

SYLLABUS :-

Understanding databases, understanding NCBI Entrez, Pairwise alignment and multiple alignment, BLAST analysis of nucleotide and protein sequences, Gene finding (Genescan, ORF finder, Translation etc.), Sequence analysis (restriction map, repeat sequence identification, secondary structure prediction etc.), Primer design for PCR, Genome analysis (ongoing and completed genome), Phylogenetic tree constructions, protein structure prediction and functional analysis.