution  Configure Galaxy to use plain brew dependency resolution.
--shed_dependency_resolution  Configure Galaxy to use brewed Tool Shed dependency resolution.
--no_dependency_resolution  Configure Galaxy with no dependency resolvers.
--conda_prefix DIRECTORY  Conda prefix to use for conda dependency commands.
--conda_exec FILE  Location of conda executable.
--conda_debug  Enable more verbose conda logging.
--conda_channels, --conda_ensure_channels TEXT  Ensure conda is configured with specified comma separated list of channels.
--conda_use_local  Use locally built packages while building Conda environments.
--conda_dependency_resolution  Configure Galaxy to use only conda for dependency resolution.
--conda_copy_dependencies  Conda dependency resolution for Galaxy will copy dependencies instead of attempting to link them.
--conda_auto_install / --no_conda_auto_install  Conda dependency resolution for Galaxy will attempt to install requested but missing packages.
--conda_auto_init / --no_conda_auto_init  Conda dependency resolution for Galaxy will auto install conda itself using miniconda if not available on conda_prefix.
--profile TEXT  Name of profile (created with the profile_create command) to use with this command.
--postgres  Use postgres database type.
--database_type [postgres|postgres_docker|sqlite|auto]  Type of database to use for profile - 'auto', 'sqlite', 'postgres', and 'postgres_docker' are available options. Use postgres to use an existing postgres server you can access without a password via the psql command. Use postgres_docker to have Planemo manage a docker container running postgres. Data with postgres_docker is not yet persisted past when you restart the docker container launched by Planemo so be careful with this option.
--postgres_psql_path TEXT  Name or or path to postgres client binary (psql).
--postgres_database_user TEXT  Postgres username for managed development databases.
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(continued from previous page)

--postgres_database_host TEXT  Postgres host name for managed development databases.
--postgres_database_port TEXT  Postgres port for managed development databases.
--file_path DIRECTORY         Location for files created by Galaxy (e.g. database/files).
--database_connection TEXT    Database connection string to use for Galaxy.
--shed_tool_conf TEXT        Location of shed tools conf file for Galaxy.
--shed_tool_path TEXT        Location of shed tools directory for Galaxy.
--galaxy_single_user / --no_galaxy_single_user
                           By default Planemo will configure Galaxy to run in single-user mode where there is just one user and this user is automatically logged it. Use --no_galaxy_single_user to prevent Galaxy from running this way.
--daemon                   Serve Galaxy process as a daemon.
--pid_file FILE            Location of pid file is executed with --daemon.
--ignore_dependency_problems When installing shed repositories for workflows, ignore dependency issues. These likely indicate a problem but in some cases may not prevent a workflow from successfully executing.
--shed_install / --no_shed_install
                           By default Planemo will attempt to install repositories needed for workflow testing. This may not be appropriate for production servers and so this can disabled by calling planemo with --no_shed_install.
--help                     Show this message and exit.

9.58. workflow_edit command
Best Practices for Creating Galaxy Tools

This page is written by experienced tool developers and contains information about what practices in Galaxy tool development tend to be the most successful ones.

10.1 Why you might read this

If you need to maintain existing tools or develop new tools for Galaxy, this programmer oriented guide, contributed by the community, will detail current collected best practice guidelines for building and maintaining automatically installing reproducible Galaxy tools.

10.2 Definitions

Follows a short summary of the key parts when it comes to Galaxy Tools.

- **ToolShed**, The Galaxy AppStore - companion Galaxy web server for tools. E.g. https://toolshed.g2.bx.psu.edu or localhost:9009 for Mercurial based source code management and automated installation of all components described below through any Galaxy admin interface.

- **Galaxy Tool** - An application specific, XML defined interface and associated documentation exposing any command line application as a form-driven Galaxy tool - e.g. BWA or bamtools. Ideally, as a shareable tool shed repository, supporting automated Galaxy installation with revision/version specific control of dependency binaries for reproducible analyses.

- **Tool Dependency Package** - Tool Shed tools in the Tool Dependency Packages category whose names start with package_ such as package_samtools_1_0_0, automate the installation of a specific version of some command line application software that other tools depend on. Each dependency package may be shared by many tools and are only available to users through tool forms that populate command lines and execute them.

- **Datatypes** - Galaxy has a flexible and extensible internal representation for specialised data formats such as fasta sequences, fastq short read data or tabular text persisted in Galaxy histories. Tools and packages can extend Galaxy by installing new datatypes when needed.
• DataManagers - Large scale scientific analyses often involve local copies of canonical reference data such as reference genomes and application specific index files for annotation and mapping in genomics. In most cases these are rapidly evolving and a constant drain on highly skilled resources to keep up to date manually. Data Managers can be built and shared to automate reference data maintenance by the local Galaxy administrators. Data Manager repositories should start with data_manager_.

10.3 Tools

10.3.1 Tools

Before you start writing a new tool please search the Main Tool Shed (MTS) and the Test Tool Shed (TTS) because it’s possible that someone has already created a wrapper for the same third party executable you are looking for. Consider announcing your tool project on galaxy-dev to see if anyone has already created a wrapper.

Tool versions

Tool versions are mandatory to enable reproducibility. Version is an attribute of the XML tool element, e.g.

```xml
<tool id="rgTF" name="Tool Factory" version="1.11">
```

and should be incremented with each change of the wrapper that is released to the Tool Shed (except for cosmetic modifications).

Tool ids

Should be meaningful and unique also in a larger context. If your tool is called grep try to prefix that name with something meaningful. Objective is to make it easier for Galaxy admins to identify a tool based on the short ID. Otherwise they would need to use the long toolshed/xx/id.

Some simple rules for generating tool IDs:

- Tool IDs should contain only [a-z0-9_-].
- Multiple words should be separated by underscore or dashes
- Suite tools should prefix their ids with the suite name. E.g. bedtools_*

Tool Names

Names are important! Names are how users and admins find your tools. Names should strive to be unique within a suite of tools, and may wish to include the suite name if it is a well known suite. Some instructional examples:

- Cufflinks, Cuffdiff, Cuffmerge are in a suite together.
- The vsearch suite contains tools with names like “VSearch Alignment”, “VSearch Clustering”, etc.

In the cufflinks example, everyone knows the functionality of the cufflinks command, and can easily guess as the use of a tool named “cuffdiff” in their tool panel.

With VSearch however, a tool named “Alignment” would not be useful, as users would have a hard time finding it and gathering context about its functionality. With the VSearch prefix, once a user learns what one VSearch tool does, they can quickly apply that to the other available VSearch tools.
**Tool Descriptions**

Tool names are not your only tool for making your tool discoverable to end users, and conveying information regarding the functionality of said tool. Tool descriptions are displayed directly after the tool name and generally conform to a “sentence” like structure.

- **bowtie2** is a short read aligner
- **Cuffmerge** merges together several Cufflinks assemblies
- **NCBI BLAST+ database info** shows BLAST database information from blastdbcmd

In the above examples the tool name is rendered in fixed width text, and the rest is the tool description.

**Parameter help**

The help section should include the long argument name (but this should not be in the tool label). E.g. `help="(--max)"`. This is useful to give the user the chance to go to the original documentation and map the Galaxy UI element to the actual parameter. It also makes debugging easier if the user is talking to non-Galaxy developers.

**Tests**

All Galaxy Tools should include functional tests. In their simplest form, you provide sample input files and expected output files for given parameter values. Where the output file is not entirely reproducible you can make assertions about the output file contents.

Testing error conditions is also important. Recent development now allows tests say if the test should fail, and to make assertions about the tool’s stdout and stderr text (e.g. check expected summary text or warning messages appear).

**Booleans**

truevalue and falsevalue should have the actual parameter included. This makes it really easy to reference the param name in the Cheetah command section.

```xml
<param name="strict" truevalue="--enable-strict" falsevalue=""/>
$strict
```

Boolean should not be used as conditionals. For conditionals please use a select type as described in Dynamic Options below.

**Dynamic Options**

Certain options such as “Advanced Options” should be a select box and not a boolean. A checkbox is not expected to change the content of the mask from a user point of view.

**Command tag**

The command tag is one of the most important parts of the tool, next to the user-facing options. It’s important that it be highly legible.
Command Formatting

The command tag should be started and finished by a CDATA tag, allowing direct use of characters like the ampersand (&) without needing XML escaping (&amp;).

```xml
<![CDATA[ your lines of Cheetah here ]]> 
```

Wikipedia has more on CDATA

If you need to execute more than one shell command, concatenate them with a double ampersand (&&), so that an error in a command will abort the execution of the following ones.

Exit Code Detection

Unless the tool has special requirements, you should take advantage of the exit code detection provided by Galaxy, in lieu of using the `<stdio/>` tags. This can be done by adding a `detect_errors` tag to your `<command/>` block like so:

```xml
<command detect_errors="aggressive">
  ...
</command>
```

This will automatically fail the tool if the exit code is non-zero, or if the phrases `error:` or `exception:` appear in STDERR.

Help tag

The help tag should be started and finished by a CDATA tag.

```xml
<![CDATA[ your lines of restructuredText here ]]> 
```

http://en.wikipedia.org/wiki/CDATA

Inside the help tag you should describe the functionality of your tool. The help tag is to the `help=""` attribute as a man page is to the `--help` flag. The help tag should cover the tools functionality, use cases, and even known issues in detail. The help tag is a good place to provide examples of how to run the tool and discuss specific subcases that your users might be interested in.

Including Images

If you have produced images detailing how your tool works (e.g. bedtools), it might be nice for those images to be included in the Galaxy tool documentation!

Images should be placed in a subdirectory, `.static/images/`, and referenced in your tool help as `.. image:: my-picture.png`. This can be seen in the IUC’s wrappers, such as the one for the bedtools slop command.

Tool Dependency Package

If you are using perl/ruby/python/R packages, use the corresponding `*_environment` tags to depend on a specific version of Perl/Ruby...
Generating Indices

Occasionally data needs to be indexed (e.g. bam, fasta) files. When data is indexed, those indices should be generated in the current working directory rather than alongside the input dataset. This is part of the tool contract, you can read from your inputs, but only write to your outputs and CWD.

It’s convenient to do something like:

```
ln -sfn "$input_fasta" tmp.fa;
```

before data processing in order to be able to easily generate the indices without attempting to write to a (possibly) read-only data source.

Datatypes

TODO

DataManagers

TODO

Coding Style

- 4 spaces indent
- Order of XML elements:
  - description
  - macros
  - requirements
  - [code]
  - stdio
  - version_command
  - command
  - environment_variables
  - configfiles
  - inputs
  - outputs
  - tests
  - help
  - citations
- Cheetah code should be mainly PEP8 conform
- Large XML tags should be broken into several lines
  - label and help can be on a new line
- param names should be readable and understandable, e.g. using the long option name of the wrapped tool
• All Cheetah variables for text params, input and output files must be quoted with “${var_name}”

• Order of parameter attributes
  – name
  – type
  – value | truevalue | falsevalue
  – [checked]
  – label
  – help

10.4 Packages

10.4.1 Packages

Before you start writing a new tool please search the Main Tool Shed (MTS) and the Test Tool Shed (TTS) because it’s possible that someone has already created an installer for the same third party executable you are looking for. Consider announcing your packaging project on galaxy-dev to see if anyone has already created a wrapper.

