Instructor: Prof. Tiffani L. Williams, HRBB 328C (office), 845-7977 (phone)
Email: tlw@cs.tamu.edu
Meeting: MWF 12:40-1:30pm, ZACH 105B
Office Hours: MWF 4:00 - 5:00pm and by appointment
Course Webpage: http://faculty.cs.tamu.edu/tlw/

Course Information

This course will focus on algorithmic techniques for reconstructing evolutionary trees or phylogenies. A phylogeny is a reconstruction of the evolutionary history of a group of organisms. Phylogenies are used throughout the life sciences, as they offer a structure around which to organize the knowledge and data accumulated by researchers. A phylogeny usually takes the form of a tree, although certain evolutionary events, such as hybridization, may cause it to assume the form of a directed acyclic graph. Phylogenetic reconstruction is a crucial tool in forensic studies, in security applications for networks and computers, and in a variety of disciplines such as historical linguistics.

Course topics will include:

- Optimization criteria (e.g., maximum parsimony and maximum likelihood)
- Local-search heuristics used in phylogenetic software such as PAUP and TNT.
- Distance-based approaches such as neighbor-joining and UPGMA.
- High-performance computing and phylogenetics
- Non-biological uses of evolutionary trees (e.g., historical linguistics, computer viruses, chain letters)
- Consensus and supertree methods
- Models of sequence evolution
- Assessment of phylogenetic reconstruction methods

Grading:

The course grade will be composed of a research project and assignments. The weighting of each of the components is given below.

- Assignments (20%)
- Class Discussions (20%)
- Research project (60%)

Assignments will be composed of homework questions based on class lectures and material from course readings. Since this course is a research seminar, each student is expected to participate in class discussions. Furthermore, each student will also be required to lead a discussion of a research paper assigned to the class. The research project is an opportunity for you to explore a topic in greater-depth. The range of topics is
wide-open as long as it deals with phylogenetics and involves "hands-on” training (e.g., implementing an algorithm and testing its performance, using existing phylogenetic software to analyze data, etc.).

More details concerning the research project and leading a class discussion will be given during the semester.

Academic Integrity

Aggie Code of Honor (http://www.tamu.edu/aggiehonor)

"Aggies do not lie, cheat, or steal nor do they tolerate those who do.” Students are expected to attend all classes, complete assignments on time, and participate fully in class discussions and group projects. Violations will be handled in accordance with the Texas A&M University Regulations governing academic integrity.

Plagiarism

As commonly defined, plagiarism consists of passing off as ones own the ideas, words, writings, etc., which belong to another. In accordance with this definition, you are committing plagiarism if you copy the work of another person and turn it in as your own, even if you should have permission of that person. Plagiarism is one of the worst academic sins, for the plagiarist destroys the trust among colleagues without research cannot safely communicated. If you have any questions regarding plagiarism, please consult the latest issue of the Texas A&M University Student Rules, under the section Scholastic Dishonesty.

American with Disabilities Act

The Americans with Disabilities Act (ADA) is a federal antidiscrimination statute that provides comprehensive civil rights protection for persons with disabilities. Among other things, this legislation requires that all students with disabilities to be guaranteed a learning environment that provides for reasonable accommodation of their disabilities. If you believe you have a disability requiring an accommodation, please contact the Department of Student Life, services for students with disabilities in Room 126 of Koldus Building, or call 845-1637.