

# Sequence Alignment and Tree Building

## UGENE

The following video illustrates the tree building process using MUSCLE and PhyML in [UGENE](#).

## Command Line

The following requires:

- A UNIX-like environment like Linux or MacOS
- [MUSCLE](#) to perform a multiple sequence alignment
- [PhyML](#) to generate Maximum Likelihood
- [FigTree](#) to manipulate the tree

Download the example file [oranges](#). In the download directory, perform the following:

```
unzip orange.zip cd orange cat ./*txt >> oranges.fasta ## merges all files into a single fasta file muscle -in oranges.fasta -phyiout oranges.phy ## -phyiout tells muscle to use the interleaved phylip format for output phyml -i oranges.phy -m HKY85 ## -m is for method and HKY85 is the default nucleotide method we used in UGENE mv oranges.phy_phyml_tree.txt oranges.nwk ## change the name of the output to reflect it is a nwk file
```