PG DIPLOMA IN BIOINFORMATICS

Program Outcomes

Bioinformatics is an interdisciplinary program offering substantial training in both the biological sciences and computer sciences.PG Diploma in Bioinformatics emphasizes the integration of computer science with genomics, proteomics and molecular biology. Students attracted to this program have dual interests.in computer science and biology and find it an excellent choice for their broad interests. Students who complete this program enter the top graduate programs in bioinformatics and computational biology in the world, enter leading professional institutes or find employment in biotechnology, pharmaceutical, or drug designing and drug development companies.

Paper I – Basic Cellular and Molecular Biology

Scope

This course – Basic Cellular and Molecular Biology is designed to provide the knowledge to the PG diploma Bioinformatics students in invaluable areas of advanced microbiology and biotechnology which plays a crucial role in determining its future use and applications in medicine, drug discovery and in pharmaceutical industry.

Objectives

At the completion of this course it is expected that the students will get an understanding about the following aspects;

- Central dogma of molecular biology

- Structure and function of cell and cell communication

- Identify appropriate sources of enzymes

- Understand and perform genetic engineering techniques in gene manipulation, r-DNA technology and gene amplification.

- Understand the overview of pharmacogenomics

Course outcomes

- Students will understand the various techniques used in microbiology and biotechnology

- Students can be able to provide examples of current applications of bio-technology and advances in the different areas like medical, microbial and forensic sciences

- Students can able to explain cell-cell interaction, cell cycle and regulation and mutation process

- Students can explain the concept and application of Genomics

Unit wise program

Unit No.	Chapter	No. of Credits
I	**Biology of cells:** Cells as a unit of life, structure of prokaryotic and eukaryotic cells, function of cell organelles. **Cellular membrane:** structure, transport, channels, Carriers, receptors, endocytosis, membrane potentials **Molecules of Life:** Introduction to carbohydrates, proteins and lipids Nucleic acids-Purines, pyrimidines, Nucleosides and Nucleotides, structure of DNA, denaturation and renaturation of DNA	4
II	**DNA replication:** Protein synthesis-Eukaryotic and Prokaryotic, Transcription and Translation Cell-Cell interactions and signal transductions: Intercellular junctions, signaling by hormones and neurotransmitters: receptors, G-proteins, protein kinases and Second messengers. Cell Cycle and regulation-Mitosis, Meiosis	4
III	Mutation- Types of mutations, types of mutagenic agents and their molecular mechanism; DNA repair, Chromosomal types and structure Enzymes: coenzymes and metal cofactors, temperature and Ph effects, Michaelis-Menten kinetics, inhibitors and activators, active site and mechanism of enzyme Action, Isoenzyme, allosteric enzymes	4
IV	Genomics: Definition of genome, Genome sequencing, Genome map: Types of Genome maps And their uses. Map repositories: NCBI-Entrez Human genome map viewer, OMIM- Online Mendelian Inheritance in Man. Linkage map resources. Practical uses of genome maps: Locating genomic regions, target identification, arrangement of genes, SNP diagnosis, positional specific cloning.	4
V	Annotation of the Genome: Structural Annotation. Various approaches in gene Prediction: ORF prediction, Gene prediction in prokaryotes and eukaryotes, Hidden Markov Model, pattern discrimination, Evaluation of gene prediction methods, prediction of promoter sequences, Functional annotation: Employing the similarity in the sequence, gene family and metabolic pathway. Employing the Conserved domain, profile and motif comparison, EST Comparison, Analysis of Human Genome.	4

PG DIPLOMA IN BIOINFORMATICS

Paper II – Bioinformatic and In Silico Biology

Scope

Graduation in bioinformatics can engage in any combination of research, teaching, clinical service, and consultation. There is a growing need for bioinformatics researchers who can analyze new sources of high-throughput experimental data in biology, medicine, and bioengineering. Biotechnology and pharmaceutical companies also seek bioinformatics graduates for applied research on disease and drug discovery. Medical centers are also increasingly hiring bioinformatics graduates as genomics data become important in medical research and clinical applications.

