19BSP706					Introduction to Bio-Informatics					
Teaching Scheme					Examination Scheme					
L	T	P	C	Hrs/Week	Theory		Internal	Team Work	Practical/ Viva	Total Marks
					MS	ES				
3	0	0	3	3	25	50	25	-	-	100

COURSE OBJECTIVES

- ⬚ To study inherent structure of biological information.
- ⬚ To give students knowledge of organizing biological data in form of database.
- ⬚ To make them understand various biological techniques.
- ⬚ To give them knowledge of comparing and analyzing biological data.
- ⬚ To get introduced to the basic concepts of Bioinformatics and its significance in Biological data analysis.

UNIT I INTRODUCTORY BIOINFORMATICS   **9 Hrs.**
Bioinformatics: History and scope, branches of bioinformatics, career in bioinformatics, bioinformatics industry. Human genome Project (HGP), Robotics, DNA Microarray, Polymerase chain reaction (PCR), Computational evolutionary biology.

UNIT II STRUCTURAL BIOINFORMATICS   **12 Hrs.**
Structure of protein: Primary, secondary, tertiary, quaternary, protein secondary structure prediction method- Chou fasman, GOR method. Protein tertiary structure prediction method-homology/comparative modeling, fold recognition and threading approaches, ab initio (de novo). Computational resource for protein structure prediction. Nucleic acid: DNA, RNA, RNA structure prediction method- RNA fold, ALIDOT. DNA structure prediction method- MEME (Multiple EM for Motif Elicitation).

UNIT III BIOLOGICAL DATABASE IN BIOINFORMATICS   **14 Hrs.**
Sequence analysis: protein sequence analysis, nucleic acid sequence analysis, applications of sequence analysis. Data, Database, purpose, types of biological database: Sequence database: Nucleotide database- NCBI, Gene bank, EMBL, DDBL, Protein Database- primary databases (PIR, UNIPROT, PFAM) and secondary databases (PDB, CATH, SCOP).

UNIT IV SOFTWARE TOOLS OF BIOINFORMATICS AND BIODIVERSITY MEASURING   **10 Hrs.**
Sequence alignment: Types, methods, uses. FASTA, BLAST, GGSEARCH, GLSEARCH, DNA/RNA GC content calculator, ORF finder. Measuring Biodiversity: species richness, species evenness, Simpson's index of diversity. Overview of Bioinformatics applications in different fields.
                                                                                         Max. 45 Hrs.

COURSE OUTCOMES

On completion of the course, student will be able to

CO1 - Analyze new sources of experimental data in biology and medicine.
CO2 - Determine the basis of sequence alignment and analysis.
CO3 - Apply basic principles of biology, computer science and mathematics to address complex biological problem.
CO4 - Analysis and development of models for better interpretation of biological data to extract knowledge.
CO5 - Determine the protein function from sequence through analyzing data.
CO6 - Understanding the methodologies used for database searching, and determining the accuracies of database search.

TEXT/REFERENCE BOOKS

1. Basics of bioinformatics, Rui Jiang, Xuegong Zang and Michael Q. Zhang.
2. Essential Bioinformatics, Jin Xiong.
3. Structure and Mechanism in protein structure, Fresh WH Freeman
4. Bioinformatics- A Beginners' guide, John Wiley & Sons.
5. Structural bioinformatics, Jehnny Gu. And Philips E. Bourne.
6. Introduction to bioinformatics, M. Lesk.
7. Bioinformatics: A Practical guide to the analysis of genes and protein, Andreas D. baxevanis and B. F. Francis Quellette.
8. Bioinformatics computing, B. Bergeron.
9. Bioinformatics: Principles and application, Bibekanand Mallick and Zhumur Ghosh.
10. Fundamentals of Bioinformatics, Harisha S.
11. Bioinformatics: Sequence and Genome analysis, David W. Mount.
12. Introduction of bioinformatics, Arthur Lesk, Oxford University Press, latest edition, 2002.
13. Instant notes in Bioinformatics, Westhead D.R., Parish, J.H., Twyman, R.M.