

M.Phil., Bioinformatics

With effect from 2014 – 2015

PAPER – I: RESEARCH METHODOLOGY

UNIT-I

Biological database-Sequence databases-Other specialized databases– Microarray databases, Database browsers and search engines. Data mining definition – Classification and clustering of data – Association rules – Data visualization.

UNIT-II

Introduction to Microarrays - Oligonucleotide and Spotted cDNA arrays – Design considerations for microarray experiments – Goals of a microarray experiment. Basic research with DNA microarrays – Microarrays and Cancer - Myeloid leukemia (AML) vs. acute lymphoblastic leukemia (ALL) data analysis. Use of array analysis programs – SAM - TIGR programs – MEV.

UNIT-III

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 –IV

Biological background for sequence analysis. Searching for database for similar to a new sequence. Identification of protein primary sequence from DNA sequence. Database search for similar to a new sequence. Calculation of sequence alignment for evolutionary interferences and to aid in structural and functional analysis. Construction of phylogenetic guide tree-Distance and similarity.The evolutionary basis for sequence alignment. Substitution scores and gap penalties.

UNIT –V

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

Reference Books:

1. Jin Xiong, 2006, Essential Bioinformatics, Cambridge University Press UK.
2. N.Gowtham, 2006, Bioinformatics – Databases and algorithms, Alpha Science Intel LTD UK.
3. U.R.Muller and D.V.Nicolau, 2005, Microarray technology and its applications, Springer publications, USA.
4. Kin-N.King, 2008, C-Programming – A modern approach II Edition, W.W. Norton & Company New York.
5. Jason T.L. Wang, Mohammed J. Zaki, Hannu.T.T. Tolonen and Dennies Shasha, 2005, Data Mining in Bioinformatics, Springer-Verlag London limited.
6. David W. Mount, 2004, Bioinformatics- Sequence and Genome analysis, Cold spring harbor laboratory press, USA.
7. Francesco Falciani and Frederics Falciani, 2007, Microarray technology Through application, Taylor & Francis group, UK.
8. Wing-kin Sung, 2009, Algorithms in Bioinformatics CRC Press, Taylor & Francis Group, N.W USA.

PAPER – II: ADVANCES IN BIOINFORMATICS

UNIT -I

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-II

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

UNIT-III

Protein Primary, 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

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, insilico vector construction.

UNIT-V

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

Reference Books:

1. R.Hatti-Kaul and B.Mattiasson, 2003, Isolation and Purification of proteins, CRC Press, Taylor & Francis Group, NW USA.
2. Corrado Tringali, 2001, Bioactive Compounds from natural sources, Taylor & Francis, group NW USA.
3. R.M.Kamp, J.J.Calvete and T.Choli-Papaodopoulou, 2004, Methods in proteome & Protein Analysis, Springer publications, USA.
4. David W. Mount, 2004, Bioinformatics-Sequence and Genome analysis, Cold Spring Harbor Laboratory Press, USA.

5. S.B. Primerose and R.M. Twyman – 2003, Principles of Genome analysis and Genomics, III Edition, Black Well Publisher, UK.
6. Jonathan Pevsner and Wiley. 2009, Bioinformatics and Functional Genomics II Edition. Black Well Publishers, UK.
7. M. Tomita and T Nishioka, 2003, Metabolism the frontiers of system Biology, Springer- Verlag, Tokyo.