**Creating a Phylogenetic Tree from DNA Sequences (.fasta files)**

1. Remove all the gaps (eg. “------”) from the DNA (a quick search and replace will do the job.)

*Optional step: Having a text editor could make this job easier if you do not already have one. I've heard* [*text wrangler*](https://www.barebones.com/products/textwrangler/download.html) *is a good program for macs.*

2. Add the sequences you trimmed to this file in fasta format

3. Align them all in [mafft](https://mafft.cbrc.jp/alignment/server/).

4. Check them on an alignment viewer of your choice for quality control.

5. If all looks good then upload them to [IQTree](http://iqtree.cibiv.univie.ac.at/)

6. View your final tree on a tree viewer. I use [figtree](http://tree.bio.ed.ac.uk/software/figtree/).