Packaging software is something of a more advanced topic, and due to the complexities of the syntax, somewhat harder to validate.

Downloads

Packages generally must download one or more files from the internet in order to function. We require checksums on all of our package downloads from multiple reasons:

• Download integrity.

• Insecure transport methods, like http:// and ftp://

• The packages come from the untrusted internet, we don’t know if anyone has modified the software in transit. This software is installed directly to large university clusters. We must make an effort to ensure that what is being installed is what the user actually asked for, and not a version of bowtie that has been modified unexpectedly.

The checksums take the form of sha256sums attached as attributes to <action type="download_by_url">
and other elements, e.g.

```
<action type="download_by_url" sha256sum="ab060325...">
  http://mbio-serv2.mbioekol.lu.se/ARAGORN/Downloads/aragorn1.2.36.tgz
</action>
```

This XML snippet will cause the file aragorn1.2.36.tgz to be downloaded, and to be validated. If the sha256sums match, then the package installs. Otherwise, it fails immediately.

10.5 Repository Layout

10.5.1 Github Repositories

Most tool developers are on GitHub, and have chosen to lay out their repositories in a structure similar to the following:
The highest level directory contains only a few folders for the major types of Galaxy repositories: tools, packages, data managers, and sometimes visualizations and datatypes.

**ToolShed Repositories**

A Github repository many correspond to any number of published ToolShed repositories. Every unrestricted tool shed repository should contain a README file - named either README or README.txt (if plain text) or README.rst (if reStructuredText). A reStructuredText README.rst is generally preferred. For a good example of such a file - please see Peter Cock’s NCBI Blast+ Suite’s README.rst.

The Tool Shed recognizes many more types of README files than this - but these are not encouraged and may be deprecated in the future. Markdown is not supported by the Tool Shed at this time and so README.md are not recognized at all.

**Package Repositories**

These may only contain a tool_dependencies.xml file

**Suites**

The Toolshed offers the concept of a suite which is simply a meta-package listing several other packages. For example the suite_hmmer_3 provides a package that depends on all of the individual hmmer_* packages, defined by a repository_dependencies.xml file:

```
<repositories description="HMMER v3 HMM based sequence alignment and database search tools">
  <repository changeset_revision="ddda6eae7b23" name="hmmer_hmemmit" owner="iuc">
    <toolshed>https://testtoolshed.g2.bx.psu.edu</toolshed>
  </repository>
  <repository changeset_revision="5ec773098cb9" name="hmmer_hmmconvert" owner="iuc">
    <toolshed>https://testtoolshed.g2.bx.psu.edu</toolshed>
  </repository>
  ...
</repositories>
```

Manually curated suites are most commonly used to package together related pieces of software by different groups, when that functionality all serves a common purpose.

Suites should NOT be used for a single set of highly related tools from the same group, like the hmmer example above, or bedtools. Instead, a suite can be automatically created for those sets of tools by Planemo.
Tools

Tool often contain:

- Tool XML files
- `macros.xml` file for use in keeping tools DRY
- `test-data/` directory, because all tools need test data
- `tool-data/` directory, for things like `*.loc` files
- `tool_dependencies.xml` file for specifying associated packages

10.6 `.shed.yml`

10.6.1 Toolshed Yaml File

The `.shed.yml` file provides a way for developers using the awesome `planemo` to easily push their tools to toolshed repositories.

```yaml
name: package_aragorn_1_2_36
owner: iuc
description: Contains a tool dependency definition that downloads and extract version 1.2.36 of Aragorn.
homepage_url: http://mbio-serv2.mbioekol.lu.se/ARAGORN/
long_description: |
  ARAGORN, tRNA (and tmRNA) detection.
remote_repository_url: https://github.com/galaxyproject/tools-iuc/tree/master/packages/package_aragorn_1_2_36
type: tool_dependency_definition
categories:
- Tool Dependency Packages
```

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>name</td>
<td>This is the package or tool’s name. It is usually the name of the</td>
</tr>
<tr>
<td></td>
<td>folder that contains the <code>.shed.yml</code> file. This should be package_</td>
</tr>
<tr>
<td></td>
<td><em>Name</em> <em>Version</em> for packages, and $name for tools</td>
</tr>
<tr>
<td>owner</td>
<td>Your toolshed username</td>
</tr>
<tr>
<td>description</td>
<td>A short description of the package or tool set</td>
</tr>
<tr>
<td>homepage_url</td>
<td>This value is currently under debate, but we recommend reading over</td>
</tr>
<tr>
<td></td>
<td>#1.</td>
</tr>
<tr>
<td>long_description</td>
<td>A longer README type description of the package, as tool dependencies</td>
</tr>
<tr>
<td></td>
<td>do not currently support README files.</td>
</tr>
<tr>
<td>remote_repository_url</td>
<td>This should be the path to the folder in your github</td>
</tr>
<tr>
<td></td>
<td>repository, on the branch you create releases from (usually master).</td>
</tr>
<tr>
<td></td>
<td>This will eventually be used with the toolshed for update hooks.</td>
</tr>
<tr>
<td>type</td>
<td>The repository type, one of <code>unrestricted</code>, <code>tool_dependency_definition</code>, or <code>repository_suite_definition</code></td>
</tr>
<tr>
<td>categories</td>
<td>Toolshed categories that are relevant to the tool or package.</td>
</tr>
</tbody>
</table>

A note on the `name` attribute: as periods are disallowed in repository names, we recommend replacing periods in the version number with underscores.
### Advanced Parameters

Currently there exists a tension between what is best for developers (storing all tools in a single repository - e.g. `ncbi_blast_plus` or `bedtools`) and what is best for Galaxy users (storing a single repository per tool and collecting them together with a suite - e.g. `samtools` or `gatk`).

Thus a number of advanced parameters were added for helping developers manage suites of tools.

```yaml
auto_tool_repositories:
  name_template: "{{ tool_id }}"
  description_template: "Wrapper for samtools application {{ tool_name }}."
suite:
  name: "suite_samtools_1_2"
  description: "A suite of Galaxy tools designed to work with version 1.2 of the SAMTools package."
  long_description:
    > SAM (Sequence Alignment/Map) format is a generic format for storing large nucleotide sequence alignments. This repository suite associates selected repositories containing Galaxy utilities that require version 1.2 of the SAMTools package. These associated Galaxy utilities consist of a Galaxy Data Manager contained in the repository named data_manager_sam_fasta_index_builder and Galaxy tools contained in several separate repositories.
```

This example assumes the `.shed.yml` file is placed in a “flat” directory with each samtools tool wrapper. Planemo will create and update repositories for each individual tool given the specified templates in `auto_tool_repositories`. The suite key here will auto-generate a suite repository for all of these tools and will automatically created the corresponding repository_dependencies.xml to populate it with (this is generated during shed_upload and never needs to exist in your repository).

Again this example is admittedly idealized, but if `auto_tool_repositories` is not specified, a repositories list can be specified instead. There are some examples of this in the planemo’s test data:

- This `.shed.yml` is a simple example of specifying custom repositories for individual tools.
- This demonstrates complex inclusions files from sub-directories and renaming.

The test data also includes some more advanced usages of the suite key as well - specifically using it without `auto_tool_repositories` as a generic replacement for `repository_dependencies.xml` and adding additional dependent repositories in addition to the ones defined by the `.shed.yml` file.

### Shed Upload Includes/Excludes

Sometimes it is of interest to have shared data in a single directory, and then to include that when needed. A good example of this are the `blast` wrappers which take advantage of the feature in order to share test data amongst a number of directories which all need the data.
This snippet informs planemo that it should include specific datasets from `../../test-data` and that as part of the include process it should strip the first two path components.

The `exclude` functionality works similarly, just specify a list of paths you wish to exclude:

```yaml
exclude:
  - test-data/my-gigantic-test-dataset.fastq
```

layout: true class: inverse, middle

class: title
11.1 John Chilton

This document describes changes to Galaxy’s tooling framework over recent releases.

11.1.1 16.04

Full Galaxy changelog.

Tool Profile Version (PR #1688)

Tools may (and should) now declare a `profile` version (e.g. `<tool profile="16.04" ...>`).

This allows Galaxy to fire a warning if a tool uses features too new for the current version and allows us to migrate away from some undesirable default behaviors that were required for backward compatibility.

`set -e` by default (d020522)

From the IUC best practices documentation:

“If you need to execute more than one shell command, concatenate them with a double ampersand (&&), so that an error in a command will abort the execution of the following ones."

The job script generated with profile 16.04+tools will include a `#set -e` statement causing this behavior by default.

Older-style tools can enable this behavior by setting `strict="true"` on the tool `command` XML block.
Using Exit Codes for Error Detection (b92074e)

Previously the default behavior was for Galaxy to ignore exit codes and declare a tool in error if issued any output on standard error. This was a regrettable default behavior and so all tools were encouraged to declare special XML blocks to force the use of exit codes.

For any tool that declares a profile version of 16.04 or greater, the default is now just to use exit codes for error detection.

Unrobust Features Removed (b92074e)

A few tool features have been removed from tools that declare a version of 16.04 or newer.

- The `interpreter` attribute on `command` blocks has been eliminated. Please use `$_tool_directory_` from within the tool instead.
- `format="input"` on output datasets has been eliminated, please use `format_source=` to specify an exact input to derive datatype from.
- Disables extra output file discovery by default, tools must explicitly describe the outputs to collect with `discover_dataset` tags.
- Tools require a `version` attribute - previously an implicit default to 1.0.0 would be used.
- `$param_file` has been eliminated.

Clean Working Directories

Previously, Galaxy would fill tool working directories with files related to metadata and job metric collection. Tools will no longer be executed in the same directory as these files.

This applies to all tools not just profile 16.04+ tools.

11.1.2 16.01

Full Galaxy changelog.

Conda Dependency Resolution (PR #1345)

```
<tool>
  ...
  <requirements>
    <requirement type="package" version="0.11.4">FastQC</requirement>
  </requirements>
  ...
</tool>
```

- Dependency resolvers tell Galaxy how to translate requirements into jobs.
• The Conda dependency resolver forces Galaxy to create a conda environment for the job with `FastQC` at version 0.11.4 installed.

• Only dependency resolver that can be installed at runtime - great for Docker images, heterogeneous clusters, and testing tools.

• Links Conda and BioConda

---

**ToolBox Enhancements - Labels (PR #1012)**

![ToolBox Labels]

**ToolBox Enhancements - Monitoring (PR #1398)**

• The Galaxy toolbox can be reloaded from the Admin interface.

• Tool conf files (e.g. `tool_conf.xml`) can be monitored and automatically reloaded by Galaxy.

