Global B

BIOINFORMATICS		
(Theory)		
Course Code: 16G5B01		CIE Marks:100
Credits : L:T:P:S: 4:0:0:0		SEE Marks:100
Hrs/Week::04		SEE Duration(Theory) : 3 Hrs
Course Learning Objectives: The students will be able to		
1. Understand the underlying technologies of Bioinformatics and Programming		
2. Explore the various algorithms behind the computational genomics and proteomic structural bioinformatics, modeling and simulation of molecular systems.		
3. Apply the tools and techniques that are exclusively designed as data analytics to investigate the significant meaning hidden behind the high throughput biological data.		
4. Analyze and evaluate the outcome of tools and techniques employed in the processes of biological data preprocessing and data mining.		
5. Use effective tools and powerful techniques to compose innovative ideas to tackle potential challenges in the field of Biotechnology and chemical engineering.		
UNIT-I		**9hrs**
Biomolecules: Introduction to Biomolecules. Structure, Types and Functions of Carbohydrates, Lipids, Nucleic Acids and Proteins. Genetic code, Codon degeneracy, Genes and Genomes. **Bioinformatics & Biological Databases:** Introduction to Bioinformatics, Goals, Scope, Applications in biological science and medicine. Biological databases – Sequence, structure, Special Databases and applications - Genome, Microarray, Metabolic pathway, motif, and domain databases. Mapping databases – genome wide maps. Chromosome specific human maps.		
UNIT II		**9hrs**
Sequence Alignment: Introduction, Types of sequence alignments - Pairwise and Multiple sequence alignment, Alignment algorithms (Needleman & Wunch, Smith & Waterman and Progressive global alignment). Database Similarity Searching- Scoring matrices – BLOSSUM and PAM, Basic Local Alignment Search Tool (BLAST), and FASTA. Next Generation Sequencing – Alignment and Assembly. **Molecular Phylogenetics:** Introduction, Terminology, Forms of Tree Representation. Phylogenetic Tree Construction Methods - Distance-Based & Character-Based Methods and Phylogenetic Tree evaluation.		
UNIT III		**9hrs**
Predictive methods: Predicting secondary structure of RNA, Protein and Genes – algorithms to predict secondary structure of RNA, Protein and Gene. Prediction of Tertiary structure of Protein, Protein identity and Physical properties of protein. **Molecular Modeling and Drug Designing:** Introduction to Molecular Modeling. Methods of Molecular Modeling and Force Fields used in Molecular Modeling. Drug designing process - deriving Pharmacophore, Receptor Mapping, Estimating Receptor-Ligand interactions and Molecular Docking.		
UNIT IV		**9 hrs**
Perl: Introduction to Perl, writing and executing a Perl program. Operators, Variables and Special variables. Data Types – Scalar, Array and Associative array. Regular Expressions (REGEX),		

Components of REGEX - Operators, Metacharacters and Modifiers. Subroutines – types of functions, defining and calling functions in Perl, calling function - call by value and call by reference. Object Oriented Programming in Perl – Class and object, Polymorphism, inheritance and encapsulation. Perl Package – writing and calling package. Perl Module – writing and calling module.

UNIT V	9 hrs

BioPerl: Introduction to BioPerl, BioPerl Modules, Applications of BioPerl – Sequence retrieval from Database and submission of sequence to online Database, Indexing and accessing local databases, Transforming formats of database record, Sequence alignments BioPerl and Sequence Analysis - Pair wise and Multiple sequence alignment, Restriction mapping. , Identifying restriction enzyme sites, acid cleavage sites, searching for genes and other structures on genomic DNA, Parsing BLAST and FASTA results. BioPerl and phylogenetic analysis, BioPerl and Phylogenetic tree manipulation, creating graphics for Sequence display and Annotation.

Course Outcomes: After completing the course, the students will be able to

CO1	Understand the Architecture and Schema of online databases including structure of records in these databases.
CO2	Explore the Mind crunching Algorithms, which are used to make predictions in Biology, Chemical Engineering, and Medicine.
CO3	Apply the principles of Bioinformatics and Programming to the problems related to process simulation and process engineering in Biological system.
CO4	Use Bioinformatics tools and Next Generation Technologies to model and simulate biological phenomenon.

Text Books

1. T. Christiansen, B. D. Foy, L. Wall, J. Orwant, Programming Perl: Unmatched power for text processing and scripting, O'Reilly Media, Inc., 4th edition, 2012, ISBN-13: 978-0596004927
2. B. Haubold, T. Weihe, Introduction to Computational Biology: An Evolutionary Approach, new age publishers, Paperback Edition, 2009, ISBN-13: 978-8184890624
3. C. Bessant, I. Shadforth, D. Oakley, Building Bioinformatics Solutions: with Perl, R and MySQL, Oxford University Press, 1st edition, 2009, ISBN
4. D. C. Young. Computational Drug Design: A Guide for Computational and Medicinal Chemists,Wiley-Interscience, 1st edition, 2009, ISBN-13: 978-0470126851.

Continuous Internal Evaluation (CIE)	
(Theory – 100 Marks)	
Evaluation method	**Course with assignment**
Quiz -1	10
Test -1	30
Quiz -2	10
Quiz -3	10
Test -2	30
Assignments	10
Total	**100**

Semester End Evaluation (SEE)	
Theory (100 Marks)	
Part- –A	**20**
Objective type questions	
Part –B	
There should be five questions from five units. Each question should be for maximum of 16 Marks.	
The UNIT-2 and UNIT-3 should have an internal choice. Both the questions should be of the same complexity in terms of COs and Bloom's taxonomy level.	80
Total	**100**

Note: The faculty teaching the course may adapt additional methods for evaluation within the total maximum marks.

		What	To whom	Frequency of conduction	Max Marks	Evidence	Contribution to Course Outcome		
Direct Assessment Methods	CIE	Quiz	Students	Three	30	Answer Scripts	80%	100%	90%
		Test		Two	60				
		Assignment		2 phases	10	Reports			
	SEE	Semester End Examination		End of every semester Consisting of Part-A and Part-B	100	Answer Scripts	20%		
Indirect Assessment		Course End Survey	Students	End of course		Questionnaire Based on COs	10%		

CO-PO Mapping												
CO/PO	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PO12
CO1	2	3	2	3	2	3	3			1	2	
CO2	3	3	3	2	3	3	2		2			
CO3	3	2	2	2	2	1	1				1	
CO4	1	2	3	3	3	2	1			2		

High-3 : Medium-2 : Low-1