

Bioinformatics

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Bioinformatics provides in depth coverage of the principles and applications of bioinformatic analyses of nucleic acid and protein sequences, databases and data mining. Dynamic programming algorithms of Needleman-Wunsch and Smith-Waterman, amino acid exchange matrices such as Dayhoff PAM series matrices and BLOSSUM series matrices and DOT matrix are discussed in detail along with pair-wise sequence alignment tools such as BLAST, FASTA and their variants, multiple sequence alignment tools such as CLUSTAL-W, CLUSTAL-X, SAGA, and progressive alignment and profile alignment. The book describes methods of detection and prediction of genes, ORFs, promoters, motifs, mRNA, tRNA, miRNA, their structure and function and protein structure and function using ab initio HMM and Neural Networks. Software programs like GeneID, Genescan, Genie, GeneModeler, GRAIL and GeneMARK for gene detection and visual mining tools available are discussed while Gene Ontology (GO) and use of sequence information for phylogenetic inferences are illustrated.

KEY FEATURE:

- Presents key databases, analytical tools and software programmes for analyzing biological sequence data



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