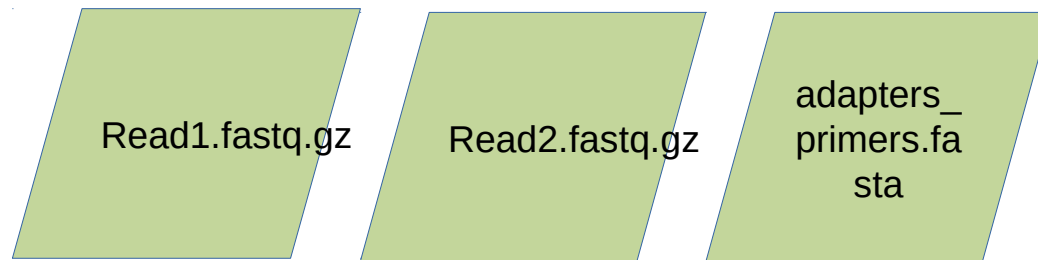


Input:



Raw read files. List of sequences added during the library

java program to run

Paired-end mode

Save log file.

Raw read files

Command Line:

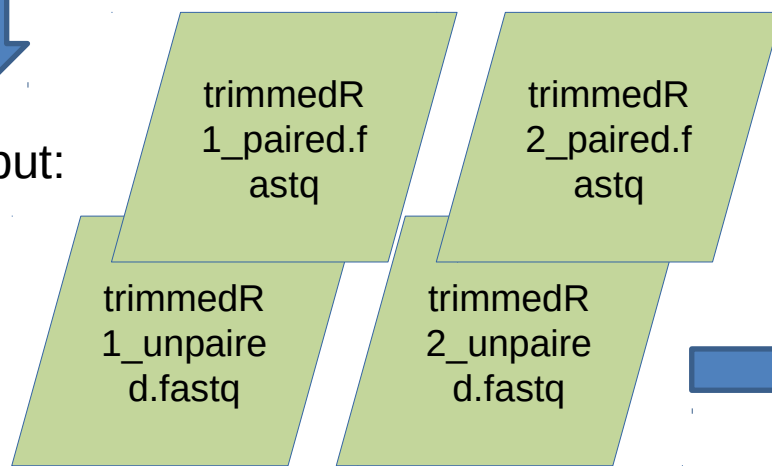
```
java -jar trimmomatic-0.33.jar PE -threads 10 -trimlog trim.log Read1.fastq.gz Read2.fastq.gz \
trimmedR1_paird.fastq trimmedR1_unpaired.fastq trimmedR2_paird.fastq trimmedR2_unpaired.fastq \
ILLUMINACLIP:adapters_primers.fasta:2:30:10 LEADING:3 TRAILING:3 SLIDINGWINDOW:4:15 MINLEN:30
```

Output files

Remove these sequences from reads

Trim reads based on quality

Output:



De novo  
assembly

Discard for  
this  
analysis

High quality reads, containing only viral sequence.  
Ready for de novo assembly.