

MBS-506: Metagenomics & Proteomics

40 h

Unit I

13h

Structure and organization of Genomes in Prokaryotes and Eukaryotes: gene structure, Open reading frames, Conceptual translation, Termination sequences and GC content. **Genome Sequencing:** High throughput sequencing, clone-by-clone approach, Whole genome shot gun approach, quality of genome sequence, human genome sequencing project.

Unit II

13h

Comparative Genomics of prokaryotes and eukaryotes, Comparative genomics of organelles, Large scale mutagenesis and interference. Analysis of Transcriptomes: Introduction, **DNA microarray technology,** Functional genomics, Expressed Sequence Tags (ESTs) and Serial Analysis of Gene Expression (SAGE,) Allele mining and SNPs, Applications of genomics.

Unit III

14h

Metagenomics: Introduction to sequence based and function based metagenomics. Analyses of community composition and change, Metabolic reconstruction analyses, metatranscriptome and metaproteome analyses. Proteomics: Introduction to proteomics, **Proteomics Technologies** - Protein Arrays, Protein Chips and their applications, 2D Gel Electrophoresis and its application, Mass Spectrometry and Protein identification, Shotgun proteomics.