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260.841 Protein Bioinformatics (JHSPH registrar)

Description

Provides students with an overview of protein bioinformatics including computational and experimental approaches. The course will introduce amino acid and protein physical properties as well as the alignment and evolution of protein sequences. Protein structure and methods of structure determination will be presented as well as the use of protein databases and software for visualizing proteins. Methods for secondary and tertiary protein structure prediction will be discussed as well as methods for modeling small/molecule-protein interactions and protein-protein interactions. The course will also cover mass spectrometry and the analysis of high-throughput mass spectrometry data. A survey of mass spectrometry ionization techniques and instrument types will be followed by an overview of data analysis techniques for protein identification, *de novo* protein sequencing, and the analysis of post-translational modifications. Finally, students will be introduced to experimental and computational aspects of mapping protein interaction networks.

Objectives

The objective of the course is to provide students with the ability to analyze and understand data from high-throughput proteomics experiments. At the conclusion of the course the students will be able to:

1. Define protein physical properties and analyze protein structure.
2. Explain how proteins are studied experimentally and how data is generated in high-throughput experiments.
3. Describe the computational methods used to study protein structure and interactions.
4. Explain the algorithms, statistical techniques and software tools used to analyze high-throughput proteomics data.

Intended audience: Students enrolled in the MHS in Bioinformatics program as well as others interested in protein bioinformatics.

Instructors: Ingo Ruczinski, Sean Prigge, Akhilesh Pandey, Jonathan Pevsner, Robert Cotter, Joel Bader, Heng Zhu

Prerequisites

Introduction to Molecular Biology (120.602) or permission of the instructor

Texts: Hand-outs and readings

Grading Policy: 5 homework assignments + Final exam.

Time: T-Th 3-4:30 W2033

Protein Bioinformatics

Tentative Schedule
4th Term 2005

T Mar. 29	Introduction to physical properties of amino acids	Prigge
Th Mar. 31	Protein Structure (level of Branden and Tooze)	Prigge
T Apr. 5	Protein sequence alignment and evolution	Pevsner
Th Apr. 7	Principles of mass spectrometry	Cotter
T Apr. 12	Applications of mass spectrometry to proteomics	Pandey
Th Apr. 14	Applications of mass spectrometry to proteomics	Pandey
T Apr. 19	Protein structure determination	Prigge
Th Apr. 21	Protein databases, structural classification of proteins, visualization	Ruczinski
T Apr. 26	Protein secondary structure prediction	Ruczinski
Th Apr. 28	Protein structure prediction	Ruczinski
T May 3	Protein structure prediction (CASP)	Ruczinski
Th May 5	Protein networks	Bader
T May 10	High throughput approaches to proteomics	Zhu
Th May 12	Protein-protein docking	Gray
T May 17	Lab	
Th May 19	Final exam	