Lahore University of Management Sciences
BIO 435 – Computational Proteomics
Fall 2014

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Course URL (if any)	

Course Basics				
Credit Hours	3			
Lecture(s)	Nbr of Lec(s) Per Week	2	Duration	1 hr 15 mins
Recitation (per week)	Nbr of Rec (s) Per Week		Duration	
Lab (if any) per week	Nbr of Session(s) Per Week	1	Duration	1 hr 30 mins
Tutorial (per week)	Nbr of Tut(s) Per Week		Duration	

Course Distribution	
Core	
Elective	Yes
Open for Student Category	
Closed for Student Category	

COURSE DESCRIPTION

This course covers experimental (20%) and computational (80%) methods in proteomics. Within the wide area of proteomics, the course will focus on protein sequence analysis and algorithms used to sequence unknown proteins. The experimental emphasis will be on protein mass spectrometry using top down proteomics. Besides the role of mass spectrometry in proteomics, an overview of its important role in basic science will also be surveyed. The course aims to impart the enrolled students with a very strong foundation in protein sequence analysis and prepare them for advanced courses. An extensive background in mass spectrometry or biology is not required.

COURSE PREREQUISITE(S)

- CS100
- BIO231 or BIO212 OR BIO216

COURSE OBJECTIVES

- To explore protein sequence analysis and associated computational techniques for an improved identification
- To provide hands-on training of using and developing a protein sequence search engine

Learning Outcomes

After the course, the student should:

- Understand the common computational proteomic techniques.
- Be able to apply these techniques to proteomics data.
- Be able to develop MATLAB code for an improved protein sequence search.

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Grading Breakup and Policy
Assignment(s): 15% Home Work: Quiz(s): 10% Class Participation: 5% Attendance: Midterm Examination: 20% Project: 20% Final Examination: 30%

Examination Detail	
Midterm Exam	Yes/No: Yes Combine Separate: Combine Duration: 2 hrs Preferred Date: Exam Specifications:
Final Exam	Yes/No: Yes Combine Separate: Combine Duration: 2 hrs Exam Specifications:

COURSE OVERVIEW

Week/ Lecture/ Module	Topics	Recommended Readings	Objectives/ Application
1	Introduction		
2	Protein, Proteome, and Proteomics		
3	Protein Separation - 2D Gel Electrophoresis		
4	Protein Digestion.		
5	Literature Based Discussion		
6	Peptide Separation		
7	Fundamentals of Mass Spectrometry		
8	Mass Spectrometry - MALDI-TOF		
9	Protein Identification and Characterization by MS		
10	Tandem MS or MS/MS Analysis		
11	Literature Based Discussion		
12	Fragmentation Models		
13	Identification and Characterization by MS/MS		
14	Spectral Comparisons		
15	Sequential Comparison - de novo Sequencing		
16	Database Searching for De Novo Sequences		
17	Large-Scale Proteomics		
18	Quantitative Mass Spectrometry-Based Proteomics		
19	Literature Based Discussion		
20	Peptides to Proteins		
21	Top-Down Proteomics		
22	Standards		
23	Literature Based Discussion		
24	Literature Based Discussion		
25	Literature Based Discussion		

26	Literature Based Discussion		
27	Literature Based Discussion		

Textbook(s)/Supplementary Readings

- Introduction to Computational Proteomics, by Golan Yona, (Chapman & Hall/CRC Mathematical & Computational Biology)
- Principles of Proteomics, 2nd Edition by Richard Twyman. ISBN: 9780815344728.