

OEB 181: Systematic Fall 2017
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WHEN & WHERE: Mo, Wed, Fr. 9–9.59 AM; Lectures with integrated lab component

SYLLABUS AND REQUIRED SOFTWARES:

August 30th: Introduction to systematics and its applications. Motivation.

September 1st: Species and taxa.

September 6th: A brief history of systematics.

Chapter 1 in: Wheeler, W. C. 2012. *Systematics: A course of Lectures*. Wiley-Blackwell, Chichester.

September 8th: Representing genealogies. *Software: FigTree*.

September 11th: Morphology, phenotypic characters and homology.

September 13th: Coding morphological characters and selecting terminals.

September 15th: Creating data matrices. *Software: Morphobank and Mesquite*.

September 18th: Fundamentals of molecular evolution.

Chapter 1 in: Graur, D. and W. H. Li. 2000. *Fundamentals of Molecular Evolution*. Sinauer Associates, Sunderland.

Chapter 2 in: Page, R. D. M. and E. C. Holmes. 1998. *Molecular evolution. A phylogenetic approach*. Blackwell Science, Boston.

September 20th: Homology in molecular characters and DNA sequence alignments.

September 22nd: Editing molecular data matrices. *Software: Geneious*.

September 25th: Optimality criteria: Parsimony and character optimization.

September 27th: Parsimony tree searches.

September 29th: Searching for the most parsimonious trees. *Software: TNT and Cipres*.

October 2nd: Introduction to evolutionary models and distance methods for tree inference.

October 4th: Optimality criteria: Maximum likelihood and evolutionary models.

October 6th: Model selection. *Software: jModeltest and PartitionFinder.*

October 11th: Guest Lecturer, Ward Wheeler, American Museum of Natural History: Single step phylogenetics [1.5 hours]

October 13th: Maximum likelihood calculations and types of likelihood. Searching for the most likely trees. *Software: RAxML and IQTree.* [2 hours]

October 16th: Calculating nodal support: bootstrapping, jackknifing, Bremer support.

October 18th: Calculating tree support: topology tests. Tree stability.

October 20th: Calculating support. *Software: RAxML and TNT.*

October 23rd: Bayesian phylogenetics I.

October 25th: Bayesian phylogenetics II. Analyzing data under DO. *Software: POY.* [2 hours]

October 27th: Analyzing data with Bayesian methods. *Software: MrBayes and Tracer*

October 30th: Estimating divergence times. [1.5 hours]

November 1st: Molecular clocks and calibrations. Node calibration or tip calibration? [1.5 hours]

November 3rd: Divergence dating. *Software: BEAST.*

November 6th: Genomic data sets: Genomes, transcriptomes, target enrichment, RADseq. [1.5 hours]

November 8th: Data matrices and phylogenomic data. [1.5 hours]

November 10th: Phylogenomic analyses. *ExaML*

November 13th: Species delimitation methods. Automated criteria for species designations? [1.5 hours]

November 15th: *Software: BPP and PTP* [2 hours]

November 17th: No class

November 20th: No class

November 27th: No class

November 29th: No class

December 1st: No class

ASSESSMENT:

40% Class assignments (4) and class participation

60% Final exam