

# RADish

Scripts aiding file processing and analysis of RADseq and GBS data

## LICENSE

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## CITATION

If you use scripts from this repository as part of your published research, I require that you cite the repository as follows (also see DOI information below):

- Bagley, J.C. 2017. RADish. GitHub repository, Available at: <http://github.com/justincbagley/RADish>.

Alternatively, please provide the following link to this software repository in your manuscript:

- <https://github.com/justincbagley/RADish>

### fastq\_ReadLengthChecker

Example usage code and output to screen during a `fastq_ReadLengthChecker.sh` run, in which reads were discovered to range from 78 bp to 140 bp in length:

```
$ ./fastq_readLengthChecker.sh .

#####
#                               fastq_ReadLengthChecker v0.1.0, February 2018                               #
#####

INFO      | Wed Feb 21 17:58:12 EST 2018 | Found 1123 .fastq files in current working directory.
INFO      | Wed Feb 21 17:58:12 EST 2018 | Shortest read length: 78 bp
INFO      | Wed Feb 21 17:58:12 EST 2018 | Longest read length: 140 bp
INFO      | Wed Feb 21 17:58:12 EST 2018 | Results output to 'fastq_lengths_summary.txt' in current working direc
INFO      | Wed Feb 21 17:58:12 EST 2018 |
INFO      | Wed Feb 21 17:58:12 EST 2018 | ...Cleaning up workspace...
INFO      | Wed Feb 21 17:58:12 EST 2018 |
INFO      | Wed Feb 21 17:58:12 EST 2018 | Done checking fastq read lengths.
INFO      | Wed Feb 21 17:58:12 EST 2018 | Bye.
```

### fastqTrimmer

Example usage code and output to screen during a `fastqTrimmer.sh` run, in which all fastq files within the working directory were trimmed down to the first 1-91 bases:

```
$ ./fastqTrimmer.sh -l 91 .

#####
```

```
#                               fastqTrimmer v0.1.0, February 2018                               #
#####

INFO      | Thu Feb 22 09:32:59 MST 2018 | STEP #1: SETUP.
INFO      | Thu Feb 22 09:32:59 MST 2018 |           Setting working directory to: .
INFO      | Thu Feb 22 09:32:59 MST 2018 | STEP #2: TRIMMING READS.
INFO      | Thu Feb 22 09:32:59 MST 2018 |           Trimming reads in all .fastq files in current directory. Trim
INFO      | Thu Feb 22 09:32:59 MST 2018 |           ./trimmed_fastq/, and original fastq files will be moved to .,
./APA1_1.R1.fastq
./APA1_2.R1.fastq
./APA1_3.R1.fastq
./APA1_4.R1.fastq
./APA1_5.R1.fastq
./APA1_6.R1.fastq
./APA1_7.R1.fastq
./APA1_8.R1.fastq
./CAP1H_10.R1.fastq
./CAP1H_1.R1.fastq
./CAP1H_2.R1.fastq
./CAP1H_3.R1.fastq
./CAP1H_4.R1.fastq
./CAP1H_5.R1.fastq
./CAP1H_6.R1.fastq
./CAP1H_7.R1.fastq
./CAP1H_8.R1.fastq
./CAP1H_9.R1.fastq
./CAP1L_10.R1.fastq
./CAP1L_1.R1.fastq
.
.
.
```

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