**Learning Objectives**

After this week’s class you are expected to able to do the following:

1. Apply the scientific definition of a **model** to identify or describe types of models
2. Demonstrate comprehension of basic model components. Including…
   1. Parameters
   2. Relationships/operations
   3. Assumptions
3. Evaluate models based on the criteria…
   1. Interpolative ability
   2. Extrapolative ability
   3. Simplicity
   4. ~~Congruence~~
4. Apply the definition of parsimony to the problem of finding the best model
5. Compare and contrast frequentist and Bayesian approaches to statistics
6. Compare parsimony to statistical methods in the context of finding the best model
7. Demonstrate comprehension of (computational) heuristics and explain why they are necessary.
8. Build a Markov-Chain Monte-Carlo (MCMC) simulation for the purpose of finding the maximum likelihood model for a given problem
9. Describe “model space” (or tree space). ~~and how it relates to three major methods of searching for the best model in the context of phylogenetics~~ Additionally…
   1. Compare and contrast **local maxima** versus **global maxima** and what it means to be “trapped in a local maxima”
10. Compare and contrast **parsimony**, **likelihood** and **Bayesian** in their relationship and application to modelling
11. Identify some evolutionary patterns that models can be applied to infer. Including…
    1. Nucleotide substitution
    2. Morphological change
    3. Ancestral states
    4. Phylogenetic relationships
    5. Divergence times
    6. ~~Selection pressure~~
12. Demonstrate a basic comprehension of some common components of evolutionary models. Including…
    1. Parsimony
    2. Symmetrical or asymmetrical nucleotide substitutions
    3. Brownian motion
    4. Rate heterogeneity
    5. Codon position
    6. Phylogenetic relationships
    7. ~~Coalescence~~
13. Utilize the **phangorn** and **ape** R packages to apply evolutionary models to DNA (or protein) data and assess their fit