Objectives

- The basic objective is to give students an introduction to the basic theory knowledge on techniques of Biology and bioinformatics.

- Emphasis will be given to the application of bioinformatics and biological databases to problem solving in real research problems.

- The students will become familiar with the use of a wide variety of internet applications, biological database and will be able to apply these methods to research problems.

Course outcomes:

- Students will be able to identify strengths and weaknesses in a variety of systems biology.
- Entire course will instruct a range of bioinformatics and modeling software to develop predictive and mechanistic models.

- Students can access, query and retrieve models from public repositories for systems biology, and structural biology.

- Students will be able to Identify an appropriate modeling approach for a given biological question and dataset.

Unit wise program:

Unit No.	Chapter	No. of Credits (total = 20)
I	Introduction to bioinformatics, classification of biological databases, Biological data formats, Application of bioinformatics in various field. Introduction to single letter code of amino acids, symbols used in nucleotides, data retrieval- Entrez.	3
II	Introduction to sequence alignment. Substitution matrices, scoring matrices-PAM and BLOSUM. Local and Global alignment concept, Dot plot. Dynamic programming methodology: Needleman and Wunsch algorithm. Smith Waterman algorithm. Statistics of alignment score. Multiple sequence alignment. Progressive alignment. Database search for similar sequences using FASTA and BLAST programs. Evolutionary analysis: distances, Cladistic and phenetic method. Clustering method. Rooted and uprooted tree representation. Use of cluster and PHYLIP.	5
III	Protein Prediction method: Concepts of secondary structure prediction of RNA and protein. Probabilistic model: Markov chain, Hidden Markov Models-other applications. Gene prediction: Analysis and prediction of regulatory regions. Fragment assembly. Genome sequence assembly, Restriction Mapping, Repeat sequence finder.	4
IV	Comparative Genomics: purpose and Method of comparison, Tools for genomic comparison: Application of comparative Genomics, Reconstruction of metabolic pathway, predicting regulatory elements, Identifying targets, examination of domain function, analysis of conserved regions. Genome projects and Model Organism research –Yeast; C. Elegans; and Mouse – a comparative analysis.	4
V	Functional Genomics: Gene expression analysis by cDNA microarrays, SAGE, strategies for generating ESTs and full-length inserts; EST clustering and assembly. EST databases (DBEST, UNIGENE).	4

Recommended Books/Sources:

- Bioinformatics Sequence and Genome Analysis. 2001. David W. Mount. Cold spring Harbour, Laboratory Press.

- Comparative genetics. Ann Gibbons, 1998. Science. 281: 1432-1434.

- The Molecular Biology Database Collection: Updated Compilations of Biological

- Database Resources. Baxevanis A.D. 2001. Nucleic acids Research. 29 p 1-10.

- Genomes. T. A Brown, 2001. Taylor and Francis Group.

Course outcomes

- The students will be able to describe the contents and properties of the most important bioinformatics databases, perform text and sequence based searches, and analyze and discuss the results in light of molecular biological knowledge

- The students will be able to explain the major steps in pair wise and multiple sequence alignment, explain the principle for, and execute pair wise sequence alignment by dynamic programming

- The students will be able to predict the secondary and tertiary structures of protein sequences.

15 Assignments

1. Data retrieval tools and methods

2. Protein sequence analysis(ExPASy proteomics tools)

3. Sequence similarity searching (NCBI BLAST)

4. Multiple sequence alignment(Clustal W)

5. Molecular phylogeny(PHYLIP)

6. Sub cellular localization prediction

7. Analysis of protein and nucleic acids sequences

8. Protein structure prediction

9. Gene structure and function prediction
10. DNA, Protein, drug binding studies using docking tools

11. Staining technique – Simple, Gram's and Negative

12. Isolation of plasmid DNA, protein

13. Estimation of DNA and protein

14. Agarose Gel Electrophoresis

15. SDS PAGE system