

A Primer In Biological Data Analysis And Visualization Using R

While it is true that members of most sexually reproducing species can be defined as either male or female, those who belong to the rest of the biological world are not so simply understood. Hermaphroditic creatures reproduce both as male and as female individuals, providing a fascinating glimpse into alternative sexual practices in nature and their ecological and evolutionary successes and failures. Eloquently written by an award-winning biologist and pioneer in molecular ecology, this primer on hermaphroditism traces the phenomenon throughout Earth's myriad species, accounting for the adaptive significance of alternative sexual systems. Accessible and richly illustrated, the text maps the evolutionary origins of hermaphroditism, as well as its historical instances and fictional representations, underscoring the relevance of dual sexuality to our biological, intellectual, and cultural making. John C. Avise describes the genetics, ecology, phylogeny, and natural history of hermaphroditic plants, fish, and invertebrate animals and details organisms that either produce simultaneously as male and female or switch routinely between one sex and the other. Filled with surprising creatures and compelling revelations, this textbook stands alone in its clear yet comprehensive treatment of hermaphroditism and its unique challenge to the supremacy of separate sexes.

Synthetic Biology — A Primer (Revised Edition) presents an updated overview of the field of synthetic biology and the foundational concepts on which it is built. This revised edition includes new literature references, working and updated URL links, plus some new figures and text where progress in the field has been made. The book introduces readers to fundamental concepts in molecular biology and engineering and then explores the two major themes for synthetic biology, namely 'bottom-up' and 'top-down' engineering approaches. 'Top-down' engineering uses a conceptual framework of systematic design and engineering principles focused around the Design-Build-Test cycle and mathematical modelling. The 'bottom-up' approach involves the design and building of synthetic protocells using basic chemical and biochemical building blocks from scratch exploring the fundamental basis of living systems. Examples of cutting-edge applications designed using synthetic biology principles are presented, including: the production of novel, microbial synthesis of pharmaceuticals and fine chemical/the design and implementation of biosensors to detect infections and environmental waste. The book also describes the Internationally Genetically Engineered Machine (iGEM) competition, which brings together students and young researchers from around the world to carry out summer projects in synthetic biology. Finally, the primer includes a chapter on the ethical, legal and societal issues surrounding synthetic biology, illustrating the integration of social sciences into synthetic biology research. Final year undergraduates, postgraduates and established researchers interested in learning about the interdisciplinary field of synthetic biology will benefit from this up-to-date primer on synthetic biology. Contents:List of ContributorsPrefaceIntroduction to BiologyBasic Concepts in Engineering BiologyFoundational TechnologiesMinimal Cells and Synthetic LifeParts, Devices and SystemsModelling Synthetic Biology SystemsApplications of Designed Biological SystemsiGEMThe Social Impact of Synthetic BiologyAppendices:Proforma of Common Laboratory TechniquesGlossaryIndex Readership: Students, professionals, researchers in biotechnology and bioengineering. Keywords:Synthetic Biology;Engineering Principles;Biosociety;Biological Engineering;BiotechnologyKey Features:The book is written in a way that is accessible to students and researchers from different disciplinesThe authors are part of the internationally recognised Centre for Synthetic Biology and Innovation and are among the leaders in this field

This book presents the foundations of phylogeny estimation and technical material enabling researchers to develop improved computational methods.

