



### TIPS FOR FINAL PROJECT

#### FINAL PROJECT

I hope you had a great time during Dr. Dentinger's talk! And I hope you had an epiphany during the week and are already playing around with your final dataset. To ensure adequate progress is being made, you are still expected to put on some work outside of scheduled class times throughout the rest of the semester and contact me (anytime!) if progress can be improved. The Project is expected to contain:

- Introduction (with the question of interest or what are you investigating): 2-3 short paragraphs
- Material & Methods: 4 paragraphs, be verbose
- Results and Discussion (including phylogenetic tree(s) edited as **publication-ready** figure(s) – legends required!): 4-5 paragraphs
- References (list with at least five solid literature sources – no Wikipedia accepted, but Wikipedia does provide direct links to sources. I recommend [Google Scholar](#))

The final Project is expected to have at least three pages of text plus three figures, or 2,500 words plus three figures.

The **two most important sections** are M&M and Results. For M&M, you are required to:

- List the repository from where you have retrieved the sequences (for example, GenBank) and also how did you conduct the search for said sequences;
- How many ingroup terminals, how many outgroups;
- How did you align your data and algorithms (including the program you used to translate nucleotides to protein, etc.)
- What methods did you utilize to analyze your data. You must use at least two reconstruction methods: MP, ML, or BI. Preference should be given to ML and BI, considering you'd probably be working with molecular data (including all parameters you utilize, how many partitions (if using more than one marker), how many runs, what measure of support, etc. Be verbose here as I will attempt to replicate your runs! Include references for the programs you used.
- What comparative method did you utilize to analyze your data. You must use at least one comparative method (e.g., mapping traits into trees, co-phylogeny, character evolution).
- Where did you run your analyses (local computer, CIPRES, lab, etc.)
- How did you organize your outputs (FigTree, R packages, etc.). If using R, mention package (with reference) and functions/commands.

For Results & Discussion, you are required to:

- At least: size of your final alignment, how many terminals, how many parsimony-informative sites
- Topology: spend time describing the topology, then the support for clades. For example, X and Y were recovered as sister taxa with high support (UFB: 100, PP: 95).
- Figures (emphasis on figures!)
- What did you reveal with the comparative method. Important discoveries, speculation

For references, please format them uniformly. I suggest using [the APA](#) style.

### **Important Dates for Final Project:**

**Step 1:** Make sure to have your analyses done by the end of the month. Please reach out if you need any kind of feedback!

**Step 2:** The Final Project should be uploaded to Canvas or emailed to me as a PDF before the deadline of May 4. Late assignments will only be worth 80%. NO extensions, NO exceptions. Further, it is up to you to check and ensure that you uploaded the correct file on time. You are also expected to submit your final dataset (i.e., aligned and ready-to-run matrix; if you ran MrBayes or any other program that uses Nexus blocks, please send those NEXUS files as well) so I can replicate your analyses. You can (and are expected to) request progress checks during any time of the Project (besides a day before the submission). The Final Project is worth 400 points.

**Step 3:** The final projects will be presented as a short (5-10 minutes per student) seminar to the class during a "Phylogenetics Symposium" (April 27), where students are expected to present five slides (PowerPoint, PDF, or preferred format) mirroring their written Final Project. It is worth 70 points, so make sure it looks nice!

### **IMPORTANT POINTS**

Analyses: please **do not** wait until the last week to analyze your data. I won't be able to help you troubleshoot if you send me stuff a day before the deadline.

We will use classes on the 18th and 20th of this month – and the 27th if we have time – to troubleshoot analyses or make them run. We can also set up extra hours or office hours to work together on your analyses if needed. You are expected to be proactive – but don't stress too much; the goal here is to design a small paper where you can showcase your understanding of molecular phylogenetics 😊