Term Project

This course is designed to teach you the theory behind phylogenetic analysis, the methods used to infer evolutionary relationships, and the critical skills required to interpret phylogenetic trees.

Throughout the semester, you will **analyze a phylogenetic dataset** in order to complete a term project which is divided into three assignments: an outline, an explanation of your methods, and a final paper. In addition to the fundamental goals of this course, these assignments will help you develop writing skills

If you have questions, or need help with any aspect of the project, you can email the instructors to arrange a meeting.

All assignments should be handed in via Quercus by 11:59 PM on the due date.

Assignment	Due Date
Choose Datasets	27 January 2021
Outline	10 February 2021
Methods	10 March 2021
Final Paper	13 April 2021

Datasets

Datasets for this project will be provided - please **sign up for a dataset using the discussion board on Quercus** by **January 27th**. If you have your own data that you would prefer to work with, email the professors with a description of the dataset as soon as possible.

Although **we encourage you to discuss your work with your peers**, each student must complete their own project in accordance with the University of Toronto's Academic Integrity Policy.

Assignment One: Outline

In the form of an outline, address the following questions. Be sure to cite the literature where necessary. Do not write in full paragraphs; your outline should be **250-500 words** long.

> i) Why is it important to consider phylogenetic relationships when studying evolution? What are some potential risks of failing to consider a phylogeny?

> ii) What questions can be answered using a phylogenetic tree? Provide 2-3 examples of specific questions that could be answered about the taxa in your dataset using a tree alone, or in combination with other data for those taxa. Why is a phylogenetic approach valuable/necessary for these questions?

Goals: As with any outline, the purpose of this assignment is to evaluate the hierarchy, structure, and logic of your writing. Outlines should **focus on the content** of your argument rather than the way your arguments are communicated. This outline will ultimately be used as the introductory portion of your final paper: the more complete the outline, the easier it will be to write.

Due Date: 10 February 2021

Assignment Two: Methods

In **500 words or less**, describe your dataset and the reasoning behind the methods you have chosen, and explain the methods you will use to analyse your data. The format should follow that of the Material and Methods section of a scientific publication, and you should give enough detail to ensure your analyses are **reproducible**. Include the following information, as well as appropriate justification for, and explanation of, any additional analyses you may wish to perform (*e.g.* topology tests, constrained tree searches, etc.):

> i) Give a brief description of your dataset, including the number and type of loci, as well as accession numbers for publicly available data; the taxa included; and the outgroup(s) you have chosen
>
> ii) Explain your analyses:
>   a) Alignment
>   b) Model testing
>   c) Infer a phylogeny using at least two optimality criteria; explain the relative strengths of each criterion, and the advantage of inferring trees using multiple methods
>
> iii) Be sure to give version numbers and citations for all programs you use

Goals: Demonstrate your understanding of the most commonly used phylogenetic methods, in terms of their utility and their practical application. Your methods section will guide you in your analyses, and be incorporated into your final paper.

Due Date: 10 March 2021

Assignment Three: Final Paper

After using your dataset to complete the analyses you specified in assignment two, write a **4 - 6 page** paper explaining **the importance of evolutionary relationships** and phylogenetic analyses to the study of ecology and evolutionary biology, as well as the **results and implications of your own analyses**. As always, cite the literature wherever necessary. Include the following components:

i) Introduction
This should be fleshed out from the outline you created for **Assignment One**, incorporating any feedback from the professors

ii) Materials & Methods
For this section, you may use **Assignment Two**, incorporating any feedback you received. If you have added additional analyses or made changes to the methods laid out in your initial assignment, make sure those changes are reflected here.

iii) Results
Describe your results. You should list the models used in your analyses; give an impression of support values; include the relevant scores (e.g. tree length, likelihood…) for your trees; and detail notable results from any other analyses you may have done. Your results do not have to be comprehensive: choose **3 - 6 of the most interesting findings** to focus on.

iv) Discussion
Interpret the results of your analyses and what can be learned from them. Compare trees inferred under different optimality criteria, and discuss the robustness, evolutionary implications, and potential significance of your results.

v) Figures and Tables
Show your **trees and tables/figures for any other analyses you may have conducted** (e.g. topology tests, pairwise distances, etc.). Trees should be included as a PDF or image file and must display support values. All figures should be accompanied by captions which include enough information that they can be understood without reading the paper. **Figures and tables will not contribute to the page count** of your paper.

vi) References
In-text citations and reference list should follow APA format. Your **reference list will not contribute to the final page count** of your paper.

vii) Appendix
Include .tre files and log files for all phylogenetic analyses.

Goals: This project allows you to demonstrate your knowledge and understanding of the importance of phylogenetic systematics (both in its own right, and as a tool for exploring other evolutionary questions); your knowledge of the theory and methods used in phylogenetic analysis, including the relative strengths and weaknesses of those methods; and your ability to interpret phylogenetic trees.

Due Date: 13 April 2021