• Tool conf files can now be specified as YAML (or JSON).
Process Inputs as JSON (PR #1405)

```python
<command>python "$__tool_directory/script.py" "$json_inputs"</command>
<configfiles>
  <inputs name="json_inputs" />
</configfiles>
```

This will produce a file referenced as $json_inputs that contains a nested JSON structure corresponding to the tools inputs. Of limited utility for simple command-line tools - but complex tools with many repeats, conditional, and nesting could potentially benefit from this.

For instance, the JBrowse tool generates a complex JSON data structure using a configfile inside the XML. This is a much more portable way to deal with that.

---

**Collections**

- data_collection tool parameters (params) can now specify multiple collection_types for consumption (PR #1308).
  - This mirrors the format attribute which allows a comma-separated list of potential format types.
- Multiple collections can now be supplied to a multiple="true" data parameter (PR #805).
- Output collections can specify a type_source attribute (again mirroring format_source) (PR #1153).

---

**11.1.3 15.10**

Full Galaxy changelog.

---

**Collections**

- Tools may now produce explicit nested outputs PR #538. This enhances the discover_dataset XML tag to allow this.
- Allow certain output actions on collections. PR #544.
- Allow discover_dataset tags to use format instead of ext when referring to datatype extensions/formats.
- Allow min/max attributes on multiple data input parameters PR #765.

---

**Whitelist Tools that Generate HTML (PR #510)**

Galaxy now contains a plain text file that contains a list of tools whose output can be trusted when rendering HTML.
11.1.4 15.07

Full Galaxy changelog.

Parameterized XML Macros (PR #362)

Macros now allow defining tokens to be consumed as XML attributes. For instance, the following definition

```xml
<tool>
  <expand macro="inputs" foo="hello" />
  <expand macro="inputs" foo="world" />
  <expand macro="inputs" />
  <macros>
    <xml name="inputs" token_foo="the_default">
      <inputs>@FOO@</inputs>
    </xml>
  </macros>
</tool>
```

would expand out as

```xml
<tool>
  <inputs>hello</inputs>
  <inputs>world</inputs>
  <inputs>the_default</inputs>
</tool>
```

Tool Form

The workflow editor was updated to the use Galaxy’s newer frontend tool form.
Environment Variables (PR #395)

Tools may now use inputs to define environment variables that will be set during tool execution. The new environment_variables XML block is used to define this.

```xml
<command>
  echo "\$INTVAR" > $out_file1;
  echo "\$FORTEST" >> $out_file1;
</command>
<environment_variables>
  <environment_variable name="INTVAR">$inttest</environment_variable>
  <environment_variable name="FORTEST">#for i in ['m', 'o', 'o']#$i#end for#</environment_variable>
</environment_variables>
```
Test tool demonstrating the use of the environment_variables tag.

Collections

- Explicit output collections can now be used in workflows. (PR #311)
- The filter tag has been implemented for output dataset collections (PR #455. See the example tool output_collection_filter.xml.)
Planemo Project Code of Conduct

This code of conduct outlines our expectations for participants within the Planemo community, as well as steps to reporting unacceptable behavior. We are committed to providing a welcoming and inspiring community for all and expect our code of conduct to be honored. Anyone who violates this code of conduct may be banned from the community.

Our open source community strives to:

• **Be friendly and patient.**

• **Be welcoming:** We strive to be a community that welcomes and supports people of all backgrounds and identities. This includes, but is not limited to members of any race, ethnicity, culture, national origin, colour, immigration status, social and economic class, educational level, sex, sexual orientation, gender identity and expression, age, size, family status, political belief, religion, and mental and physical ability.

• **Be considerate:** Your work will be used by other people, and you in turn will depend on the work of others. Any decision you take will affect users and colleagues, and you should take those consequences into account when making decisions. Remember that we’re a world-wide community, so you might not be communicating in someone else’s primary language.

• **Be respectful:** Not all of us will agree all the time, but disagreement is no excuse for poor behavior and poor manners. We might all experience some frustration now and then, but we cannot allow that frustration to turn into a personal attack. It’s important to remember that a community where people feel uncomfortable or threatened is not a productive one.

• **Be careful in the words that we choose:** We are a community of professionals, and we conduct ourselves professionally. Be kind to others. Do not insult or put down other participants. Harassment and other exclusionary behavior aren’t acceptable. This includes, but is not limited to: Violent threats or language directed against another person, Discriminatory jokes and language, Posting sexually explicit or violent material, Posting (or threatening to post) other people’s personally identifying information (“doxing”), Personal insults, especially those using racist or sexist terms, Unwelcome sexual attention, Advocating for, or encouraging, any of the above behavior, Repeated harassment of others. In general, if someone asks you to stop, then stop.

• **Try to understand why we disagree:** Disagreements, both social and technical, happen all the time. It is important that we resolve disagreements and differing views constructively. Remember that we’re different. Diversity contributes to the strength of our community, which is composed of people from a wide range of backgrounds. Different people have different perspectives on issues. Being unable to understand why someone...
holds a viewpoint doesn’t mean that they’re wrong. Don’t forget that it is human to err and blaming each other doesn’t get us anywhere. Instead, focus on helping to resolve issues and learning from mistakes.

### Diversity Statement
We encourage everyone to participate and are committed to building a community for all. Although we will fail at times, we seek to treat everyone both as fairly and equally as possible. Whenever a participant has made a mistake, we expect them to take responsibility for it. If someone has been harmed or offended, it is our responsibility to listen carefully and respectfully, and do our best to right the wrong.

Although this list cannot be exhaustive, we explicitly honor diversity in age, gender, gender identity or expression, culture, ethnicity, language, national origin, political beliefs, profession, race, religion, sexual orientation, socioeconomic status, and technical ability. We will not tolerate discrimination based on any of the protected characteristics above, including participants with disabilities.

### Reporting Issues
If you experience or witness unacceptable behavior, or have any other concerns, please report it by contacting Dave Clements (clementsgalaxy@gmail.com). To report an issue involving Dave Clements please email James Taylor (james@taylorlab.org). All reports will be handled with discretion. In your report please include:

- Your contact information.
- Names (real, nicknames, or pseudonyms) of any individuals involved. If there are additional witnesses, please include them as well. Your account of what occurred, and if you believe the incident is ongoing. If there is a publicly available record (e.g. a mailing list archive or a public IRC logger), please include a link.
- Any additional information that may be helpful.

After filing a report, a representative will contact you personally, review the incident, follow up with any additional questions, and make a decision as to how to respond. If the person who is harassing you is part of the response team, they will recuse themselves from handling your incident. If the complaint originates from a member of the response team, it will be handled by a different member of the response team. We will respect confidentiality requests for the purpose of protecting victims of abuse.

### Attribution & Acknowledgements
This code of conduct is based on the Open Code of Conduct from the TODOGroup.
Contributing

Please note that this project is released with a Contributor Code of Conduct. By participating in this project you agree to abide by its terms.

Contributions are welcome, and they are greatly appreciated! Every little bit helps, and credit will always be given.
You can contribute in many ways:

13.1 Types of Contributions

13.1.1 Report Bugs

If you are reporting a bug, please include:

• Your operating system name and version, versions of other relevant software such as Galaxy or Docker.
• Links to relevant tools.
• Any details about your local setup that might be helpful in troubleshooting.
• Detailed steps to reproduce the bug.

13.1.2 Fix Bugs

Look through the GitHub issues for bugs. Anything tagged with “bug” is open to whoever wants to implement it.

13.1.3 Implement Features

Look through the GitHub issues for features. Anything tagged with “enhancement” is open to whoever wants to implement it.
13.1.4 Write Documentation

Planemo could always use more documentation, whether as part of the official Planemo docs, in docstrings, or even on the web in blog posts, articles, and such.

13.1.5 Submit Feedback

The best way to send feedback is to file an issue at https://github.com/galaxyproject/planemo/issues.

If you are proposing a feature:

- Explain in detail how it would work.
- Keep the scope as narrow as possible, to make it easier to implement.
- This will hopefully become a community-driven project and contributions are welcome :)

13.2 Get Started!

Ready to contribute? Here’s how to set up planemo for local development.

1. Fork the planemo repo on GitHub.

2. Clone your fork locally:

   $ git clone git@github.com:your_name_here/planemo.git

3. Install your local copy into a virtualenv. Assuming you have virtualenvwrapper installed, this is how you set up your fork for local development:

   $ make setup-venv

4. Create a branch for local development:

   $ git checkout -b name-of-your-bugfix-or-feature

   Now you can make your changes locally.

5. When you’re done making changes, check that your changes pass flake8 and the tests

   $ make lint
   $ make test

   If the modification doesn’t affect code that configures and runs Galaxy - skipping a couple tests that will cause Galaxy and its dependencies to be downloaded results in a significant speed up. This subset of tests can be run with make quick-test.

6. Commit your changes and push your branch to GitHub:

   $ git add .
   $ git commit -m "Your detailed description of your changes."
   $ git push origin name-of-your-bugfix-or-feature

7. Submit a pull request through the GitHub website.
13.3 Pull Request Guidelines

Before you submit a pull request, check that it meets these guidelines:

1. If the pull request adds functionality, the docs should be updated. Put your new functionality into a function with a docstring.

2. The pull request should work for Python 2.7 and 3.4. Check [https://travis-ci.org/galaxyproject/planemo/pull_requests](https://travis-ci.org/galaxyproject/planemo/pull_requests) and make sure that the tests pass for all supported Python versions.

13.4 Tips

To run a subset of tests:

```
% make tox ENV=py27 ARGS='--tests tests/test_shed_upload.py'
```

This will use Tox to run the specified tests using Python 2.7. `ENV` here can be used to specify different Python version (e.g. `py27` and `py34`). Python 3.4 is a work in progress.

Even more granularity is also possible by specifying specific test methods:

```
make tox ENV=py27 ARGS='--tests tests/test_shed_upload.py:ShedUploadTestCase.test_tar_from_git'
```

tox can be used to run tests directly also (use `.venv/bin/activate` to ensure it is on your PATH).

```
tox -e py27 -- --tests tests/test_shed_upload.py
```

Tox itself is configured to wrap nose. One can skip Tox and run nosetests directly.

```
nosetests tests/test_shed_upload.py
```

13.4.1 Tox

Tox is a tool to automate testing across different Python versions. The tox executable can be supplied with a `--e` argument to specify a testing environment. Planemo defines the following environments:

- `py27-lint` Lint the planemo code using Python 2.7.
- `py34-lint` Lint the planemo code using Python 3.4 (also ensures valid Python 3 syntax).
- `py27-lint-readme` Lint the README reStructuredText.
- `py27` Run planemo tests in Python 2.7.
- `py34` Run planemo tests in Python 3.4 (not currently working).

13.4.2 Pre-commit Hooks

Planemo pull requests are automatically linted and tested using TravisCI. A git pre-commit hook can be setup to lint and/or test Planemo before committing to catch problems that would be detected by TravisCI as early as possible.

