

Gene Clustering Application 1

Darina Dicheva, Danail Dochev

Data Clustering: Theory, Algorithms, and Applications, Second Edition Guojun Gan,Chaoqun Ma,Jianhong Wu,2020-11-10 Data clustering, also known as cluster analysis, is an unsupervised process that divides a set of objects into homogeneous groups. Since the publication of the first edition of this monograph in 2007, development in the area has exploded, especially in clustering algorithms for big data and open-source software for cluster analysis. This second edition reflects these new developments, covers the basics of data clustering, includes a list of popular clustering algorithms, and provides program code that helps users implement clustering algorithms. Data Clustering: Theory, Algorithms and Applications, Second Edition will be of interest to researchers, practitioners, and data scientists as well as undergraduate and graduate students.

Practical Guide to Cluster Analysis in R Alboukadel Kassambara,2017-08-23 Although there are several good books on unsupervised machine learning, we felt that many of them are too theoretical. This book provides practical guide to cluster analysis, elegant visualization and interpretation. It contains 5 parts. Part I provides a quick introduction to R and presents required R packages, as well as, data formats and dissimilarity measures for cluster analysis and visualization. Part II covers partitioning clustering methods, which subdivide the data sets into a set of k groups, where k is the number of groups pre-specified by the analyst. Partitioning clustering approaches include: K-means, K-Medoids (PAM) and CLARA algorithms. In Part III, we consider hierarchical clustering method, which is an alternative approach to partitioning clustering. The result of hierarchical clustering is a tree-based representation of the objects called dendrogram. In this part, we describe how to compute, visualize, interpret and compare dendrograms. Part IV describes clustering validation and evaluation strategies, which consists of measuring the goodness of clustering results. Among the chapters covered here, there are: Assessing clustering tendency, Determining the optimal number of clusters, Cluster validation statistics, Choosing the best clustering algorithms and Computing p-value for hierarchical clustering. Part V presents advanced clustering methods, including: Hierarchical k-means clustering, Fuzzy clustering, Model-based clustering and Density-based clustering.

Multiobjective Genetic Algorithms for Clustering Ujjwal Maulik,Sanghamitra Bandyopadhyay,Anirban Mukhopadhyay,2011-09-01 This is the first book primarily dedicated to clustering using multiobjective genetic algorithms with extensive real-life applications in data mining and bioinformatics. The authors first offer detailed introductions to the relevant techniques – genetic algorithms, multiobjective optimization, soft computing, data mining and bioinformatics. They then demonstrate systematic applications of these techniques to real-world problems in the areas of data mining, bioinformatics and geoscience. The authors offer detailed theoretical and statistical notes, guides to future research, and chapter summaries. The book can be used as a textbook and as a reference book by graduate students and academic and industrial researchers in the areas of soft computing, data mining, bioinformatics and geoscience.

Handbook of Cluster Analysis Christian Hennig,Marina Meila,Fionn Murtagh,Roberto Rocci,2015-12-16 Handbook of Cluster Analysis provides a comprehensive and unified account of the main research developments in cluster analysis. Written by active, distinguished researchers in this area, the book helps readers make informed choices of the most suitable clustering approach for their problem and make better use of existing cluster analysis tools.The

Research Anthology on Artificial Neural Network Applications Management Association, Information Resources,2021-07-16 Artificial neural networks (ANNs) present many benefits in analyzing complex data in a proficient manner. As an effective and efficient problem-solving method, ANNs are incredibly useful in many different fields. From education to medicine and banking to engineering, artificial neural networks are a growing phenomenon as more realize the plethora of uses and benefits they provide. Due to their complexity, it is vital for researchers to understand ANN capabilities in various fields. The Research Anthology on Artificial Neural Network Applications covers critical topics related to artificial neural networks and their multitude of applications in a number of diverse areas including medicine, finance, operations research, business, social media, security, and more. Covering everything from the applications and uses of artificial neural networks to deep learning and non-linear problems, this book is ideal for computer scientists, IT specialists, data scientists, technologists, business owners, engineers, government agencies, researchers, academicians, and students, as well as anyone who is interested in learning more about how artificial neural networks can be used across a wide range of fields.

Biotechnology: Concepts, Methodologies, Tools, and Applications Management Association, Information Resources,2019-06-07 Biotechnology can be defined as the manipulation of biological process, systems, and organisms in the production of various products. With applications in a number of fields such as biomedical, chemical, mechanical, and civil engineering, research on the development of biologically inspired materials is essential to further advancement. Biotechnology: Concepts, Methodologies, Tools, and Applications is a vital reference source for the latest research findings on the application of biotechnology in medicine, engineering, agriculture, food production, and other areas. It also examines the economic impacts of biotechnology use. Highlighting a range of topics such as pharmacogenomics, biomedical engineering, and bioinformatics, this multi-volume book is ideally designed for engineers, pharmacists, medical professionals, practitioners, academicians, and researchers interested in the applications of biotechnology.

