

Trimmomatic installation and usage example

Installing Trimmomatic on AWS (t2.micro instance size):

```
$ wget http://www.usadellab.org/cms/uploads/supplementary/Trimmomatic/Trimmomatic-0.38.zip
```

```
$ unzip Trimmomatic-0.38.zip
```

The above generates the folder Trimmomatic-0.38

Running Trimmomatic:

General command:

```
$ java -jar trimmomatic-0.35.jar PE -phred33 input_forward.fq.gz input_reverse.fq.gz  
output_forward_paired.fq.gz output_forward_unpaired.fq.gz output_reverse_paired.fq.gz  
output_reverse_unpaired.fq.gz HEADCROP:20 SLIDINGWINDOW:4:30 MINLEN:30
```

Note that two output files per input file are generated *paired.fq.gz and *unpaired.fq.gz. In the *paired.fq.gz files you will find the reads for which both reads in the pair survived the processing. In the *unpaired.fq.gz files are the reads for which the other read in the pair did not survive the processing. You will typically only need the *paired.fq.gz files for your downstream analyses.

Specific command (using the same data as in Exercise 3):

```
$ java -jar trimmomatic-0.35.jar PE -phred33 SRR4114395_1.fastq.gz SRR4114395_2.fastq.gz  
SRR4114395_1_paired.fq.gz SRR4114395_1_unpaired.fq.gz SRR4114395_2_paired.fq.gz  
SRR4114395_2_unpaired.fq.gz HEADCROP:20 SLIDINGWINDOW:4:30 MINLEN:30
```