The following command will install a pre-commit hook that lints the Planemo code:
To also run the faster planemo tests, the following command can be used to setup a more rigorous pre-commit hook:

```
make setup-git-hook-lint-and-test
```
CHAPTER 14

Project Governance

This document informally outlines the organizational structure governing the Planemo code base hosted at https://github.com/galaxyproject/planemo. This governance extends to code-related activities of this repository such as releases and packaging and related Planemo projects such planemo-machine. This governance does not include any other Galaxy-related projects belonging to the galaxyproject organization on GitHub.

14.1 Benevolent Dictator for Now (BDFN)

John Chilton (@jmchilton) is the benevolent dictator for now (BDFN) and is solely responsible for setting project policy. The BDFN is responsible for maintaining the trust of the developer community and so should be consistent and transparent in decision making processes and request comment and build consensus whenever possible.

The BDFN position only exists because the developers of the project believe it is currently too small to support full and open governance at this time. In order to keep things evolving quickly, it is better to keep procedures and process to a minimum and centralize important decisions with a trusted developer. The BDFN is explicitly meant to be replaced with a more formal and democratic process if the project grows to a sufficient size or importance.

The committers group is the group of trusted developers and advocates who manage the Planemo code base. They assume many roles required to achieve the project’s goals, especially those that require a high level of trust.

The BDFN will add committers as he or she see fits, usually after a few successful pull requests. Committers may commit directly or merge pull requests at their discretion, but everyone (including the BDFN) should open pull requests for larger changes.

In order to encourage a shared sense of ownership and openness, any committer may decide at any time to request a open governance model for the project be established and the BDFN must replace this informal policy with a more formal one and work with the project committers to establish a consensus on these procedures.

14.2 Committers

- Dannon Baker (@dannon)
• Bérénice Batut (@bebatut)
• Martin Cech (@martenson)
• John Chilton (@jmchilton)
• Peter Cock (@peterjc)
• Björn Grüning (@bgruening)
• Helena Rasche (@erasche)
• Nicola Soranzo (@nsoranzo)
• James Taylor (@jxtx)
• Marius van den Beek (@mvdbeek)
This page describes the process of releasing new versions of Planemo.

This release checklist is based on the Pocoo Release Management Workflow.

This assumes ~/.pypirc file exists with the following fields (variations) are fine.

```
[distutils]
index-servers =
  pypi
  test

[pypi]
username:<username>
password:<password>

[test]
repository:https://testpypi.python.org/pypi
username:<username>
password:<password>
```

- Review `git status` for missing files.
- Verify the latest Travis CI builds pass.
- `make open-docs` and review changelog.
- Ensure the target release is set correctly in `planemo/__init__.py` (version will be a devN variant of target release).
- `make clean` & `make lint` & `make test`
- `make release`

This process will push packages to test PyPI, allow review, publish to production PyPI, tag the git repository, push the tag upstream, and modify the Homebrew recipe. If changes are needed, such as manual changes to the homebrew recipe, this can be broken down into steps such as:

- `make release-local`
- make push-release
- make release-brew
16.1 0.61.0.dev0

16.2 0.60.0 (2019-05-31)

- Return validation error if doi is empty Pull Request 937
- Add junit as test reporter (thanks to @selten). Pull Request 935
- Update galaxy.xsd for new python 3 compatibility attribute (thanks to @martenson). Pull Request 931
- Documentation: add a little warning for <param ... multiple="true"/> (thanks to @bernt-matthias). Pull Request 930

16.3 0.59.0 (2019-05-09)

- Add ability to test data manager tools (thanks to @mvdbeek). Pull Request 912
- Update Training for new requirement definition (thanks to @bebatut). Pull Request 913
- Drop amqp workaround (thanks to @mvdbeek). Pull Request 917
- Use yaml.safe_load() instead of deprecated load() (thanks to @nsoranzo). Pull Request 921
- Allow converting tool_test_report.json to xunit (thanks to @mvdbeek). Pull Request 918
- Fix error if testcase.data.job does not exist (thanks to @mvdbeek). Pull Request 924
- Fix deprecated getchildren() (thanks to @nsoranzo). Pull Request 925

16.4 0.58.2 (2019-03-01)

- Fix display of tool ids in planemo html report (thanks to @mvdbeek). Pull Request 908
Planemo Documentation, Release 0.61.0.dev0

• Single quotes for file names (thanks to @bernt-matthias). Pull Request 909
• Fix doc linting (thanks to @mvdbeek). Pull Request 910
• Update TS categories (thanks to @nsoranzo). 07dc6e0
• Close tag in doc help, to help with copy&paste (thanks to @blankenberg). Pull Request 914
• Update the tool XSD file (thanks to @bgruening). Pull Request 915

16.5 0.58.1 (2019-01-03)

• Update galaxy-lib requirement to 18.9.2 to add Python 3.7 support (thanks to @nsoranzo). Pull Request 906
• Fix command run by planemo test --skip_venv (thanks to @nsoranzo). Pull Request 907

16.6 0.58.0 (2019-01-01)

• Remove deprecated sudo: false from .travis.yml (thanks to @nsoranzo). Pull Request 902
• Do not skip Galaxy client build for planemo serve. Install Galaxy when the directory specified with --galaxy_root does not exist or is empty. (thanks to @nsoranzo). Pull Request 895, Issue 845

16.7 0.57.1 (2018-11-23)

• Fix username validation for shed linting (thanks to @martenson). Pull Request 899, Issue 898

16.8 0.57.0 (2018-11-19)

• Allow workflow_convert to convert a native .ga workflows to format 2 (yaml). Pull Request 896
• New command (workflow_edit) to open workflow in a synchronized graphical editor. Pull Request 894
• Conda tutorial fixes (thanks to @nsoranzo). Pull Request 876
• Enable --conda_use_local option for planemo test (thanks to @nsoranzo). Pull Request 876
• When testing, skip workflow outputs that do not have a label set (thanks to @bgruening). Pull Request 893
• Add __repr__ for TestCase to improve debugging Planemo (thanks to @bgruening). Pull Request 892
• Increase IO polling interval over time (thanks to @martenson). Pull Request 891
• Sync galaxy xsd and fix tests (thanks to @mvdbeek). Pull Request 889
• Linting fix for W605 (thanks to @martenson). Pull Request 888
• Add icon for repeat parameters in training (thanks to @bebatut). Pull Request 887
16.9 0.56.0 (2018-10-30)

- Allow selection of Python version when starting managed Galaxy (thanks to @mvdbeek). Pull Request 874
- Change the channel priority of conda (again). (thanks to @bgruening). Pull Request 867
- Some small English corrections (thanks to @erasche). Pull Request 868
- Print the list of excluded paths when running `ci_find_repos` (thanks to @nsoranzo). Pull Request 877
- Improved XSD lint reporting. Pull Request 871
- Fix Planemo writing a file called `gx_venv_None`. Pull Request 870
- Update cwltool and galaxy-lib dependencies for Python 3.7 (thanks to @nsoranzo). Pull Request 864
- Fix to make workflow testing more robust. Pull Request 882

16.10 0.55.0 (2018-09-12)

- Add commands to create Galaxy training materials (thanks to @bebatut). Pull Request 861
- Fix `planemo test` when TEMP env variable contain spaces (thanks to @nsoranzo). Pull Request 851
- Support testing a completely remote galaxy instance (thanks to @erasche). Pull Request 856
- Allow naming history from command line (thanks to @erasche). Pull Request 860
- Sync galaxy.xsd from galaxy repo (thanks to @nsoranzo). Pull Request 866
- Fix ServeTestCase.test_shed_serve test (thanks to @nsoranzo). bad810a

16.11 0.54.0 (2018-06-06)

- Better support for testings against different versions of Galaxy efficiently and robustly. Pull Request 849
- New database version (thanks to @bgruening). Pull Request 847
- Hyperlink DOIs against preferred resolver (thanks to @katrinleinweber). Pull Request 850
- Tests for collection inputs to workflows. Pull Request 843
- Bring in Ephemeris sleep function - hopefully makes serve tests a bit more robust. b12b117
- More tutorial testing, tutorial updates. 016b923, 324c776, 2002b49
- More isolated `test_shed_upload.py` tests. 72d2ca7
- Add filetype support for workflow test inputs (thanks to @bgruening). Pull Request 842
- Add `--no_shed_install` option, to prevent shed installs as part of workflow testing. Pull Request 841
- Small docs fix (thanks to @erasche). Pull Request 848

16.12 0.53.0 (2018-05-22)

- Make Planemo testing easier for CWL tools and workflows in various ways and update tutorials to reflect these simplifications. Pull Request 837
• Test and fix running workflow tests against externally managed Galaxy servers. Pull Request 833, Pull Request 836
• Allow using URIs for inputs of workflow test. Pull Request 840
• Slide Galaxy testing window to include 18.05 and drop 17.09. Pull Request 838

16.13 0.52.0 (2018-05-20)

• Allow optional disabling of Galaxy single user mode. Pull Request 835
• Fix for path pasting options during workflow testing. Pull Request 834

16.14 0.51.0 (2018-05-19)

• Fix essentially all Conda and BioContainers related functionality to allow parity between CWL and existing Galaxy functionality - fixes and enhances many commands including lint, conda_install, conda_env, test, run, and mull. Pull Request 828
• Add two new tutorials for Conda and Container development with CWL tools that mirrors the existing tutorials for Galaxy tools - including new CWL exercises, answers, and example project templates. 347c622
• Improve the CWL generated by the tool_init command to properly deal with SoftwareRequirements and generate more idiomatic CWL. Pull Request 820, a5c72e3
• Add new engine type (--engine toil) for testing and running CWL tools (requires manually installing Toil with pip install toil in Planemo’s environment). Pull Request 831
• Add documentation for the Galaxy Workflow and CWL test format files (includes information on configuring various test engines). Pull Request 832
• Better default logging config for CWL development. Pull Request 830
• Various fixes for the conda_search command. Pull Request 826
• Fix test coverage configuration. Pull Request 822
• Reorganize .travis.yml for clarity. Pull Request 829
• More isolated, robust unit tests that use git. Pull Request 827, Pull Request 818
• Fix default list of best-practice Conda channels. Pull Request 825
• Refactor tests to speed up quick tests - fewer buggy URLs fetched in “quick” mode. Pull Request 823
• Fix upload configuration of workflow testing to default (overrideable) external Galaxies to not use path pasting. Pull Request 816
• Fix test number parsing for workflow tests. Pull Request 817

16.15 0.50.1 (2018-05-11)

• Fix the process of waiting on Galaxy to boot up for the Docker Galaxy container --engine.
16.16 0.50.0 (2018-05-10)

- Fixes and small CLI tweaks to get the Docker Galaxy container working as an `--engine` for the run, serve, and test commands.

16.17 0.49.2 (2018-05-09)

- Various small fixes for new external Galaxy engine type.

16.18 0.49.1 (2018-05-06)

- Fix PyPI README rendering for 0.49.0 release changes.

