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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
phym1 -i oranges.phy -m HKY85
## -m is for method and HKY85 is the default nucleotide method we used
in UGENE
mv oranges.phy_phym1_tree.txt oranges.nwk
## change the name of the output to reflect it is a nwk file
```