

Course Code	Course Name	Teaching Scheme (Hrs/week)			Credits Assigned			
		L	T	P	L	T	P	Total
MCA5054	Bioinformatics	3	1	--	3	--	--	3
		Examination Scheme						
		ISE		MSE		ESE		
		10		30		100 (60% Weightage)		

Pre-requisite Course Codes	Mathematics	
Course Outcomes	Student will be able to	
	CO1	To impart knowledge on introduction and historical and academic perspective to the field of bioinformatics
	CO2	To learn the key methods and tools used in bioinformatics
	CO3	To influence of biological science on computing science
	CO4	To Understand the theoretical basis behind bioinformatic
	CO5	To relates Informatics and explore the tools and techniques used in Bioinformatics

Module No.	Unit No.	Topics	Ref.	Hrs.
1		<b>Bioinformatics</b>	1	4
	1.1	Bioinformatics as multidisciplinary domain		
	1.2	Goal and scope of bioinformatics		
	1.3	Future prospectus of bioinformatics		
	1.4	Use of computers to biologists		
2		<b>Biological research on the web</b>	1, 2, 3	6
	2.1	Public biological databases : Primary sequence database		
	2.2	Protein sequence databases		
	2.3	Secondary databases		
	2.4	Protein pattern databases		
	2.5	Searching biological databases- depositing data into public Databases		
	2.6	Finding software , Judging the quality of information		
3		<b>Introduction to Protein structure</b>	2,3,4	9
	3.1	Chemistry of proteins : 1D to 3D		
	3.2	Peptide bond		
	3.3	Amino Acid		
	3.4	Web based protein structure tools : Structure visualization		
	3.5	Cn3D, RasMol		
	3.6	Structure modeling, MolMol, Jmol		
	3.7	Structure classification : Types of classification, Databases (SCOP,CATH)		
4	4.1	Composition of DNA and RNA	2, 3	6
	4.2	Watson and Crick Solve the Structure of DNA		

	4.3	Importance and features of DNA sequence analysis ,		
	4.4	Development of DNA Sequencing Methods,		
	4.5	Gene finders and Feature Detection in DNA		
5	5.1	Pairwise Sequence Comparison,	3, 4	9
	5.2	Pairwise Sequence alignment methods : Dot plot		
	5.3	Dynamic programming, Local and Global similarities, Word and K-tuple		
	5.4	BLAST, FASTA		
	5.5	Multiple sequence alignment methods : Progressive		
	5.6	ClustalW, Iterative, DiAlign		
6	6.1	Phylogenetic Analysis : Phylogenetic Trees Based on Pairwise Distances	5	6
	6.2	Phylogenetic Trees Based on Neighbor Joining		
	6.3	Phylogenetic Trees Based on Maximum Parsimony		
	6.4	Phylogenetic Trees Based on Maximum Likelihood Estimation Introduction to motif		
7	7.1	Automating data analysis using Perl	4	5
	7.2	Perl basics		
	7.3	Pattern matching and regular expressions		
	7.4	Parsing BLAST output using Perl		
<b>Total</b>				<b>45</b>

#### References:

- [1] Cynthia Gibas, Per Jambeck “Developing Bioinformatics Computer Skills”, O'Reilly.
- [2] T Kattwood& D J Parry-Smith “Introduction to Bioinformatics”Addison Wesley Longman
- [3] Machael “Bioinformatics A beginners Guide” Wiley-Dreamtech
- [4] Rehm and Reed “Biotechnology: a multi-volume comprehensive treatise” Volume 5b
- [5] Neil C. Jones,Pavel A. Pevzner “An Introduction to Bioinformatics Algorithms”