**Introduction:** Biology is currently undergoing a revolution in which computational methods play a central role. Advances in high-throughput molecular biology have resulted in huge amounts of biological data that offer new insights into the function of genes, proteins, and cells. Effective use of this information critically depends upon the development of novel computational methods for biological data analysis. The emerging field of bioinformatics has arisen in response to these challenges.

**Course objectives:** The course is devoted to the design and analysis of efficient algorithms in bioinformatics. We will emphasize general algorithmic techniques and fundamental data structures, although relevant biological background and applications will be introduced as needed.

**Course time/place:** MW 2-3:15pm, Engineering II, Room 322

**Instructor:** Ion Mandoiu (261 ITE Building, Tel: 486-3784, E-mail:/ion@engr.uconn.edu)

**Office hours:** MW 12:30-1:30pm and by appointment

**Textbooks:**

**Topics to be covered:** physical mapping, fragment assembly, sequence alignment, similarity search, gene prediction, evolutionary trees, genome rearrangements, gene expression analysis, and computational proteomics. The list of topics may change according to class progress.

**Grading policy:** Grading will be based on bi-weekly homework assignments (50%) and a term project on a topic approved by the instructor (50%). The projects may involve algorithm implementations and empirical studies, in-depth surveys of bioinformatics topics not covered in class, original solutions to open research problems (see Chapter 12 of the textbook for a list of open problems), non-trivial improvements of known results, etc.

**Academic Honesty:** You are expected to adhere to the highest standards of academic honesty. Collaboration on the homework is not allowed. Collaboration and teamwork are encouraged on the term projects; however, teamwork requires instructor’s prior approval and must be justified by the difficulty of the project.