



Lahore University of Management Sciences
BIO 331 – Computational Biology II
 Fall 2013

Instructor	Dr Aziz Mithani and Dr Safee Ullah Chaudhary
Room No.	9-419A and 9-420A
Office Hours	12:00-13:00
Email	aziz.mithani@lums.edu.pk and safeeullah@lums.edu.pk
Telephone	8397 and 8352
Secretary/TA	Ashar J Malik and Roop Omar
TA Office Hours	
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	Yes
Elective	
Open for Student Category	Any
Closed for Student Category	

COURSE DESCRIPTION
The primary focus of the course is to understand theoretical foundation of some of the most widely used computational biology techniques. The principles and methods for pair-wise and multiple sequence analysis using hidden Markov models, phylogenetic analysis, protein sequence analysis and structure prediction are extensively covered. In addition systems biology is introduced at a glance with a significant amount of time spent on microarray analysis. The tutorials will provide hands-on training of programming in R with the aim of developing problem solving skills in computational biology research using scripting languages

COURSE PREREQUISITE(S)
<ul style="list-style-type: none"> • BIO 213 or BIO 231 • MATH 230 (Probability and Statistics)

COURSE OBJECTIVES
<ul style="list-style-type: none"> • To understand theory behind of some of the most widely used computational biology techniques. • To provide in depth knowledge of sequence and evolutionary analyses. • To provide hands-on training of programming in Python and Perl for computational biology.

Learning Outcomes
<ul style="list-style-type: none"> • After the course, the student should: • Understand the inner working of some of the most widely used computational biology techniques. • Be able to apply the techniques to biological data. • Be able to solve moderate complexity problems related to bioinformatics using Python and Perl.



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Grading Breakup and Policy
Assignment(s): 20% Quiz(s): 10% Lab: 10% Midterm Examination: 30% 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				
No.	Topic	Instructor	Key Dates	Objectives/ Application
1	Introduction to Probability & Markov Chains	AM		
2	Hidden Markov Models I	AM		
3	Hidden Markov Models II	AM	HW1 handed out	
4	Pair HMM I	AM		
5	Pair HMM II	AM		
6	Profile HMM	AM		
7	Molecular Evolution I	AM		
8	Molecular Evolution II	AM		
9	Microarrays - Introduction	AM	Quiz 1	
10	Microarrays - Image Processing & Normalisation	AM	HW 1 due, HW 2 handed out	
11	Microarrays - Differential Expression	AM		
12	Microarrays - Clustering	AM		
13	Microarrays - Classification	AM	Quiz 2	
14	Microarrays - Experimental Design	AM	HW 2 due	
	Mid Term			
15	Protein Sequence Analysis	CSU	HW 3 handed out	
16	Techniques for Sequencing Protein	CSU		
17	Protein Sequence Search Engines	CSU		
18	Scoring Schemes for Protein Searching	CSU		
19	RNA Structure Prediction I	CSU		
20	RNA Structure Prediction II	CSU	HW 3 due, HW 4 handed out	
21	Solving Structures using X-ray Crystallography and NMR	CSU	Quiz 3	
22	Protein Secondary Structures Prediction	CSU		
23	Homology Modelling	CSU		
24	Ab initio Structure Prediction	CSU		
25	Threading	CSU		
26	Multiscale modelling I	CSU	Quiz 4	
27	Multiscale modelling II	CSU	HW 4 due	



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	Final			
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Textbook(s)/Supplementary Readings
<ul style="list-style-type: none">• Biological Sequence Analysis. Probabilistic Models of Proteins and Nucleic Acids, Richard Durbin, Sean R. Eddy, Anders Krogh, Graeme Mitchison. Cambridge University Press, 1998.• Inferring Phylogenies, 2nd Edition, Joseph Felsenstein. Sinauer Associates, 2003.• Introduction to Computational Biology. An Evolutionary Approach. Bernhard Haubold, Thomas Wiehe. Birkhauser, Verlag 2006.• Microarray Bioinformatics. Dov Sketel. Cambridge University Press. 2003