Biologists are stepping up their efforts in understanding the biological processes that underlie disease pathways in the clinical contexts. This has resulted in a flood of biological and clinical data from genomic and protein sequences, DNA microarrays, protein interactions, biomedical images, to disease pathways and electronic health records. To exploit these data for discovering new knowledge that can be translated into clinical applications, there are fundamental data analysis difficulties that have to be overcome. Practical issues such as handling noisy and incomplete data, processing compute-intensive tasks, and integrating various data sources, are new challenges faced by biologists in the post-genome era. This book will cover the fundamentals of state-of-the-art data mining techniques which have been designed to handle such challenging data analysis problems, and demonstrate with real applications how biologists and clinical scientists can employ data mining to enable them to make meaningful observations and discoveries from a wide array of heterogeneous data from molecular biology to pharmaceutical and clinical domains. Contents:Sequence Analysis:Mining the Sequence Databases for Homology Detection: Application to Recognition of Functions of Trypanosoma brucei brucei Proteins and Drug Targets (G Ramakrishnan, V S Gowri, R Mudgal, N R Chandra and N Srinivasan)Identification of Genes and Their Regulatory Regions Based on Multiple Physical and Structural Properties of a DNA Sequence (Xi Yang, Nancy Yu Song and Hong Yan)Mining Genomic Sequence Data for Related Sequences Using Pairwise Statistical Significance (Yuhong Zhang and Yunbo Rao)Biological Network Mining:Indexing for Similarity Queries on Biological Networks (Günhan Gülsöy, Md Mahmudul Hasan, Yusuf Kavurucu and Tamer Kahveci)Theory and Method of Completion for a Boolean Regulatory Network Using Observed Data (Takeyuki Tamura and Tatsuya Akutsu)Mining Frequent Subgraph Patterns for Classifying Biological Data (Saeed Saleem)On the Integration of Prior Knowledge in the Inference of Regulatory Networks (Catharina Olsen, Benjamin Haibe-Kains, John Quackenbush and Gianluca Bontempi)Classification, Trend Analysis and 3D Medical Images:Classification and Its Application to Drug-Target Prediction (Jian-Ping Mei, Chee-Keong Kwoh, Peng Yang and Xiao-Li Li)Characterization and Prediction of Human Protein-Protein Interactions (Yi Xiong, Dan Szymanski and Daisuke Kihara)Trend Analysis (Wen-Chuan Xie, Miao He and Jake Yue Chen)Data Acquisition and Preprocessing on Three Dimensional Medical Images (Yuhua Jiao, Liang Chen and Jin Chen)Text Mining and Its Biomedical Applications:Text Mining in Biomedicine and Healthcare (Hong-Jie Dai, Chi-Yang Wu, Richard Tzong-Han Tsai and Wen-Lian Hsu)Learning to Rank Biomedical Documents with Only Positive and Unlabeled Examples: A Case Study (Mingzhu Zhu, Yi-Fang Brook Wu, Meghana Samir Vasavada and Jason T L Wang)Automated Mining of Disease-Specific Protein Interaction Networks Based on Biomedical Literature (Rajesh Chowdhary, Boris R Jankovic, Rachel V Stankovics, John A C Archer, Xiangliang Zhang, Xin Gao, Vladimir B Bajic) Readership: Students, professionals, those who perform biological, medical and bioinformatics research. Keywords:Healthcare;Data Mining;Biological Data Mining;Protein Interactions;Gene Regulation;Text Mining;Biological Literature Mining;Drug Discovery;Disease Network;Biological Network;Graph Mining;Sequence Analysis;Structure Analysis;Trend Analysis;Medical Images;Key Features:Each chapter of this book will include a section to introduce a specific class of data mining techniques, which will be written in a tutorial style so that even non-computational readers such as biologists and healthcare researchers can appreciate themThe book will disseminate the impact research results and best practices of data mining approaches to the cross-disciplinary researchers and practitioners from both the data mining disciplines and the life sciences domains. The authors of the book will be well-known data mining experts, bioinformaticians and cliniciansEach chapter will also provide a detailed description on how to apply the data mining techniques in real-world biological and clinical applications. Thus, readers of this book can easily appreciate the computational techniques and how they can be used to address their own research issues

Calculus, Modeling, Probability, and Dynamical Systems

Bioinformatics and Computational Biology

Synthetic Biology - a Primer (revised Edition)

Maps, Sequences and Genomes

Data Mining for Bioinformatics Applications

Hermaphroditism

Introducing Biological Rhythms is a primer that serves to introduce individuals to the area of biological rhythms. It describes the major characteristics and discusses the implications and applications of these rhythms, while citing scientific results and references. Also, the primer includes essays that provide in-depth historic and other background information for those interested in more specific topics or concepts. It covers a basic cross-section of the field of chronobiology clearly enough so that it can be understood by a novice, or an undergraduate student, but that it would also be sufficiently technical and detailed for the scientist.

