Bayesian Methods In Structural Bioinformatics Statistics For Biology And Health

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Bayesian Analysis for the Social Sciences - Simon Jackman 2009-10-27
Bayesian methods are increasingly being used in the social sciences, as the problems encountered lend themselves so naturally to the subjective qualities of Bayesian methodology. This book provides an accessible introduction to Bayesian methods, tailored specifically for social science students. It contains lots of real examples from political science, psychology, sociology, and economics, exercises in all chapters, and detailed descriptions of all the key concepts, without assuming any background in statistics beyond a first course. It features examples of how to implement the methods using WinBUGS – the most-widely used Bayesian analysis software in the world – and R – an open-source statistical software. The book is supported by a Website featuring WinBUGS and R code, and data sets.

Structural Bioinformatics - Jenny Gu 2009-03-16
Structural Bioinformatics was the first major effort to show the application of the principles and basic knowledge of the larger field of bioinformatics to questions focusing on macromolecular structure, such as the prediction of protein structure and how proteins carry out cellular functions, and how the application of bioinformatics to these life science issues can improve healthcare by accelerating drug discovery and development. Designed primarily as a reference, the first edition nevertheless saw widespread use as a textbook in graduate and undergraduate university courses dealing with the theories and associated algorithms, resources, and tools used in the analysis, prediction, and theoretical underpinnings of DNA, RNA, and proteins. This new edition contains not only thorough updates of the advances in structural bioinformatics since publication of the first edition, but also features eleven new chapters dealing with frontier areas of high scientific impact, including: sampling and search techniques; use of mass spectrometry; genome functional annotation; and much more. Offering detailed coverage for practitioners while remaining accessible to the novice, Structural Bioinformatics, Second Edition is a valuable resource and an excellent textbook for a range of readers in the bioinformatics and advanced biology fields. Praise for the previous edition: "This book is a gold mine of fundamental and practical information in an area not previously well represented in book form." —Biochemistry and Molecular Education "... destined to become a classic reference work for workers at all levels in structural bioinformatics...recommended with great enthusiasm for educators, researchers, and graduate students." —BAMBED "...a useful and timely summary of a rapidly expanding field." —Nature Structural Biology "...a terrific job in this timely creation of a compilation of articles that appropriately addresses this issue." —Briefings in Bioinformatics

Bayesian Analysis with Python - Osvaldo Martin 2016-11-25
Unleash the power and flexibility of the Bayesian framework About This Book Simplify the Bayes process for solving complex statistical problems using Python; Tutorial guide that will take the you through the journey of Bayesian analysis with the help of sample problems and practice exercises; Learn how and when to use Bayesian analysis in your applications with this guide. Who This Book Is For Students, researchers and data scientists who wish to learn Bayesian data analysis with Python and implement probabilistic models in their day to day projects. Programming experience with Python is essential. No previous statistical knowledge is assumed. What You Will Learn Understand the essentials Bayesian concepts from a

practical point of view Learn how to build probabilistic models using the Python library PyMC3 Acquire the skills to sanity-check your models and modify them if necessary Add structure to your models and get the advantages of hierarchical models Find out how different models can be used to answer different data analysis questions When in doubt, learn to choose between alternative models. Predict continuous target outcomes using regression analysis or assign classes using logistic and softmax regression. Learn how to think probabilistically and unleash the power and flexibility of the Bayesian framework In Detail The purpose of this book is to teach the main concepts of Bayesian data analysis. We will learn how to effectively use PyMC3, a Python library for probabilistic programming, to perform Bayesian parameter estimation, to check models and validate them. This book begins presenting the key concepts of the Bayesian framework and the main advantages of this approach from a practical point of view. Moving on, we will explore the power and flexibility of generalized linear models and how to adapt them to a wide array of problems, including regression and classification. We will also look into mixture models and clustering data, and we will finish with advanced topics like non-parametrics models and Gaussian processes. With the help of Python and PyMC3 you will learn to implement, check and expand Bayesian models to solve data analysis problems. Style and approach Bayes algorithms are widely used in statistics, machine learning, artificial intelligence, and data mining. This will be a practical guide allowing the readers to use Bayesian methods for statistical modelling and analysis using Python.

