
process*fastqDocumentation*

Release 2.1.3

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PROCESS_FASTQ

This package will help process, merge and link fastq in user specified directory from manifest file

- Free software: Apache Software License 2.0
- Documentation: <https://process-fastq.readthedocs.io>.

1.1 Usage

Usage can be found here: <https://process-fastq.readthedocs.io/en/latest/usage.html>

1.2 Features

1. Given Manifest file, path to location of raw fastq, path to where they need to linked:
 - a. Get all the folders for the samples and the fastq file
 - b. Check quickly the lenght of the reads if read length is not the same use the shorter read length and trim the fastq
 - c. Merge the final fastq if comming from multiple runs.
 - d. Link all the fastq with the folder structure in user provided location

1.3 Credits

This package was created with [Cookiecutter](#) and the [audreyr/cookiecutter-pypackage](#) project template.

INSTALLATION

2.1 Stable release

To install `process_fastq`, run this command in your terminal:

```
$ pip install process_fastq
```

This is the preferred method to install `process_fastq`, as it will always install the most recent stable release.

If you don't have `pip` installed, this [Python installation guide](#) can guide you through the process.

2.2 From sources

The sources for `process_fastq` can be downloaded from the [Github repo](#).

You can either clone the public repository:

```
$ git clone git://github.com/rhshah/process_fastq
```

Or download the [tarball](#):

```
$ curl -OL https://github.com/rhshah/process_fastq/tarball/master
```

Once you have a copy of the source, you can install it with:

```
$ python setup.py install
```


USAGE

To use `process_fastq` in a project:

```
import process_fastq
process_fastq.run(sample_id, request_id, run_id, fastq_path, output_path, cutadapt_
↳ path)
```

To use `process_fastq` from cli:

```
Usage: process_fastq [OPTIONS]

Options:
  -s, --sample-id TEXT          Sample id to get the fastq files can be
                                either IGO sample id or Investigator sample
                                id (eg: -s EDD_ret_pt049_cf02) [required]
  -p, --request-id TEXT         IGO request id to get the fastq files.
                                (eg: -p Project_05500_GB or -p 05500_GB)
  -r, --run-id TEXT             Run id to get the fastq files, can be
                                specified multiple times (eg: -r PITT_0376 -r
                                PITT_0378)
  -fp, --fastq-path PATH        Full path to fastq files [required]
  -op, --output-path PATH       Full path to where we link the output files
                                [required]
  -cp, --cutadapt-path PATH     Full path to location of cutadapt executable
                                [required]
  -l, --expected-read-length INTEGER Expected read length from the fastq file
  --version                     Show the version and exit.
  -v, --verbosity LVL          Either CRITICAL, ERROR, WARNING, INFO or
                                DEBUG
  --help                       Show this message and exit.
```

Example commandline:

```
$ process_fastq \
-p request_id \
-s smaple_name \
-r RunID \
-fp /path/to/fastq/directory \
-op /path/to/output/directory \
-cp /path/to/cutadapt
```

To use `link_fastq_juno.py` from cli:

Usage: `link_fastq_juno.py` [OPTIONS]

Options:

- m, --manifest-file PATH** Manifest file having information about run id and sample id to get the fastq files (eg: -m Project_05500_GB_manifest.xlsx) [required]
- p, --request-id TEXT** IGO request id to get the fastq files. (eg:-p Project_05500_GB or -p 05500_GB) [required]
- fp, --fastq-path PATH** Full path to fastq files [required]
- op, --output-path PATH** Full path to where we link the output files [required]
- cp, --cutadapt-path PATH** Full path to location of cutadapt executable [required]
- pfp, --process-fastq-path PATH** Full path to location of cutadapt executable [required]
- l, --expected-read-length INTEGER** Expected read length from the fastq file
- version** Show the version and exit.
- v, --verbosity LVL** Either CRITICAL, ERROR, WARNING, INFO or DEBUG
- help** Show this message and exit.

Example commandline:

```
$ python3 link_fastq_juno.py \  
-p request_id \  
-m /path/to/manifest.xlsx \  
-pfp /path/to/process_fastq \  
-fp /path/to/fastq/directory \  
-op /path/to/output/directory \  
-cp /path/to/cutadapt
```

CONTRIBUTING

Contributions are welcome, and they are greatly appreciated! Every little bit helps, and credit will always be given. You can contribute in many ways:

4.1 Types of Contributions

4.1.1 Report Bugs

Report bugs at https://github.com/rhshah/process_fastq/issues.

If you are reporting a bug, please include:

- Your operating system name and version.
- Any details about your local setup that might be helpful in troubleshooting.
- Detailed steps to reproduce the bug.

4.1.2 Fix Bugs

Look through the GitHub issues for bugs. Anything tagged with “bug” and “help wanted” is open to whoever wants to implement it.

4.1.3 Implement Features

Look through the GitHub issues for features. Anything tagged with “enhancement” and “help wanted” is open to whoever wants to implement it.

4.1.4 Write Documentation

`process_fastq` could always use more documentation, whether as part of the official `process_fastq` docs, in docstrings, or even on the web in blog posts, articles, and such.

4.1.5 Submit Feedback

The best way to send feedback is to file an issue at https://github.com/rhshah/process_fastq/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.
- Remember that this is a volunteer-driven project, and that contributions are welcome :)

4.2 Get Started!

Ready to contribute? Here's how to set up *process_fastq* for local development.

1. Fork the *process_fastq* repo on GitHub.
2. Clone your fork locally:

```
$ git clone git@github.com:your_name_here/process_fastq.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:

```
$ mkvirtualenv process_fastq
$ cd process_fastq/
$ python setup.py develop
```

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, including testing other Python versions with tox:

```
$ flake8 process_fastq tests
$ python setup.py test or py.test
$ tox
```

To get flake8 and tox, just pip install them into your virtualenv.

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.

4.3 Pull Request Guidelines

Before you submit a pull request, check that it meets these guidelines:

1. The pull request should include tests.
2. If the pull request adds functionality, the docs should be updated. Put your new functionality into a function with a docstring, and add the feature to the list in README.rst.
3. The pull request should work for Python 2.7, 3.4, 3.5 and 3.6, and for PyPy. Check https://travis-ci.org/rhshah/process_fastq/pull_requests and make sure that the tests pass for all supported Python versions.

4.4 Tips

To run a subset of tests:

```
$ python -m unittest tests.test_process_fastq
```

4.5 Deploying

A reminder for the maintainers on how to deploy. Make sure all your changes are committed (including an entry in HISTORY.rst). Then run:

```
$ bumpversion patch # possible: major / minor / patch
$ git push
$ git push --tags
```

Travis will then deploy to PyPI if tests pass.

CREDITS

5.1 Development Lead

- Ronak Hasmukh Shah <rons.shah@gmail.com>

5.2 Contributors

None yet. Why not be the first?

HISTORY

6.1 2.1.0 (2020-03-12)

- Modifying to suite new access workflow.

6.2 0.1.0 (2019-07-25)

- First release on PyPI.

INDICES AND TABLES

- `genindex`
- `modindex`
- `search`