

IB 467 - Principles of Systematics

CRN 40508

4 hrs credit, offered in alternate years

Lec TuTh (80 min); Lab Tu (3 hr)

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Prerequisite: IB 302 and IB 335 or IB 468; or consent of instructor.

Course Description

General: Comprehensive survey of the theory and methodology of systematics, with an emphasis on molecular phylogenetics as applied to any group of organisms or data, including practical experience in the acquisition and analysis of data (genes to morphology) for phylogenetic inference.

Systematics is an ever-changing discipline that examines the diversity of organisms, their genealogical relationships, and patterns of evolution. Thus, it constitutes the underlying basis for organizing our knowledge of modern biology. This course provides a comprehensive survey of the theory and methods of systematics, focusing on modern methods of phylogenetics. This course is directed at those advanced undergraduate and graduate students interested in studies of organismal biology, evolutionary biology, biodiversity and conservation, and phylogenetics. Phylogenetics is concerned with the reconstruction and analysis of trees to examine the evolution of organisms, from species to populations to genes. It is fundamental to discovering the evolutionary interrelationships among all living organisms and the patterns of evolution, including rapid radiations of organisms in the 'tree of life'. It is used widely in molecular biology, anthropology and linguistics, and has advanced rapidly via the development of new statistical and computational techniques. With the availability of a wealth of new biological data, from genes to genomes, phylogenetics has become an essential foundation for all of biology. Some specific topics to be discussed include the major contemporary schools of systematics, the methodologies of phylogenetic inference, including maximum likelihood and Bayesian techniques, molecular phylogenetics, phylogenomics, the use of databases, research collections and other resources, and the application of the results of systematic studies in the areas of biogeography, speciation, co-evolution, and biodiversity and conservation. The laboratory will provide hands-on experience in the acquisition and analysis of various types of biological data, from molecules to morphology. You will gain familiarity with the use of multiple contemporary computer programs currently used in phylogenetic inference.

Learned Skills - skills tailored to student interest

- How to make informed decisions about the next steps in your career development
- How to align large DNA datasets (nucleotide and protein alignments)
- How to use GenBank and other DNA databases
- How to assess appropriate models for analysis of diverse datasets
- Understanding the basic theory and analytical methods of phylogenetic inference, including Bayesian Inference, Maximum Likelihood and Parsimony
- How to conceive, plan and write a phylogenetics research project, using original data
- The methods of scientific writing and presentation of independent project research

Shared Learning

Students have the opportunity to work together in lab, which is run like a workshop. Students work closely with the instructor to complete weekly lab exercises, which are often completed by working in pairs.

For end-of-semester project oral presentations, each student will be critiqued by the rest of the students and the instructor, receiving written feedback on both the substantive science and the visual aspects. *The course is designed to have some degree of flexible content to consider, in part, the needs and desires of the students.*

Learn by Doing

Each student will collect either original data or data from the literature to work with throughout the course, ultimately resulting in a thorough phylogenetic analysis by the end of the course. Learning will be hands-on and students grapple with the unique aspects of their own datasets— no two students will be working with the same data for their projects. Students will learn to think critically about their data and how best to analyze it through all the steps of a phylogenetic analysis.

Who needs the course?

Students interested in this course are from diverse fields, including evolutionary biology, ecology, taxonomy, population genetics and bioinformatics. They will have the opportunity to learn the procedures of tree estimation and to use trees to gain insights into the evolution of phenotypic traits

Textbook (required)

Baum, DA, and Smith, SD. 2013. Tree Thinking, An Introduction to Phylogenetic Biology. Roberts and Co., Greenwood Village, CO

In addition to the textbook, many supplemental books are on reserve in the Cameron Lab for student use.

