

MANONMANIAM SUNDARANAR UNIVERISTY,
TIRUNELVELI-12



SYLLABUS

CERTIFICATE COURSE IN COMPUTATIONAL BIOLOGY

Subject Status	Subject Title	Subject Code
Core	MOLECULAR BIOLOGY GENETIC ENGINEERING	RCCB1
Core	COMPUTATIONAL METHODS FOR SEQUENCE ANALYSIS	RCCB2
Practical	Practical	RCCVL
Project	Project	RCCBP

MOLECULAR BIOLOGY GENETIC ENGINEERING

Unit – 1

DNA : Structure, Replication : eukaryotes, Repair – different methods & Recombination – different methods, Nucleic acids – structure, function and properties, A-, B-, Z- and triplex DNA. Mutation – Types of mutations.

Unit – 2

Mechanism of DNA polymerase – DNA synthesis at the replication fork, initiation of DNA replication, RNA polymerase structure and assembly; RNA polymerase I, II, III; Eukaryotic promoters and enhancers; Processing of mRNA. tRNA. rRNA; 5'-Cap formation; 3' –end processing and polyadenylation; Splicing; RNA editing;

Unit – 3

Tools in rDNA technology: Restriction endonucleases and other enzymes used in recombinant DNA technology – Cloning vectors – Plasmid cloning vector pBR322, plasmid vectors, Bacteriophage vectors – Cosmids, Phagemids – YAC and BAC vectors – Genetic transformation of prokaryotes – Transferring DNA into E. coli – Chemical induction and Electroporation.

Unit – 4

Primers; Fidelity of thermostable enzymes; Types of PCR – multiplex, nested, reverse transcriptase, real time PCR, colony PCR; Proof reading enzymes; PCR in molecular diagnostics; Viral and bacterial detection; PCR based mutagenesis, Mutation detection: SSCP, DGGE.

Unit – 5

DNA sequencing – Chemical cleavage and dideoxy methods – Automated DNA sequencing – Next generation sequencing. Applications : Southern and Northern blotting – DNA Diagnostic system – random amplified polymorphic DNA (RAPD), RFLP, DNA finger printing, their applications – Transgenic animals.

References :

1. Watson, J.D., Tania A. Baker, Stephen P. Bell, Alexander Gann, Michael Levine, Richard Losick, “Molecular Biology of the Gene”. Benjamin Cummings, London, 3rd Edition, 2003.
2. Weaver, R.F., Hedrick, P.W., “Molecular Biology”. William C. Brown, Illinois, 5th Edition, 2003.
3. Malacinski G.M., Freifelder D., “Essentials of Molecular Biology”, Jones & Bartlett Pub, Boston, 4th Edition, 2002.
4. Primrose, S.B., Twyman, R.M., Bob Old, “Principles of Gene Manipulation and Genomics”, Blackwell Publishing, 7th Edition, Boston, 2006.

5. James Watson, Jan Witkowski, Myers Richard, Amy Caudy, "Recombinant DNA: Genes and Genomics; A short course", F.H. Freeman, San Francisco, 3rd Edition, 2006.
6. Bernard R. Glick & Jack J. Pasternak, "Molecular Biotechnology", ASM Press, Washington, 3rd Edition, 2003.
7. Joseph Sambrook & David W. Russel, "Molecular Cloning", Cold Spring Harbor Laboratory, New York, 3rd Edition, 2001.
8. Robert F. Weaver, "Molecular Biology", MGH Publication, London, 5th Edition, 2005.
9. Grosveld, F., Kollias, G., (Eds). "Transgenic Animals", Academic Press, New York, 1st Edition, 1992.

COMPUTATIONAL METHODS FOR SEQUENCE ANALYSIS

Unit – 1

Introduction to bioinformatics : Definitions and concepts, Emergence of bioinformatics as a separate discipline. Classification of biological databases: Primary nucleotide sequence databases (EMBL, GenBank, DDBJ), Secondary nucleotide sequence databases (Unigene, SGD), Protein sequence databases (SwissPro, TrEMBL, PIR) and Protein structure databases (PDB, SCOP, CATH).

Unit – 2

Introduction to sequence alignment. Substitution matrices, Scoring matrices – PAM and BLOSUM. Local and Global alignment concepts, Dot plot. Dynamic programming methodology: Needleman and Wunsch algorithm. Smith – Waterman algorithm. Multiple sequence alignment – Clustal W. Database search for similar sequences using FASTA and BLAST. DATA retrieval using Entrez and SRS, ExPASy.

Unit – 3

Gene finding methods. Gene prediction : Fragment assembly, Genome sequence assembly, Restriction Mapping, Repeat Sequence finder, ORF, Biological data formats. Introduction to single letter code of aminoacids, codon usage, Symbols used in nucleotides. Sequence polymorphisms – Types, dbSNP, ALFRED and JANP.

Unit – 4

Protein structure prediction – Secondary Structure Prediction : Chou and Fasman method and PHD. Transmembrane – Top Pred and TMHMM. Tertiary Structure modeling: Homology modeling, threading, Ab Initio structure prediction, protein structure evaluation – SPDBV, Ramachandran plot. Visualizing proteins using Rasmol, SPDBV.

Unit – 5

Methods of phylogenetics analysis : Rooted and unrooted tree representation. Bootstrapping strategies, Distance matrix method – UPGMA and Neighbour method and Character – based methods – maximum parsimony and maximum likelihood. Phylogenetics software like MEGA

References:

1. David Mount, “Bioinformatics : Sequence and Genome Analysis,” (1st Edition), Cold Spring Harbor Laboratory Press.
2. Andrea’s D. Baxevanis. B.F. Francis Ouellette, “Bioinformatics – Concepts, Skills, Applications, Bioinformatics : A Practical Guide to the Analysis of Genes and Proteins” (2nd Edition), John Wiley & Son.
3. Teresa. K, Atwood and David J. Parry – Smith. “Introduction to Bioinformatics”. Prentice Hall Publishers.
4. Arthur M. Lesk, “Introduction to Bioinformatics”, 1st Edition, Oxford University.
5. Christopher Fall, Eric marland, John Wagner, John Tyson, “Computational Cell Biology”, Springer.
6. Peter Clote and Roif Backofen, “Computational Molecular Biology: An Introduction”, Wiley.
7. Michael S. Waterman, “Introduction to Computational Biology: Maps, Sequences and Genomes:, CRC.

PRACTICAL’S

1. Isolation of DNA from prokaryotes
2. Isolation of DNA from animal tissue
3. PCR amplification
4. Identification of DNA amplification using agarose gel
5. Restriction enzyme analysis
6. Cloning (demonstration only)
7. Identification of transformant (demonstration only)
8. Internet access to software and databases
9. Retrieving and analysis of protein and nucleic acids sequences
10. Converting sequences between different formats
11. Detecting ORFs, Codon usage
12. Protein sequence analysis (ExPASy proteomics tools)
13. Multiple sequence alignment (Clustal W)
14. Similarity search using BLAST
15. Composition analysis, Hydrophobicity
16. Transmembrane predictions;
17. Molecular visualization – Rasmol, SPDBV – Basic operations.
18. Boot strapping strategies, MEGA.

Preparation of record and submission.

PROJECT

- Group project – Maximum of five students
- Dissertation 50 + Viva voce 50 marks
- Project should not be wet Lab oriented