

BHARATHIAR UNIVERSITY, COIMBATORE - 641 046

M.Phil Degree Course

Part I - Syllabus

**PAPER-I TEACHING TECHNIQUES / PEDAGOGICAL TECHNIQUES IN  
BIOINFORMATICS**

**Objectives:**

At the end of the course, the scholars will be able to

1. Understand the meaning, scope and concept of Education, Educational Technology, Instructional Technology & Educational Evaluation.
2. Appreciate the contributions made by philosophers and educationalist to the field of education.
3. Review the relative effectiveness among the different methods and techniques of teaching and learning in Higher Education.
4. Discriminate among different types of tests meant for students evaluation, diagnose the learning problems of the students and take remedial measures.
5. Be aware of the web based communication strategies for professional development and be benefited of the e-resources in Bioinformatics.

**UNIT-I Teaching Technology: Designs**

Meaning, concept and scope - Instructional Designs-Objective based, Skill based, Competency based, Learning style based and Model based.

**UNIT-II Methods and Techniques of Teaching**

Large Group Techniques: Lecture, Modified Lecture, Seminar, Symposium, Panel Discussion, Team Teaching, Project Approach and Workshop ...

Small Group Techniques: Group Discussion, Simulation, Role Playing Buzz Technique, Brain Storming, Case Discussion and Assignment.

**UNIT-III Electronic Media in Bioinformatics**

Instructional Media: Concept, Selection and Use; Variety of learning; e-Learning, e-books, e-journals, web-based Learning, Systematic approaches in Bioinformatics

- Access and Teaching Issues.

**UNIT-IV Hypothesis and Statistical evaluation**

Basic concepts of Hypothesis; Procedure for Hypothesis testing; Probability: Markov models and Hidden Markov models; Probability distribution. Binomial, Poisson, Normal distribution, and Multiple testing methods. ANOVA; Test of significance: T-test, F-test.

**UNIT -V Interpretation and Report writing**

Meaning of Interpretations; Techniques of Interpretation, Precautions in Interpretations, Significance of Report writing; Different steps in Report writing; Layout of the Research project; Types of reports and Oral presentation.

## **Books for References**

1. Kumar K.L, Educational Technology, New Age International (P) Ltd (1997), New Delhi.
2. Sampathkumar, K.Paneerselvam.A and Santhanam.S, Introduction to Educational Technology, Sterling Publishers (Pvt.) Ltd (1990), New Delhi.
3. Tony Bates A.W, Technology, e-Learning and Distance Education, New York (2005), Routledge.
4. Kothari C.R, Research Methodology - Methods and Techniques, New Age International (P) Ltd, 2004.

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**Part I- Syllabus**

**PAPER-II RESEARCH METHODOLOGY AND TRENDS IN  
BIOINFORMATICS**

**UNIT-I Research Methodology**

Introduction; Definition; Objectives of research; Types of research; Research approaches; Significance of research; Research methods; Research and scientific method; Importance of knowing how research is done; Research process; Criteria of good research; Problem encountered by researchers in India; Need for research design: Features of good design; Important concepts relating to design; Different research designs; Basic principles of experimental design.

**UNIT-II Elements of C Programming**

Features of C, Variables, Constants, Keywords, Data types, Operators, Statements, Loops-Simple programs using Loops, Arrays-Integer arrays, Character arrays, Simple programs using arrays. Introduction to Functions - Simple programs using functions, Introduction to Pointers, Structures - String manipulations using Pointers and Arrays. Files: Defining & Opening a file, Closing a file, Input/Output operations on files.

**UNIT-III High throughput Technology**

High throughput genome and Protein sequencing, Genome and Proteome assembly; DNA and Protein micro arrays, Gene and Protein expression data sets.

**UNIT-IV Algorithms**

Protein and Nucleic acid sequence Algorithms: Sequence Databases, Use of the algorithms BLAST, Multiple sequence alignments and Clustering algorithms. Phylogeny: Evolutionary trees; Biological networks: Pathway analysis.

**UNIT-V Protein structure analysis**

Protein structure databases; Protein structure comparison; Fold recognition; 3D-1D Profiles; Threading and Comparative structure modeling.

**Books for References**

1. Kothari C.R, Research Methodology - Methods and Techniques, New Age International (P) Ltd, 2004.
2. E.Balagurusamy, Programming in ANSI C, Tata McGraw Hill Publication.
3. Andrews D.Baxevanis and BF. Francis Ouellette, Bioinformatics-A Practical guide to the Analysis of Genes and Proteins, A John Wiley & Sons Pub, 2001.
4. David W.Mount, Bioinformatics-Sequence and Genome Analysis, CBS Publishers, 2003.
5. Ian Korf, Mark Xandell & Joseph Bedell, BLAST (O'REILLY), SPD Private Ltd, 2003.

## **ANNEXURE-III**

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Part I-Syllabus

### **PAPER-III BIOLOGICAL DATABASES, DATA MINING AND MICROARRAYS**

#### **UNIT-I**

Biological database - Sequence databases - Other specialized databases – Microarray databases - Database browsers and search engines.

