Name of the Programme: M.Sc. Biotechnology

Course Code: GBT–526

Title of the Course: LAB VI: LAB IN BIOINFORMATICS

Number of Credits: 2

Effective from AY: 2022-23

Pre-requisites for the Course:	NIL	
Course Objectives:	The aim is 1) to provide practical training in bioinformatics and statistical methods 2) learn to access and search the major public databases for data retrieval.	
Content:		**No. of hours**
	1. Using NCBI and Uniprot web resources. 2. Introduction and use of various genome databases. 3. Sequence information resource: Using NCBI, EMBL, Genbank, Entrez, Swissprot/ TrEMBL, UniProt. 4. Similarity searches using tools like BLAST and interpretation of results. 5. Multiple sequence alignment using ClustalW. 6. Phylogenetic analysis of protein and nucleotide sequences. 7. Use of gene prediction methods (GRAIL/Genscan,/Glimmer). 8. Use of various primer designing and restriction site prediction tools.	30
	9. Use of different protein structure prediction databases (PDB, SCOP, CATH). 10. Construction and study of protein structures using RASMOL/Deepview/PyMol. 11. Homology modelling of proteins. 12. Whole-genome assembly from NGS raw data sequence 13. 16S rRNA sequence analysis and use of Bioedit 14. Molecular docking	30
Pedagogy:	Hands-on experiments in the laboratory, video, online data	
References/ Readings:	1. A.D. Baxevanis, G.D. Bader, D.S. Wishart, Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins Wiley Publisher, 2020. 2. S. Shui Qing, Bioinformatics: A Practical Approach (Chapman;	

	Hall/CRC Mathematical and Computational Biology), 2007. 3. W. Even, and G. Grant, Statistical methods in Bioinformatics: An introduction, 2005. 4. N.C. Jones, and P.A. Pevzner; Introduction to Bioinformatics Algorithms; Ane Books, India, 2004. 5. D.W. Mount, Bioinformatics: Sequence and Genome Analysis, Cold Spring Harbor Laboratory Press, 2001.
Course Outcomes:	On completion of this course, students should be able to: 1. describe contents and properties of important bioinformatics databases, perform text- and sequence-based searches, analyse and discuss results in the light of molecular biology knowledge; 2. explain major steps in pairwise and multiple sequence alignment, explain its principles and execute pairwise sequence alignment by dynamic programming; 3. predict secondary and tertiary structures of protein sequences; 4. perform various statistical tools available to analyse the data.

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