BIT3001	COMPUTATIONAL BIOLOGY	L	T	P	J	C
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Pre-requisite	**BIT2001**	**Syllabus version**				
		1.0				

Course Objectives:

1. Students will learn about the computational problems in the emerging areas of Bioinformatics, Computational Biology, andGenomics.

2. The students will gain insights from varied backgrounds of engineering, computer science, and the lifesciences

Expected Course Outcome:

At the end of the course, students should be able to:
1) Explain mathematical concepts involved inbiology
2) Gain basic knowledge of modern molecular biology andgenomics
3) Develop an algorithm for analysis of biological sequences.
4) Gain knowledge to identify and develop in silico models appropriate to the different biologicalprojects
5) Apply molecular methods to study genetic variation within and betweenspecies
6) Explain and evaluate different phylogenetic optimalcriteria
7) Correctly select systems biology tools that will help them in re-constructing and re-defining complex biologicalprocesses

Student Learning Outcomes (SLO):	**2,7,9**

Module:1	**Introduction**	**6 hours**

How the genome is studied, maps and sequences, specific techniques, the human genome project, sequence databases. Strings, graphs, and algorithms - Understanding the Basics of NGS: From Mechanism to Variant Calling

Module:2	**Sequence Comparison and Database Search algorithms**	**6 hours**

Comparing two sequences, global comparison the basic algorithm, database search, pam matrices, blast, fast, other issues, similarity and distance, parameter choice in sequence comparison, string matching and exact sequence comparison.

Module:3	**Fragment Assembly of DNA -I**	**7 hours**

The ideal case, complications, alternative methods for DNA sequencing, shortest common superstring, reconstruction, multicontig, algorithms, representing overlaps, paths originating		
Module:4	**Fragment Assembly of DNA-II**	**7 hours**
Superstrings, shortest superstrings as paths, heuristics, findx5gding overlaps, ordering fragments, alignment and consensus, The Maximum Overlap Graph, Graph formulation of SCS		
Module:5	**Physical Mapping of DNA - I**	**7 hours**
Restriction enzymes - Restriction site mapping, hybridization mapping, models, restriction site models, interval graph models, the consecutive ones property, algorithmic implications		
Module:6	**Physical Mapping of DNA - II**	**5 hours**
An algorithm for the cp problem, an approximation for hybridization mapping with errors, a graph model, a guarantee, computational practice, heuristics for hybridization mapping. Enhanced Double Digest Problem		
Module:7	**Phylogenetic tree construction algorithms**	**5 hours**
Character states and the perfect phylogeny problem, binary character states, two characters, parsimony and compatibility in phylogenies, algorithms for distance matrices, reconstructing additive trees, reconstructing ultrametric trees, agreement between phylogenies.		
Module:8	**Contemporary issues:**	**2 hours**
Lecture by Industrial Expert		
	Total Lecture hours:	**45 hours**	

Text Book(s)

1.	João Meidanis & João Carlos Setubal PWS Publishing Company, Boston. 1997

Reference Books

1.	Konopka, Andrzej K Konopka, M James C Crabbe Compact Handbook Of Computational Biology- Science – 2004.
2.	Dan Gusfield Algorithms on Strings, Trees, and Sequences: Computer Science and Computational Biolog - Computers - 1997

3.	Michael S Waterman Introduction to Computational Biology: Maps, Sequences, and Genomes by - Science - 1995			
Recommended by Board of Studies	04-04-2014			
Approved by Academic Council	No. 37	Date	16-06-2015	