BIOL 417 – Phylogenetic Biology

General Course Syllabus (as of April 2019)

About the Course:

Course Description: Biol 417 is a course designed to help biology students to develop "tree" thinking skills and to learn about modern practices for building and making inferences from phylogenetic trees.

Course Format: Lecture and Tutorial. The course consists of 3 lecture hours per week and a 2 hour tutorial. The tutorial focuses on problem sets to reinforce material taught in lecture and hands-on computational exercises using various phylogenetics software.
Credits: 3
Pre-requisites: BIOL 200 and one of BIOL 233, BIOL 234 (BIOL 336 is recommended)

Course Learning Objectives:

By the end of the course, students should be able to:

Part A: Phylogeny basics

- Know basic tree terminology (e.g., tips / branches / nodes / root / ancestor / descendant / MRCA)
- Interpret the historical relationships between lineages given a phylogenetic tree (e.g., A is more closely related to B than it is to C)
- Recognize monophyly, paraphyly, and polyphyly
- Distinguish between rooted and unrooted trees
- Identify common misconceptions about trees (e.g., basal lineages / ancestral species)
- Recognize and define a synamorphy and homologous characters
- Describe what is meant by Linnean taxonomy and discuss some advantages and disadvantages of this system and discuss how modern taxonomy is related to phylogeny

Part B: Phylogeny estimation

- Describe the general procedure for finding the best phylogenetic tree
- Calculate probabilities using the addition and multiplication rules and identify if events are mutually exclusive
- Explain the assumptions of the common models of molecular evolution
- Write down a likelihood for a phylogeny given a model of molecular evolution
- Use Bayes Theorem and the Law of Total Probability to calculate conditional probabilities

- Describe the rules (steps) of a Markov Chain Monte Carlo (MCMC) and explain what the purpose of using this technique is (i.e., why do we need to do this?)
- Distinguish between bootstrap values and posterior probabilities and explain how each of these are obtained and what they measure
- Identify advantages and disadvantages of using Bayesian approaches to estimate phylogenies compared to using Maximum Likelihood
- Read a paragraph from the methods section of a paper and identify the major analyses that were conducted to infer the phylogeny

Part C: Making inferences from phylogenetic trees

- Describe some reasons that we may have estimated an incorrect topology
- Distinguish between gene trees and species trees
- Explain the evolutionary processes that lead to variation among gene trees
- Outline some strategies for estimating a species tree from gene trees
- Explain the idea behind the "molecular clock" and how we can estimate divergence times
- Highlight some advantages and limitations of using phylogenetic trees and the fossil record to study patterns of speciation and extinction
- Explain why phylogeny needs to be taken into account when estimating correlations between characters measured on different species
- Explain what pseudoreplication is and how the concept applies to interspecific comparisons
- Identify the method(s) that are used to test for evolutionary relationships between characters
- Calculate phylogenetic diversity (PD) and evolutionary distinctiveness (ED) from a simple tree and discuss some potential benefits of targeting conservation efforts towards evolutionarily distinct lineages

Textbooks and Additional Resources:

No textbook is necessary for the course. Primary research papers are used in this course but they will be distributed to students.

Evaluation:

The course grade is calculated as follows:

Assessment	Weight
Midterm	30%
Final exam	40%
Tutorial exercises	9%
Assignments (x3)	21%

This syllabus is a general representation of the course as previously offered and is subject to change.

Schedule of Topics:

See topics under *Course Objectives* above.

Course Policies:

There will be two exams: a midterm in class and a final exam during the exam period. If a student misses the midterm with a legitimate excuse (either by pre-arrangement or an acceptable medical emergency with doctor's note), there will be no make-up exam; rather, the final exam will count for 70% of the total grade. The instructors will not regrade questions on the tutorial exercises or assignments. If a student believes that they deserve additional marks on an exam I will regrade the entire exam.

University Policies:

UBC provides resources to support student learning and to maintain healthy lifestyles but recognizes that sometimes crises arise and so there are additional resources to access including those for survivors of sexual violence.

UBC values respect for the person and ideas of all members of the academic community. Harassment and discrimination are not tolerated nor is suppression of academic freedom.

UBC provides appropriate accommodation for students with disabilities and for religious, spiritual and cultural observances.

UBC values academic honesty and students ae expected to acknowledge the ideas generated by others and to uphold the highest academic standards in all of their actions.

Details of the policies and how to access support are available on the UBC Senate website.