Through this book, researchers and students will learn to use R for analysis of large-scale genomic data and how to create routines to automate the analytical steps. The philosophy behind the book is to start with real world raw datasets and perform all the analytical steps needed to reach final results. Though theory plays an important role, this is a practical book for graduate-level courses in bioinformatics and genomic analysis or for use in lab sessions. How to handle and manage high-throughput genomic data, create automated workflows and speed up analyses in R is also taught. A wide range of R packages useful for working with genomic data are illustrated with practical examples. The key topics covered are association studies, genomic prediction, estimation of population genetic parameters and diversity, gene expression analysis, functional annotation of results using publicly available databases and how to work efficiently in R with large genomic datasets. Important principles are demonstrated and illustrated through engaging examples which invite the reader to work with the provided datasets. Some methods that are discussed in this volume include: signatures of selection, population parameters (LD, FST, FIs, etc.) use of a genomic relationship matrix for population diversity studies; use of SNP data for parentage testing; snpBLUP and gBLUP for genomic prediction. Step-by-step, all the R code required for a genome-wide association study is shown: starting from raw SNP data, how to build databases to handle and manage the data, quality control and filtering measures, association testing and evaluation of results, through to identification and functional annotation of candidate genes. Similarly, gene expression analyses are shown using microarray and RNAseq data. At a time when genomic data is decidedly big, the skills from this book are critical. In recent years R has become the de facto tool for analysis of gene expression data, in addition to its prominent role in analysis of genomic data. Benefits to using R include the integrated development environment for analysis, flexibility and control of the analytic workflow.

Included topics are core components of advanced undergraduate and graduate classes in bioinformatics, genomics and statistical genetics. This book is also designed to be used by students in computer science and statistics who want to learn the practical aspects of genomic analysis without delving into algorithmic details. The datasets used throughout the book may be downloaded from the publisher 's website.

Artificial Intelligence in Bioinformatics: From Omics Analysis to Deep Learning and Network Mining reviews the main applications of the topic, from omics analysis to deep learning and network mining. The book includes a rigorous introduction on bioinformatics, also reviewing how methods are incorporated in tasks and processes. In addition, it presents methods and theory, including content for emergent fields such as Sentiment Analysis and Network Alignment. Other sections survey how Artificial Intelligence is exploited in bioinformatics applications, including sequence analysis, structure analysis, functional analysis, protein classification, omics analysis, biomarker discovery, integrative bioinformatics, protein interaction analysis, metabolic networks analysis, and much more. Bridges the gap between computer science and bioinformatics, combining an introduction to Artificial Intelligence methods with a systematic review of its applications in the life sciences Brings readers up-to-speed on current trends and methods in a dynamic and growing field Provides academic teachers with a complete resource, covering fundamental concepts as well as applications

At the heart of most high-throughput methods is the technique of polymerase chain reaction (PCR). This book focuses on primer design, which is critical to both the efficiency and the accuracy of the PCR. With intricate descriptions of basic approaches as well as specialized methods, "PCR Primer Design" is an exceptional reference for all those involved in studying the genome.

Handbook of Computational Molecular Biology

A Hypertextbook

A Primer on the Temporal Organization of Life, with Implications for Health, Society, Reproduction, and the Natural Environment

