- Dr.B. Hebsibah Elsie, Assistant Professor of Bio-Chemistry
- Dr. K. Shoba, Assistant Professor of Bio-Chemistry

SKILL BASED IV

BIOINFORMATICS

Sem	Sub. Code	Category	Lecture		Theory		Practical		Credit
			Hrs/ week	Hrs/ sem.	Hrs/ week	Hrs/ sem.	Hrs/ week	Hrs/ sem.	
VI	21SBC6A	Skill Based	2	30	2	30	-	-	2

COURSE OBJECTIVE:

To introduce classic bioinformatics theory to students by focusing on how computer techniques can be used for the storage, analysis, prediction and simulation of biological sequences (DNA, RNA and Proteins).

COURSE OUTCOMES:

On the successful completion of the course, students will be able to

CO Number	CO Statement	Knowledge Level ($K_1 – K_4$)
CO1	To understand the fundamentals of concepts of bioinformatics	**K1**
CO2	Provide a clear knowledge on the sequence analysis and its software tools.	**K2**
CO3	Students will analyze structural functional relationship of sequence.	**K4**
CO4	Students will have a clear knowledge on the different level of protein structure and their prediction tools.	**K4**
CO5	Provide deeper insights into protein structure. prediction and homology modeling process.	**K1**

(*CO – course Outcomes Knowledge Level: K1 – Remember; K2 – Understand; K3 – Apply; K4 – Analyze).

MAPPING WITH PROGRAMME OUTCOMES:

COS	PO1	PO2	PO3	PO4	PO5	PO6
CO1	S	M	S	M	M	M
CO2	S	S	S	S	M	M

CO3	M	M	M	S	M	S
CO4	M	S	M	S	M	M
CO5	S	S	M	M	S	S

(S- Strong; M-Medium; L-Low)

Total Hours:30

UNIT I

Introduction to Bioinformatics **5 Hours**

Introduction, definition, Aim and objectives. Branches of Bioinformatics, Scope and Research area of Bioinformatics. Sequence and Molecular file format.

UNIT II

Biological Databases **5 Hours**

Introduction, Biological Databases – Sequence, Structure and Classification of Databases.National Centre for Biotechnology (NCBI) – Introduction, General tools and Databases.

UNIT III

Sequence Analysis **7 Hours**

Introduction to Sequences, alignments and Dynamic Programming; Pair wise alignment (BLAST and FASTA Algorithm) and multiple sequence alignment (Clustal W algorithm), Online tools for Sequence analysis.

UNIT – IV

Similarity Search, Gene Identification and Prediction **6 Hours**

Similarity Search Introduction, Working with FASTA, Working with BLAST.Basis of gene prediction, Pattern recognition, Gene prediction methods, commonly available tools.

UNIT – V

Protein Classification and Structure Visualisation **7 Hours**

Overview of the Protein Structure, Protein Structure Visualization and prediction: Pymol, Rasmol, and Structure - based Protein Classification, Protein Structure databases, Protein Structure Visualization Databases and tools. Comparative modelling.

DISTRIBUTION OF MARKS: Theory - 100% and Problems – Nil

TEACHING METHODOLOGY:

- Black Board
- Power Point Presentations
- Assignments
- Models
- Demonstrations

TEXT BOOKS:

S.NO.	AUTHORS	TITLE	PUBLISHERS	YEAR OF PUBLICATION
1	Attwood.T.K. Parry D.J. and Smith	Introduction to Bioinformatics	A joint Publications	1999
2.	Baldi, P. and Brunak, S.	Bioinformatics: The Machine Learning Approach	ress,	2001
3	A.D. Baxevanis and B.F.F. Ouellette.	Bioinformatics: A practical guide to the analysis of genes and proteins	John Wiley and Sons	2002
4	Gentleman, R.	"Bioinformatics and Computational Biology Solutions using R and Bioconductor	Springer Science and Business media Inc	2005

REFERENCE BOOKS:

S.NO.	AUTHORS	TITLE	PUBLISHERS	YEAR OF PUBLICATION
1	D.W. Mount	Bioinformatics	Cold spring Press	2001
2	Lesk, A. K	Introduction to Bioinformatics, 4th Edition	University Press	2013
3	Rastogi, S.C	Bioinformatics Concepts, Skills & Applications, 2nd Edition	ublishers	2009

WEB SOURCES

- www.slideshare.net/biinoida/bioinformatics
- www.slideshare.net/PrashantTripathi59/sequence-analysis-71940516