16.19 0.49.0 (2018-05-06)

- Implement external Galaxy engine. Pull Request 781
- Restructure serve testing code for reuse. Pull Request 795
- Improve test report handling for JSON generated via galaxy-lib testing script. Pull Request 799
- Improve how various branches of Galaxy are tested. Pull Request 800
- Added documentation for `GALAXY_MEMORY_MB` (thanks to @bernt-matthias). Pull Request 801
- Log tool config in verbose logging mode. Pull Request 802
- Replace `r channel` with `conda-forge` (thanks to @bgruening). Pull Request 805
- Sync `galaxy.xsd` with latest Galaxy updates (thanks to @nsoranzo). Pull Request 806
- Use `requests.get()` when validating http URLs (thanks to @nsoranzo). Pull Request 809
- Do not consider tools with "deprecated" in the path (thanks to @bgruening). Pull Request 810
- Automatically load tools shipped with Galaxy when testing, running, or serving workflows that reference these tools. Pull Request 790
- Revise README and touch up documentation in general. Pull Request 787
- Various small changes to testing and test framework. Pull Request 792
- Various Python 3 fixes. 8fe9e9, 41f7df1
- Fixes for Galaxy 18.0X releases. Pull Request 803, dc443d6

16.20 0.48.0 (2018-02-28)

- Run all CI tests against Python 3 (thanks to @nsoranzo). Pull Request 768 and Pull Request 774
- Python 3 fix - subprocess with `universal_newlines=True` (thanks to @peterjc). Pull Request 764
- Record CWL conformance test results using JUnit xml (thanks to @mr-c). Pull Request 756
- Restore run test case for simple Galaxy tools. Pull Request 769
• Enhancements to Galaxy profiles and workflow testing. Pull Request 773
• Fix resolving & installing shed repositories from workflows for test and run commands. Pull Request 776
• Implement planemo command to convert format 2 workflows into .ga workflows. Pull Request 771
• Add a native Galaxy workflow (.ga) testing test. Pull Request 770
• Drop Brew support but add more detailed install instructions. Pull Request 761
• Clean up CWL conformance test execution. Pull Request 753
• Assorted small CWL and daemon serve fixes. Pull Request 759

16.21 0.47.0 (2017-11-18)

• Update to the latest Galaxy tool XSD (thanks to @nsoranzo). Pull Request 747
• Re-fix problem when shed_update would fail if nothing to update (thanks to @nsoranzo). Pull Request 747
• Update instructions for installation via conda (thanks to @nsoranzo). Pull Request 743
• Bug fix for MacOS chmod doesn’t support –recursive flag. (thanks to @dfornika). Pull Request 739
• Bug fix to also socket.error when linting URLs (thanks to @nsoranzo). Pull Request 738
• Disable broken tests. Pull Request 745

16.22 0.46.1 (2017-09-26)

• Rev to latest versions of bioblend and galaxy-lib for various fixes related to CWL.

16.23 0.46.0 (2017-09-15)

• Change behavior of --docker flag, for a few releases it would require Galaxy use a container for every non-upload tool. This breaks various conversion tools for instance and so was reverted. Pull Request 733
• Add ‘Accept’ header when linting doc URLs (thanks to @nsoranzo). Pull Request 725
• Fix –conda_auto_install help (thanks to @nsoranzo). Pull Request 727
• Incremental progress toward CWL support via Galaxy. Pull Request 729, Pull Request 730
• Update galaxy-lib to latest version to fix various issues. Pull Request 730
• Fix lint detected problems with documentation. Pull Request 731

16.24 0.45.0 (2017-09-06)

• Update to the latest galaxy-lib for Conda fixes. (thanks @nsoranzo) and updated CWL utilities. Pull Request 716, Pull Request 723
• Update Conda channel order to sync with Bioconda (thanks to @nsoranzo). Pull Request 715
• Experimental support running CWL workflows through the CWL fork of Galaxy.
• Mention planemo command --help in main help (thanks to @peterjc). Pull Request 709
**Bugfix handle None requirement versions when registering containers (thanks to @bgruening). Pull Request 704**

**Bugfix for dependencies by pinning ruamel.yaml version (thanks to @mvdbeek). Pull Request 720**

### 16.25 0.44.0 (2017-06-22)

- Fix and improve Galaxy root option specification options. Pull Request 701, 8a608e0
- Update *planemo mull* to use a default action of *build-and-test* since *build* no longer cleans up itself. ecc1bc2
- Add a command to pre-install *Involucro*. Pull Request 702

### 16.26 0.43.0 (2017-06-22)

- Remove stdio from generated tools - just use *exit_code* for everything. 91b6fa0
- Implement some ad-hoc documentation tests. Pull Request 699
- A large number of small enhancements and fixes for the documentation and example projects.

### 16.27 0.42.1 (2017-06-16)

- Fix Readme typos (thanks to @manabushii) 904d77a
- Fix *container_register* to create pull requests against the newly finalized home of the multi-package-containers registry repository. 9636682
- Fix *use_global_config* and *use_env_var* for options with unspecified defaults. 475104c

### 16.28 0.42.0 (2017-06-15)

- Conda/Container documentation and option naming improvements. Pull Request 684
- Sync *galaxy.xsd* with latest upstream Galaxy updates (thanks to @nsoranzo). Pull Request 687
- Fix *ci_find_repos* command to not filter repos whose only modifications where in subdirs (thanks to @nsoranzo). Pull Request 688
- Update *container_register* for mulled version 2 and repository name changes. Pull Request 689
- Better pull request messages for the *container_register* command. Pull Request 690

### 16.29 0.41.0 (2017-06-05)

- Fix *shed_update* not fail if there is nothing to update (thanks to @nsoranzo). Issue 494, Pull Request 680
- Conda documentation and option naming improvements. Pull Request 683
- Implement *container_register* for tool repositories. Pull Request 675
- Fix *hub* binary installation for Mac OS X. Pull Request 682
16.30 0.40.1 (2017-05-03)

- Fix data manager configuration to not conflict with original Galaxy at galaxy_root (thanks to @nsoranzo). Pull Request 662
- Fix filter_paths() to not partial match paths when filtering shed repositories (thanks to @nsoranzo). Pull Request 665
- Fix description when creating .shed.yml files (thanks to @RJMW). Pull Request 664

16.31 0.40.0 (2017-03-16)

- Implement instructions and project template for GA4GH Tool Execution Challenge Phase 1. 84c4a73
- Eliminate Conda hack forcing /tmp as temp directory. b4ae44d
- Run dependency script tests in isolated directories. 32f41c9
- Fix OS X bug in planemo run by reworking it to wait using urllib instead of sockets. 3129216

16.32 0.39.0 (2017-03-15)

- Implement documentation and examples for Conda-based dependency development (under “Advanced” topics). Pull Request 642, Pull Request 643
- Implement documentation and examples for container-based dependency development (under “Advanced” topics). 0a1abfe
- Implement a planemo conda_search command for searching best practice channels from the command line. Pull Request 642
- Allow Planemo to work with locally built Conda packages using the --conda_use_local command. Pull Request 643, Issue 620
- Implement an open (or just o) command to quickly open the last test results (or any file if supplied). Pull Request 641
- Linting improvements and fixes due to galaxy-lib update. * WARN on test output names not found or not matching. * INFO correct information about stdio if profile version is found. * WARN if profile version is incorrect. * INFO profile version * Fix assert_command not detected as a valid test (fixes Issue 260).
- Have lint --conda_requirements check that at least one actual requirement is found. 6638caa
- Allow conda_install to work with packages as well as just tools. 8f6f661
- Add --global option to conda_install to install requirements into global Conda setup instead of using an environment. 8f6f661
- Implement planemo lint --biocontainer that checks that a tool has an available BioContainer registered. 0a1abfe
- Add more options and more documentation to the planemo mull command. 0a1abfe
- Hack around a bug in Conda 4.2 that makes it so planemo mull doesn’t work out of the box on Mac OS X. 0a1abfe
- Allow URIs to be used instead of paths for a couple operations. ce0dc4e
- Implement non-strict CWL parsing option. 4c0f100
• Fixes for changes to cwltool and general CWL-relate functionality. 3c95b7b, 06bcf19, 525de8f, 9867c56, 9ab4a0d
• Eliminate deprecated XML-based abstraction from planemo.tools. 04238d3
• Fix MANIFEST.in entry that was migrated to galaxy-lib. ced5ce2
• Various fixes for the command conda_env. Pull Request 640
• Improved command help - both formatting and content. Pull Request 639
• Implement a --no_dependency_resolution option disabling conda dependency resolver. Pull Request 635, Issue 633
• Tests for new linting logic. Pull Request 638
• Fix bug where tool IDs needs to be lowercase for the shed (thanks to @bgruening). Pull Request 649
• Update seqtk version targeted by intro docs. e343b67
• Various other Conda usability improvements. Pull Request 634

16.33 0.38.1 (2017-02-06)

• Fix bug with shed_lint --urls introduced in 0.38.0. 84ebc1f

16.34 0.38.0 (2017-02-06)

• Trim down the default amount of logging during testing. Pull Request 629, Issue 515
• Improved log messages during shed operations. 08c067c
• Update tool XSD against latest Galaxy. fca4183, 03c9658
• Fix bug where shed_lint --tools for a suite lints the same tools multiple times. Issue 564, Pull Request 628

16.35 0.37.0 (2017-01-25)

• Update to the latest galaxy-lib release. This means new installs start with Miniconda 3 instead of Miniconda 2 and at a newer version. This fixes many Conda related bugs.
• Change defaults so that Conda automatically initializes and performs tool installs by default from within the spawned Galaxy server. The trio of flags --conda_dependency_resolution, --conda_auto_install, and --conda_auto_init are effectively enabled by default now. 4595953
• Use the Galaxy cached dependency manager by default (thanks to @abretaud). Pull Request 612
• Test Conda dependency resolution for more versions of Galaxy including the forthcoming release of 17.01.
• Update to the latest Galaxy tool XSD for various tool linting fixes. 32acd68
• Fix pip ignores for bioconda_scripts (thanks to @nturaga) Pull Request 614
16.36 0.36.1 (2016-12-12)

- Fix move error when using `project_init`. Issue 388, Pull Request 610
- Improved integration testing for `test` command. Pull Request 609
- Update CWL links to v1.0 (thanks to @mr-c). Pull Request 608

16.37 0.36.0 (2016-12-11)

- Bring in latest tool XSD file from Galaxy (thanks to @peterjc). Pull Request 605
- PEP8 fixes for various linting problems (thanks to @peterjc). Pull Request 606
- Update tool syntax URL to new URL (thanks to @mvdbeek). Pull Request 602

16.38 0.35.0 (2016-11-14)

- Native support for building bioconductor tools and recipes (thanks to @nturaga). Pull Request 570
- Fixes for running Galaxy via docker-galaxy-stable (thanks to @bgruening). 50d3c4a
- Import order linting fixes (thanks to @bgruening).