Bayesian Methods in Structural Bioinformatics - Thomas Hamelryck 2012-03-23
This book is an edited volume, the goal of which is to provide an overview of the current state-of-the-art in statistical methods applied to problems in structural bioinformatics (and in particular protein structure prediction, simulation, experimental structure determination and analysis). It focuses on statistical methods that have a clear interpretation in the framework of statistical physics, rather than ad hoc, black box methods based on neural networks or support vector machines. In addition, the emphasis is on methods that deal with biomolecular structure in atomic detail. The book is highly accessible, and only assumes background knowledge on protein structure, with a minimum of mathematical knowledge. Therefore, the book includes introductory chapters that contain a solid introduction to key topics such as Bayesian statistics and concepts in machine learning and statistical physics.

Applied Bayesian Modelling - Peter Congdon 2014-05-23
This book provides an accessible approach to Bayesian computing and data analysis, with an emphasis on the interpretation of real data sets. Following in the tradition of the successful first edition, this book aims to make a wide range of statistical modeling applications accessible using tested code that can be readily adapted to the reader's own applications. The second edition has been thoroughly reworked and updated to take account of advances in the field. A new set of worked examples is included. The novel aspect of the first edition was the coverage of statistical modeling using WinBUGS and OPENBUGS. This feature continues in the new edition along with examples using R to broaden appeal and for completeness of coverage.

Bayesian Modeling and Computation in Python - Osvaldo A. Martin 2021-12-28

Bayesian Modeling and Computation in Python aims to help beginner Bayesian practitioners to become intermediate modelers. It uses a hands on approach with PyMC3, Tensorflow Probability, ArviZ and other libraries focusing on the practice of applied statistics with references to the underlying mathematical theory. The book starts with a refresher of the Bayesian Inference concepts. The second chapter introduces modern methods for Exploratory Analysis of Bayesian Models. With an understanding of these two fundamentals the subsequent chapters talk through various models including linear regressions, splines, time series, Bayesian additive regression trees. The final chapters include Approximate Bayesian Computation, end to end case studies showing how to apply Bayesian modelling in different settings, and a chapter about the internals of probabilistic programming languages. Finally the last chapter serves as a reference for the rest of the book by getting closer into mathematical aspects or by extending the discussion of certain topics. This book is written by contributors of PyMC3, ArviZ, Bambi, and Tensorflow Probability among other libraries.

Object Oriented Data Analysis - J. S. Marron 2021-11-18
Object Oriented Data Analysis is a framework that facilitates inter-disciplinary research through new terminology for discussing the often many possible approaches to the analysis of complex data. Such data are naturally arising in a wide variety of areas. This book aims to provide ways of thinking that enable the making of sensible choices. The main points are illustrated with many real data examples, based on the authors' personal experiences, which have motivated the invention of a wide array of analytic methods. While the mathematics go far beyond the usual in statistics (including differential geometry and even topology), the book is aimed at accessibility by graduate students. There is deliberate focus on ideas over mathematical formulas. J. S. Marron is the Amos Hawley Distinguished Professor of Statistics, Professor of Biostatistics, Adjunct Professor of Computer Science, Faculty Member of the Bioinformatics and Computational Biology Curriculum and Research Member of the Lineberger Cancer Center and the Computational Medicine Program, at the University of North Carolina, Chapel Hill. Ian L. Dryden is a Professor in the Department of Mathematics and Statistics at Florida International University in Miami, has served as Head of School of Mathematical Sciences at the University of Nottingham, and is joint author of the acclaimed book Statistical Shape Analysis.

Experiments and Simulations: A Pas de Deux to Unravel Biological Function - Massimiliano Bonomi 2022-01-19

Advance in Structural Bioinformatics - Dongqing Wei 2014-11-11
This text examines in detail mathematical and physical modeling, computational methods and systems for obtaining and analyzing biological structures, using pioneering research cases as examples. As such, it emphasizes programming and problem-solving skills. It provides information on structure bioinformatics at various levels, with individual chapters covering introductory to advanced aspects, from fundamental methods and guidelines on acquiring and analyzing genomics and proteomics sequences, the structures of protein, DNA and RNA, to the basics of physical simulations and methods for conformation searches. This book will be of immense value to researchers and students in the fields of bioinformatics, computational biology and chemistry. Dr. Dongqing Wei is a Professor at the Department of Bioinformatics and Biostatistics, College of Life Science and Biotechnology, Shanghai Jiaotong University, Shanghai, China. His research interest is in the general area of structural bioinformatics.