An Introduction to Perl for Biologists

An Introduction to Statistical Genetic Data Analysis

From Omics Analysis to Deep Learning and Network Mining

A Primer for Computational Biology aims to provide life scientists and students the skills necessary for research in a data-rich world. The text covers accessing and using remote servers via the command-line, writing programs and pipelines for data analysis, and provides useful vocabulary for interdisciplinary work. The book is broken into three parts: Introduction to Unix/Linux; The command-line is the "natural environment" of scientific computing, and this part covers a wide range of topics, including logging in, working with files and directories, installing programs and writing scripts, and the powerful "pipe" operator for file and data manipulation. Programming in Python: Python is both a premier language for learning and a common choice in scientific software development. This part covers the basic concepts in programming (data types, if-statements and loops, functions, loops and when to use them) as well as techniques for large-scale, multi-test analyses. Other topics include 53 classes and data visualization with ggplot2. Encyclopedia of Bioinformatics and Computational Biology: ABC of Bioinformatics combines elements of computer science, information technology, mathematics, statistics and biotechnology, providing the methodology and in silico solutions to mine biological data and processes. The book covers Theory, Topics and Applications, with a special focus on Integrative -omics and Systems Biology. The theoretical, methodological underpinnings of BC, including phylogeny are covered, as are more current areas of focus, such as translational bioinformatics, cheminformatics, and environmental informatics. Finally, Applications provide guidance for commonly asked questions. This major reference work spans basic and cutting-edge methodologies authored by leaders in the field, providing an invaluable resource for students, scientists, professionals in research institutes, and a broad swath of researchers in biotechnology and the biomedical and pharmaceutical industries. Brings together information from computer science, information technology, mathematics, statistics and biotechnology Written and reviewed by leading experts in the field, providing a unique and authoritative resource Focuses on the main theoretical and methodological concepts before expanding on specific topics and applications Includes interactive images, multimedia tools and crosslinking to further resources and databases

Bioinformatics for Everyone provides a brief overview on currently used technologies in the field of bioinformatics–interpreted as the application of information science to biology– including various online and offline bioinformatics tools and softwares. The book presents valuable knowledge in a simplified way to help students and researchers easily apply bioinformatics tools and approaches to their research and lab routines. Several protocols and case studies that can be reproduced by readers to suit their needs are also included. Explains the most relevant bioinformatics tools available in a didactic manner so that readers can easily apply them to their research Includes several protocols that can be used in different types of research work or in lab routines Discusses upcoming technologies and their impact on biological/biomedical sciences

In today's data driven biology, programming knowledge is essential in turning ideas into testable hypothesis. Based on the author's extensive experience, Python for Bioinformatics, Second Edition helps biologists get to grips with the basics of software development. Requiring no prior knowledge of programming-related concepts, the book focuses on the easy-to-use, yet powerful, Python computer language. This new edition is updated throughout to Python 3 and is designed not just to help scientists master the basics, but to do more in less time and in a reproducible way. New developments added in this edition include NoSQL databases, the Anaconda Python distribution, graphical libraries like Bokeh, and the use of Github for collaborative development.

A Field Guide for the Life Sciences (and Other Data-rich Pursuits)

Introduction to Computational Biology

The Gene Ontology Handbook

Python for Bioinformatics

Beginning Perl for Bioinformatics

Standard and Super-Resolution Bioimaging Data Analysis

This text is an engaging, practical, and lab-oriented introduction to R for students in the life sciences. This second edition has been revised to be current with the versions of R software released since the book's original publication. It features updated terminology, sources, and examples throughout.

Clings to the headlines of news coverage, this book examines the potential agents, delivery methods, and toxic and nontoxic effects of possible nuclear, biological, and chemical terrorist attacks. Providing countermeasures for governmental and emergency first-response teams, the book covers the impact of WMDs on public health, agriculture, and eco

What every neuroscientist should know about the mathematical modeling of excitable cells, presented at an introductory level.

Written especially for computer scientists, all necessary biology is explained. Presents new techniques on gene expression data mining, gene mapping for disease detection, and phylogenetic knowledge discovery.

Artificial Intelligence in Bioinformatics

Introducing Biological Rhythms

Biological Data Mining in Protein Interaction Networks

An Introduction to Designing Methods for Phylogeny Estimation

A Primer on the Biology, Ecology, and Evolution of Dual Sexuality

Bioinformatics for Everyone

A Primer in Biological Data Analysis and Visualization Using R

This textbook introduces fundamental concepts of bioinformatics and computational biology to the students and researchers in biology, medicine, veterinary science, agriculture, and bioengineering. The respective chapters provide detailed information on biological databases, sequence alignment, molecular evolution, next-generation sequencing, systems biology, and statistical computing using R. The book also presents a case-based discussion on clinical, veterinary, agricultural bioinformatics, and computational bioengineering for application-based learning in the respective fields. Further, it offers readers guidance on reconstructing and analysing biological networks and highlights computational methods used in systems medicine and genome-wide association mapping of diseases. Given its scope, this textbook offers an essential introductory book on bioinformatics and computational biology for undergraduate and graduate students in the life sciences, botany, zoology, physiology, biotechnology, bioinformatics, and genomic science as well as systems biology, bioengineering and the agricultural, and veterinary sciences.

