

Molecular Systematics and Evolution – ZOOL 6305 - Fall 2015

Recommended Pre-requisite	BIOL 5305, ZOOL 6302, or consent of instructor.
Learning Objectives	<p>After completing this course, students will be able to:</p> <ul style="list-style-type: none"> - Describe the methods and principle of modern molecular systematics including: parsimony, distance, maximum likelihood, Bayesian analyses - Relate systematics analysis to the evolution of the taxa under investigation - Implement the major software packages associated with performing molecular systematics
Lectures	TTh 3:30-4:50. You are expected to attend all lectures. Failure to attend will be detrimental to your grade.
Professor and Co-instructor	<p>Dr. David Ray, ESB 206, 806-834-1677, david.a.ray@ttu.edu Office Hrs: MTW (3:00-4:00)</p> <p>Dr. Roy N Platt, ESB 216, 806-834-7128, neal.platt@gmail.com Office Hrs: TWTh (2:00-3:00)</p>
Textbook and Lecture Notes	<p>Class lectures and supplementary information in the form of animations, FAQs, and extra reading will be available on the class website (http://davidraylab.com).</p> <p>Several sources were used to develop this course. Most information comes from The Phylogenetic Handbook 2nd Ed., edited by Lemey, Salemi and Vandamme. Additional information comes from Tree Thinking by Baum and Smith. We recommend having a copy of the first and getting the second if you feel the need.</p>
Course Format	The course will consist of two parts. During the first half of the semester, Dr. Ray will lecture on the theory and history of molecular systematics, data types, tree interpretation, etc. In an effort to make the course more useful (and less esoteric) to students, the second half of the course, led by Dr. Platt, will consist of hands-on analyses and experience with particular software packages and data sets.
Learning Assessment Methods	Three exams (variable formats) worth 100 points each. The first two will take place during the first half of the course. The third will be at the end of the course. A final project covering the various phylogenetic methods/tools will be turned in at the end of the course.
Grading	<p>Final averages will be calculated as a percentage of the available points (Only a single letter grade will be issued). Letter grades will be determined as:</p> <p>Graduate students: A (93-100%), B (83-92%), C (73-82%), D (65-72%), F (≤65%)</p> <p>Make-up exams will ONLY be given to those who present documentation explaining their absence immediately upon their return to class. Please inform me of absences in advance so that arrangements for a make-up exam can be made. Make-up exams will be of a different format and have different questions from the regularly scheduled exam. Students who miss an exam without a valid excuse will receive a ZERO for that exam.</p> <p>Point scale: 3 x 100 pts (exams) + 100 pts (project) = 400 pts</p>
Evacuation Plan	In the event of an emergency, leave the classroom in an orderly manner. Leave the building through the nearest outside door and quickly move as far away as possible. Do not gather near building or parking lots.
Honor Statement	Dishonesty on tests, quizzes, written work, or connected with your attendance in lab or lecture will have serious consequences. Students are expected to be aware of, and abide by, the University's Honor code. Plagiarism on written lab reports or essays (copying/paraphrasing from other students or from other sources without giving due credit) will result in the loss of all points for that exercise, at the very least.

Special Student Considerations	Any student who, because of a disability, may require special arrangements in order to meet the course requirements should contact the instructor as soon as possible to make any necessary arrangements. Students should present appropriate verification from Student Disability Services (AccessTECH). No requirement exists that accommodations be made prior to completion of this approved university process.
Topics	<p>Part 1: Unit 1. Introduction & Tree Thinking Unit 2. Molecular Evolution and Data Unit 3. Taxonomic Units Unit 4. Sequence Alignment Unit 5. Tree Inference/Models of DNA Evolution Unit 6. Clustering Methods Unit 7. Maximum Likelihood Unit 8. Bayesian Analysis Unit 9. Parsimony Unit 10. Tree Confidence & Support Unit 11. Whole Genome Phylogenetics</p> <p>Part 2: Unit 12. Introduction to the CLI, Data Formats, & Trouble Shooting Unit 13. Obtaining Data & Sequence Alignment Unit 14. Substitution Models Unit 15. Distance Methods Unit 16. Parsimony Unit 17. Maximum Likelihood Unit 18. Bayesian Methods Unit 19. Hypothesis testing & Ancestral State Reconstruction</p> <p>Topics are issued for general information, and deviations from the schedule will likely occur. The Instructor reserves the right to make corrections and/or changes, and you will, of course, be informed about these.</p>