Assessment

Course Component	Percent Grade
Lecture Exam 1	15%
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Final Exam	25%
Student-Led Paper Discussion	5%
Student Oral Presentation	10%
Laboratory Projects	20%
Laboratory Assignments & Homework	10%

Required Laboratory Exercises

Laboratory attendance is mandatory. Laboratory Exercises for IB 467 will be uploaded to moodle at least a few days prior to lab sessions. Please print and read each week's exercise before coming to lab

Participation includes showing up (!), participating in class discussion—giving feedback on other student's presentations, filling out evaluation forms with thoughtful and constructive feedback, bringing in questions for class discussion.

Academic Integrity

This course assumes that all students will abide by the policies of honesty and integrity, which is fundamental to the process of teaching and learning. The university and this class assumes that you will pursue all assignments with personal integrity so that we can maintain an environment in which all can succeed via their own efforts.

Disability

If any student anticipates or experiences barriers to learning or full participation in this course based on a physical, learning, or mental health disability, please contact the instructor immediately to discuss possible accommodations.

Lecture Syllabus (Sample)

#	Date	Lecture Topic	Req. Readings	Optional Readings
		<i>Documents posted in Moodle</i>		
1		Course Organization and Overview of Systematics: Nomenclature, Classification, and Schools of Phylogenetics Overview of Systematics Outline Systematics Terms Nomenclature Outline Nomenclature Terms	Baum & Smith, ch. 1 and 2; Quicke 1993, ch. 6	Felsenstein 2001; Winston chs. 2&7, and pp. 103-105, 346, 424; Hull 1988, ch. 5; Mayr 1982, pp 147-208; Felsenstein 2004, ch. 10 (ref)
2		Paper Discussion 1 - Future of Taxonomy	Godfray 2002 Deans et al. 2012	
3		Principles of Phylogenetics: Reading Trees, Characters, Character States, Polarity and rooting of trees Char State and Polarity Handout Phylogenetic Terms Handout	Baum & Smith, ch. 4 and 5; pp. 61-64, 175	
4		Principles of Phylogenetics: Tree Thinking, Hennigian Concepts, and Character Conflict Notes on Hennig, Character Conflict & Cladistics	Baum & Smith, ch. 3; Kitching et al. 1998, ch. 1	Hennig 1966; Farris 1970 (ref)
5		Inferring Trees with Maximum Parsimony Parsimony Notes	Baum & Smith, ch. 7; Hillis et al. 1996, ch. 11, pp. 415-426	Kitching et al., ch. 3, pp 38-48; ch. 4, 70-79 Edwards 2009; Hennig 1966; Farris 1970 (ref)

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6	Paper Discussion 2 - Species Concepts	Smith et al. 2008	Hausdorf 2011
7	Diversity of Systematic Data and Uses Data Diversity Notes	Quicke 1993, ch 8, pp 32-41	Systematics and Biological Characteristics
8	Molecular Markers Markers Notes	Avise 2004, ch 3; Downton 2003	Rokas 2000; Genetic marker (wiki)
9	Alignment of DNA Sequences Alignment Notes	jRNA website; MUSCLE website; SQUINT website	
10	Issues with Sequence Data Sequence Data Notes	Page & Holmes 1998, ch. 2	Boussau et al. 2008; Boussau et al. 2009; Steel 2005; Penny et al. 2001
11	Paper Discussion 3 - Computer Alignment Review Session 1 (Study Guide)	Morrison 2009	Edgar 2004; Martin et al. 2007; Kjer et al. 2009
12	EXAM - Midterm 1		
13	Inferring Trees with Maximum Likelihood and Models of Molecular Evolution ML Handout	Baum & Smith ch. 8, pg 1-20; Page & Holmes 1998, ch. 6 pp.193-201	Broman, ch. 8, pp.282-296; Felsenstein 2004, ch. 16 (ref)
14	Inferring Trees by Distance Methods Distance Notes Distance Homework	Baum & Smith ch. 8, pp 1-15	Lemey et al. 2009 ch 5, pp 142-154
15	Inferring Trees with Bayesian Methods Bayesian Notes	Baum & Smith, ch. 8, pg. 20-28; Huelsenbeck et al. 2002	Ronquist & Deans 2009
16	Paper Discussion 4 - TBA	<i>TBA</i>	
17	Evaluating Results and Measures of Support Support Measures notes	Baum & Smith, ch. 9; Page & Holmes, ch 6 pp. 209-214, 218-227	Sanderson & Schaffer 2002
18	Supertrees and Networks: Phylogenetic Congruence (guest lec: Jim Whitfield)	<i>TBA</i>	McBreen & Lockhart 2006; Bininda-Emonds et al. 2002
19	Phylogeny Estimation with Big Data (guest lec: Nam Nguyn)	<i>TBA</i>	
20	Paper Discussion 5 - Bootstrap vs. Posterior Probability	Alfaro et al. 2003; Douady et al. 2003	

