

- **Align the final assembly to the reference genome.**
- **This alignment will be used as input for the phylogenetic analysis.**

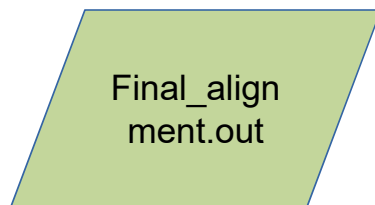
Read in the preliminary assembly

Run another aligner: mafft

Reference Genome

Save the alignment file.

```
cat final_assembly.fasta | mafft ebola_ref.fasta > Final_alignment.out
```



SNP-analysis,  
phylogenetics