



Read, Analyze, and Visualize Genomic and Proteomic Data with MATLAB (Paperback)

By J Perkins

Createspace Independent Publishing Platform, 2018. Paperback. Condition: New. Language: English . Brand New Book ***** Print on Demand *****. Bioinformatics Toolbox provides algorithms and apps for Next Generation Sequencing (NGS), microarray analysis, mass spectrometry, and gene ontology. Using toolbox functions, you can read genomic and proteomic data from standard file formats such as SAM, FASTA, CEL, and CDF, as well as from online databases such as the NCBI Gene Expression Omnibus and GenBank. You can explore and visualize this data with sequence browsers, spatial heatmaps, and clustergrams. The toolbox also provides statistical techniques for detecting peaks, imputing values for missing data, and selecting features. You can combine toolbox functions to support common bioinformatics workflows. You can use ChIP-Seq data to identify transcription factors; analyze RNA-Seq data to identify differentially expressed genes; identify copy number variants and SNPs in microarray data; and classify protein profiles using mass spectrometry data. The essential content of this book is the following: -Next Generation Sequencing analysis and browser - Sequence analysis and visualization, including pairwise and multiple sequence alignment and peak detection -Microarray data analysis, including reading, filtering, normalizing, and visualization -Mass spectrometry analysis, including preprocessing, classification, and marker identification -Phylogenetic tree analysis -Graph theory functions,...



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