CAP 5510 Introduction to Bioinformatics

Catalog Description
Introduction to bioinformatics; algorithmic, analytical and predictive tools and techniques; programming and visualization tools; machine learning; pattern discovery; analysis of sequence alignments, phylogeny data, gene expression data, and protein structure. (3 credits)

Prerequisites
COP 3530, or equivalent and STA 3033 or equivalent.

Type
Elective for MSCS, MSIT, MSTN, and Ph.D. students

Course Objectives
This is an introductory graduate course in Bioinformatics. Students will learn standard tools and techniques used to analyze and interpret biomedical data. There is considerable overlap with areas such as data mining, machine learning, pattern recognition, and algorithms. No prerequisite knowledge in molecular and cell biology, genetics, or biochemistry will be assumed.

Topics
Fundamentals of Biology, Statistics, the Internet, and Bioinformatics
• Databases and Software Packages, BioPerl.
• Sequence Alignment, Multiple Sequence Alignment
• Sequencing; Next Generation Sequencing & Applications
• Predictive Methods: Nucleotide Sequences and Protein Sequences
• Pattern Discovery Techniques and applications
• Machine Learning: NN, HMM, SOM, SVM, etc.
• Gene Regulation; Predicting Regulatory Elements
• Analysis of Gene Expression Data
• Gene Ontology and Pathways; Protein-protein interactions
• Genomics, Proteomics, Comparative Genomics
• Phylogenetic Analysis
• Molecular Structural Analysis: RNA and Proteins
• Genetics and Genome-Wide Association Schemes
• Single Nucleotide Polymorphisms
• Advanced Topics: RNAi, Alternative Splicing, Epigenetics
The course will contain a lab component to learn Bioinformatics analysis tools.

Textbook
Bioinformatics and Functional Genomics, J. Pevsner, Wiley-Blackwell, 2nd Edition, **ISBN**: 978-0-470-08585-1

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