

CGS 5166 Introduction to Bioinformatics Tools

Catalog Description

Introduction to bioinformatics; analytical and predictive tools; practical use of tools for sequence alignments, phylogeny, visualizations, pattern discovery, gene expression analysis, and protein structure. (2 credits)

Prerequisites

Prerequisites: PCB 6025 or equivalent.

Type

Elective for non-CS and non-IT majors

Course Objectives

This course will introduce computational tools and techniques for analyzing biomolecular (DNA, RNA, protein) sequences, structures, and quantitative data arising from biological experiments. Students will also learn about the major databases and repositories of bioinformatics information. No background in Computer Science will be expected. However, knowledge of basic molecular biology and genetics will be useful.

Topics

Fundamentals of Biology, Statistics, the Internet, and Bioinformatics

- Databases and Software Packages: GenBank, SwissProt, BioPerl.
- Sequence Alignment, Multiple Sequence Alignment: BLAST, CLUSTAL
- Sequencing, Assembly & Applications: VELVET
- Pattern Discovery: PROSITE, Pfam,
- Predictive Machine Learning Tools: HMMPro, GeneCluster, SVMLite.
- Gene Regulation; Predicting Regulatory Elements: RegulonDB
- Analysis of Gene Expression Data: MAS, GeneSpring
- Ontology and Pathways – Databases and Analysis: GO, KEGG
- Genomics, Proteomics, Comparative Genomics: GreenGenes
- Phylogenetic Analysis: PHYLIP, PAUP
- Molecular Structural Analysis – RNA & Proteins: RASMOL, DALI
- Genetics and Genome-Wide Association Schemes
- Single Nucleotide Polymorphisms and SNP Databases
- 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

Last Update

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