- dN/dS methods can be used to both handle some residual MSA error during selection screens and also find it in alignments
- The structure of the underlying substitution model can be adjusted to reflect more biological realism (e.g. MNM)
- Can identify specific genes and/or species which have higher putative errors

- Implemented in the HyPhy package
- Not computationally cheap, but delivers a useful result while screening for errors
  - The main cost growth dimension is the # of genomes
  - For 32 genomes, per MSA run time is on the order of 1-10 minutes per core

# Break