

CS 5263 • Bioinformatics

Fall 2008 • MW 7-8:15pm

Large-scale genome sequencing projects and other high-throughput technologies have generated large amounts of complex data that challenge the effective storage, analysis and interpretation of biological information. This has created entirely new fields and industries, and a need for trained bioinformaticians who are able to apply statistical and computational techniques to the analysis of difference kinds of biological data.

This course is designed for both CS/math/engineering students who wish to learn some advanced algorithms and their applications to biology (applications to other areas will also be discussed to some extent), and biological/medical students who wish to have a better understanding of the fundamental concepts underlying common bioinformatics tools.

Topics covered

- Sequence comparison (dynamic programming, string matching)
- Gene prediction (hidden Markov models)
- Motif finding (probabilistic optimization algorithms)
- RNA secondary structure prediction (context free grammar models)
- Microarray data analysis (data mining)
- Biological networks, social networks and the Internet (complex networks, graph algorithms)
- Other interesting/hot topics requested by students

Prerequisite

- Graduate students or senior undergrads with permission.
- Basic knowledge of algorithms and some statistics
- Experience in at least one programming language, such as C/C++/Java, perl, or matlab.
- **Background in Biology is NOT required.**

About the instructor

Dr. Jianhua Ruan joined the CS department at UTSA as an assistant professor in Fall 2007. He has a BS in Biology, a MS and a PhD in Computer Science. His research area is in bioinformatics and computational biology. For further information about the instructor and the course check the instructor's webpage at <http://cs.utsa.edu/~jruan> or email him at jruan@cs.utsa.edu.

