(LS 478): Computational Biology and Bioinformatics

Course Faculty: Prof. Samudrala Gourinath, Prof. Ajay Saxena, Dr. Nirala Ramchiary, Dr. Karunakar Kar*

Credits: 2 credits, 29 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 softwaretools. 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 (in hours)	Name of faculty
1	Brief description of the Course - Overview of Computational Biology: History, definition, applications – Research trajectory	1	AKS
2	Definition and concepts of Bioinformatics - biological data, databases, Examples of different databases and sources - Database searching using Boolean operators- Practical on database searching and data retrieval	3	AKS/SGN/KK
3	Overview of Prokaryotes and Eukaryotes - Mapping a DNA biomolecule to strings (4 letter, 2 letter and binary codes) – Gene and genome structure and sequence makeup	2	KK/NR
4	Overview of sequence analysis in practice – Compositions, Codon usage analysis, pattern finding, alignments, motifs, RNA secondary structure	2	SGN
5	Pairwise alignment – PAM and BLOSUM scoring matrices – Scoring models, with gaps and affine gaps - Global (Needleman and Wunsch) and local alignment (Smith – waterman) algorithms	2	AKS/KK
6	Multiple Sequence alignment – Progressive methods – Consensus model – Position weight matrices. Protein sequence analysis, and predictions of important characteristics.	2	NR/KK
7	Database alignment – Overview of BLAST suite of programs – Computational approach – Statistical significance	2	NR
8	Practical demonstration of alignments with real DNA Sequence Data sets	1	NR
9	Amino acids and its analysis – Secondary structure prediction methods – methods –Motif finding – Protein Structure – Basics of Homology Modelling	4	AKS
10	RNA-structure and analysis: lncRNA, mRNA, SiRNA	1	NR
11	Phylogenetic tree construction, theory and practical	2	NR
12	Genome data – high throughput sequencing (NGS Platform) – Assembly and mapping of reads, and annotation with functional features – Practical use of scripts for NGS data analysis	3	NR
13	Overview of R-Seq, Chip-Seq data and its analysis	1	NR
14	Molecular Docking, Protein-ligand and Protein-protein interactions. Online tools, Data generation and analysis.	3	SGN, 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