21		Review Session (Study Guide 2)		
22		EXAM - Midterm 2		
23		Comparative Method: Testing Evolutionary Correlations Among Traits Comparative Method Notes	Baum & Smith, ch. 10; Felsenstein 1985;	Harvey & Pagel 1991 ch. 4, pp 78-100; Pagel 1999; Pagel, Atkinson & Meade 2007
24		Host Parasite Coevolution Host Parasite Coevolution Notes	Clayton et al. 2003; Johnson et al. 2003	
25		Gene Tree/Species Tree Issues for Phylogenetic inference (guest lec: Pranjal Vachaspati)	Rosenberg & Nordberg 2002	Cheviron & Brumfield 2009; Domingues et al. 2012
26		Paper Discussion 6 - Issues with Gene Trees	<i>TBA</i>	
--		Thanksgiving Break		
27		Historical Biogeography and Divergence Times Historical Biogeography and Divergence Times Notes	Baum & Smith, ch. 11	Hines 2008; Rutschmann 2006; Landis et al. 2013; Ree and Smith 2008; Ronquist and Sanmartin 2011; Tamura et al 2012
28		Rapid Radiations Radiations Handout (guest lec: Jim Whitfield)	Whitfield & Lockhart 2007	Philippe & Laurent 1998
29		Phylogenomics	Boussau 2010; Boussau 2009	Philippe et al. 2005; Rokas&Carroll 2006
		Final Exam Review		
		FINAL EXAM		

Laboratory Syllabus

August 25	1	Introduction to the Lab and Student Projects Cover Page Project Description Project Plan Project Outline Notes on Oral Presentation
September 1	2	Characters, Character States and Classifications (Caminalcules)
September 8	3	Introduction to Parsimony Analysis using PAUP*
September 15	4	Consensus Trees, Rooting, Constraints, Stepmatrices, and Bootstrapping: PAUP* continued plus GENEIOUS and SEAVIEW
September 22	5	Alignment of Molecular Data
September 29	6	Introduction to Genbank and BLAST; Working With Raw Sequence Data
October 6	7	Maximum Likelihood and Distance Methods: Models in Phylogenetics Read before lab: Posada 2008, Darriba et al. 2012 http://www.mybiosoftware.com/jmodeltest-0-1-1-1-phylogenetic-model-averaging.html
October 13	8	Bayesian Analysis: Combining Data in Mixed Model Analysis
October 20	9	Computational Skills for Phylogenetics (Guest Lab: Julie Allen)
October 27	10	Analysis of Big Data for Large Scale Phylogenies (Guest Lab: Nam Nguyn and Pranjal Vachaspati)
November 3	11	Introduction to Phylogenetic Networks
November 10	12	The Comparative Method Using R (Guest Lab: Julie Allen)
November 17	13	Free Time for Independent Projects
November 24	-	Thanksgiving Break - No Lab
December 1	14	Historical Biogeography and Divergence Time Methods: DIVA and BEAST
December 8	15	Student Presentations Projects due