Research Anthology on Bioinformatics, Genomics, and Computational Biology Management Association, Information Resources,2024-03-19 In the evolving environment of bioinformatics, genomics, and computational biology, academic scholars are facing a challenging challenge – keeping informed about the latest research trends and findings. With unprecedented advancements in sequencing technologies, computational algorithms, and machine learning, these fields have become indispensable tools for drug discovery, disease research, genome sequencing, and more. As scholars strive to decode the language of DNA, predict protein structures, and navigate the complexities of biological data analysis, the need for a comprehensive and up-to-date resource becomes paramount. The Research Anthology on Bioinformatics, Genomics, and Computational Biology is a collection of a carefully curated selection of chapters that serves as the solution to the pressing challenge of keeping pace with the dynamic advancements in these critical disciplines. This anthology is designed to address the informational gap by providing scholars with a consolidated and authoritative source that sheds light on critical issues, innovative theories, and transformative developments in the field. It acts as a single reference point, offering insights into conceptual, methodological, technical, and managerial issues while also providing a glimpse into emerging trends and future opportunities.

Bioinformatics Applications Based On Machine Learning Pablo Chamoso,Sara Rodríguez González,Mohd Saberi Mohamad,Alfonso González-Briones,2021-09-01 The great advances in information technology (IT) have implications for many sectors, such as bioinformatics, and has considerably increased their possibilities. This book presents a collection of 11 original research papers, all of them related to the application of IT-related techniques within the bioinformatics sector: from new applications created from the adaptation and application of existing techniques to the creation of new methodologies to solve existing problems.

Computational Systems Bioinformatics - Methods And Biomedical Applications Wong Stephen Tin Chi,Zhou Xiaobo,2008-01-02 Computational systems biology is a new and rapidly developing field of research, concerned with understanding the structure and processes of biological systems at the molecular, cellular, tissue, and organ levels through computational modeling as well as novel information theoretic data and image analysis methods. By focusing on either information processing of biological data or on modeling physical and chemical processes of biosystems, and in combination with the recent breakthrough in deciphering the human genome, computational systems biology is guaranteed to play a central role in disease prediction and preventive medicine, gene technology and pharmaceuticals, and other biotechnology fields.This book begins by introducing the basic mathematical, statistical, and data mining principles of computational systems biology, and then presents bioinformatics technology in microarray and sequence analysis step-by-step. Offering an insightful look into the effectiveness of the systems approach in computational biology, it focuses on recurrent themes in bioinformatics, biomedical applications, and future directions for research.

Bioinformatics Research and Applications Zhipeng Cai,Pavel Skums,Min Li,2019-05-27 This book constitutes the proceedings of the 15th International Symposium on Bioinformatics Research and Applications, ISBRA 2019, held in Barcelona, Spain, in June 2019. The 22 full papers presented in this book were carefully reviewed and selected from 95 submissions. They were organized in topical sections named: genome analysis;

systems biology; computational proteomics; machine and deep learning; and data analysis and methodology.

Computational Genomics with R Altuna Akalin, 2020-12-16 Computational Genomics with R provides a starting point for beginners in genomic data analysis and also guides more advanced practitioners to sophisticated data analysis techniques in genomics. The book covers topics from R programming, to machine learning and statistics, to the latest genomic data analysis techniques. The text provides accessible information and explanations, always with the genomics context in the background. This also contains practical and well-documented examples in R so readers can analyze their data by simply reusing the code presented. As the field of computational genomics is interdisciplinary, it requires different starting points for people with different backgrounds. For example, a biologist might skip sections on basic genome biology and start with R programming, whereas a computer scientist might want to start with genome biology. After reading: You will have the basics of R and be able to dive right into specialized uses of R for computational genomics such as using Bioconductor packages. You will be familiar with statistics, supervised and unsupervised learning techniques that are important in data modeling, and exploratory analysis of high-dimensional data. You will understand genomic intervals and operations on them that are used for tasks such as aligned read counting and genomic feature annotation. You will know the basics of processing and quality checking high-throughput sequencing data. You will be able to do sequence analysis, such as calculating GC content for parts of a genome or finding transcription factor binding sites. You will know about visualization techniques used in genomics, such as heatmaps, meta-gene plots, and genomic track visualization. You will be familiar with analysis of different high-throughput sequencing data sets, such as RNA-seq, ChIP-seq, and BS-seq. You will know basic techniques for integrating and interpreting multi-omics datasets. Altuna Akalin is a group leader and head of the Bioinformatics and Omics Data Science Platform at the Berlin Institute of Medical Systems Biology, Max Delbrück Center, Berlin. He has been developing computational methods for analyzing and integrating large-scale genomics data sets since 2002. He has published an extensive body of work in this area. The framework for this book grew out of the yearly computational genomics courses he has been organizing and teaching since 2015.

