Discovering Genomics, Proteomics And Bioinformatics (2nd Edition) Download Pdf

PGD BINF 303
Proteomics and Genomics
(2 Credits)

Unit-I

Genomics and Metagenomics: 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 lac 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. Basic concepts in identification of Drought stress response genes, insect resistant genes, nutrition enhancing genes

Unit-II

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

Unit-III

Comparative genomics: Basic concepts and applications, whole genome alignments: understanding the significance; Artemis, BLAST2, MegaBlast algorithms, PipMaker, AVID, Vista, MUMmer, applications of suffix tree in comparative genomics, synteny and gene order comparisons Comparative genomics databases: COG, VOG

Unit-IV

Functional genomics: Application of sequence based and structure-based approaches to assignment of gene functions – e.g. sequence comparison, structure analysis (especially active sites, binding sites) and comparison, pattern identification, etc. Use of various derived databases in function assignment, use of SNPs for identification of genetic traits. Gene/Protein function prediction using Machine learning tools viz. Neural network, SVM etc

Unit-V

Proteomics: Protein arrays: basic principles. Computational methods for identification of polypeptides from mass spectrometry. Protein arrays: bioinformatics-based tools for analysis of proteomics data (Tools available at ExPASy Proteomics server); databases (such as InterPro) and analysis tools. Protein-protein interactions: databases such as DIP, PPI server and tools for analysis of protein-protein interactions

Text Books:

1. Discovering Genomics, Proteomics and Bioinformatics 2nd edition - by A. Malcolm Campbell and Laurie J. Heyer. by Cold Spring Harbor Laboratory Press 2006.

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Bioinformatics and Computational Biology Solutions Using R and ... Comparative Community Proteomics Demonstrates the Unexpected. in Computer Science ... D) 2§, Jose Diaz-Romero (Ph. The pipeline begins with FASTQ files and outputs both a gene count. ... Bioconductor and transparent png images free download.. Genomics, Proteomics & Bioinformatics ... applied to the study of proteins involved in carcinogenesis, as well as to discover biomarkers for clinical use (1).. This resource is powered by the Protein Data Bank archive-information about the ... in molecular biology, structural biology, computational biology, and beyond.. [SHARE] Fulfilled Request Megathread 4 FREE DOWNLOAD ... And Protein Folding (Structural Biology) Reprint Edition(self) 1 [BOOK] Genetic Analysis: Genes, Genomes, and Networks in Eukaryotes 2nd Edition by Philip Meneely(self) 2 ... Exploring the Boundaries of Environmental and State-Corporate Crime in Bolivia, ... integrate large quantities of genomic, proteomic, and other data. ... 2. Bioinformatics. The term bioinformatics was coined by Paulien Hogeweg in 1979 for the study of informatic processes in biotic ... Gene finding is an important application of comparative genomics, as is discovery of new, non-coding ... [19] Aluru, S., ed.. Completion of the human genome project and explosion of genomic information ... 2. Term work (40%) and University examination (60%) will be separate ... Campbell, A.M & Heyer, L.J., Discovering genomics, proteomics and ... Mount, D.W., Bioformatics sequence and genome analysis, 2nd Ed., 2004.. Discovering Genomics Proteomics And Bioinformatics 2nd Edition Pdf.pdf beach head 2010.rar station cash generator.rar download mozilla .... in genomics, transcriptomics, proteomics, metabolomics, and bioinformatics. 121. U n it 2. Ch a p te r. 7. UNIT 2. BIOMARKERS: PRACTICAL ASPECTS. CHAPTER 7. Platforms for biomarker analysis ... colleagues, the discovery of DNA ... isotopic or label-free methods can also be used that include spectral counting and. cfec45ee80