



# The Analysis Of Biological

**S Marginson**



## **The Analysis Of Biological:**

**The Analysis of Biological Data** Michael Whitlock, Dolph Schluter, 2009 This text emphasizes intuitive understanding rather than an over reliance on formulas The focus is on data and graphical displays rather than the mathematical foundations of statistics and students do not need knowledge of mathematics beyond simple algebra Analysis of Biological Data Sanghamitra Bandyopadhyay, 2007 Bioinformatics a field devoted to the interpretation and analysis of biological data using computational techniques has evolved tremendously in recent years due to the explosive growth of biological information generated by the scientific community Soft computing is a consortium of methodologies that work synergistically and provides in one form or another flexible information processing capabilities for handling real life ambiguous situations Several research articles dealing with the application of soft computing tools to bioinformatics have been published in the recent past however they are scattered in different journals conference proceedings and technical reports thus causing inconvenience to readers students and researchers This book unique in its nature is aimed at providing a treatise in a unified framework with both theoretical and experimental results describing the basic principles of soft computing and demonstrating the various ways in which they can be used for analyzing biological data in an efficient manner Interesting research articles from eminent scientists around the world are brought together in a systematic way such that the reader will be able to understand the issues and challenges in this domain the existing ways of tackling them recent trends and future directions This book is the first of its kind to bring together two important research areas soft computing and bioinformatics in order to demonstrate how the tools and techniques in the former can be used for efficiently solving several problems in the latter Sample Chapter s Chapter 1 Bioinformatics Mining the Massive Data from High Throughput Genomics Experiments 160 KB Contents Overview Bioinformatics Mining the Massive Data from High Throughput Genomics Experiments H Tang An Introduction to Soft Computing A Konar Biological Sequence and Structure Analysis Reconstructing Phylogenies with Memetic Algorithms and Branch and Bound J E Gallardo et al Classification of RNA Sequences with Support Vector Machines J T L Wang Beyond String Algorithms Protein Sequence Analysis Using Wavelet Transforms A Krishnan Filtering Protein Surface Motifs Using Negative Instances of Active Sites Candidates N L Shrestha Distill A Machine Learning Approach to Ab Initio Protein Structure Prediction G Pollastri et al In Silico Design of Ligands Using Properties of Target Active Sites S Bandyopadhyay et al Gene Expression and Microarray Data Analysis Inferring Regulations in a Genomic Network from Gene Expression Profiles N Noman A Reliable Classification of Gene Clusters for Cancer Samples Using a Hybrid Multi Objective Evolutionary Procedure K Deb et al Feature Selection for Cancer Classification Using Ant Colony Optimization and Support Vector Machines A Gupta et al Sophisticated Methods for Cancer Classification Using Microarray Data S B Cho Multiobjective Evolutionary Approach to Fuzzy Clustering of Microarray Data A Mukhopadhyay et al Readership Graduate students and researchers in computer science bioinformatics computational and molecular biology

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