Spiking neural networks (SNN) are biologically inspired computational models that represent and process information internally as trains of spikes. This monograph book presents the classical theory and applications of SNN, including original author's contribution to the art. The book introduces for the first time not only deep learning and deep knowledge representation in the human brain and in brain-inspired SNN, but takes that further to develop new types of AI systems, called in the book brain-inspired AI (BI-AI). BI-AI systems are illustrated on: cognitive brain data, including EEG, fMRI and DTI; audio-visual data; brain-computer interfaces; personalized modeling in bio-neuroinformatics; multisensory streaming data modelling in finance, environment and ecology; data compression; neuromorphic hardware implementation. Future directions, such as the integration of multiple modalities, such as quantum-, molecular- and brain information processing, is presented in the last chapter. The book is a research book for postgraduate students, researchers and practitioners across wider areas, including computer and information sciences, engineering, applied mathematics, bio- and neurosciences.

An introduction to the world of bioinformatics Massive increases in computing power and the ability to routinely sequence whole genomes of living organisms have begun to fundamentally alter our understanding of biology, medicine, and agriculture. At the intersection of the growing information and genomics revolutions sits bioinformatics, which uses modern computational power to reveal patterns in biological data sets, especially DNA, RNA, and protein sequences. Computational Biology: A Hypertextbook, by Scott Kelley and Dennis Didulo, provides a wonderful introduction for anyone who wants to learn the basics of bioinformatics. This book is more than a textbook because of the wealth of online ancillary materials and how the print and electronic components are integrated to form a complete educational resource. Aspects that make Computational Biology: A Hypertextbook a unique and valuable tool for teaching and learning bioinformatics include Clear explanations of the basic biology of DNA, RNA, and proteins and how the related bioinformatics algorithms work Extensive exercises that enable students to practice with the same bioinformatics applications that are used by scientists worldwide Tutorials, sample data sets, and interactive learning tools developed with teachers in mind and field-tested by hundreds of students Online tutorials and curated web links that are accurate (instead of frustrating!) and won't lead to dead ends Online resources that work on multiple platforms and electronic devices Computational Biology: A Hypertextbook is written in an accessible voice, punctuated with humor, and designed to significantly increase computational competencies. Biology and computer science undergraduate and graduate students will thoroughly enjoy learning from this unique hypertextbook, as will anyone with an interest in exploring this burgeoning topic.

Computational Phylogenetics

Geometric Morphometrics for Biologists

Mathematics for the Life Sciences

Time-Space, Spiking Neural Networks and Brain-Inspired Artificial Intelligence

Science and Technology of Terrorism and Counterterrorism

A Primer for Biologists

Mathematics for the Life Sciences provides present and future biologists with the mathematical concepts and tools needed to understand and use mathematical models and read advanced mathematical biology books. It presents mathematics in biological contexts, focusing on the central mathematical ideas, and providing detailed explanations. The author assumes no mathematics background beyond algebra and precalculus. Calculus is presented as a one-chapter primer that is suitable for readers who have not studied the subject before, as well as readers who have taken a calculus course and need a review. This primer is followed by a novel chapter on mathematical modeling that begins with discussions of biological data and the basic principles of modeling. The remainder of the chapter introduces the reader to topics in mechanistic modeling (deriving models from biological assumptions) and empirical modeling (using data to parameterize and select models). The modeling chapter contains a thorough treatment of key ideas and techniques that are often neglected in mathematics books. It also provides the reader with a sophisticated viewpoint and the essential background needed to make full use of the remainder of the book, which includes two chapters on probability and its applications to inferential statistics and three chapters on discrete and continuous dynamical systems. The biological content of the book is self-contained and includes many basic biology topics such as the genetic code, Mendelian genetics, population dynamics, predator-prey relationships, epidemiology, and immunology. The large number of problem sets include some drill problems along with a large number of case studies. The latter are divided into step-by-step problems and sorted into the appropriate section, allowing readers to gradually develop complete investigations from understanding the biological assumptions to a complete analysis.

