

GUJARAT TECHNOLOGICAL UNIVERSITY

MASTER OF COMPUTER APPLICATIONS (MCA)

SEMESTER: V

Subject Name: **Bioinformatics (Bio-I) (Elective-III)**

Subject Code: **650015**

Objective:

- Use of information technology to accomplish the challenges in the field of Biology

Prerequisites:

Knowledge of DBMS, Data Structure, Unix/Linux, Scripting Languages

Contents:

Unit 1: Introduction of Bioinformatics:

Biology in the Computer Age, Computational Approaches to Biological Questions

Unit 2: Tools for Bioinformatics:

Biological Research on the Web, Sequence Analysis, Pairwise Alignment and Database Searching, Multiple Sequence Alignments, Trees, and Profiles

Unit 3: Protein Structure and Prediction:

Visualizing Protein Structures and Computing Structural Properties, Predicting Protein Structure and Function from Sequence, Tools for Genomics and Proteomics

Unit 4: Databases and Visualization:

Building Biological Databases, Visualization and Data Mining (20%)

Text Book:

(An introduction to Software Tools for Biological Applications)

Cynthia Gibas & Perl Jambeck, "Developing Bioinformatics Computer Skills", O'Reilly Publications

Chapter wise Coverage:

Unit 1: Chapters 1, 2

Unit 2: Chapters 6, 7, 8

Unit 3: Chapters 9, 10, 11

Unit 4: Chapter 13, 14

Reference Books:

1. Orpita Bosu & Simminder Kaur Thukral, "BIOINFORMATICS Databases, Tools and Algorithms", Oxford Publications

2. Jean-Michel Claverie & Cedric Notredame, “Bioinformatics – A Beginner’s Guide”, Wiley Publications
3. Zhumar Ghosh & Bibekanand Mallick, “BIOINFORMATICS Principles and Applications”, Oxford Publications
4. Kenneth Baclawski and Tianhua Niu, “Bioinformatics”, JAICO BOOKS Publications

Accomplishments of Students:

- Learn to create Biological database of available sequences
- Learn how to search for similar sequences
- Learn the concept of available computerized biological databases & Software tools
- Learn how to visualize the architecture of a biological input data
- Learn the need for sequence analysis
- Understanding of tools for Identification, Prediction, Visualization and Pattern Matching from biological sequences and structure of proteins
- Can classify the structure of protein with the help of available software tools
- Learn how to develop the tools for pattern matching from available sequences
- Able to develop software for data transfer into biological database and execution of tools

Suggested Continuous Evaluation Components (CEC):

A. Tools and Applications:

1. Learning of Specialized languages, available to support bioinformatics like Biojava, Bioperl, Biocorba, BioXML, Bioruby, Biopython and open source like BSMML (Bioinformatics Sequence Markup Language)
2. Constructing biological databases : Design and build a Database of biological sequences for any organization or research group
3. Preprocess and visualize Biological data
4. Explanation of Protein Modeling Project
5. Improving diagnosis, screening and drug discovery through bioinformatics
6. Discovering evolutionary relationship between sequences
7. Accessing Genome Information the Web
8. Building phylogenetic trees
9. Networks and pathway visualization
10. Annotating and Analyzing Whole Genome Sequences
11. Bioinformatics applications in the field of
 - DNA fingerprinting
 - DNA chip (Microarray) technology
 - Single Nucleotide Polymorphism
 - Drug discovery
 - Simulation of Biological problems
 - Development of diagnostic techniques based on genetic background
 - Personalized Medicine

B. Case study on:

- The Whole human genome project
- Genome sequencing of living organisms
- Efficient utilization of PubMad for Bioinformatics
- Hybrid technologies for helping the farmers with Bioinformatics

- Identification of disease pattern from sequences
- Animal tissue engineering using Bioinformatics
- Grid based resources for Bioinformatics

C. Laboratory Exercise

- Development of Data Warehouse for biological databases
- Developing Web-Based Software that interacts with databases
- Development of tools based on data mining techniques for pattern recognition from sequences
- Development of software for sequence conversion from one database form to another
- Development of sequence submission tool to the database
- Microarray Database creation and its management
- Identification of Single Nucleotide Polymorphism
- Identification of structure from sequences
- Identification and recognition of mutation from database
- Development of sequence comparison tools
- Development of Grid for bioinformatics
- Development of Structure Prediction tools
- Write a programs for DNA:
 - DNA Replication
 - DNA Transcription
 - DNA Translation
 - For given DNA sequence, find start codon and stop codon