

We can now align the viral reads to a known reference sequence.

Sequence of the reference strain (already known).



Quality Viral Reads,
from the previous step.

- **Use the “bwa” program to map the viral reads to the known reference assembly.**

trimmed
R1_pair
ed.fastq

trimmed
R2_pair
ed.fastq

Reference
genome,
indexed for
use with bwa

- Start with quality reads and a reference genome.
- Use bwa mem to align the reads to the reference.
- Save the output in a .sam file, which links the read to a location in the reference genome where the read aligns.

Mapping
algorithm

Name of
reference.

Name of files to
process

```
bwa mem ebola_ref trimmedR1_paired.fastq trimmedR2_paired.fastq \  
> Prelim_alignment.sam
```

Save output in a .sam file.

Prelim_alig
nment.sam



Continue Reference
Based Assembly