

Title: Genomics and Proteomics [3-0-0-3]

Content :

Brief overview of prokaryotic and eukaryotic genome organization; extra-chromosomal DNA: bacterial plasmids, mitochondria and chloroplast.

Genetic and physical maps; markers for genetic mapping; methods and techniques used for gene mapping, physical mapping, linkage analysis, cytogenetic techniques, FISH technique in gene mapping, somatic cell hybridization, radiation hybrid maps, in situ hybridization, comparative gene mapping.

Human Genome Project, genome sequencing projects for microbes, plants and animals, accessing and retrieving genome project information from the web.

Identification and classification of organisms using molecular markers- 16S rRNA typing/sequencing, SNPs; use of genomes to understand evolution of eukaryotes, track emerging diseases and design new drugs; determining gene location in genome sequence.

Aims, strategies and challenges in proteomics; proteomics technologies: 2D-PAGE, isoelectric focusing, mass spectrometry, MALDI-TOF, yeast 2-hybrid system, proteome databases.

Transcriptome analysis for identification and functional annotation of gene, Contig assembly, chromosome walking and characterization of chromosomes, mining functional genes in genome, gene function- forward and reverse genetics, gene ethics; protein-protein and protein- DNA interactions; protein chips and functional proteomics; clinical and biomedical applications of proteomics; introduction to metabolomics, lipidomics, metagenomics and systems biology.

Texts / References:

1. Primrose, S. B., Twyman, R. M., Primrose, S. B., & Primrose, S. B. (2006). Principles of Gene Manipulation and Genomics. Malden, MA: Blackwell Pub.
2. Liebler, D. C. (2002). Introduction to Proteomics: Tools for the New Biology. Totowa, NJ: Humana Press. Campbell, A. M., & Heyer, L. J. (2003). Discovering Genomics, Proteomics, and Bioinformatics. San Francisco: Benjamin Cummings.