Principles of Systematic Biology - Biology 545 - Spring 2013

Professor: Dr. Jack Sullivan Office: LSS 257 Phone: 5-9049 email: jacks@uidaho.edu Office Hours: Tuesdays, 10:30 – 11:30 & Wednesdays, 8:30 – 9:30

Research Interests: Theoretical systematics; Molecular evolution, Comparative phylogeography, Speciaition.

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Text: Felsenstein, J. 2003. *Inferring Phylogenies*. Sinauer, Sunderland, Massachusetts. This is by far the best book out there for a graduate course. Joe has been the main driving force behind the statistical approach to phylogenetics and the book is amazing.

Course Website: http://www.webpages.uidaho.edu/~jacks/Biol545.html. I will post lecture notes, lab handouts, old exams, and papers from the primary literature on this site. The lecture notes will be in pdf format, and will actually be the notes I lecture from. This is my sixth time through this course and the notes are in pretty good shape. However, the field is incredibly dynamic and you can expect some delays.

Goals (a.k.a., Learning Outcomes): The goals for the course are as follows: a. Provide you with an understanding of the central role that systematics plays across the biological disciplines. b. Provide you with the historical and, especially, theoretical background that will facilitate your understanding of current controversies in systematic biology. c. Provide the expertise and experience that will enable you to address questions in biology using modern, cutting-edge phylogenetic analyses.

Make-up Policy: Make-up exams will be given only if I have been contacted prior to the exam.

Late Assignments: Five points will be deducted for every day that an assignment is late.

Grading:

Exams (there are three, each worth 100 pts.)	300
Participation in discussions of primary literature	
Exercises (6 assignments, each worth 10 pts.)	
Final Project: Presentation	

Total 430

Lecture & Lab Schedules (Tentative)

01/10 – 1. Introduction: Importance of Phylogeny	
01/15 – 2. History of Phylogenetic Inference: Schools 01/17 – 3. Characters: Homology, Morphology	1/14 Lab 1: Intro & Paper Discussion
01/22 – 4. Characters: Molecular 01/24 – 5. Alignment Strategies	1/21 Lab 2: Character Coding
01/29 – 6. Optimality Criteria – Parsimony 01/31 – 7. Optimality Criteria –ML/ME	1/31 Lab 3: Paper Discussion
02/04 – 8. Optimality Criteria – ML/ME 02/06 – 9. Optimality Criteria – ML/ME	2/4 Lab 4: Alignments
02/12 – 10. "Algorithmic" Approaches 02/14 – 11. "Algorithmic" Approaches	2/14 Lab 5: Paper Discussion
02/19 – 12.Searching Tree Space 02/21 – Exam I	2/18 Lab 6: Parsimony analyses
02/26 – 13. Why Models of Sequence Evolution Matter 02/28 – 14. Simple Models of Sequence Evolution	2/25 Lab 7: Paper Discussion
03/05 – 15. Increasing Model Complexity 03/07 – 16. Model Complexity/Model Selection	3/4 Lab 8: Model-based Methods
Spring Break	
03/19 – 17. Model Selection 03/21 – 18. Method Performance	3/18 Lab 9: Paper Discussion
03/26 – 19. Support: Decay &Bootstrap Analysis 03/28 – 20. Support: Bayesian Nodal Probabilities	3/25 Lab 10: Nodal Support
04/05 – 21. Hypothesis Testing: Paired Sites 04/07 – 22. Hypothesis Testing: Parametric Methods	4/1 Lab 11: Paper Discussion
04/09 – 23. Molecular Clocks 04/11 – Exam II	4/08 Lab 12: Project Help
04/16 – 24. Multiple Data Sets: Partitioned and Mixture Models 04/18 – 25. Multiple Data Sets: Partitioned and Mixture Models	4/15 Lab 13: Paper Discussion
04/23 – 26. Species Trees: MP, ML, & Bayesian Approaches 04/25 – 27. Non Tree-Based Methods: Networks & Spectra	4/22 Lab 14: Project Help
04/30 – 28. Ancestral Character State Reconstruction 05/02 – 29. Taxon sampling	4/29 Lab 15: Paper Discussion

Internet Resources

There is an ever-growing array of resources available to those wishing to estimate phylogenies. Some of these are web-based, whereas others are downloadable. This array is constantly changing, but there are a few sites on the Internet that provide updated lists, descriptions, and links.

http://evolution.genetics.washington.edu/phylip/software.html. Joe Felsenstein provides one of the best compilations of a diverse array of phylogeny programs (at least 194 of them) at this site. Programs included in this listing are those that do some type of phylogenetic analysis.

<u>http://www.ebi.ac.uk/Tools/msa/</u>
. This site provides access to lots of different alignment programs (ClustalW, TCoffee, Kalign, MAFFT, and Muscle). It allows you to do alignments online.