B.Sc Biotechnology: Semester-VI BST 604: Bioinformatics	
Teaching Scheme Lectures: 3 hrs/Week Tutorials: 1 hr/Week Credits: 4	**Examination Scheme** Class Test -12Marks Teachers Assessment - 6Marks Attendance – 12 Marks End Semester Exam – 70 marks

Prerequisite: - BST302 Molecular Biology, BST404 Enzymology

Course Objectives:

1 To give basic overview of databases and tools used in bioinformatics.

2. To give complete knowledge of DNA and protein sequencing techniques.

3. To explain the concept of different bioinformatic tools such as BLAST, ClustalX, MEGA, Pymol, RASMOL, CHIME.

4. To explain the importance of homology modeling and molecular docking.

5. To explain and emphasize on the concept of computer Aided drug designing, ORF prediction, Gene prediction and analysis.

Course Outcomes:

After completing the course, students will be able to:

CO1: To give practical and hands-on experience with common bioinformatics tools and databases like as BLAST, ClustalX, MEGA, Pymol, RASMOL, CHIME.

CO2: To understand basic theory and application of programs used for database searching, protein and DNA sequence analysis, prediction of protein function, and building phylogenetic trees.

CO3: To determine and execute basic competences in the use of bioinformatics tools.

CO4: To analyze and compare different bioinformatics tools.

CO5: To evaluate information networks and bioinformatics tools on the internet.

CO6: To explain and the knowledge of bioinformatics tools for computer Aided drug designing, ORF prediction, Gene prediction and analysis.

CO7: To explain the concept of homology modeling, molecular docking and protein-protein interaction.

Detailed syllabus:

UNIT-1 Introduction of Bioinformatics
Introduction of Bioinformatics and its role in biotechnology, NCBI, EBI, PDB, Searching and retrieval of DNA and protein, protein structure (PDB), DNA sequencing (chemical chain termination, Dideoxy chain termination method, Automatic sequencer), Generation and analysis of biological data and their submission. Protein sequencing (Edmand degradation method).

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UNIT-2 Sequence alignment

BLAST, ClustalX, MEGA, Sequence alignment (pairwise and multiple, global and local), Phylogenetic analysis. Extraction of phylogenetic data set. Tree building methods and tree evaluation. Comparative genome analysis. Reconstruction of metabolic pathways. Computationaltools for expression analysis. Prediction and designing of primers & probes for diagnosis and analysis, Prediction of RNA secondary structure, codon optimization, computer Aided drug designing, ORF prediction, Gene prediction and analysis.

UNIT-3 Identification of target protein

Identification of target protein for disease, identification and analysis of epitope, identification of promoter, transcription factor, gene designing, prediction and analysis of protein structure (primary, secondary and tertiary), Homology modeling, protein threading. *In silico* protein validation, protein folding and activity, Basic of molecular docking. Structure visualization methods (Pymol, RASMOL, CHIME etc.), protein-protein interaction, construction of metabolic gene network, drug target, vaccine designing.

Text and Reference Books

1. Bioinformatics: Principles and applications by Ghosh and Mallick (oxford) university press)

2. Bioinformatics by Andreas D Boxevanis (Wiley Interscience)

3. Fundamental concept of bioinformatics by Dan e. krane

4. Introduction to bioinformatics by Attwood and Parry Smith (Pierson educationPublication)

5. Instant notes in Bioinformatics by Westhead, parish and Tweman (Bios scientific publishers)

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