SIO147/SIO293-Applications in Phylogenetics
6 units Winter 2014: Tues & Thurs
Lecture: 12:30-1:50pm; Lab: 2-5:50pm.
Location: Main Campus: Lecture= Center Hall 201; Lab= Center Hall 315

Course Instructor: Greg Rouse: grouse@ucsd.edu
Office hour Friday 1.30-2.30pm; SIO Hubbs Hall room 2170

Teaching Assistant: Josefin Stiller: jstiller@ucsd.edu

This course will review some of the tremendous variety of methods for constructing phylogenetic trees using morphological and molecular data.The various options are outlined and critically examined, along with relevant software. There will be a lectures on a series of relevant topics followed by practical classes where both morphological and molecular data will be explored through a series of exercises. The uses of the resulting phylogenetic trees (e.g., evolutionary and ecological transformations, biodiversity measurements, biogeography, systematics and taxonomy) are further examined through an independent project. A 10-minute presentation and a short write-up of the project are required at the end. For graduate students an additional review of a contemporary issue in phylogenetics is is required.

There is no textbook required. Reading will be assigned as needed. If you want to do some background reading, have a look at the free electronic resource available through the UCSD library:

E.O. Wiley & Bruce S. Lieberman 2011. Phylogenetics: theory and practice of phylogenetics systematics. 2nd edition http://roger.ucsd.edu/record=b7094662~S9

Assessment

Midterm Quiz at the beginning of Week 5 = 10%; there will be a short 'practice' (no marks) quiz in week 4 to familiarize students with exam question style and content.

Project write-up (~5 page max.; 30%) and **presentations** (10%) = 40% for **UG**; Project write-up (~5 page max.; 20%) and presentations (10%) = 30% for **Grads.**

Graduate students write a **review** (~5 page max.) on a contemporary issue in phylogenetics (10%; due end of week 8).

Final exam = 50%. **Likely to be March 17**

The project writeup is due March 14 (end of week 10).

Lectures

Week 1.
January 7 Introduction to systematics, tree-thinking, basic terminology.
January 9 Morphology, characters and parsimony analysis, similarity and homology-statements, basic tree calculations, tree rooting.

Week 2.
January 14 Parsimony, tree searching, multiple equally parsimonious trees & consensus. Assessing support for trees; bootstrap, jackknife and Bremer support.
January 16 Character coding. Transformations, Acctran, Deltran.

Week 3.
January 21 Molecular sequence data 1. Alignment, Clustal Muscle, MAFFT etc.
January 23 Molecular Sequence Data 2. Alternatives to Parsimony: Distance methods, Models and Maximum Likelihood.

Week 4.
January 28 Molecular sequence data 3. Bayesian methods. **(Practice quiz)**
January 30 Combining data.

Week 5.
February 4 Hypothesis testing **(Midterm Quiz =10%)**
February 6 The comparative method and phylogenetic trees.

Week 6.
February 11 Historical biogeography.
February 13 Phylogeography.

Week 7.
February 18 Current Nomenclature; Biodiversity measurement; taxonomic surrogacy.
February 20 Species.

Week 8.
February 25 Fossils, molecular clocks and dating on trees.
February 27 Key innovations/diversification rates/cospeciation **(Graduate essays due).**

Week 9.
March 4 Biodiversity and DNA barcoding.
March 6 Josefin TBA.

Week 10.
March 11 No lecture work on projects.
March 13 Presentations.

Practicals

Week 1
January 7. Parsimony analysis. Hand exercises using Caminalacules &
Parrots;Taxonomy exercises involving trees.
January 9. Introduction to PAUP* and Mesquite. Data entry, Nexus format,Tree
manipulation, Character tracing. Executing files, Managing data (include exclude taxa,
characters, annotations footnotes and images). Defining assumptions, Searching for
trees. Describing trees, Searching methods under parsimony, Saving trees.Vertebrates,
Parrots.

Week 2.
January 14. Continue using PAUP, Mesquite & FigTree to become familiar with the
programs. Tree Searching, Consensus trees and Tree support methods; Bootstrap and
Jacknife analysis; Running Autodecay for Bremer support. Beardworms and
Ventworms,Vertebrates, Parrots.
January 16. Tracing the history of character evolution Concentrated changes test and
correlated evolution. Cirratuliform worms, Sharks and Rays.

Week 3.
January 21. Molecular data 1. Basic Alignment and Parsimony Analysis. GenBank.
Using Clustal and MUSCLE in Mesquite. Species exercise.What is the status of the Polar
bear? Relationships of bears (Ursidae) based on mitochondrial *cytochrome b* nucleotide
sequences.
January 23. Molecular data 2. Distance and Neighbor-Joining. Incorporating models of
molecular evolution into datasets. Using jModelTest. Maximum Likelihood in RaXML.
Long branch attraction. Ursidae; Strepsiptera.

Week 4.
January 28 (Practice quiz) Phylogenetic analysis of molecular data 3. MP and
Likelihood (Anglerfish) and then Bayesian Statistical approaches to tree building;
jModelTest and Bayesian approaches (MrBayes). Primates.
January 30 Review of methods to date. Giant clams.

Week 5.
February 4 Midterm Quiz for 10%. Combining Data and Hypothesis testing.
Featherworms.
February 6 Comparative method and trees exercises. Concentrated changes again and
correlated evolution revisited. Syngnathidae and Sea dragons.

Week 6.
February 11 Integrating geography & DNA I: Historical biogeography Crayfish and Iguanas.
February 13 Integrating geography and & DNA II: Phylogeography. Sea slugs, featherstars, seastars.

Week 7.
February 18 Taxonomy exercise; Linnaean and Phylocode. Revisit the clown worm data.
February 20 Molecular clocks and divergence times (Primates and bone worms).

Week 8.
February 25 Diversification rates (*Conus*), and cospeciation.
February 27 Revise methods session: Penguins.

Week 9.
March 4 Individual projects.
March 6 Individual projects.

Week 10.
March 11 Individual projects.
March 13 Presentations: 10 minutes each.