

Computational Biology Assignment

[Section: B]

*Dear students please submit your assignment on 25 Jan 2012.

Enrollment No.	Topic
A7100210055	Information Resources: NCBI, EBI, ExPasy Entrez & SRS System
A7100210056	Primary Sequence & Structure Databases: Genbank, SwissProt/Uniprot,
A7100210057	EMBL, PIR, PDB, MMDB,NDB, CSD, KEGG
A7100210058	Derived (Secondary) Databases of Sequences and structure: Prosite, PRODOM, PRINTS, Pfam, BLOCK, INTERPRO.
A7100210059	Derived (Secondary) Databases of Sequences and structure: SCOP, CATH, DSSP, FSSP, RNAbase.
A7100210060	Genome Databases (at NCBI, EBI, TIGR, SANGER),
A7100210062	High-throughput genomics sequence (EST, STS,GSS), ENSEMBL.
A7100210063	Sequence File formats: Fasta, GenBank, embl, Swiss-prot, pdb, nbrf, pir
A7100210066	Sequence File formats: multiple sequences formats (Aln, Mega, Pileup, phylip etc.)
A7100210067	Sequence Similarity Basics: Similarity, Identity, Homology, Scoring, selectivity/Sensitivity,
A7100210068	Gap cost, Linear and Affine Gap Penalty, Basic of scoring system and matrices (PAM, BIOSUM, GONNET etc.)
A7100210069	Pairwise Sequences Alignment: Brute Force method, Dot matrix method.
A7100210070	Scoring Matrices: Substitution Matrices, Concept log-odds, PAM & BLOSUM Series
A7100210071	Similarity Searching Tools: BLAST and FASTA, Theory and Algorithms.
A7100210072	Variants of BLAST and FASTA, PSI-BLAST and PHI BLAST, Statistical Significance.
A7100210073	Sequence Pattern and Profiles: Concepts of motif, pattern and profile
A7100210074	Profile construction and its application in Bioinformatics.
A7100210075	Scoring methods of MSA (sum of pair, Multidimensional DP, Progressive, Iterative, Probabilistic)
A7100210076	Phylogenetics prediction methods: Basics, molecular clock, Substitution Models of evolution
A7100210077	Tree reconstruction methods (Distance based, character based method, statistical), Bootstrapping.
A7100210078	Suffix tree and its applications in Bioinformatics
A7100210079	Gene Identification Methods
A7100210080	Predictive Methods using DNA and Protein sequences.
A7100210081	Statistical Modeling: Log-likelihood, Bayesian network, Markov and hidden markov models
A7100210082	Clustering Algorithms: K-means, Hierarchical and Mixture of Gaussion.

A7100210084	Phylogenetics analysis software
A7100210085	Molecular Structure drawing tool
A7100210087	Molecular modeling/Docking.
A7100210088	Application of computational biology/Bioinformatics in Agriculture,
A7100210089	Application of computational biology/Bioinformatics in Human health,
A7100210090	Application of computational biology/Bioinformatics in Environment.
A7100210091	Application of computational biology/Bioinformatics in Biotechnology.
A7100210092	Application of computational biology/Bioinformatics in Molecular Biology.
A7100210093	Global (Needleman- Wunsch) and Local Alignment (Smith-Waterman) using Dynamic programming.
A7100210094	Application of computational biology/Bioinformatics in Drug Designing.
A7100210095	Application of computational biology/Bioinformatics in Veterinary Science.
A7100210096	Introduction to Computational Biology.
A7100210097	History of Bioinformatics.
A7100210098	Profile construction and its application in Bioinformatics.
A7100210099	Molecular Structure drawing tool
A7100210100	Gene Identification Methods
A7100210101	Statistical Modeling: Log-likelihood, Bayesian network, Markov and hidden markov models
A7100210102	Phylogenetics analysis software
A7100210103	Global (Needleman- Wunsch) and Local Alignment (Smith-Waterman) using Dynamic programming.
A7100210104	Derived (Secondary) Databases of Sequences and structure: Prosite, PRODOM, PRINTS, Pfam, BLOCK, INTERPRO.
A7100210105	Application of computational biology/Bioinformatics in Neurobiology.
A7100210106	Predictive Methods using DNA and Protein sequences.
A7100210107	Suffix tree and its applications in Bioinformatics.