Your research has generated gigabytes of data and now you need to analyse it. You hate using spreadsheets but it is all you know, so what else can you do? This book will transform how you work with large and complex data sets, teaching you powerful programming tools for slicing and dicing data to suit your needs in a fun and accessible style, this step-by-step guide will inspire and inform non-programmers about the essential aspects of Unix and Perl. It shows how, with just a little programming knowledge, you can write programs that could save you hours, or even days. No prior experience is required and new concepts are introduced using numerous code examples that you can try out for yourself. Going beyond the basics, the authors touch upon many broader topics that will help those new to programming, including debugging and how to write in a good programming style.

Biology is in the midst of a era yielding many significant discoveries and promising many more. Unique to this era is the exponential growth in the size of information-packed databases. Inspired by a pressing need to analyze that data, Introduction to Computational Biology explores a new area of expertise that emerged from this fertile field: the combination of biological and information sciences. This introduction describes the mathematical structure of biological data, especially from sequences and chromosomes. After a brief survey of molecular biology, it studies restriction maps of DNA, rough landmark maps of the underlying sequences, and clones and clone maps. It examines problems associated with reading DNA sequences and comparing sequences to finding common patterns. The author then considers that statistics of pattern counts in sequences, RNA secondary structure, and the inference of evolutionary history of related sequences. Introduction to Computational Biology exposes the reader to the fascinating structure of biological data and explains how to treat related combinatorial and statistical problems. Written to describe mathematical formulation and development, this book helps set the stage for even more, truly interdisciplinary work in biology.

R is the most widely used open-source statistical and programming environment for the analysis and visualization of biological data. Drawing on Gregg Hartvigsen's extensive experience teaching biostatistics and modeling biological systems, this text is an engaging, practical, and lab-oriented introduction to R for students in the life sciences. Underscoring the importance of R and RStudio in organizing, computing, and visualizing biological statistics and data, Hartvigsen guides readers through the processes of correctly entering and analyzing data and using R to visualize data using histograms, boxplots, barplots, scatterplots, and other common graph types. He covers testing data for normality, defining and identifying outliers, and working with non-normally distributed data. Students are introduced to common one- and two-sample tests as well as one- and two-way analysis of variance (ANOVA), correlation, and linear and nonlinear regression analyses. This volume also includes a section on advanced procedures and a chapter outlining algorithms and the art of programming using R. This second edition has been revised to be current with the versions of R software released since the book's original publication. It features updated terminology, sources, and examples throughout.

Primer to Analysis of Genomic Data Using R

Kernel Methods in Computational Biology

PCR Primer Design

Synthetic Biology — A Primer

Biological Data Mining and Its Applications in Healthcare

Data Mining for Bioinformatics Applications provides valuable information on the data mining methods have been widely used for solving real bioinformatics problems, including problem definition, data collection, data preprocessing, modeling, and validation. The text uses an example-based method to illustrate how to apply data mining techniques to solve real bioinformatics problems, containing 45 bioinformatics problems that have been investigated in recent research. For each example, the entire data mining process is described, ranging from data preprocessing to modeling and result validation. Provides valuable information on the data mining methods have been widely used for solving real bioinformatics problems Uses an example-based method to illustrate how to apply data mining techniques to solve real bioinformatics problems Contains 45 bioinformatics problems that have been investigated in recent research

This book covers several of the statistical concepts and data analytic skills needed to succeed in data-driven life science research. The authors proceed from relatively basic concepts related to computed p-values to advanced topics related to analyzing highthroughput data. They include the R code that performs this analysis and connect the lines of code to the statistical and mathematical concepts explained.

