

(LS 478): Computational Biology and Bioinformatics

(Theory 2 credit)

Course Faculty: Prof. Nirala Ramchiary, Devinder Kaur, Dr. Karunakar Kar

Credits: 2 credits, 32 Lectures

Method of Evaluation: Mid-semester and sessional – 50% End semester - 50% (weightage)

Objective of the course: This course will be primer to DNA and RNA sequence Analysis using computational methods and software tools. Overview of data analysis carried out by biologists will be covered with examples.

Learning outcomes from this course:

1. Students get Practical Exposure to access and use of database resources and software tools
2. Enable students to perform DNA sequence data analysis using publicly available software tools
3. Will motivate students to understand primary research concepts and undertake simple projects on bioinformatics.

S. No.	Topics	No. of lectures	Name of faculty
1	Brief description of the Course - Overview of Computational Biology: History, definition, applications – Research trajectory	1	NR
2	Definition and concepts of Bioinformatics - biological data, databases, Examples of different databases and sources - Database searching using Boolean operators, Database alignment	2	DK
3	Overview of Prokaryotes and Eukaryotes - Gene and genome structure and sequence makeup.	2	NR
4	Overview of sequence analysis – Compositions, Codon usage analysis, pattern finding, alignments, motifs analysis	2	DK
5	Pairwise alignment– concepts of homology – Scoring models, with gaps and affine gaps - Global (Needleman and Wunsch) and local alignment (Smith – waterman) algorithms, – PAM and BLOSUM scoring matrices, dot plot and its relevance. Theory and Practical	3	DK
6	Multiple Sequence alignment – Progressive methods – Consensus model – Position weight matrices. Protein sequence analysis, and predictions of important characteristics.	4	NR/KK
7	Overview of BLAST suite of programs – Computational approach – Statistical significance	2	NR
8	Amino acids and its analysis – Secondary structure prediction methods – Motif finding – Protein Structure – Basics of Homology Modelling	2	DK
9	RNA-structure and analysis: lncRNA, mRNA, SiRNA	2	NR
10	Phylogenetic tree construction	1	DK
11	Genome/Transcriptome data – high throughput sequencing (NGS Platform) – Assembly and mapping of reads, annotation with functional features and Visualization of data	5	NR/DK
12	Overview of Chip-Seq data and its analysis	2	NR
13	Molecular Docking, Protein-ligand and Protein-protein interactions. Online tools, Data generation and analysis.	4	KK

Textbook:

1. Jonathan Pevsner. Bioinformatics and functional genomics. Wiley Blackwell, Third Edition, 2015

2. Des Higgins and William Taylor. Bioinformatics: Sequence, Structure, and databanks. Oxford University Press, 2001

Reference Book:

1. Richard Durbin, Sean R. Eddy, Anders Krogh, Graeme Mitchison. Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids. Cambridge University Press, 1998