Bayesian Methods in Structural Bioinformatics - Thomas Hamelryck 2014-04-13
This book is an edited volume, the goal of which is to provide an overview of the current state-of-the-art in statistical methods applied to problems in structural bioinformatics (and in particular protein structure prediction, simulation, experimental structure determination and analysis). It focuses on statistical methods that have a clear interpretation in the framework of statistical physics, rather than ad hoc, black box methods based on neural networks or support vector machines. In addition, the emphasis is on methods that deal with biomolecular structure in atomic detail. The book is highly accessible, and only assumes background knowledge on protein structure, with a minimum of mathematical knowledge. Therefore, the book includes introductory chapters that contain a solid introduction to key topics such as Bayesian statistics and concepts in machine learning and statistical physics.

Structural Equation Modeling - Sik-Yum Lee 2007-04-04
Winner of the 2008 Ziegel Prize for outstanding new book of the year Structural equation modeling (SEM) is a powerful multivariate method allowing the evaluation of a series of simultaneous hypotheses about the impacts of latent and manifest variables on other variables, taking measurement errors into account. As SEMs have grown in popularity in recent years, new models and statistical methods have been developed for more accurate analysis of more complex data. A Bayesian approach to SEMs allows the use of prior information resulting in improved parameter estimates, latent variable estimates, and statistics for model comparison, as well as offering more reliable results for smaller samples. Structural Equation Modeling introduces the Bayesian approach to SEMs, including the selection of prior distributions and data augmentation, and offers an overview of the subject's recent advances. Demonstrates how to utilize powerful statistical computing tools, including the Gibbs sampler, the Metropolis-Hasting algorithm, bridge sampling and path sampling to obtain the Bayesian results. Discusses the Bayes factor and Deviance Information Criterion (DIC) for model comparison. Includes coverage of complex models, including SEMs with ordered categorical variables, and dichotomous variables, nonlinear SEMs, two-level SEMs, multisample SEMs, mixtures of SEMs, SEMs with missing data, SEMs with variables from an exponential family of distributions, and some of their combinations. Illustrates the methodology through simulation studies and examples with real data from business management, education, psychology, public health and sociology. Demonstrates the application of the freely available software WinBUGS via a supplementary website featuring computer code and data sets. Structural Equation Modeling: A Bayesian Approach is a multi-disciplinary text ideal for researchers and students in many areas, including: statistics, biostatistics, business, education, medicine, psychology, public health and social science.

Handbook of Sport Psychology - Gershon Tenenbaum 2020-03-31
The fourth edition of a classic, leading resource for the field of sport, exercise, and performance psychology Now expanded to two volumes, and featuring a wealth of new chapters from highly respected scholars in the field, this all-new edition of the Handbook of Sports Psychology draws on an international roster of experts and scholars in the field who have assembled state-of-the-art knowledge into this thorough, well-rounded, and accessible volume. Endorsed by the International Society of Sport Psychology, it represents an invaluable source of theoretical and practical information on our understanding of the role of psychology in sport, exercise, and performance—and how that understanding can be applied in order to improve real-world outcomes. Presented in eight parts, the Handbook of Sports Psychology, 4th Edition adds new material on emerging areas such as mindfulness, brain mapping, self-consciousness, and mental toughness, and covers special topics such as gender and cultural diversity, athletes with disabilities, and alcohol and drug use in sports. In addition, it covers classic topics such as what motivates an athlete to perform; why do some choke under pressure; how do top performers handle leadership roles; what does one do to mentally train; how an athlete deals with injury; and much more. Fourth edition of the most influential reference work for the field of sport psychology New coverage includes mindfulness in sport and exercise psychology, ethics, mental toughness, sport socialization, and making use of brain technologies in practice Endorsed by the International Society of Sport Psychology (ISSP) Handbook of Sports Psychology, 4th Edition is an indispensable resource for any student or professional interested in the field of sports psychology.