#### **UNIT-II**

Data mining definition – Classification and clustering of data – Association rules – Data visualization.

#### **UNIT-III**

Introduction to Microarrays - Oligonucleotide and Spotted cDNA arrays - Design considerations for microarray experiments – Goals of a microarray experiment.

#### **UNIT-IV**

Basic research with DNA microarrays – Microarrays and Cancer - Myeloid leukemia (AML) vs. acute lymphoblastic leukemia (ALL) data analysis.

#### **UNIT-V**

Use of array analysis programs – SAM - TIGR programs – MEV.

#### **Books for References**

1. Analysis of DNA Microarray Data by Steen Knudsen.
2. Discovering Genomics, Proteomics, and Bioinformatics by A.M. Campbell and L.J. Heyer.

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**Part I - Syllabus**

**PAPER- III COMPUTATIONAL BIOLOGY**

**UNIT I: DATA MINING AND SEQUENCE ANALYSIS**

- Biological background for sequence analysis.
- Searching for database for similar to a new sequence.
- Identification of protein primary sequence from DNA sequence.
- Searching for database for similar to a new sequence.
- Calculation of sequence alignment for evolutionary interferences and to aid in structural and functional analysis.

**UNIT II: SIMILARITY SEARCHES & CONSTRUCTION OF PHYLOGENETIC GUIDE TREE**

- Distance and similarity.
- The evolutionary basis for sequence alignment.
- Substitution scores and gap penalties.
- Optimal alignment method.
- Database similarity searching.
- FASTA and BLAST.
- Conclusion and internet software availability.

**UNIT III: PRACTICAL ASPECT OF MULTIPLE SEQUENCE ALIGNMENT**

- Introduction.
- MULT ALIN.
- BLOCKS.
- MOST.
- Probe.
- MacBoxshade.

**UNIT IV: PHYLOGENETIC ANALYSIS**

- Introduction.
- Phylogenetic tree building methods.
- Multiple tree alignment procedures.
- Searching for trees.
- Evaluating trees and data.
- Phylogenetic software's.
- Internet resources.

## **UNIT V: PREDICTIVE METHODS USING PROTEIN AND NUCLEIC ACID SEQUENCES**

- Introduction.
- Detecting functional sites in DNA.
- Internet tools for identification of protein coding genes.
- Internet resources for repeat analysis.
- Predictive methods using protein sequences.
- AACompIdent and AACompsin.
- Secondary structures and folding classes.
- nnPredict, predict protein, ssPRED, SOPMA.
- Tertiary structures.

### **Books for References**

1. Computer methods for macromolecular sequence analysis. Doolittle R.F (Ed.). Academic Press, San Diego (1996).
2. Introduction to Bioinformatics. Teresa K. Attwood and David J. Parry-Smith.
3. Bioinformatics-concepts, skills, applications. S.C. Rastogi, Namita Mendiratta, Parag Rastogi.
4. Bioinformatics – A practical approach 2004. K. Mani and N. Vijayaraj. Aparna publications.
5. Hand book of computational Molecular Biology. Edited by Srinivas Aluru. Chapman and Hall 2006.
6. Computational Methods in Molecular Biology Edited by S. Salzberg, D. Searls, and S. Kasif. Elsevier Science, 1998.
7. Sequence and Genome Analysis. By David W. Mount Published 2004 CSHL Press Science.
8. Trends in Bioinformatics. By Dr. P. Shanmughavel. 2006 Pointer publishers, Jaipur, India.
9. Principles of Bioinformatics. By Dr. P. Shanmughavel. 2005 Pointer publishers, Jaipur, India.

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**Part I - Syllabus**

**PAPER- III “OMICS” COMPLEXES IN PHYTOMATICS**

**UNIT-I Purification of Macromolecules**

Moving boundary and zonal sedimentations, Partion and Ion-exchange Chromatography; Electrophoresis Principles, Electrophoresis of Nucleic acids; SDS gel Electrophoresis; Capillary Electrophoresis and Purification.

**UNIT-II Structural Proteomics**

Experimental Techniques for Protein Structure Elucidation, X-ray Crystallography, 2-D Electrophoresis, MALDI-TOF, Mass Spectrometry, Protein Microarrays & Bioseparation, Structure Visualization & Manipulation.

**UNIT-III Biological Databases**

Secondary & Tertiary Structure Prediction Tools: FASTA, BLAST, PSI-BLAST, CLASTALW, Multialign, Dialign, Gene Bee, Motif Scan, TMPred, GOR, Chou-Fasman, Neural Network Prediction, Promoter Finder, NEB cutter, Genscan, ORF Finder and Intron- Exon Finder.

**UNIT-IV Pointers in Sequence analysis**

Usage of Sequence alignment & Searching Tools for Gene Identification ,Genome Annotation, ORFs, ESTs, Codon Biases, Redundancy, Conserved Motifs, Patterns, Blocks & Domains.

**UNIT-V Metabolomics**

Understanding the Metabolic Pathways of Cyanobacteria, Microbes and Medicinal Plants. Metabolic analysis and Tools.

