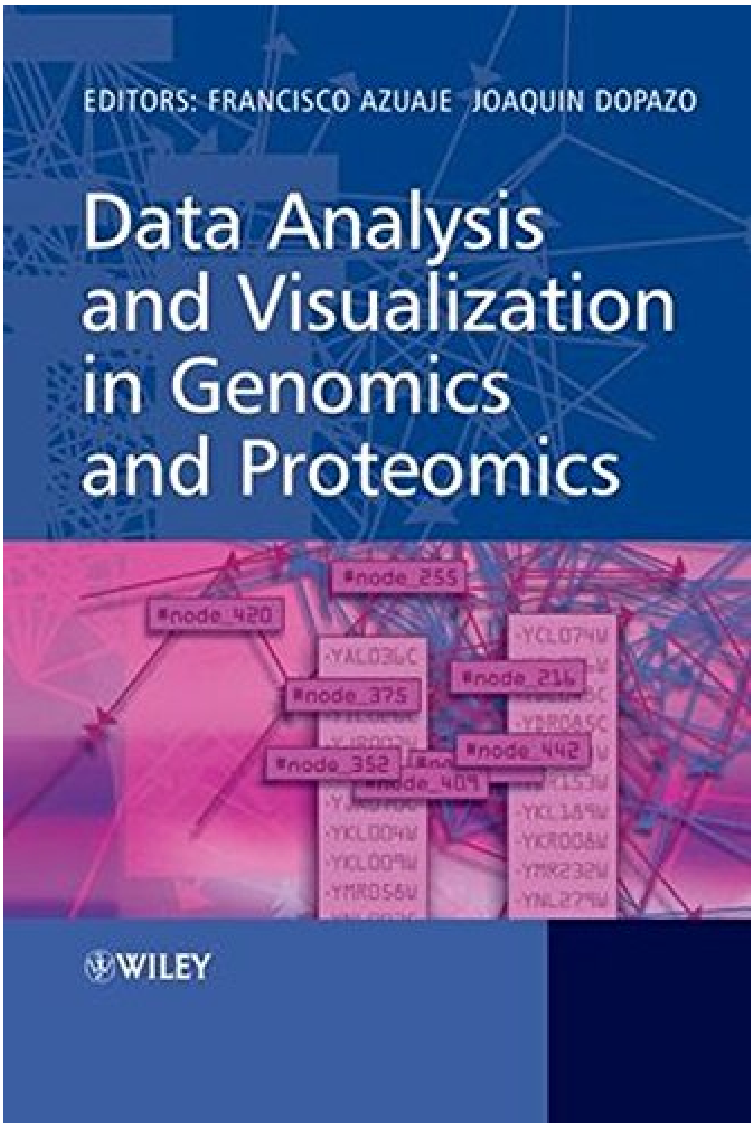
Data Analysis and Visualization in Genomics and Proteomics

From Azuaje



#5548575 in Books Azuaje 2005-04-29Original language:EnglishPDF # 1 9.96 x .96 x 6.14l, 1.51 #File Name: 0470094397284 pagesData Analysis And Visualization | File size: 52.Mb

From Azuaje : Data Analysis and Visualization in Genomics and Proteomics before purchasing it in order to gage whether or not it would be worth my time, and all praised Data Analysis and Visualization in Genomics and Proteomics:

2 of 2 people found the following review helpful. Nice overview, but lacks detailBy Eric JainThis book provides a nice overview of some important genomics and proteomics databases and analysis techniques, but doesn't go into much detail anywhere, especially not on data visualization.

Data Analysis and Visualization in Genomics and Proteomics is the first book addressing integrative data analysis and visualization in this field. It addresses important techniques for the interpretation of data originating from multiple sources, encoded in different formats or protocols, and processed by multiple systems. One of the first systematic overviews of the problem of biological data integration using computational approaches

From the Back CoverThis book provides scientists and students with the basis for the development of integrative computational approaches to analysing biological data on a systemic scale. It emphasises the processing of multiple data and knowledge resources, and the combination of different prediction models and systems. It covers different data analysis and visualisation techniques for studying the roles of genes and proteins at a systems level. A fairly broad definition for the areas of genomics and proteomics is adopted, which also encompasses a wider spectrum of omic approaches required to understand the functions of genes and their products. From a bioinformatics point of view, the book illustrates: how data analysis techniques can facilitate more comprehensive, user-friendly data visualisation tasks; how data visualisation methods may make data analysis a more meaningful and biologically relevant process; and how to approach the overabundance of data in genomic studies, in which spurious associations often occur, with the proper statistical tools. The book describes how this synergy may support integrative approaches to functional genomics. The book will be of interest to all bioinformaticians, from students to researchers, as well as to many scientists working in genomics, proteomics, systems biology and related areas.