This book provides a practical and self-contained overview of the Gene Ontology (GO), the leading project to organize biological knowledge on genes and their products across genomic resources. Written for biologists and bioinformaticians, it covers the state-of-the-art of how GO annotations are made, how they are evaluated, and what sort of analyses can and cannot be done with the GO. In the spirit of the Methods in Molecular Biology book series, there is an emphasis throughout the chapters on providing practical guidance and troubleshooting advice. Authoritative and accessible, The Gene Ontology Handbook serves non-experts as well as seasoned GO users as a thorough guide to this powerful knowledge system. This work was published by Saint Philip Street Press pursuant to a Creative Commons license permitting commercial use. All rights not granted by the work's license are retained by the author or authors.

""The goal of this book is to disseminate research results and best practices from cross-disciplinary researchers and practitioners interested in, and working on bioinformatics, data mining, and proteomics"--Provided by publisher.

UNIX and Perl to the Rescue!

A Primer for Librarians

Cellular Biophysics and Modeling

Bioinformatics for Geneticists

Practical Computing for Biologists

ABC of Bioinformatics

The enormous complexity of biological systems at the molecular level must be answered with powerful computational methods. Computational biology is a young field, but has seen rapid growth and advancement over the past few decades. Surveying the progress made in this multidisciplinary field, the Handbook of Computational Molecular Biology of the first edition of Geometric Morphometrics for Biologists has been the primary resource for teaching modern geometric methods of shape analysis to biologists who have a stronger background in biology than in multivariate statistics and matrix algebra. These geometric methods are appealing to biologists who approach the study of shape from a variety of perspectives, from clinical to evolutionary, because they incorporate the geometry of organisms throughout the data analysis. The second edition of this book retains the emphasis on accessible explanations, and the copious illustrations and examples of the first, updating the treatment of both theory and practice. The second edition represents the current state-of-the-art and adds new examples and summarizes recent literature, as well as provides an overview of new software and step-by-step guidance through details of carrying out the analyses. Contains updated coverage of methods, especially for sampling complex curves and 3D forms and a new chapter on applications of geometric morphometrics to forensics Offers a reorganization of chapters to streamline learning basic concepts Presents detailed instructions for conducting analyses with freely available, easy to use software Provides numerous illustrations, including graphical presentations of important theoretical concepts and demonstrations of alternative approaches to presenting results

To help with the increasingly large data sets that many scientists deal with, this book illustrates how to use many freely available computing tools to work more powerfully and effectively. The book was born out of the authors' experiences developing tools for their research and to fix other biologist's computational problems.

A comprehensive introduction to modern applied statistical genetic data analysis, accessible to those without a background in molecular biology or genetics. Human genetic research is now relevant beyond biology, epidemiology, and the medical sciences, with applications in such fields as psychology, psychiatry, statistics, demography, sociology, and economics. With advances in computing power, the availability of data, and new techniques, it is now possible to integrate large-scale molecular genetic information into research across a broad range of topics. This book offers the first comprehensive introduction to modern applied statistical genetic data analysis that covers theory, data preparation, and analysis of molecular genetic data, with hands-on computer exercises. It is accessible to students and researchers in any empirically oriented medical, biological, or social science discipline; a background in molecular biology or genetics is not required. The book-first provides foundations for statistical genetic data analysis, including a survey of fundamental concepts, primers on statistics and human evolution, and an introduction to polygenic scores. It then covers the practicalities of working with genetic data, discussing such topics as analytical challenges and data management. Finally, the book presents applications and advanced topics, including polygenic score and gene-environment interaction applications, Mendelian Randomization and instrumental variables, and ethical issues. The software and data used in the book are freely available and can be found on the book's website.

