

alignment
.sam

- Read in the preliminary assembly.
- Use “bcftools consensus” to make a new fasta with the corrected sequences.

Read in the
preliminary assembly

Make a new fasta
containing the corrected
sequences

The .vcf file containing
list of changes to make.

Save the new assembly

```
cat prelim_assembly.fasta | bcftools consensus mpileup.vcf.gz > final_assembly.fasta
```

Assemble the
viral genome.



SNP-analysis,
phylogenetics