

Branch Name:	M.Sc. Biotechnology / Microbiology
Program Code:	SC201 / SC202
Course Name:	Principles of Bioinformatics
Course Code:	3SC2000103
Pre-requisite Course:	

Course Objectives:

- To introduce the fundamental concepts of computers relevant to bioinformatics.
- To provide information about bioinformatics, and biological databases
- To explain methods for retrieval and analysis of biological information.
- To develop skills for use of various basic and advance bioinformatics tools.

Teaching and Examination Scheme:

Teaching Scheme (Hours per week)				Evaluation Scheme (Marks)				
Lecture (L)	Tutorial (T)	Practical (P)	Credit	Theory (Marks)		Practical (Marks)		Total (Marks)
				University Assessment	Continuous Assessment	University Assessment	Continuous Assessment	
4	--	--	4	50	50	--	--	100

Subject Contents:

Unit	Content	Lectures	Weightage
1	Introduction to Computers Components of computer (CPU, memory, I/O devices) Types of computers: workstation, clusters, supercomputers Introduction to high performance computing (HPC) in biology Modern Computers: Workstations, parallel processing computers, supercomputers. Operating systems and basic functions: Windows, Linux/Unix environment, File systems and directories, Basic Linux commands (ls, cd, mkdir, cp, rm, grep) Computer Networks & Internet: WWW, HTTP, FTP; Cloud computing in bioinformatics	15	25%
2	Programming Basics for Bioinformatics • Number systems (brief) • Introduction to scripting languages • Basics of Python and R for biological data analysis Bioinformatics: Introduction, Overview, History, Scope/ needs and Applications of bioinformatics, Biological data types (DNA, RNA, protein), Introduction to Omics (Genomics, Proteomics, Transcriptomics, Metabolomics, Metagenomics, Metaproteomics, Metatranscriptomics) Mode of data storage - Sequence formats and retrieval, requirements of tools and software, File formats - FASTA, Genbank and Uniprot, Data submission & retrieval from NCBI, EMBL, DDBJ, Uniprot, PDB.	15	25%

3	In Silico Resources for the Information Biological Databases: Introduction, significance, types of databases Nucleotide sequence database: EMBL, gene bank, DDBJ Protein Database Protein sequence database: PIR, Swiss-Prot, CDD Structure database: PDB, MMDB, Classification database: CATH, SCOPE\ Metabolic pathway Database: KEGG Chemical Database: ZINC, PUBCHEM Mechanism of submitting the biological data to the database: Data Standardization & Formatting, Validation, Deposition, Accession Primary Tools of bioinformatics Sequence Alignment & Similarity Search: Pair wise sequence Alignment: Dynamic programming Algorithm, Multiple sequence alignments (MSA): Global Multiple sequence alignments and introduction to CLUSTALW and PileUp, Local Multiple sequence alignments and introduction to BLOCKS, eMOTIF, MEME, GIBBS, HMM	15	25%
4	Molecular Visualization & Structural Analysis: PyMOL, Swiss-Pdb Viewer (DeepView), RasMol Secondary structure prediction: Computation methods for secondary structure prediction: Chou Fasman, GOR and Softwares for Secondary structure prediction Protein Modeling: Methods for Protein Modeling, Homology Modeling; fold recognition and threading approaches, and Ab-initio structure prediction methods. Molecular Interaction and Docking: Simulation techniques, Softwares for Structure based drug design and molecular docking, Autodock and Drug Bank	15	25%

Text Books:

1. Developing Bioinformatics Computer Skills C. Gibas and P. Jamback.
2. Pevzner, P., & Shamir, R. (2011). *Bioinformatics for biologists*. Cambridge University Press.

Reference Books:

1. Bioinformatics A machine learning approach P. Baldi & S. Bruna
2. Bioinformatics: A Practical guide to the analysis of genes and Proteins A. D. Buxevanis and B. F. Onellette
3. Bioinformatics Methods and protocols: Methods in molecular biology Vol. 132: S. Misener and S. A. Krawetz (Eds)

List of Open Source Software/learning website:

- <https://www.youtube.com/watch?v=lhU3CzslFqw>
- <https://www.ncbi.nlm.nih.gov/>
- <https://www.ncbi.nlm.nih.gov/home/learn/>
- <https://www.bioinformatics.org/>
- <https://www.genome.jp/kegg/>
- <https://www.expasy.org/>
- <https://www.ddbj.nig.ac.jp/index-e.html>

Course Learning Outcomes (CLO): On completion of this course, the students will be able to:

CLO	Description	Bloom's Taxonomy Level
CLO1	Explain the fundamental concepts of computers, operating systems, number systems, and basic programming relevant to bioinformatics.	1 Remember 2 Understand
CLO2	Describe the scope, applications, and need of bioinformatics and omics technologies	2 Understand
CLO3	Identify and retrieve biological data from biological databases.	3 Apply
CLO4	Demonstrate the use of bioinformatics tools for sequence similarity search and sequence alignment.	3 Apply
CLO5	Analyze protein structures and predict secondary structures using computational tools and visualization software.	4 Analyze
CLO6	Apply computational approaches such as homology modeling and molecular docking in structure-based drug design studies.	5 Evaluate 6 Create

Mapping of CLO s with POs & PSOs

Course Learning Outcomes	Programme Outcomes (POs)																Programme Specific Outcome (PSOs)		
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	PSO1	PSO2	PSO3
CLO1						1			3	3								1	
CLO2		2	1		2	1			3	3								1	1
CLO3	1	2	1		2	1			3	3									1
CLO4	2	2	1		2	1			3	3								1	1
CLO5	3	3	3		3	3			3	3									1
CLO6	3	3	3		3	3			3	3								1	

3: High, 2: Medium, 1: Low