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Data Protection

for Illumina NGS data

Citations

Bolger, A. M., Lohse, M., & Usadel, B. (2014). Trimmomatic: A flexible trimmer for Illumina Sequence Data. *Bioinformatics*, btu170.

Downloading Trimmomatic

starting on version 0.40 we also offer a [github page](#) (as well as older versions)

Version 0.39: [binary](#), [source](#) and [manual](#)

Version 0.36: [binary](#) and [source](#)

Quick start

Paired End:

With most new data sets you can use gentle quality trimming and adapter clipping.

You often don't need leading and traling clipping. Also in general setting *keepBothReads* to True can be useful when working with paired end data, you will keep even redunfant information but this likely makes your pipelines more manageable. Note the additional :2 in front of True (for keepBothReads) this is the minimum adapter length in palindrome mode, you can even set this to 1. (Default is a very conservative 8)

If you have questions please don't hesitate to contact us, this is not necessarily one size fits all. (e.g. RNAseq expression analysis vs DNA assembly).

```
java -jar trimmomatic-0.39.jar PE input_forward.fq.gz
input_reverse.fq.gz output_forward_paired.fq.gz
output_forward_unpaired.fq.gz
```