BIOINFORMATICS SYLLABUS

Scoring matrices: Detailed method of derivation of the PAM and BLOSUM matrices

Pair wise sequence alignments: Needleman and Wunsch, Smith and Waterman algorithms and their implementation

Multiple sequence alignments (MSA):

Use of HMM-based Algorithm for MSA (e g. SAM method)

Sequence patterns and profiles:

Repeats: Tandem and Interspersed repeats, repeat finding, Motifs, consensus, position weight matrices

Algorithms for derivation of and searching sequence patterns: MEME, PHI-BLAST, Scan Prosite and PRATT

Algorithms for generation of sequence profiles: Profile Analysis method of Gribskov, HMMer, PSIBLAST

Protein and nucleic acid properties: e g. Proteomics tools at the ExPASy server and EMBOSS

Taxonomy and phylogeny: Phylogenetic analysis algorithms such as maximum Parsimony, UPGMA, Transformed Distance, Neighbors-Relation, Neighbor-Joining, Probabilistic models and associated algorithms such as Probabilistic models of' evolution and maximum likelihood algorithm, Bayesian inference algorithm, Bootsoapping methods, use of tools such as PHYLIP, MEGA, PAUP. Analysis of regulatory RNA's: Databases and tools

Structural Biology

Experimental methods for Biomolecular structure determination: X-ray and NMR, Prediction Of secondary structure: PHD and PSI-PRED methods

Tertiary Structure prediction: Fundamentals of the methods for 3D structure prediction (sequence similarity/identity of target proteins of known structure, fundamental principles of protein folding etc.) Homology Modeling, fold recognition, threading approaches, and ab-initio structure prediction methods

Structure analysis and validation: Pdbsum, Whatcheck, Procheck, Verify3D and ProsaII, Critical Assessment of Structure Prediction (CASP), Structures of oligomeric proteins and study of interaction interfaces

Molecular modeling and simulations

Macro-molecular force fields, salvation, long-range forces, and Geometry optimization algorithms: Steepest descent, conjugate gradient, Various simulation techniques: Molecular mechanics, conformational searches, Molecular Dynamics, Monte Carlo, genetic algorithm approaches, Rigid and Semi-Flexible Molecular Docking

Genomics

Large scale genome sequencing strategies: Genome assembly and annotation, Genome databases of Plants, animals and pathogens Metagenomics

Gene networks: basic concepts, computational model such as Lambda receptor and/oc operon, Prediction of genes, promoters, splice sites, regulatory regions: basic principles, application of methods to prokaryotic and eukaryotic genomes and interpretation of results

Basic concepts on identification of disease genes, role of bioinformatics-OMIM database, reference genome sequence, integrated genomic maps, gene expression profiling; identification of SNPs, SNP database (DbSNP). Role of SNP in Pharmacogenomics, SNP arrays

DNA microarray: database and basic tools, Gene Expression Omnibus (GEO), ArrayExpress, SAGE databases, understanding of' microarray data, normalizing microarray data, detecting differential gene expression, correlation of gene expression data to biological process and computational analysis.