proatac Documentation

Release 0.2.1

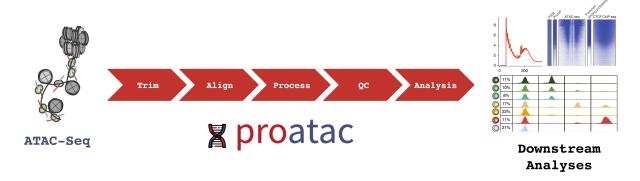
Caleb Lareau

Contents

1	About	1
_	Installation2.1Install stable version through PyPi2.2Install via GitHub	3 3 3
3	Dependencies 3.1 Getting proatac running	5 5
	Revisions 4.1 Revision history	7 7
5	Author	9
6	Citation	11
7	Bugs / Errors	13

About

proatac is an open-source command-line toolkit that performs robust and scalable preprocessing of ATAC-Seq data. Specifically, we've implemented our workflow using



2 Chapter 1. About

Installation

Install stable version through PyPi

There are a few dependencies needed to get **proatac** to run. All are very common bioinformatics tools / languages and should be readily available in most systems. However, **note that the current implementation of proatac is not supported on Windows platforms**.

Depending on your python environment, we generally recommend using a virtual environment to keep python dependencies tidy. An example of installing **proatac** inside a new python virtual environment called venv3 using the following sequence of commands—

```
python3 -m venv venv3
source venv3/bin/active
pip3 install proatac
```

Install via GitHub

Though **not recommended**, a bleeding-edge (development) version can be installed directly from Git. Again using a virtual environment—

```
python3 -m venv venv3
source venv3/bin/active
pip3 install git+ssh://git@github.com/buenrostrolab/search/tree/master/proatac
```

While installing **proatac** is obviously a great first step, make sure that all of the dependencies are met. Check out the next page for more detail.

Dependencies

Getting proatac running

proatac has a few dependencies that are listed below with relevant hyperlinks for installation instructions from the source. To quickly determine what may be lacking in your system, try running **proatac** with the default.yaml file (more on that *here*) using the --check flag. To do this, we'll first clone the repository

```
git clone https://github.com/buenrostrolab/proatac.git
proatac yaml/default --check
```

If you get a message saying that the check was successful, then you're most likely ready to begin analyzing data. However, if you run into one or more error messages, you are likely missing the necessarily software. Make sure that

- · bedtools
- bowtie2 and relevant index for analysis.
- java language
- macs2

We note that macs2 though also a PyPi package is only compatible with Python 2.7 whereas **proatac** is a Python 3 package. There's a good chance that macs2 is already living in your environment if you are reading this help page, which can be tested using the following—

```
which macs2
```

and hopefully seeing a valid path. If not, one solution for macs2 install is to create a separate python2 virtual environment using the following commands –

```
python2 -m venv venv2
source venv2/bin/active

pip install numpy
pip install wheel
pip install macs2
```

- R language and package dependencies (see wiki/Rpackages for more information).
- samtools

Revisions

Revision history

Maybe **bold** *this* will work?

New header?

two

three

four

CHAPTER \$	_)
------------	--------

Author

The primary developer is Caleb Lareau in the Buenrostro Lab.

10 Chapter 5. Author

CHAP	TED	h
UNAL		V

Citation

If you use **proatac** in your research, please cite our tool at the following URL:

http://buenrostrolab.com/proatac

12 Chapter 6. Citation

	CHAPTER 7
	Bugs / Errors