**Learning Objectives**

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

1. Apply the definition of **bioinformatics** to various research in biology. Additionally, …
   1. Demonstrate comprehension of the definition in the context of phylogenetics
   2. Explain that bioinformatics is not just applicable to phylogenetics
2. Define **BLAST**, and utilize it for…
   1. **Identifying molecular sequences** of unknown origin
   2. **Annotation** of single sequences (or sets of sequences)
3. Evaluate the process of **annotation**, how it applies to different types of molecular data, and how certain methods might differ
4. Evaluate the importance of **BLAST and genome annotation** for modern applications in bioinformatics
5. Utilize **NCBI GenBank** to obtain desired molecular sequence data
6. Synthesize your knowledge to carry out **a phylogenetic analysis** on a given set of taxa or genes. This includes knowledge of…
   1. Phylogenetic pipelines
   2. **MCMC**
   3. **Heuristics**
   4. **Maximum likelihood**
   5. Coding in R
7. ~~Evaluate the importance of assessing support for phylogenetic relationships using multiple methods~~
8. ~~Interpret metrics of statistical support for relationships and trees~~