16.39 0.34.1 (2016-10-12)

- Mimic web browser to validate user help URLs fixing Issue 578 (thanks to @peterjc). Pull Request 591
- Fix for Bioconda recipes depending on `conda-forge` (thanks to @nsoranzo). Pull Request 590

16.40 0.34.0 (2016-10-05)

- Implement `mull` command to build containers for tools based on Conda recipes matching requirement definitions. 08cef54
- Implement `--mulled_containers` flag on `test`, `serve`, and `run` commands to run tools in “mulled” containers. Galaxy will first search locally cache containers (such as ones built with `mull`), then search the mulled namespace of quay.io, and finally build one on-demand if needed using galaxy-lib and Involucro developed by @thriqon.
- Implement `--conda_requirements` flag on `lint` command to ensure requirements can be resolved in best practice channels. 9da8387
- Allow `conda_install` command over multiple tool paths. 2e4e5fc
- Update `pip` as part of setting virtual environment in `Makefile` target. 19b2ee9
- Add script to auto-update Bioconda recipe for Planemo and open a pull request. f0da66f
16.41 0.33.2 (2016-09-28)

- Fix HISTORY.rst link problem that prevented correct display of content on PyPI.

16.42 0.33.1 (2016-09-28)

- Fix lint --urls false positives by being more restrictive with what is considered a URL (fixed by @erasche after detailed report from @peterjc). Issue 573, Pull Request 579

16.43 0.33.0 (2016-09-23)

- Enable XSD validation of tools by default (restore old behavior with planemo lint --no_xsd). lef05d2
- Implement a conda_lint command to lint Conda recipes based on anaconda-verify. 6a6f164
- Implement clone and pull_request commands to ease PRs (with documentation fixes from @martenson). e925ba1, ea5324f
- Update galaxy.xsd to allow version_command's to have an interpreter attribute. 7cca2e4
- Apply improvement from @nsoranzo for Planemo's use of git diff. 6f91719
- Pull in downstream refactoring of tool_init code from @nturaga's Bioconductor work. ccdd2d5
- Update to latest Tool Factory code from tools-iuc. ca88b0c
- Small code cleanups. b6d8294, d6da3a8
- Fixup docs in planemo.xml.validation.
- Allow skipping newly required lxml dependency in setup.py. 34538de

16.44 0.32.0 (2016-09-16)

- Enhance planemo lint --xsd to use a fairly complete and newly official XSD definition. Pull Request 566
- Migrate and update documentation related to tool XML macros and handling multiple outputs from the Galaxy wiki (with help from @bgruening, @mvdbeek, and @nsoranzo). Pull Request 559
- Documentation fixes (thanks to @ramezrawas). Pull Request 561
- Do not fail URL linting in case of too many requests (thanks to @nsoranzo). Pull Request 565

16.45 0.31.0 (2016-09-06)

- Implement new commands to ci_find_repos and ci_find_tools to ease CI scripting. Pull Request 555
16.46 0.30.2 (2016-09-01)

• Fix another problem with Conda prefix handling when using --conda_dependency_resolution. f7b6c7e

16.47 0.30.1 (2016-09-01)

• Fix a problem with Conda prefix handling when using --conda_dependency_resolution. f7b6c7e
• Fix for quote problem in update_planemo_recipe.bash. 6c03de8
• Fix to restore linting of tests/ directory and fix import order throughout module. ef4b9f4

16.48 0.30.0 (2016-09-01)

• Update to the latest galaxy-lib release and change Conda semantics to match recent updates to Galaxy. For the most robust Conda usage - use planemo 0.30+ with Galaxy 16.07 or master. 07d94bd
• Implement the --conda_auto_init flag for conda_install. ca19910
• Allow the environment variable PLANEMO_CONDA_PREFIX to set a default for --conda_prefix. 24008ab
• Fixup documentation regarding installs and Conda. ce44e87
• Fix and lint Python module import order throughout project. Pull Request 550
• Use cp rather than symlink to $DOWNLOAD_CACHE in the dependency_script command (thanks to @peterjc). c2204b3
• Fixes for the Homebrew recipe updater. c262b6d

16.49 0.29.1 (2016-08-19)

• Improved handling of Python 2.7 specific dependencies.

16.50 0.29.0 (2016-08-19)

• Look for sha256sum checksums during shed_lint (thanks to @peterjc). Pull Request 539
• An assortment fixes and enhancements to the dependency_script command (thanks to @peterjc). Pull Request 541, Pull Request 545
• Fix shed_build to respect exclude: in .shed.yml (thanks to @nsoranzo). Pull Request 540
• Fix linting of tool URLs (thanks to @nsoranzo). Pull Request 546

16.51 0.28.0 (2016-08-17)

• Fixes for bioblend v0.8.0 (thanks to @nsoranzo). 9fd4f90
• Enable shed repo type update (thanks to @nsoranzo). 3ceaa40
• Create suite repositories with repository_suite_definition type by default (thanks to @nsoranzo). 057f4f0
• Include shed_lint in script run by travis_init (thanks to @peterjc). Pull Request 528
• Minor polish to the travis_init command (thanks to @peterjc). Pull Request 512
• Update pip and setuptools on TravisCI; fix travis_init (thanks to @peterjc). Pull Request 521
• Shorten command one line descriptions for main help (thanks to @peterjc). Pull Request 510
• Use planemo test --no_cache_galaxy under TravisCI (thanks to @peterjc). Pull Request 513
• Improve and fix docs ahead of GCC 2016 (thanks to @martenson). Pull Request 498, 725b232
• Add description of expect_num_outputs to planemo FAQ. a066afb
• Revise planemo tools docs to be more explicit about collection identifiers. a811e65
• Add more docs on existing dynamic tool output features. Pull Request 526
• Fix serve command doc (thanks to @nsoranzo). 8c088c6
• Fix make lint-readme (RST link errors) (thanks to @peterjc). Pull Request 525
• Add union bedgraph example to project templates (for GCC demo example). d53bcd6
• Add Flow Cytometry Analysis, Data Export, and Constructive Solid Geometry as shed categories (thanks to @bgruening, @gregvonkuster, and @nsoranzo). e890ab5, 08bb354, e2398fb
• Remove duplicated attribute in docs/writing/bwa-mem_v5.xml (thanks to Paul Stewart @pstew). Pull Request 507

16.52 0.27.0 (2016-06-22)

• Use ephemeris to handle syncing shed tools for workflow actions. 1c6cfbb
• More planemo testing enhancements for testing artifacts that aren’t Galaxy tools. Pull Request 491
• Implement docker_galaxy engine type. eb039c0, Issue 15
• Enhance profiles to be Dockerized Galaxy-aware. Pull Request 488
• Add linter for DOI type citation - thanks to @mvdbeek. Pull Request 484

16.53 0.26.0 (2016-05-20)

• Implement Engine and Runnable abstractions - Planemo now has beta support for testing Galaxy workflows and CWL tools with Galaxy and any CWL artifact with cwltool. Pull Request 454, 7be1bf5
• Fix missing command_line in test output json. e38c436
• More explicit Galaxy job_conf.xml handling, fixes bugs caused by galaxy_root having existing and incompatible job_conf.xml files and makes it possible to specify defaults with fixed server name. e4dfd55
• Introduce profile commands (profile_create, profile_delete, and profile_list) and profile improvements (automatic postgres database creation support). Pull Request 480, a87899b
• Rework Galaxy test reporting to use structured data instead of XUnit data. 4d29bf1
• Refactor Galaxy configuration toward support for running Galaxy in docker-galaxy-stable. Pull Request 479
16.54 0.25.1 (2016-05-11)

- Tweak dependencies to try to fix cwltool related issues - such as Issue 475.

16.55 0.25.0 (2016-05-11)

- Implement Galaxy “profiles” - the ability to configure persistent, named environments for serve and test. 5d08b67
- Greatly improved serve command - make test-data available as an FTP folder, (on 16.07) automatically log in an admin user, and many more options (such as those required for “profiles” and a --daemon mode).
- Two fixes to ensure more consistent, dependable test output. Pull Request 472, f3c6917
- Add code and documentation for linting (lint) and building (tool_init) CWL tools. a4e6958, b0b867e, 4cd571c
- If needed for Conda workaround, shorten config_directory path (thanks to @mvdbeek). efc5f30
- Fix --no_cache_galaxy option (thanks to Gildas Le Corguillé). d8f2038
- Target draft 3 of CWL instead of draft 2. 775bf49
- Fix cwltool dependency version - upstream changes broke compatibility. 65b999d
- Add documentation section and slides about recent Galaxy tool framework changes (with fix from @remi-marenco). 069e7ba
- Add IUC standards to Planemo docs. 2ae2b49
- Improve collection-related contents in documentation (thanks in part to @martenson), fea51fc, 13a5ae7
- Add documentation on GALAXY_SLOTS and running planemo on a cluster. 45135ff, e0acf91
- Revise command-line handling framework for consistency and extension - allow extra options to be configured as defaults ~/.planemo.yml including --job_config_file and Conda configuration options. e769118, 26e378e
- Fix tool_init commons options typos (thanks to Nitesh Turaga). 826d371
- Refactor galaxy-related modules into submodules of a new planemo.galaxy package. 8e96864
- Fix error message typo (thanks to @blankenberg). b1c8f1d
- Update documentation for recent command additions. 3f4ab44
- Rename option --galaxy_sqlite_database option to --galaxy_database_seed and fix it so it actually works. f7554d1
- Add --extra_tools option to serve command. 02a08a0
- Update project testing to include linting documentation (docs/), Python import order, and docstrings. a13a120, 6e1e726, 95d5cba

16.56 0.24.2 (2016-04-25)

- Revert “check .shed.yml owner against credentials during shed creation”, test was incorrect and preventing uploads. Pull Request 425, Issue 246
16.57 0.24.1 (2016-04-08)

- Fix test summary report. Pull Request 429
- Improve error reporting when running `shed_test`. ce8e1be
- Improved code comments and tests for shed related functionality. 89674cb
- Rev `galaxy-lib` dependency to 16.4.1 to fix wget usage in newer versions of wget. d76b489

16.58 0.24.0 (2016-03-29)

- Drop support for Python 2.6. 93b7bda
- A variety of fixes for `shed_update`. Pull Request 428, Issue 416
- Fix reporting of metadata updates for invalid shed updates. Pull Request 426, Issue 420
- Check `.shed.yml` owner against credentials during shed creation. Pull Request 425, Issue 246
- Fix logic error if there is a problem with `shed_create`. 358a42c
- Tool documentation improvements. 0298510, a58a3b8

16.59 0.23.0 (2016-02-15)

- Fix duplicated attributes with Conda resolver (thanks to Björn Grüning). Pull Request 403
- Upgrade to latest version of `galaxy-lib` for more linting.
- Attempt to better handle conditional dependency on cwltool.

16.60 0.22.2 (2016-01-14)

- Fixed bug targeting forthcoming release of Galaxy 16.01.

16.61 0.22.1 (2016-01-14)

- Fixed problem with PyPI build artifacts due to submodule’s not being initialized during previous release.

