

**Phylogenetic Biology**  
**Biol 1425**  
**SPRING 2013**  
**BROWN UNIVERSITY**

**Professor:** Casey Dunn

**Time:** Monday 3:00-4:00 (section), Wednesday 2:30-4:50pm (seminar)

**Location:** First floor conference room, Walter Hall (80 Waterman St.)

**Contact:** casey\_dunn@brown.edu. Please prefix the subject line of e-mails related to the class with “phylobio:”

**Office Hours:** W 12:30-2:00pm, Walter Hall (80 Waterman St.) Room 301

## Overview and Objectives

Phylogenetic Biology is the study of the evolutionary relationships between organisms, and the use of evolutionary relationships to understand other aspects of organism biology. This course will survey phylogenetic methods, providing a detailed picture of the statistical, mathematical, and computational tools for building phylogenies and using them to study evolution. We will also examine the application of these tools to particular problems in the literature and emerging areas of study.

This seminar will include lectures by the professor, as well as student presentations and frequent open discussions.

## Enrollment

Enrollment is capped at 16 students, and registration requires instructor permission. To request a spot, please fill out the online form at <http://goo.gl/v6w0E> before November 6, 2012.

## Prerequisites

Students are expected to have taken classes in:

- Statistics (eg Biol 0495)
- Evolutionary Biology (eg Biol 0480, 0410, 0430, 1430, 1485)

Exceptions will be made if students can demonstrate proficiency in these areas, or in closely related areas such as computer science and math.

## Assignments and grading

- **Final Project, 40%** . Each student will conduct their own phylogenetic study, which could include development of a new method, reconstructing the phylogeny of a particular group of organisms, examining the evolution of one more more characters on a tree, or examination of the behavior of a particular method. The final project will be summarized as a scientific paper in PLoS One format, see <http://www.plosone.org/static/guidelines.action> for formatting details. In addition, each student will make a 10 minute presentation summarizing their work.
- **Analysis assignments, 20%** . There will be several take-home phylogenetic analysis assignments. These will provide you with the opportunity to apply your new skills to example datasets.
- **Class participation, 15%** . Takes attendance and participation in class discussions into account.
- **Group presentation, 15%**. Groups of 4 students will lead discussions of papers that describe particular methods and applications. Groups are expected to summarize the methods and results of the paper, tie the paper to other topics covered in class, and lead a discussion that examines its strengths, weaknesses, and implications. The prepared presentation should last 15 minutes, and will be followed by discussion for 5-10 minutes. Everyone in the class should read each paper prior to the presentation.
- **Individual presentation, 10%**. Each student will make a 10 minute presentation about a scientific paper.

## Reading

- **Required:** . This text covers many of the principles of tree thinking and phylogenetic methods.
- **Suggested:** . You will perform a variety of phylogenetic analyses, which will require running programs at the command line and editing text files. If you are not familiar with these skills already, this book will provide the necessary background.
- **Primary literature.** Scientific papers from the primary literature are a critical component of this course. These will be assigned over the course of the semester as they are selected by students and the professor. 2–4 papers a week will be assigned.

## Computing

The assignments and final project will require that you have access to a computer running Unix or Linux. If you have an Apple Mac or a computer with Linux installed, you are already set. If your computer runs Microsoft Windows you have a couple options. You can run your analyses in a computer lab with Apple Macs or Linux computers, or you can install Linux

on your windows computer within a virtual machine. This page has links that explain how to set up a virtual machine: <http://practicalcomputing.org/preworkshop>

## Course Outline

### **Tree Thinking** (Week 1)

1. Understanding what phylogenetic trees are
2. Reading phylogenetic trees
3. An overview of example applications
4. Gene trees and species trees

### **Inferring phylogenies** (Week 2-5)

1. Tree space
2. Characters and homology
3. Multiple sequence alignment
4. Optimality Criteria
5. Heuristics for finding trees
6. Summarizing trees
7. Measuring tree support
8. Dating trees

### **Model-based approaches revisited** (Week 6)

1. Models of molecular evolution
2. Calculating the likelihood of a tree
3. Bayesian inference
4. Relationship between Bayesian and likelihood approaches
5. Models of morphological evolution

## **Real-world applications** (Week 7)

1. Designing a phylogenetic study
2. Taxon and character sampling
3. Missing data
4. Sources of systematic error

## **Testing phylogenetic hypotheses** (Week 8)

1. Common scenarios
2. KH Test
3. SH Test
4. Other tests

## **Character evolution on phylogenies** (Week 9-10)

1. Reconstructing discrete and continuous characters
2. Testing evolutionary scenarios
3. Characterizing patterns of character evolution, including phylogenetic signal
4. Examining the co-evolution of multiple characters, including independent contrasts
5. Accounting for phylogenetic uncertainty

## **Populations and phylogenies** (Week 11)

1. Coalescence
2. Incomplete lineage sorting
3. Phylogeography
4. Speciation

## **Phylogenomics** (Week 12)

1. Project design
2. Sequence assembly
3. Identifying homologs
4. Identifying orthologs
5. Simultaneous estimation of gene trees and species trees

## **Final Project Presentations** (Week 13)

1. Final Project presentations