SEMESTER II
CORE THEORY II
NUCLEIC ACIDS & BIOINFORMATICS

Unit 1: Nucleic Acids and Genome organization

1.1 DNA as the genetic material- Griffith's experiments on transformation in Streptococcus pneumoniae, Hershey-Chase experiments with radio labeled T2 bacteriophage, Avery, MacLeod and McCarty's experiments
1.2 RNA as genetic material- Tobacco Mosaic Virus
1.3 Structure and forms of DNA (A, B and Z)
1.4 Genome organization in prokaryotes
1.5 Genome organization in eukaryotes, C-value and C-value paradox, Reassociation kinetics-cot curve, Denaturation, Renaturation, Tm curve
1.6 Kinetic classes of DNA- unique sequences, moderately repeated and highly repeated sequences; tandem repeats (satellite, minisatellite and micro satellites), interspersed repeats (SINES-eg: Alu repeats, LINES); palindromic sequences and transposable genetic elements

Unit 2: DNA Replication, Recombination and Repair

2.1 DNA replication- enzymes; semi conservative DNA replication-Messelson and Stahl experiment; Linear, Circular, Rolling circle, Theta, D loop models
2.2 Mutation- spontaneous, induced (frame shift, transition, transversion)
2.3 Physical and chemical mutagens
2.4 DNA damage- intrinsic and extrinsic factors
2.5 DNA repair-Direct, Excision and methyl mediated mismatch, recombinational and SOS repair
2.6 DNA recombination-homologous, site specific recombination and NHEJ (Non-Homologous End Joining)

Unit 3: Concepts of Bioinformatics

3.1 Bioinformatics – a historical perspective
3.2 Internet and its role in bioinformatics
3.3 Bioinformatics Data: Genomes, nucleic acids, proteins, protein structures
3.4 Storage of databases in DNA (GenBank, EMBL, DDBJ)
3.5 Protein data banks (PDB, SWISS-PROT, UNIPROT, PIR) and their utilization
3.6 Data retrieval tools-BLAST, ENTREZ

Unit 4: Applications of Bioinformatics

4.1 Genome annotation: Gene identification tools
4.2 Basics of sequence alignment, Pairwise alignment (global and local)
4.3 Multiple sequence alignment and phylogenetic analysis
4.4 Structural classification of proteins and homology model building
4.5 Applications of Bioinformatics- drug targets, overview of drug designing
4.6 Concepts of Phramacogenomics

CORE-II: PRACTICALS

1. Isolation of DNA from Plant cells
2. Isolation of DNA from Animal cells
3. Estimation of DNA by Diphenylamine method
4. Estimation of RNA by Orcinol method
5. Exploring data bases: Genbank and Uniprot
6. Exploring the structural data bases: PDB, MMDB
7. Visualization of Protein structures-RASMOL
8. Database searching and downloading bioinformatics data- DNA (Gen bank, DDBJ, ENA) Protein (Uniprot)
9. Pairwise sequence alignment (global and local) of DNA and proteins
10. Multiple sequence alignment of DNA & protein sequences using ClustalW
11. Database searching with heuristic algorithms: BLAST

REFERENCE BOOKS

1. Genes VII. Benjamin Lewin, Oxford Univ. Press, Oxford
2. Molecular Biology by D, Freifelder Narosa Publishing house New York, Delhi
3. Molecular Cell Biology Lodish, H., Baltimore, D; fesk, A., Zipursky S.L., Matsudaride, P. and Darnel. American Scientific Books. W.H. Freeman, NewYork
4. Molecular Biology by Brown
5. Essentials of Molecular Biology. D. Freifelder, Panima Publishing Corporation.
6. Bioinformatics: Sequence and Genome Analysis by David W. Mount, Cold Spring Harbor Laboratory Press
7. Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids by Richard Durbin, Sean R. Eddy, Anders Krogh, Graeme Mitchison, Cambridge University Press
8. Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins, Andreas D. Baxevanis, B. F. Francis Ouellette, Wiley-Interscience
9. Bioinformatics tools and Resources – free online tools, downloadable free tools, software packages, internet, Bioinformatics books and Journals, Bioinformatics web-portals