

Phylogenetics - Biology 545 - Spring 2023

Professor: Dr. Jack Sullivan Office: LSS 345 Phone: 5-9049 email: jacks@uidaho.edu
Office Hours: Tuesdays, 10:30 – 11:30 & Wednesdays, 8:30 – 9:30

Research Interests: Theoretical systematics, Conservation genetics, Comparative phylogeography, Speciation.

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Supplemental 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 excellent.

Course Website: <http://www.webpages.uidaho.edu/~jacks/Biol545.html>. I will post lecture notes, lab handouts, old exams, problem sets, and papers from the primary literature on this site. The lecture notes will be in pdf format and will be the very notes I lecture from. This is my 12th time teaching this course and the notes are in pretty good shape. However, the field is incredibly dynamic, and you can expect some minor delays as I update lectures to incorporate emerging material. I'll also post links to recorded lectures here.

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 phylogenetics plays across the biological disciplines. **b.** Provide you with the historical and, especially, theoretical background that will facilitate your understanding of controversies in phylogenetics. **c.** Provide the expertise and experience that will enable you to address questions in biology using modern, cutting-edge phylogenetic analyses.

Zoom Links: I will use Zoom to transmit my lectures if you can't attend or don't feel comfortable doing so. I would prefer that you watch these synchronously so that you can participate in lecture. However, I will also post links to recorded lectures as well as my lecture notes and slides. Papers discussions and labs *must* be attended synchronous if you choose to participate via Zoom.

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

Late Assignments: One point will be deducted for every day that an assignment is late.

Grading:

Exams (there are two, each worth 100 pts.)	200
Participation in discussions of primary literature	50
Exercises (5 assignments, each worth 10 pts.)	50
Final Project Presentation	50

Total 350

Lecture & Lab Schedules (Tentative)

01/12 – 1. Introduction: Importance of Phylogeny	
01/17 – 2. History of Phylogenetic Inference: Schools	1/16 – MLK Day
01/19 – 3. No Class (NSF Panel)	
01/24 – 4. Characters: Homology	1/23 - Paper Discussion
01/26 – 5. Alignment Strategies	
01/31 – 6. Optimality Criteria – Parsimony	1/30 - Lab 1: Alignments
02/02 – 7. Optimality Criteria –ML/ME	
02/07 – 8. Optimality Criteria – ML/ME	2/6 - Paper Discussion
02/09 – 9. Optimality Criteria – ML/ME	
02/14 – 10. “Algorithmic” Approaches	2/13 - Lab 2: Parsimony analyses
02/16 – 11. “Algorithmic” Approaches	
02/21 – 12. Searching Tree Space	2/20 - Review for Exam
02/23 – Exam I	
02/28 – 13. Why Models of Sequence Evolution Matter	0/27 - Lab 3: Model-based Analyses
03/02 – 14. Simple Models of Sequence Evolution	
03/07 – 15. Increasing Model Complexity	3/6 - Paper Discussion
03/09 – 16. Model Complexity/Model Selection	
Spring Break	
03/21 – 17. Model Selection	3/20 Lab 4: Nodal Support
03/23 – 18. Method Performance	
03/28 – 19. Consensus and Nodal Support	3/27 - Paper Discussion
03/30 – 20. Consensus and Nodal Support	
04/04 – 21. Hypothesis Testing	4/3 - Lab 5: Species Trees
04/06 – 22. Molecular Clocks	
04/11 – 23. Multiple Data Sets: Partitions/Mixtures	4/10 - Review for Exam
04/13 – Exam II	
04/18 – 24. Multiple Data Sets: Partitions/Mixtures	4/17 - Paper Discussion
04/20 – 25. Species Trees	
04/25 – 26. Species Trees	4/24 - Project Help
04/27 – 27. Non-Tree Approaches: Networks & Spectra	
05/02 – 28. Ancestral Character State Reconstruction	5/01 - Project Presentations
05/04 – 29. Taxon sampling	

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.

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