Handbook of Research on Computational Intelligence Applications in Bioinformatics Dash, Sujata, Subudhi, Bidyadhar, 2016-06-20 Developments in the areas of biology and bioinformatics are continuously evolving and creating a plethora of data that needs to be analyzed and decrypted. Since it can be difficult to decipher the multitudes of data within these areas, new computational techniques and tools are being employed to assist researchers in their findings. The Handbook of Research on Computational Intelligence Applications in Bioinformatics examines emergent research in handling real-world problems through the application of various computation technologies and techniques. Featuring theoretical concepts and best practices in the areas of computational intelligence, artificial intelligence, big data, and bio-inspired computing, this publication is a critical reference source for graduate students, professionals, academics, and researchers.

Artificial Intelligence: Methodology, Systems, and Applications Darina Dicheva, Danail Dochev, 2010-09-03 The 14th International Conference on Artificial Intelligence: Methodology, Systems, Applications (AIMSA 2010) was held in Varna, Bulgaria, during September 8-10, 2010. The AIMSA conference series has provided a biennial forum for the presentation of artificial intelligence research and development since 1984. The conference covers the full range of topics in artificial intelligence (AI) and related disciplines and provides an ideal forum for international scientific exchange between Central/Eastern Europe and the rest of the world. The 2010 AIMSA edition continued this tradition. For AIMSA 2010, we decided to place special emphasis on the application and leverage of AI technologies in the context of knowledge societies where knowledge creation, accessing, acquiring, and sharing empower individuals and communities. A number of AI techniques play a key role in responding to these challenges. AI is intensively used in the development of systems for effective management and flexible and personalized access to large knowledge bases, in the Semantic Web technologies that enable sharing and reuse of and reasoning over semantically annotated resources, in the emerging social Semantic Web applications that aid humans to collaboratively build semantics, in the construction of intelligent environments for supporting (human and agent) learning, etc. In building such intelligent applications, AI techniques are typically combined with results from other disciplines such as the social sciences, distributed systems, databases, digital libraries, information retrieval, service-oriented applications, etc.

Computational Methods With Applications In Bioinformatics Analysis Tsai Jeffrey J P, Ng Ka-lok, 2017-06-09 This compendium contains 10 chapters written by world renowned researchers with expertise in semantic computing, genome sequence analysis, biomolecular interaction, time-series microarray analysis, and machine learning algorithms. The salient feature of this book is that it highlights eight types of computational techniques to tackle different biomedical applications. These techniques include unsupervised learning algorithms, principal component analysis, fuzzy integral, graph-based ensemble clustering method, semantic analysis, interolog approach, molecular simulations and enzyme kinetics. The unique volume will be a useful reference material and an inspirational read for advanced undergraduate and graduate students, computer scientists, computational biologists, bioinformatics and biomedical professionals.

Evolutionary Data Clustering: Algorithms and Applications Ibrahim Aljarah, Hossam Faris, Seyedali Mirjalili, 2021-02-20 This book provides an in-depth analysis of the current evolutionary clustering techniques. It discusses the most highly regarded methods for data clustering. The book provides literature reviews about single objective and multi-objective evolutionary clustering algorithms. In addition, the book provides a comprehensive review of the fitness functions and evaluation measures that are used in most of evolutionary clustering algorithms. Furthermore, it provides a conceptual analysis including definition, validation and quality measures, applications, and implementations for data clustering using classical and modern nature-inspired techniques. It features a range of proven and recent nature-inspired algorithms used to data clustering, including particle swarm optimization, ant colony optimization, grey wolf optimizer, salp swarm algorithm, multi-verse optimizer, Harris hawks optimization, beta-hill climbing optimization. The book also covers applications of evolutionary data clustering in diverse fields such as image segmentation, medical applications, and pavement infrastructure asset management.

