Course Name: Bioinformatics

ABOUT THE COURSE:

TOTAL DURATION:	45HRS
MODE OF DELIVERY	PHYSICAL CLASSROOM TRAINING AT RESPECTIVE COLLEGES
TRAINER TO STUDENT RATIO:	1:50
TOTAL MARKS:	75

TABLE 1	
OVERALL COURSE OBJECTIVE:	This is an immersive course designed to provide students with foundational skills in bioinformatics. Throughout this program, students will explore the principles behind sequencing techniques, gaining insight into various sequencing methods and their significance in modern biology. Delve into the world of gene prediction algorithms and tools, understanding how they play a crucial role in deciphering genomic information. Additionally, the course will cover essential topics such as sequence analysis, homology modeling, and database access, offering a deep understanding of biological databases, data mining techniques, and genomic sequence analysis. Students will also acquire practical Python scripting skills, enabling them to read and write scripts and efficiently use functions for repetitive tasks. Furthermore, the course will guide students in the application of key bioinformatics tools like Knime, clustalW, and blast for tasks such as creating phylogenetic trees, contributing to drug discovery processes, and analyzing genome variants. By the end of this journey, students will emerge with a comprehensive understanding of bioinformatics principles, ready to apply their knowledge to real-world scenarios in genomics and drug discovery.
LEARNING OUTCOME:	1. Sequencing Techniques: - Define the principles underlying DNA sequencing techniques.

	- Distinguish between different sequencing methods and explain their respective importance in biological research. 2. Exploring Gene Prediction: - Identify and describe the key concepts of gene prediction. - Utilize gene prediction algorithms and tools to interpret genomic information. 3. Mastering Sequence Analysis and Database Access: - Demonstrate proficiency in analyzing biological sequences, including homology modeling. - Navigate and query diverse biological databases, understanding the information formats they employ. - Apply data mining techniques to extract relevant information from biological databases. 4. Developing Python Scripting Skills: - Read and comprehend Python scripts relevant to bioinformatics. - Write Python scripts for basic bioinformatics applications. - Implement functions in Python and apply them for repetitive tasks in bioinformatics. 5. Application of Bioinformatics Tools: - Utilize bioinformatics tools such as Knime, clustalW, and blast for specific tasks. - Create phylogenetic trees using appropriate tools.

	- Apply tools in drug discovery processes and analyze genome variants. 6. Real-world Application: - Apply acquired knowledge to solve practical problems in genomics and drug discovery. - Complete a final project integrating multiple aspects of bioinformatics. 7. Critical Thinking and Problem Solving: - Develop critical thinking skills to assess and solve bioinformatics challenges. - Apply problem-solving strategies in diverse bioinformatics scenarios. 8. Communication and Collaboration: - Effectively communicate bioinformatics findings. - Collaborate with peers on bioinformatics projects, fostering teamwork and shared learning.

TABLE 2: MODULE WISE COURSE CONTENT AND OUTCOME

SL. NO	MODULE NAME	MODULE CONTENT	MODULE LEARNING OUTCOME	DURATION (HRS)
1.	BASICS - Introduction to bioinformatics	Analysing sequences, Homology modelling & Accessing Databases Understand different databases and their information format. - Data Mining and Comparison.	Expertise in Data retrieval and Data comparison	15

		- Analysing Genomic Sequences. - Basics of Molecular biology and Systems Function.		
2.	CONSTRUCTION- Sequencing pathways	- Understand the principle behind sequencing technique. - Different sequencing methods and their importance. - Knowledge of gene prediction algorithms and tools. - Familiarity with assembly software packages and understanding their parameters and limitations. - Comparative Genomics.	Proficiency in Genome Assembly and Annotation	15
3.	CODING - Developing pipelines using Knime tool	- How to read and write python script and call a function for repetitive tasks	Identify patterns and make predictions related drugs and new compound discovery	15

TABLE 3: OVERALL COURSE LEARNING OUTCOME ASSESSMENT CRITERIA AND USECASES		
LEARNING OUTCOME	**ASSESSMENT CRITERIA**	**USE CASES**
Understand basics of Python programming language	MCQ (real-time problem solving applications	Python programming is used in a variety of bioinformatics applications, including: Python programming is used in genome analysis. It is used to align DNA and protein sequences, identify

		genetic variations, and perform gene expression analysis. Biopython is widely used for this purpose.
Create phylogenetic tree using CLUSTALW to map the genome	Assessments & assignments	Phylogenetic trees can be used to study the evolutionary relationships between different species and to understand the evolutionary processes over time. Phylogenetic trees can be used to study the diversity and distribution of species and to develop conservation strategies to protect endangered species and ecosystems.

TABLE 4: LIST OF FINAL PROJECTS	
SL.NO	**FINAL PROJECT**
1	Identification of alternate target drugs for Leukemia using Knime & PyRX

TABLE 5: COURSE ASSESSMENT RUBRICS (TOTAL MARKS: 75)				
ASSESSMENT CRITERIA	**DESCRIBE THE CRITERIA OF THE BELOW CATEGORY PERFORMANCE**			**TOTAL MARKS**
	FAIR	**GOOD**	**EXCELLENT**	
MCQ (real-time problem-solving applications (30 marks)	5	10	15	15
AMA (Ask me Anything) sessions (15 marks)	5	7	10	10

Assessment	7	12	20	20
Project (30 marks)	10	20	30	30