SwiftSeq Documentation

Release 1.0.3

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Aug 27, 2018

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CHAPTER 1

Getting Started

To install with pip:

```
$ pip install swiftseq
```

Or to get the latest development version:

```
$ pip install git+https://github.com/PittGenomics/SwiftSeq@dev
```

> **Caution:** The development version may not be stable

Once SwiftSeq is install, software dependencies can be installed with Bioconda:

```
$ swiftseq install-env
```

This will produce an `executables.config` file that the user can pass directly into a SwiftSeq run.

> **Note:** The above command will only work if the user has Anaconda/Miniconda installed. It's provided as a convenience; if the user would rather install software dependencies manually, Swiftseq only needs an `executables.config` at runtime and is indifferent to where it comes from.

The user can then run Swiftseq:

```
swiftseq run --exe-config /path/to/executables.config [options]
```