

Bioinformatics

BIOL 5005.005 MATH 5220.001 CSCE 5933.008

Course Information (Spring 2020)

Instructor: Rajeev Azad (Rajeev.Azad@unt.edu)

Lectures: Tuesday & Thursday 11:00 AM – 12:20 PM, LANG 210

Office hours: Tuesday 12:25 – 2:25 PM, GAB 434

Recommended Textbooks: The course content will be based on selected Bioinformatics textbooks considering diverse background of the prospective students and with no expectation of the prior exposure to this interdisciplinary area. The recommended textbooks are Biological Sequence Analysis by Durbin *et al.*, Bioinformatics and Functional Genomics by Pevsner, and Statistical Methods in Bioinformatics by Ewens & Grant. New research developments will also be covered in this course, based mainly on research articles and review papers.

Course objective: The aim of this course is to familiarize students with state-of-the-art methodologies in Bioinformatics and Computational Biology, and help them understand how to apply these techniques to solving biological and biomedical problems. This course will include the following topics:

- An introduction to Bioinformatics
- An introduction to probability and probabilistic models for interpreting biological sequence data
- Biological Databases and Genome Browsers
- Markov chain models, hidden Markov models, profile hidden Markov models
- Genome architecture, genome assembly, gene prediction, protein topology prediction
- Pairwise and multiple sequence alignment
- Molecular phylogeny
- Genome evolution: vertical and horizontal modes of gene transfer
- Microarray, RNA-Seq, and next generation sequencing data analysis
- Metagenomics and Metatranscriptomics
- Human genomic variations: detection of structural variations and copy number polymorphisms, identification of disease-associated genes

Course outcomes: Appreciation of the interdisciplinary approaches to solving problems in biology; understanding of the essence of computational and mathematical methods in biology and medicine; familiarization with principles and models underlying standard bioinformatics methods/algorithms; practical experience of using bioinformatics tools for biological data analysis.

Grading: Based on in-class discussions and presentation, homework assignments, exam and project. Above 90% ≡ A, 80-89.99% ≡ B, 70-79.99% ≡ C, 60-69.99% ≡ D, and Below 60% ≡ F