

Analysis Of Biological Data Solutions Whitlock

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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 s kim an introduction to soft computing a konar s das 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 x wu beyond string algorithms protein sequence analysis using wavelet transforms a krishnan k b li filtering protein surface motifs using negative instances of active sites candidates n l shrestha t ohkawa 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 h iba 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 h s park 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 artificial intelligence data mining machine learning electrical engineering system science researchers in pharmaceutical industries

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

biochemical and biophysical characteristics genetics cytogenetics and reproducton

development and morphology nutrition digestion and metabolism respiration and circulation other physiological activities and performances biologically active compounds environment and survival symbiosis and parasitism ecology and biogeography

this volume maps the areas of ethical concern in the debate regarding the governance of genetic information and suggests alternative ethical frameworks and models of regulation in order to inform its restructuring genetic governance is at the heart of medical and scientific developments and is connected to global exploitation issues of commodification commercialisation and ownership the concepts of property and intellectual property and concerns about individual and communal identity thus the decisions that are made in the next few years about appropriate models of genetic governance will have knock on effects for other areas of governance in short the final answer to who decides in the context of genetic governance will fundamentally shape the ethical constructs of individuals and their networks and relationships in the public sphere

the first comprehensive overview of preprocessing mining and postprocessing of biological data molecular biology is undergoing exponential growth in both the volume and complexity of biological data and knowledge discovery offers the capacity to automate complex search and data analysis tasks this book presents a vast overview of the most recent developments on techniques and approaches in the field of biological knowledge discovery and data mining kdd providing in depth fundamental and technical field information on the most important topics encountered written by top experts biological knowledge discovery handbook preprocessing mining and postprocessing of biological data covers the three main phases of knowledge discovery data preprocessing data processing also known as data mining and data postprocessing and analyzes both verification systems and discovery systems biological data preprocessing part a biological data management part b biological data modeling part c biological feature extraction part d biological feature selection biological data mining part e regression analysis of biological data part f biological data clustering part g biological data classification part h association rules learning from biological data part i text mining and application to biological data part j high performance computing for biological data mining combining sound theory with practical applications in molecular biology biological knowledge discovery handbook is ideal for courses in bioinformatics and biological kdd as well as for practitioners and professional researchers in computer science life science and mathematics

the study of biological data is constantly undergoing profound changes firstly the volume of data available has increased considerably due to new high throughput techniques used for experiments secondly the remarkable progress in both computational and statistical analysis methods and infrastructures has made it possible to process these voluminous data the resulting challenge concerns our ability to integrate these data i e to use their complementary nature effectively in the hope of advancing our knowledge therefore a major challenge in studying biology today is integrating data for the most exhaustive analysis possible biological data integration deals in a pedagogical way with research work in biological data science examining both computational approaches to data integration and statistical approaches to the integration of omics data

a manual to teach people to use the statistical software package s plus and to support the process of learning statistical concepts and methods it is a useful workbook to accompany the

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