16.62 0.22.0 (2016-01-13)

- Add `--skip_venv` to support running Galaxy 16.01 inside of conda environments. 9f3957d
- Implement conda support. f99f6c1, ad3b2f0, 5e0b6d1
- Update LICENSE for Planemo to match Galaxy. 15d33c7
- Depend on new `galaxy-lib` on PyPI instead of previous hacks... Pull Request 394
- Fix egg caching against master/15.10. 6d0f502
• Fix bug causing shed publishing of .svn directories. Issue 391
• Bug fixes for Conda support thanks to @bgruening. 63e456c
• Fix document issues thanks to @eion. Pull Request 390
• Improve client for shed publishing to support newer shed backend being developed by @erasche. Pull Request 394
• Tool Shed repo_id change, @erasche. Pull Request 398
• Various other small changes to testing, project structure, and Python 3 support.

16.63 0.21.1 (2015-11-29)

• Fix serious regression to test command. 94097c7
• Small fixes to release process. 4e1377c, 94645ed

16.64 0.21.0 (2015-11-29)

• If virtualenv not on PATH, have Planemo create one for Galaxy. 5b97f2e
• Add documentation section on testing tools installed in an existing Galaxy instance. 1927168
• When creating a virtualenv for Galaxy, prefer Python 2.7. e0577e7
• Documentation fixes and improvements thanks to @martenson. 0f8cb10, 01584c5, b757791
• Specify a minimum six version requirement. 1c7ee5b
• Add script to test a planemo as a wheel. 6514ff5, Issue 184
• Fix empty macro loading. Issue 362
• Fix an issue when you run shed_diff --shed_target local thanks to Gwendoline Andres and Gildas Le Corguillé at ABiMS Roscoff. Pull Request 375
• Fix shed_diff printing to stdout if -o isn’t specified. f3394c7
• Small shed_diff improvements to XML diffing and XUnit reporting. a17448c, 83e227a
• More logging of shed_diff results if --verbose flagged. 9427b47
• Add test_report command for rebuilding reports from structured JSON. 99ee51a
• Fix option bug with Click 6.0 thanks to @bgruening. 2a7c792
• Improved error messages for test commands. fdce74c
• Various fixes for Python 3. 2f666c3, 7572e99, 8eda729, 764ce01
• Use newer travis container infrastructure for testing. 6d81a94
• Test case fixes. 98fde8c, 0e4f70a
16.65 0.20.0 (2015-11-11)

- More complete I/O capturing for XUnit. 6409449
- Check for select parameter without options when linting tools. Issue 373
- Add \--cwl_engine argument to cwl_run command. dd94ddc
- Fixes for select parameter linting. 8b31850
- Fix to demultiplexing repositories after tool uploads. Issue 361
- Fix to update planemo for Galaxy wheels. 25ef0d5
- Various fixes for Python 2.6 and Python 3. c1713d2, 916f610, c444855

16.66 0.19.0 (2015-11-03)

- Initial implementation of cwl_run command that runs a CWL tool and job file through Galaxy. 49c5c1e
- Add \--cwl flag to serve to experimentally serve CWL tools in Galaxy. Pull Request 339
- Implement highly experimental cwl_script command to convert a CWL job to a bash script. 508dce7
- Add name to all XUnit reports (thanks to @erasche). Pull Request 343
- Capture stdout and stderr for shed_diff and shed_update XUnit reports. Pull Request 344
- More tool linting (conditionals) thanks to @erasche. Pull Request 350
- UTF-8 fixes when handling XUnit reports. Pull Request 345
- Add Epigenetics as Tool Shed category. Pull Request 351
- Merge changes to common modules shared between Galaxy, Planemo, and Pulsar (thanks to @natefoo). Pull Request 356
- Add \--cite_url to tool_init. fdb1b51
- tool_init bug fix. f854138
- Fix setup.py for cwltool and bioblend changes. 1a157d4
- Add option to specify template sqlite database locally. c23569f
- Add example IPython notebooks to docs. c8640b6

16.67 0.18.1 (2015-10-22)

- Fix issue with test reporting not being populated. 19900a6

16.68 0.18.0 (2015-10-20)

- Improvements to docker_shell usability (thanks to @kellrott). Pull Request 334
- Add docker pull attempt when missing Dockerfile (thanks to @kellrott). Pull Request 333
- Fix bug inferring which files are tool files (thanks to @erasche). Pull Request 335, Issue 313
Planemo Documentation, Release 0.61.0.dev0

- Initial work toward automating brew recipe update. 4d6f7d9, Issue 329

16.69 0.17.0 (2015-10-19)

- Implement basic XUnit report option for shed_update (thanks to @martenson), Pull Request 322
- Fix issues with producing test outputs. 572e754
- XUnit reporting improvements - refactoring, times, diff output (thanks to @erasche), Pull Request 330
- Implement project governance policy and update developer code of conduct to match that of the Galaxy project, Pull Request 316
- Update filters for account for new .txt and .md test outputs (thanks to @erasche), Pull Request 327
- Add verbose logging to galaxy test output handling problems. 5d7db92
- Flake8 fixes (thanks to @martenson), 949a36d
- Remove uses of deprecated mktemp Python standard library function (thanks to @erasche), Pull Request 330

16.70 0.16.0 (2015-10-07)

- Adding new command dependency_script to convert Tool Shed dependencies into shell scripts - thanks to @peterjc, Pull Request 310, f798c7e, Issue 303
- Implement profiles in sheds section of the ~/.planemo.yml, Pull Request 314

16.71 0.15.0 (2015-10-01)

- Template framework for reporting including new markdown and plain text reporting options for testing - thanks to @erasche, Pull Request 304
- XUnit style reporting for shed_diff command - thanks to @erasche, Pull Request 305
- Add new shed_build command for building repository tarballs - thanks to @kellrott, Pull Request 297
- Fix exit code handling for lint commands - thanks to @mvdbeek, Pull Request 292
- Improved documentation for serve command - thanks to @iparsons, Pull Request 312
- Tiny backward compatible Python 3 tweaks for Tool Factory - thanks to @peterjc, dad2d9d
- Fixed detection of virtual environment in Makefile - thanks to @iparsons, Pull Request 311
- Updates to Galaxy XSD - thanks to @mr-c, Pull Request 309
- Allow reading shed key option from an environment variable. Pull Request 307
- Allow specifying host to serve Galaxy using -host - thanks in part to @chambm, Pull Request 301
- Allow specifying defaults for -host and --port in ~/.planemo.yml, Pull Request 301
- Improve ~/.planemo.yml sample comments - thanks to @martenson, Pull Request 287
- Update tool shed categories - thanks to @bgruening, Pull Request 285
- Improved output readability for diff command - thanks to @martenson, Pull Request 284
16.72 0.14.0 (2015-08-06)

- Allow \(-t\) as shorthand for \(--shed_target\) (thanks to Peter Cock). Pull Request 278
- Fix \texttt{tool_init} command to use \texttt{from_work_dir} only if file in command (thanks to bug report and initial fix outline by Gildas Le Corguillé). Pull Request 277
- Various documentation fixes (thanks in part to Peter Cock and Daniel Blankenberg). Pull Request 256, Pull Request 253, Pull Request 254, Pull Request 255, Pull Request 251, Issue 272

16.73 0.13.2 (2015-07-06)

- Fix \texttt{project_init} for missing files. cb5b906
- Various documentation improvements.

16.74 0.13.1 (2015-07-01)

- Fix for \texttt{shed_init} producing non-standard type hints. Issue 243, f0610d7
- Fix tool linting for parameters that define an argument but not a name. Issue 245, aad1eed
- Many doc updates including a tutorial for developing tools in a test-driven fashion and instructions for using the planemo appliance through Kitematic (with Kitematic screenshots from E. Rasche).

16.75 0.13.0 (2015-06-28)

- If planemo cannot find a Galaxy root, it will now automatically fetch one (specifying \(--galaxy_install\) will still force a fetch). Pull Request 235
- Documentation has been updated to reflect new and vastly improved Docker and Vagrant virtual appliances are now available, as well as a new VirtualBox OVA variant.
- Update linting for new tool XML features (including \texttt{detect_errors} and output collections). Issue 233, 334f2d4
- Fix \texttt{shed_test} \texttt{help} text. Issue 223
- Fix code typo (thanks to Nicola Soranzo). Pull Request 230
- Improvements to algorithm used to guess if an XML file is a tool XML file. Issue 231
- Fix configuration file handling bug. Issue 240

16.76 0.12.2 (2015-05-23)

- Fix \texttt{shed_test} and \texttt{shed_serve} for test and local tool sheds. f3cafaa

16.72. 0.14.0 (2015-08-06)
16.77 0.12.1 (2015-05-21)

- Fix to ensure the tab completion script is in the Python source tarball (required for setting up tab-completion for Homebrew). 6b4e7a6

16.78 0.12.0 (2015-05-21)

- Implement a --failed flag for the test command to rerun previously failed tests. Pull Request 210
- Implement shed_update to upload contents and update repository metadata. Pull Request 216
- Implement shed_test and shed_serve commands to test and view published artifacts in the Tool Shed. Pull Request 213, Issue 176
- Add shell tab-completion script. 37dcc07
- Many more commands allow specifying multiple tool and/or repository targets. Issue 150
- Add -m as alias for --message in planemo shed_upload (thanks to Peter Cock). Pull Request 200
- Add --ensure_metadata option to shed_lint to ensure .shed.yml files contain many repository. Pull Request 215
- More developer documentation, additional make targets including ones for setting up git pre-commit hooks. cc8abb6, Issue 209
- Small README improvement (thanks to Martin Čech) b53006d
- Fixes for shed operation error handling (thanks to Martin Čech). Pull Request 203, Pull Request 206
- Fix for “smart” shed_diff not in the repository root directory (thanks to Peter Cock). Pull Request 207, Issue 205
- Recursive shed_diff with directories not yet in Tool Shed. Pull Request 208
- Improve error handling and reporting for problematic --shed_target values. Issue 217
- Fix typos in lint messages. Issue 211

16.79 0.11.1 (2015-05-12)

- Fix default behavior for planemo lint to use current directory if explicit paths are not supplied. 1e3668a

16.80 0.11.0 (2015-05-12)

- More compact syntax for defining multiple custom inclusions in .shed.yml files - thanks to Peter Cock. Issue 180, Pull Request 185, Pull Request 196
- Prevent ambiguous destinations when defining custom inclusions in .shed.yml- thanks to Peter Cock. Pull Request 186
- lint now warns if tool ids contain whitespace. Pull Request 190
- Handle empty tar-balls gracefully on older Python versions - thanks to Peter Cock. Pull Request 187
- Tweak quoting in cp command - thanks to Peter Cock. 6bcf699
• Fix regression causing testing to no longer produce “pretty” test results under certain circumstances. Issue 188
• Fix for recursive shed_diff folder naming. Issue 192
• Fix output definitions to tool_init command. Issue 189

