GUJARAT TECHNOLOGICAL UNIVERSITY

Bachelor of Engineering
Subject Code: 3150407
Semester –V
Subject Name: Fundamentals and Applications of Bioinformatics

Type of course: Professional Elective course

Prerequisite: Molecular Biology and basic computer and internet knowledge

Rationale:
The objective of this course is to study fundamentals of computing focusing the processes on DNA,RNA and Proteins. The *in-silico* approaches are essential in saving the time and revenue on experimentations at first level of confirmation using global sources like NCBI. The area like evolution, phylogeny and drug designing touch the real industrial needs. The Language like PYTHON attends the need of the time by comforting tools of Bioinformatics which are used conventionally. All these features enable students to make the bioinformatics as their career choices catering pharma, foods and agricultural industries assisting various bioprocesses and design thereof.

Teaching and Examination Scheme:

Teaching Scheme			Credits	Examination Marks				Total Marks
L	T	P	C	Theory Marks		Practical Marks		
				ESE (E)	PA (M)	ESE (V)	PA (I)	
3	0	2	4	70	30	30	20	150

Content:

Sr. No.	**Content**	**Total Hrs**	**Module weightage**
	Module 1:		
1	A word on Bioinformatics (Introduction, aims, branches and scopes) [1]	1	3%
2	Bioinformatics: Applications and Research, Present Bioinformatics Scenario in India [2]		
	Module 2:		10%
3	Databases in Bioinformatics: An Introduction [1]	1	
4	Biological Sequence Databases (NCBI, EMBL, DDBJ, PIR	2	

	etc) [1]		
5	Protein 3D Structure (PDB, MMDB, CDD,Gene3D) and Classifications Databases (CATH , SCOP) [1]	2	
	Module 3:		28%
6	Data Searches and Pairwise Alignments (Dot Plots, Simple Alignments,Gaps,Scoring Matrices,Dynamic Programming: The Needleman and Wunsch Algorithm,Global and Local Alignments,Databases Searches,Multiple Sequence Alignments) [3]	5	
7	Sequence Alignments (PAM,BLOSUM Heuristic methods) [1]	2	
8	Alignment of Multiple Sequences and methods of multiple sequence alignment, Phylogenetic Analysis, Hidden Markov Models [4]	3	
9	Molecular phylogeny (Phenotypic and Molecular Phylogeny,molecular clocks and methods of phylogenetic analysis, reliability of phylogenetic analysis) [1]	2	
10	Molecular Viewers (RasMol and PDBViewer) [1]	1	
	Module 4:		26%
11	Gene identification and prediction (Introduction, Basis of Gene Prediction, Pattern Recognition, Gene prediction Methods, Other Gene Prediction Tools)	4	
12	Gene Expression and Microarrays (Introduction,Working with DNA Microarrays, Clustering Gene Expression Profiles,Data Sources and Tools for Microarray Analysis, Applications of Microarray Technology) [4]	4	
13	Protein Structure prediction and Modeling (secondary structure prediction, protein modeling, function prediction) [1] Evolution of protein structure and function and their relationship.	4	

	Module 5:		32%
14	Bioinformatics in Computer aided Drug Design (drug discovery process and structural bioinformatics, SAR and QSAR techniques) [1]	2	
15	Overview of Simulation and Statistical Protocols [1]	1	
16	PYTHON for Bioinformatics –basics of theory, BIOPYTHON –introduction, databases, graphics and applications to cover the basic uses in bioinformatics [5]	10	
17	Concepts on *Next Generation Sequencing* and any two case studies	2	

Suggested Specification table with Marks (Theory):

Distribution of Theory Marks					
R Level	**U Level**	**A Level**	**N Level**	**E Level**	**C Level**
14	15	18	9	0	14

Legends: R: Remembrance; U: Understanding; A: Application, N: Analyze and E: Evaluate C: Create and above Levels (Revised Bloom's Taxonomy)

Note: This specification table shall be treated as a general guideline for students and teachers. The actual distribution of marks in the question paper may vary slightly from above table.

Reference Books:

1. BIOINFORMATICS-Principles and Applications, Zhumur Ghosh and Bibekanand Mallick, Oxford University Press, First edition 2008
2. Bioinformatics – Databases, Tools and Algorithms, Orpita Bosu /Simminder Kaur Thakur, Oxford Higher Education, 2007
3. Fundamental Concepts of Bioinformatics,Dan E. Krane, Michael L. Raymer,Pearson Education, 2008
4. BIOINFORMATICS-Methods and Applications, S.C.Rastogi, Namita Mendiratta, Parag Rastogi, Second Edition 2006

5. PYTHON for Bioinformatics, Sebastian Bassi, Second Edition, CRC press-Taylor and Francis group.

Course Outcomes:

Students should be able to

Sr. No.	CO statement	Marks % weightage
CO-1	Describe fundamentals of bioinformatics and databases.	13%
CO-2	Explain the sequence similarities searches and their applications in fields	10%
CO-3	Explain sequence alignment, multiple sequence alignments along with their uses in the field.	18%
CO-4	Choose suitable gene prediction tools; identify the protein structure and its predictive function.	27%
CO-5	Develop/ think the skills towards computer aided drug design, logical programming in PYTHON referring current needs	32%

List of Experiments:

1. Introduction to Home Page: NCBI, DDBJ & PDB
2. Sequence Retrieval System-Entrez
3. Pair-wise Sequence Alignment-BLAST & FASTA
4. Multiple Sequence Alignment-CLUSTALW
5. Sequence Analysis Software
6. Post Translational Modification
7. Secondary Structure Prediction
8. Visualization Software
9. Generating Drug Molecule
10. Primer Design
11. Introduction to simulation software
12. Practices on PYTHON

Major Equipments:

The computers with configurations having access to internet for accessing NCBI-a global open source of bioinformatics as well as other online and offline tools/software.

List of Open Source Software/learning website:

1. Students can refer to video lectures available on the websites including NPTEL.
2. Students can perform experiments on Virtual Lab