**Books for References**

1. Andrew R Leach, Molecular Modeling-Principles and Applications, Prentice Hall Publications.
2. Andrews D.Baxevanis and BF. Francis Ouellette, Bioinformatics-A Practical guide to the Analysis of Genes and Proteins, A John Wiley & Sons Pub, 2001.
3. David W.Mount, Bioinformatics-Sequence and Genome Analysis, CBS Publishers 2003.
4. Ian Korf, Mark Xandell & Joseph Bedell, BLAST (O'REILLY), SPD Private Ltd, 2003.
5. Philip E Bourre, 2003, Structural Bioinformatics, A John Wiley & Sons Publication.
6. D.Bowtell and Sambrook, DNA Microarrays-A Molecular Cloning Manual, Cold Spring Harbor Laboratories Publication, Cold Spring Harbor, New York.
7. Robert K.Scopes, Protein Purification – Principles and Practice (3<sup>rd</sup> edition), Springer International Edition.

**ANNEXURE-III**

**BHARATHIAR UNIVERSITY, COIMBATORE – 641 046**  
**M.Phil Degree Course**  
**Part I - Syllabus**  
**PAPER III – STRUCTURAL BIOLOGY AND BIOPHYSICS**

**UNIT-I**

PERL, C+, PYTHON, MySQL, SCOP, CATH, FSSP, BIND, DIP, FASTA, BLAST, PSI, KEGG, PDB.

**UNIT-II**

Ramachandran Plot, GOR, Chou-FASMAN method, secondary tertiary Structure Prediction, TMpred, ORFs, ESTs, MOTIF, Sequence alignment.

**UNIT-III**

Structure alignment, Structure validation, Refinement, Prediction, Protein-protein interaction, membrane protein, Microarrays, Docking, QSAR, Drug discovery.

**UNIT-IV**

X-ray crystallography, nuclear magnetic resonance, UV spectrophotometry, electron microscopy, cryo electron microscopy, atomic force microscopy, MALDI-TOF, Mass spectrophotometry.

**UNIT-V**

Fundamentals of protein, carbohydrates and nucleic acids, classification, biographies, management, Intellectual property rights.

**Books for References**

- 1) Principles of Proteomics by R.M.Twyman.
- 2) Bioinformatics principles and Applications by Zhumur Ghosh.
- 3) Introduction to Systems Biology by Sangdun Choi.

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**PAPER III – COMPREHENSIVE ANALYSIS IN BIOCHEMATICS**

**UNIT-I Genome analysis**

Isolation of genomic and organelle DNA from Prokaryotes and Eukaryotes. Mapping and sequencing genes, Electrophoretic karyotyping, Construction and screening of genomic DNA libraries. Functional genomics: Sequence based, Microarray based approaches, in-silico vector construction.

**UNIT-II Techniques for Isolation and Purification of Protein & Bio-active compounds**

Extraction (soxhlet and cold percolation), Isolation of Alkaloids and Flavonoids, Protein extraction from Micro organisms, Plants and Animals. Purification: Hanging drop, Native gel, Chromatographic methods (Column, Preparative TLC, HPLC, HPTLC, Ion exchange, Gel filtration, Affinity), Crystallization.

**UNIT-III Structure elucidation of Protein and Bioactive compounds**

Crystal studies, IR, NMR, MASS, CHN analysis, X-ray diffraction, 2-D Electrophoresis, Protein microarray. Tools used for protein structure prediction: Modeler, Rosetta, 3-D-PSSM, PHD, PSIPRED, JPRED. Motif databases: BLOCKS, PROSITE, PFAM, PRINTS, COG.

**UNIT-IV Metabolomics**

Analyzing databases for Metabolic Pathways (WIT, KEGG, PathDB, BIOCARTA, PathCase). Metabolic and Cellular simulation: Gepasi, XPP, Virtual cell. Reconstruction of metabolic pathways (Biocyc, ASGARD).

**UNIT-V Molecular Interaction and Docking**

Determination of active site and hot spots, Receptor-Ligand interactions, Pharmacophore identification (Catalyst, DISCO, GASP), Denovo drug designing (Group Build, Gen Star). Tools used for docking (DOCK, FLEX, GLIDE, SLIDE, GOLD, SURFLEX).

## **Books for references**

1. Sujata V. Bhat, Bhimsen A. Nagasampagi and Meenakshi Sivakumar. Chemistry of Natural Products, Narosa Publishing House.
2. Daniel M. Bollag, Michael D. Rozycki and Stuart J. Edelstein. Protein Methods. Wiley-Liss. A John Wiley & Sons, INC, Publications.
3. Mount, David W. Sequence and Genome Analysis. Cold Spring Harbor Laboratory Press Publications.
4. S.B.Primrose and R.M.Twyman. Principles of Gene Manipulation & Genomics. Black well Publishing.
5. Cynthia Gibas and Per Jambeck. Developing Bioinformatics Computer Skills. O'Reily and Associates.
6. Jin Xiong. Essential Bioinformatics. Cambridge University Press.
7. Thomas Lengauer (Ed). Bioinformatics - From Genomes to Drugs Volume I and II. Wiley-Vch, Germany.