# BBT-405 BIOINFORMATICS

## MODULE- I

Primary and secondary databases. Specialized sequence databases of EST, TFB Sites, SNP's, gene expression. Pfam, PROSITE, BLOCK (Secondary databases). Data retrieval with ENTREZ, SRS, DBGET

Principles of DNA sequencing (chemical chain termination, Dideoxy chain termination method, Automatic sequencer). RNA sequencing . Protein sequencing ( Edmand degradation method)

## MODULE- II

Sequence alignment (pairwise and multiple, global and local). Sequence alignment algorithm (FAST , BLAST, Needleman and Wunsch, Smith Waterman ). Database similarity searches (BLAST, FASTA and PSI BLAST). Amino acid substitution matrices ( PAM BLOSUM)

## MODULE- III

Protein structure prediction ( Chou Fasman method) : Secondary and tertiary structures. Homology Modelling, ORF prediction, Gene prediction, Micro array data analysis. Profiles and motifs.

Structure visualization methods ( RASMOL, CHIME etc.) . Protein Structure alignment and analysis. Application of Bioinformatics in drug discovery and drug designing.

**Reference books & Text books:**

1. *Bioinformatics : Principles and applications by Ghosh and Mallick (oxford) university press)*
2. *Bioinformatics by Andreas D Boxevanis (Wiley Interscience)*
3. *Fundamental concept of bioinformatics by Dan e. krane*
4. *Introduction to bioinformatics by Attwood and Parry Smith ( Pierson education Publication)*
5. *instant notes in Bioinformatics by Westhead, parish and Tweman ( Bios scientific publishers)*