jbiot Documentation

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CHAPTER 1

Introduction

fastq is used to clean raw fastq data. . .

CHAPTER 2

Authors

- kongdeju <kongdeju@genehe.com>

CHAPTER 3

Status

Note: not reviewed yet.

CHAPTER 4

Installation

use git to clone code:

```
git clone git@192.168.1.251:/home/git/fastqtools.git
```

Attention: if you want to run `fastqtools` on local server without docker , try to add `config.py`.

CHAPTER 5

Usage

just type command:

```
/path/to/fastqClean.py -h
/path/to/fastqStat.py -h
/path/to/fastqSplit.py -h
```

developments followed by `Dcer` rules, script will need a yaml file,which shoud contain following key and values

5.1 must_args

- **args1** desc of args2
- **args2** desc of args2

5.2 optinal args

- **args3** desc of args3

here is a sample yaml file:

```
args1: value of args1
args2: value of args2
```

CHAPTER 6

RUN

6.1 cli way

copy and paste to your input yaml file and call script:

```
/path/of/ctpips.py -c your.yml
```

6.2 serer way

send request to jbios with `/start/ctpips/`:

```
req = requests.get("http://<server>:port/ctpips/",data=json.dumps(indict))
```

for jbios detail information check api documentation here

CHAPTER 7

Code

7.1 latest

7.1.1 fastqtools package

Subpackages

fastqtools.fastqReader package

Submodules

fastqtools.fastqReader.fastqReader module

class fastqtools.fastqReader.fastqReader.**fastqReader**(*fq1*, *fq2*)

next()

class fastqtools.fastqReader.fastqReader.**fq**(*id*, *seq*, *flag*, *qual*)

fastqtools.fastqReader.fastqWriter module

fastqtools.fastqReader.fastqWriter.**fastqWriter**(*read*, *prefix*)
write reads to fastqs

Module contents

fastqtools.fastqSplit package

Submodules

fastqtools.fastqSplit.fastqMerge module

fastqtools.fastqSplit.fastqMerge.**fastqMerge**(*fqs*, *prefix*)

fastqtools.fastqSplit.fastqSplit module

fastqtools.fastqSplit.fastqSplit.**fastqSplit**(*fq1*, *fq2*, *splitNum*, *prefix*)
split Fastq in to small ones to accelerate downstreaming analysis...

fastqtools.fastqSplit.getfileNum module

fastqtools.fastqSplit.getfileNum.**getfileNum**(*afile*)

Module contents

fastqtools.fastqStat package

Submodules

fastqtools.fastqStat.fastqStat module

fastqtools.fastqStat.fastqStat.**code2score**(*code*)

fastqtools.fastqStat.fastqStat.**fastqStat**(*fq1*, *fq2*, *prefix*)

fastqtools.fastqStat.fastqStat.**qual20**(*scores*)

fastqtools.fastqStat.fastqStat.**score2code**(*score*)

fastqtools.fastqStat.getfileNum module

fastqtools.fastqStat.getfileNum.**getfileNum**(*afile*)

Module contents

fastqtools.readprocess package

Submodules

fastqtools.readprocess.readprocess module

class fastqtools.readprocess.readprocess.**readprocess**(*read*)

autoadaptremove(*flag*)

length(*lenMin*)

nbase(*percent*)

qual(*q*, *percent*)

trim(*head1*, *tail1*, *head2*, *tail2*)

umi(*umis*)

fastqtools.readprocess.tools module

fastqtools.readprocess.tools.**autocutadaptor**(*seq1*, *seq2*)

fastqtools.readprocess.tools.**checkN**(*seq*, *percent*)

fastqtools.readprocess.tools.**checking_adaptor**(*seq1*, *seq2*, *common*, *threadhold=0.95*)

fastqtools.readprocess.tools.**checkqual**(*qual*, *q_thread*, *percent*)

fastqtools.readprocess.tools.**checkumi**(*seq*, *umis*)

fastqtools.readprocess.tools.**code2score**(*code*)

fastqtools.readprocess.tools.**diffstr**(*str1*, *str2*)

class fastqtools.readprocess.tools.**dnaseq**

static complent(*seq*)

static reverse(*seq*)

fastqtools.readprocess.tools.**enlong_and_find_common**(*seq1*, *seq2*, *seed_choosed*, *mismatchMax=5*)

return best common sequences.

fastqtools.readprocess.tools.**score2code**(*score*)

fastqtools.readprocess.tools.**seeding**(*seq1*, *seq2*, *seed_len=10*, *seed_max=3*, *seed_step=1*)

find seed candidates return seeds and locus.

Module contents

Module contents

7.1.2 setup module

Setup file for jbiot.

`setup.`**`find_bins`**`()`

`setup.`**`readfile`**`(`*filename*`)`

`setup.`**`setup_package`**`()`

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