Web-Age Information Management Yueguo Chen, Wolf-Tilo Balke, Jianliang Xu, Wei Xu, Peiquan Jin, Xin Lin, Tiffany Tang, Eenjun Hwang, 2014-10-09 This book constitutes the refereed proceedings of 5 workshops of the 15th International Conference on Web-Age Information Management, WAIM 2014, held in Macau, China, June 16-18, 2014. The 38 revised full papers are organized in topical sections on the 5 following workshops: Second International Workshop on Emergency Management in Big Data Age, BigEM 2014; Second International Workshop on Big Data Management on Emerging Hardware, HardBD 2014; International Workshop on Data Management for Next-Generation Location-based Services, DaNoS 2014; International Workshop on Human Aspects of Making Recommendations in Social Ubiquitous Networking Environment, HRSUME 2014; International Workshop on Big Data Systems and Services, BIDASYS 2014.

Recent Advances in Hybrid Metaheuristics for Data Clustering Sourav De, Sandip Dey, Siddhartha Bhattacharyya, 2020-06-02 An authoritative guide to an in-depth analysis of various state-of-the-art data clustering approaches using a range of computational intelligence techniques Recent Advances in Hybrid Metaheuristics for Data Clustering offers a guide to the fundamentals of various metaheuristics and their application to data clustering. Metaheuristics are designed to tackle complex clustering problems where classical clustering algorithms have failed to be either effective or efficient. The authors noted experts on the topic provide a text that can aid in the design and development of hybrid metaheuristics to be applied to data clustering. The book includes performance analysis of the hybrid metaheuristics in relationship to their conventional counterparts. In addition to providing a review of data clustering, the authors include in-depth analysis of different optimization algorithms. The text offers a step-by-step guide in the build-up of hybrid metaheuristics and to enhance comprehension. In addition, the book contains a range of real-life case studies and their applications. This important text: Includes performance analysis of the hybrid metaheuristics as related to their conventional counterparts Offers an in-depth analysis of a range of optimization algorithms Highlights a review of data clustering Contains a detailed overview of different standard metaheuristics in current use Presents a step-by-step guide to the build-up of hybrid metaheuristics Offers real-life case studies and applications Written for researchers, students and academics in computer science, mathematics, and engineering, Recent Advances in Hybrid Metaheuristics for Data Clustering provides a text that explores the current data clustering approaches using a range of computational intelligence techniques.

Applications of Intelligent Optimization in Biology and Medicine Aboul-Ella Hassanien,Crina Grosan,Mohamed Fahmy Tolba,2015-07-18 This volume provides updated, in-depth material on the application of intelligent optimization in biology and medicine. The aim of the book is to present solutions to the challenges and problems facing biology and medicine applications. This Volume comprises of 13 chapters, including an overview chapter, providing an up-to-date and state-of-the research on the application of intelligent optimization for bioinformatics applications, DNA based Steganography, a modified Particle Swarm Optimization Algorithm for Solving Capacitated Maximal Covering Location Problem in Healthcare Systems, Optimization Methods for Medical Image Super Resolution Reconstruction and breast cancer classification. Moreover, some chapters that describe several bio-inspired approaches in MEDLINE Text Mining, DNA-Binding Proteins and Classes, Optimized Tumor Breast Cancer Classification using Combining Random Subspace and Static Classifiers Selection Paradigms, and Dental Image Registration. The book will be a useful compendium for a broad range of readers—from students of undergraduate to postgraduate levels and also for researchers, professionals, etc.—who wish to enrich their knowledge on Intelligent Optimization in Biology and Medicine and applications with one single book.

Three Clustering Algorithms and Their Application to Microarray Data Francisco Javier Molina Lopez,2010-04 In the context of medical diagnostics, an important problem is to find the genes that are correlated with given phenotypes. These genes may reveal insights to biological processes and may be used to predict the phenotypes associated to samples of RNA. To that end, two new clustering methods are presented and studied. Our first algorithm allows us to analyze cell evolution by observing how the state of every gene changes over time. Our second algorithm cluster genes whose expression profiles are similar by using a classification of the samples utilized in the microarray experiments. This classification is based upon one or more conditions that affect the composition of the samples analyzed. By using the label of the microarray experiments, extra information is provided to cluster genes. The research reported here on the first two algorithms presented consists of three parts: 1. testing our methods on artificial datasets sampled from the probabilistic models on which our methods are based, 2. using our methods on microarray expression datasets to cluster genes, 3. and comparing results from parts 1 and 2 with the results obtained by other clustering methods on the same datasets.

Advances on Data Mining: Applications and Theoretical Aspects Petra PErner,2011-08-09 This book constitutes the refereed proceedings of the 11th Industrial Conference on Data Mining, ICDM 2011, held in New York, USA in September 2011. The 22 revised full papers presented were carefully reviewed and selected from 100 submissions. The papers are organized in topical sections on data mining in medicine and agriculture, data mining in marketing, data mining for Industrial processes and in telecommunication, Multimedia Data Mining, theoretical aspects of data mining, Data Warehousing, WebMining and Information Mining.

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