Data Analysis for the Life Sciences with R

Densifying eResearch: A Primer for Librarians

A Primer

A Primer in Biological Data Analysis and Visualization Using R

Analysis of Biological Data

Simple data analysis for biologists

A comprehensive guide to the art and science of bioimaging data acquisition, processing and analysis Standard and Super-Resolution Bioimaging Data Analysis gets newcomers to bioimage data analysis quickly up to speed on the mathematics, statistics, computing hardware and acquisition technologies required to correctly process and document data. The past quarter century has seen remarkable progress in the field of light microscopy for biomedical science, with new imaging technologies coming on the market at an almost annual basis. Most of the data generated by these systems is image-based, and there is a significant increase in the content and throughput of these imaging systems. This, in turn, has resulted in a shift in the literature on biomedical research from descriptive to highly-quantitative. Standard and Super-Resolution Bioimaging Data Analysis satisfies the demand among students and researcher scientists for introductory guides to the tools for parsing and processing image data. Extremely well illustrated and including numerous examples, it clearly and accessibly explains what image data is and how to process and document it, as well as the current resources and standards in the field. A comprehensive guide to the tools for parsing and processing image data and the resources and industry standards for the biological and biomedical sciences Takes a practical approach to image analysis to assist scientists in ensuring scientific data are robust and reliable Covers fundamental principles in such a way as to give beginners a sound scientific base upon which to build Ideally suited for advanced students having only limited knowledge of the mathematics, statistics and computing required for image data analysis An entry-level text written for students and practitioners in the bioscience community. Standard and Super-Resolution Bioimaging Data Analysis de-mythologises the vast array of image analysis modalities which have come online over the past decade while schooling beginners in bioimaging principles, mathematics, technologies and standards. eResearch presents new challenges in managing data. This book explains to librarians and other information specialists what eResearch is, how it impacts library services and collections, and how to contribute to eResearch activities at their parent institutions. • Provides librarians and other information professionals with a clear understanding of what eResearch is and how it impacts library mission, services, and collections • Defines and explains key eResearch terms and concepts • Describes eResearch library initiatives and identifies best practices • Identifies potential eResearch activities areas such as providing assistance with data management plans, depositing data, collecting and disseminating data sets, collaborating with faculty on eResearch projects, performing research consultations, and creating train-the-trainer

A Primer on Molecular Biology. A Primer on Kernel Methods. Support Vector Machine Applications in Computational Biology. Inexact Matching String Kernels for Protein Classification. Fast Kernels for String and Tree Matching. Local Alignment Kernels for Biological Sequences. Kernels for Graphs. Diffusion Kernels. A Kernel for Protein Secondary Structure Prediction. Heterogeneous Data Comparison and Gene Selection with Kernel Canonical Correlation Analysis. Kernel-Based Integration of Genomic Data Using Semidefinite Programming. Protein Classification via Kernel Matrix Completion. Accurate Splice Site Detection for Caenorhabditis elegans. Gene Expression Analysis: Joint Feature Selection and Classifier Design. Gene Selection for Microarray Data. With its highly developed capacity to detect patterns in data, Perl has become one of the most popular languages for biological data analysis. But if you're a biologist with little or no programming experience, starting out in Perl can be a challenge. Many biologists have a difficult time learning how to apply the language to bioinformatics. The most popular Perl programming books are often too theoretical and too focused on computer science for a non-programming biologist who needs to solve very specific problems.Beginning Perl for Bioinformatics is designed to get you quickly over the Perl language barrier by approaching programming as an important new laboratory skill, revealing Perl programs and techniques that are immediately useful in the lab. Each chapter focuses on solving a particular bioinformatics problem or class of problems, starting with the simplest and increasing in complexity as the book progresses. Each chapter includes programming exercises and teaches bioinformatics by showing and modifying programs that deal with various kinds of practical biological problems. By the end of the book you'll have a solid understanding of Perl basics, a collection of programs for such tasks as parsing BLAST and GenBank, and the skills to take on more advanced bioinformatics programming. Some of the later chapters focus in greater detail on specific bioinformatics topics. This book is suitable for use as a classroom textbook, for self-study, and as a reference.The book covers: Programming basics and working with DNA sequences and strings Debugging your code Simulating gene mutations using random number generators Regular expressions and finding motifs in data Arrays, hashes, and relational databases Regular expressions and restriction maps Using Perl to parse PDB records, annotations in GenBank, and BLAST output

Revised Edition

Encyclopedia of Bioinformatics and Computational Biology

Computational Biology

A Practical Biology of Excitable Cells

A Primer for Computational Biology

Data Mining in Bioinformatics