



Lahore University of Management Sciences
BIO 531 –Computational Biology
Fall 2023

Instructor	Dr Safee Ullah Chaudhary
Room No.	9-314
Office Hours	2:30 pm – 3:30 pm (Fridays)
Email	safee.ullah.chaudhary@gmail.com
Telephone	8352
Secretary/TA	Maham Hamid & Zainab Nasir
TA Office Hours	TBA
Course URL (if any)	

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

Course Teaching Methodology	
<ul style="list-style-type: none">Teaching Methodology: In personLecture details: 100% live interaction lectures	

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

COURSE DESCRIPTION
This course provides introduction to computational biology introducing the tools and techniques important to study and analyze genomic data. This course emphasises on the fundamentals of nucleic acid and protein sequence analysis, phylogenetic analysis and the analysis of biological networks.

COURSE PREREQUISITE(S)	
<ul style="list-style-type: none">	Graduate standing

COURSE OBJECTIVES	
<ul style="list-style-type: none">	<ul style="list-style-type: none">To provide introduction to computational biology and bioinformaticsTo introduce tools and techniques useful for DNA and protein sequence analysisTo enable students to program and solve problems in bioinformatics

Learning Outcomes	
<ul style="list-style-type: none">	<ul style="list-style-type: none">Have knowledge of key computational biology/bioinformatics concepts and techniques.Understand the inner working of some of the most widely-used bioinformatics methods, such as sequence analysis and comparison, and protein structure and function analysis.Be able to solve moderate complexity problems related to bioinformatics



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Grading Breakup and Policy	
Assignment(s): 20% (4 assignments, equal weightage)	
Home Work:	
Quiz(s): 20% (4 quizzes, equal weightage)	
Class Participation:	
Attendance: 5%	
Midterm Examination: 25%	
Project:	
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			
Lecture/ Module	Topics	Recommended Readings	Objectives/ Application
1	Introduction, Analysing DNA Sequences – GC Content, Base Frequencies, Codon Bias		
Module 1: Sequence Comparison and Alignment			
2	Pairwise Alignment – Global		
3	Pairwise Alignment - Local, Overlap		
4	Pairwise Alignment - Affine Gap, Scoring Matrices		
5	Multiple Sequence Alignment		
6	Markov Chains/Hidden Markov Models		
7	Probability Calculations in HMMs		
8	Sequence Alignment using Pair HMM – Global/Local		
9	Profile HMM		
Module 3: Phylogenetics			
10	UPGMA		
11	Parsimony, Evolution Models		
12	Estimating the Number of Substitutions between DNA Sequences		
13	Maximum Likelihood		
Module 4: RNA			
14	RNA Secondary Structure Prediction I		
15	RNA Secondary Structure Prediction II		
Module 5: Proteins			
16	From DNA to Protein Sequences		
17	Protein Secondary Structures		
18	Protein Structure Visualization		



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19	Protein Structure Classification		
20	Protein Structure Comparison I		
21	Protein Structure Comparison II		
22	Protein Structure Prediction		
Module 6: Biological Networks			
23	Introduction to Biological Networks		
24	Representing Biological Networks		
25	Boolean Networks		
26	Biological Networks in Diseases I		
27	Biological Networks in Diseases II		
28	Revision		

Textbook(s)/Supplementary Readings

- Bioinformatics, Sequence and Genome Analysis, Second Edition, David W Mount, Cold Spring Harbor Laboratory Press, 2004.
- Developing Bioinformatics Computer Skills, Cynthia Gibas and Per Jambeck, O'Reilly, 2001
- 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.