LS 430A Computational Biology and Bioinformatics 2 Credits Faculty: Prof. N. Ramachiary*, Dr. D. Kaur and Dr. K. Kar		
S. No.	**Topic**	**Faculty Name/ Contact Hours**
1	Overview of Computational Biology: History, definition, applications – Research trajectory	NR/1
2	Definition and concepts of Bioinformatics - biological data, databases, Examples of different databases and sources - Database searching using Boolean operators	DK/2
3	Gene and genome structure and sequence makeup in Prokaryotes and Eukaryotes	NR/2
4	Sequence analysis – Compositions, Codon usage analysis, pattern finding, alignments, motifs analysis	DK/2
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.	DK/3
6	Multiple Sequence alignment – Progressive methods – Consensus model – Position weight matrices. Protein sequence analysis, and predictions of important characteristics.	DK/4
7	Database alignment-Overview of BLAST suite of programs – Computational approach – Statistical significance	NR/2
8	Amino acids and its analysis – Secondary structure prediction methods – Protein Structure – Basics of Homology Modelling	DK/2
9	RNA-structure and analysis: lncRNA, mRNA, SiRNA	NR/2
10	Phylogenetic tree construction	DK/1
11	Genome/Transcriptome data – high throughput sequencing (NGS Platform) – Assembly and mapping of reads, annotation with functional features and Visualization of data- Practical use of scripts for NGS data analysis	NR/DK/5
12	Overview of Chip-Seq data and its analysis	NR/2
13	Molecular Docking, Protein-ligand and Protein-protein interactions. Online tools, Data generation and analysis.	KK/4

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
3. Bioinformatics and Functional Genomics. Jonathan Pevsner. ISBN-13: 978-1118581780

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