16.81 0.10.0 (2015-05-06)

• Extend shed_lint to check for valid actions in tool_dependencies.xml files. 8117e03
• Extend shed_lint to check for required files based on repository type. Issue 156
• Ignore common editor backup files during shed_upload. Issue 179
• Fix missing file when installing from source via PyPI. Issue 181
• Fix lint to verify data inputs specify a format attribute. 8117e03
• Docstring fix thanks to @peterjc. fe7ad46

16.82 0.9.0 (2015-05-03)

• Add new logo to the README thanks to @petrkadlec from puradesign.cz and @carlfeberhard from the Galaxy Project. Issue 108
• Implement smarter shed_diff command - it now produces a meaningful exit codes and doesn’t report differences if these correspond to attributes that will be automatically populated by the Tool Shed. Issue 167
• Use new smarter shed_diff code to implement a new --check_diff option for shed_upload - to check for meaningful differences before updating repositories. Issue 168
• Record git commit hash during shed_upload if the .shed.yml is located in a git repository. Issue 170
• Allow shed_operations to operate on git URLs directly. Issue 169
• Fail if missing file inclusion statements encountered during .shed.yml repository resolution - bug reported by @peterjc. Issue 158
• Improved exception handling for tool shed operations including new --fail_fast command-line option. * Issue 114, Pull Request 173
• Implement more validation when using the shed_init command. lcd0e2d
• Add -r/--recursive option to shed_download and shed_diff commands and allow these commands to work with .shed.yml files defining multipe repositories. 40a1f57
• Add --port option to the serve and tool_factory commands. 15804be
• Fix problem introduced with setup.py during the 0.9.0 development cycle - thanks to @peterjc. Pull Request 171
• Fix clone bug introduced during 0.9.0 development cycle - thanks to @bgruening. Pull Request 175

16.83 0.8.4 (2015-04-30)

• Fix for Travis CI testing picking up invalid tests (reported by @takadonet). Issue 161
• Fix tar ordering for consistency (always sort by name) - thanks to @peterjc. Pull Request 164, Issue 159
• Fix exception handling related to tool shed operations - thanks to @peterjc. Pull Request 155, b86fe1f

16.84 0.8.3 (2015-04-29)

• Fix bug where shed_lint was not respecting the -r/--recursive flag. 9ff0d2d
• Fix bug where planemo was producing tar files incompatible with the Tool Shed for package and suite repositories. a2ee135

16.85 0.8.2 (2015-04-29)

• Fix bug with config_init command thanks to @bgruening. Pull Request 151
• Fix unnessecary lint warning about parallelism tag reported by @peterjc. 9bf1eab

16.86 0.8.1 (2015-04-28)

• Fixes for the source distribution to allow installation of 0.8.0 via Homebrew.

16.87 0.8.0 (2015-04-27)

• Implement the new shed_lint command that verifies various aspects of tool shed repositories - including XSD validation of repository_dependencies.xml and tool_dependencies.xml files, best practices for README files, and the contents of .shed.yml files. This requires the lxml library to be available to Planemo or the application xmllint to be on its PATH. Pull Request 130 Issue 89 Issue 91 912df02 d26929e 36ac6d8
• Option to enable experimental XSD based validation of tools when lint is executed with the new --xsd flag. This validation occurs against the unofficial Galaxy Tool XSD project maintained by @JeanFred. This requires the lxml library to be available to Planemo or the application xmllint to be on its PATH. Pull Request 130 912df02
• Allow skipping specific linters when using the lint command using the new --skip option. 26e3cdb
• Implement sophisticated options in .shed.yml to map a directory to many, custom Tool Shed repositories during shed operaitions such shed_upload including automatically mapping tools to their own directories and automatically building suites repositories. Pull Request 143
• Make shed_upload more intelligent when building tar files so that package and suite repositories may have README files in source control and they will just be filtered out during upload. 53edd99
• Implement a new shed_init command that will help bootstrap .shed.yml files in the specified directory. cc1a447
• Extend shed_init to automatically build a repository_rependencies.xml file corresponding to a Galaxy workflow (.ga file). Issue 118 988d01d
• In addition to a single file or directory, allow lint to be passed multiple files. 343902d Issue 139
• Add -r/--recursive option to shed_create and lint commands. 63cd431 01f2af9
• Improved output formatting and option to write diffs to a file for the shed_diff command. 965511d
• Fix lint problem when using new Galaxy testing features such as expecting job failures and verifying job output. Issue 138
• Fix typo in test help thanks to first time contributor @pvanheus. Pull Request 129 1982076
• Fix NPE on empty help element when linting tools. Issue 124
• Fix lint warnings when configfiles are defined in a tool. 1a85493
• Fix for empty .shed.yml files. b7d9e96
• Fix the test command for newer versions of nose. 33294d2
• Update help content and documentation to be clear normalize should not be used to update the contents of tool files at this time. 08de8de
• Warn on unknown command attributes when linting tools (anything but interpreter). 4f61025
• Various design, documentation (including new documentation on Tool Shed publishing), and testing related improvements (test coverage has risen from 65% to over 80% during this release cycle).

16.88 0.7.0 (2015-04-13)

• Implement shed_create command to create Tool Shed repositories from .shed.yml files (thanks to E. Rasche). Pull Request 101
• Allow automatic creation of missing repositories during shed_upload with the new --force_repository_creation flag (thanks to E. Rasche). Pull Request 102
• Allow specifying files to exclude in .shed.yml when creating tar files for shed_upload (thanks to Björn Grüning). Pull Request 99
• Resolve symbolic links when building Tool Shed tar files with shed_upload (thanks to Dave Bouvier). Pull Request 104
• Add a Contributor Code of Conduct. Pull Request 113
• Omit tool_test_output.json from Tool Shed tar file created with shed_upload (thanks to Dave Bouvier). Pull Request 111
• Update required version of bioblend to 0.5.3. Fixed Issue 88.
• Initial work on implementing tests cases for Tool Shed functionality. 182fe57
• Fix incorrect link in HTML test report (thanks to Martin Čech). 4c71299
• Download Galaxy from the new, official Github repository. 7c69bf6
• Update travis_test to install stable planemo from PyPI. 39fedd2
• Enable caching on --install_galaxy by default (disable with --no_cache_galaxy). d755fe7

16.89 0.6.0 (2015-03-16)

• Many enhancements to the tool building documentation - descriptions of macros, collections, simple and conditional parameters, etc...
• Fix tool_init to quote file names (thanks to Peter Cock). Pull Request 98.
• Allow ignoring file patterns in .shed.yml (thanks to Björn Grüning). Pull Request 99
• Add --macros flag to tool_init command to generate a macro file as part of tool generation. ec6e30f

16.88. 0.7.0 (2015-04-13)
• Add linting of tag order for tool XML files. 4823c5e
• Add linting of stdio tags in tool XML files. 8207026
• More tests, much higher test coverage. 0bd4ff0

16.90 0.5.0 (2015-02-22)

• Implement --version option. Issue 78
• Implement --no_cleanup option for test and serve commands to persist temp files. 2e41e0a
• Fix bug that left temp files undeleted. Issue 80
• More improvements to release process. fba3874

16.91 0.4.2 (2015-02-21)

• Fix setup.py for installing non-Python data from PyPI (required newer for tool_factory command and reStructuredText linting). Thanks to Damion Dooley for the bug report. Issue 83

16.92 0.4.1 (2015-02-16)

• Fix README.rst so it renders properly on PyPI.

16.93 0.4.0 (2015-02-16)

• Implement tool_init command for bootstrapping creation of new tools (with tutorial.) 78f8274
• Implement normalize command for reorganizing tool XML and macro debugging. e8c1d45
• Implement tool_factory command to spin up Galaxy pre-configured the Tool Factory. 9e746b4
• Added basic linting of command blocks. b8d90ab
• Improved linting of help blocks, including verifying valid reStructuredText. 411a8da
• Fix bug related to serve command not killing Galaxy properly when complete. 53a6766
• Have serve command display tools at the top level instead of in shallow sections. badc25f
• Add additional dependencies to setup.py more functionality works out of the box. 85b9614
• Fix terrible error message related to bioblend being unavailable. Issue 70
• Various smaller documentation and project structure improvements.

16.94 0.3.1 (2015-02-15)

• Fixes to get PyPI workflow working properly.
16.95 0.3.0 (2015-02-13)

- Add option (-r) to the shed_upload command to recursively upload subdirectories (thanks to E. Rasche). Pull Request 68
- Fix diff formatting in test reports (thanks to E. Rasche). Pull Request 63
- Grab updated test database to speed up testing (thanks to approach from E. Rasche and Dannon Baker). Issue 61, dff4f33
- Fix test data command-line argument name (was test-data now it is test_data). 834bfb2
- Use tool_data_table_conf.xml.sample file if tool_data_table_conf.xml.test is unavailable. Should allow some new tools to be tested without modifying Galaxy's global tool_data_table_conf.xml file. ac4f828

16.96 0.2.0 (2015-01-13)

- Improvements to way Planemo loads its own copy of Galaxy modules to prevent various conflicts when launching Galaxy from Planemo. Pull Request 56
- Allow setting various test output options in ~/.planemo.yml and disabling JSON output. 21bb463
- More experimental Brew and Tool Shed options that should not be considered part of Planemo’s stable API. See bit.ly/gxbrew1 for more details.
- Fix project_init for BSD tar (thanks to Nitesh Turaga for the bug report.) a4110a8
- Documentation fixes for tool linting command (thanks to Nicola Soranzo). Pull Request 51

16.97 0.1.0 (2014-12-16)

- Moved repository URL to https://github.com/galaxyproject/planemo.
- Support for publishing to the Tool Shed. Pull Request 6
- Support for producing diffs (shed_diff) between local repositories and the Tool Shed (based on scripts by Peter Cock). Pull Request 33
- Use tool’s local test data when available - add option for configuring test-data target. Pull Request 1
- Support for testing tool features dependent on cached data. 44de95c
- Support for generating XUnit tool test reports. 82e8b1f
- Prettier HTML reports for tool tests. 05cc9f4
- Implement share_test command for embedding test result links in pull requests. Pull Request 40
- Fix for properly resolving links during Tool Shed publishing (thanks to Dave Bouvier). Pull Request 29
- Fix for citation linter (thanks to Michael Crusoe for the bug report). af39061
- Fix tool scanning for tool files with fewer than 10 lines (thanks to Dan Blankenberg). a2c13e4
- Automate more of Travis CI testing so the scripts added to tool repository can be smaller. 20a8680
- Documentation fixes for Travis CI (thanks to Peter Cock). Pull Request 22, Pull Request 23
- Various documentation fixes (thanks to Martin Čech). 36f7cb1, b9232e5
• Various smaller fixes for Docker support, tool linting, and documentation.

16.98 0.0.1 (2014-10-04)

• Initial work on the project - commands for testing, linting, serving Galaxy tools - and more experimental features involving Docker and Homebrew, 7d07782
 CHAPTER 17

Indices and tables

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