Geometry Driven Statistics - Ian L. Dryden 2015-09-28
A timely collection of advanced, original material in the area of statistical methodology motivated by geometric problems, dedicated to the influential work of Kanti V. Mardia This volume celebrates Kanti V. Mardia's long and influential career in statistics. A common theme unifying much of Mardia's work is the importance of geometry in statistics, and to highlight the areas emphasized in his research this book brings together 16 contributions from high-profile researchers in the field. Geometry Driven Statistics covers a wide range of application areas including directional data, shape analysis, spatial data, climate science, fingerprints, image analysis, computer vision and bioinformatics. The book will appeal to statisticians and others with an interest in data motivated by geometric considerations. Summarizing the state of the art, examining some new developments and presenting a vision for the future, Geometry Driven Statistics will enable the reader to broaden knowledge of important research areas in statistics and gain a new appreciation of the work and influence of Kanti V. Mardia.

Hybrid Biomolecular Modeling - Slavica Jonic 2019-01-24

Models of biomolecular structure and dynamics are often obtained by combining simulation or prediction approaches (e.g., comparative modeling, Molecular Dynamics (MD) simulations, Normal Mode Analysis (NMA), etc.) with experimental approaches (e.g., Nuclear Magnetic Resonance (NMR), X-ray crystallography, Small-Angle X-ray Scattering (SAXS), Electron Microscopy (EM), etc.). Such hybrid modeling extends the capabilities of experimental techniques, by enriching structural information and facilitating dynamics studies of biomolecules. This eBook contains articles on methodological developments, applications, and challenges of hybrid biomolecular modeling that have been collected in the framework of the Frontiers Research Topic entitled "Hybrid Biomolecular Modeling".

Directional Statistics for Innovative Applications - Ashis SenGupta 2022-06-15

In commemoration of the bicentennial of the birth of the "lady who gave the rose diagram to us", this special contributed book pays a statistical tribute to Florence Nightingale. This book presents recent phenomenal developments, both in rigorous theory as well as in emerging methods, for applications in directional statistics, in 25 chapters with contributions from 65 renowned researchers from 25 countries. With the advent of modern techniques in statistical paradigms and statistical machine learning, directional statistics has become an indispensable tool. Ranging from data on circles to that on the spheres, tori and cylinders, this book includes solutions to problems on exploratory data analysis, probability distributions on manifolds, maximum entropy, directional regression analysis, spatio-directional time series, optimal inference, simulation, statistical machine learning with big data, and more, with their innovative applications to emerging real-life problems in astro-statistics, bioinformatics, crystallography, optimal transport, statistical process control, and so on.

Big Data Analytics in Bioinformatics and Healthcare - Wang, Baoying 2014-10-31

As technology evolves and electronic data becomes more complex, digital medical record management and analysis becomes a challenge. In order to discover patterns and make relevant predictions based on large data sets, researchers and medical professionals must find new methods to analyze and extract relevant health information. Big Data Analytics in Bioinformatics and Healthcare merges the fields of biology, technology, and medicine in order to present a comprehensive study on the emerging information processing applications necessary in the field of electronic medical record management. Complete with interdisciplinary research resources, this publication is an essential reference source for researchers, practitioners, and students interested in the fields of biological computation, database management, and health information technology, with a special focus on the methodologies and tools to manage massive and complex electronic information.

Essential Computing Skills for Biologists - Wang Ziling 2013-10-10

This is a handbook of methods and protocols for biologists. It aimed at undergraduate, graduate students and researchers originally trained in biological or medical sciences who need to know how to access the data archives of genomes, proteins, metabolites, gene expression profiles and the questions these data and tools can answer. For each chapter, the conceptual and experimental background is provided, together with specific guidelines for handling raw data, including preprocessing and analysis. The content is structured into three parts. Part one introduces basic knowledge about popular bioinformatics tools, databases and web resources. Part two presents examples of omics bioinformatics applications. Part three provides basic statistical analysis skills and programming skills needed to handle and analyze omics datasets.

Medical Imaging: Concepts, Methodologies, Tools, and Applications - Management Association, Information Resources 2016-07-18

Medical imaging has transformed the ways in which various conditions, injuries, and diseases are identified, monitored, and treated. As various types of digital visual representations continue to advance and improve, new opportunities for their use in medical practice will likewise evolve. Medical Imaging: Concepts, Methodologies, Tools, and Applications presents a compendium of research on digital imaging technologies in a variety of healthcare settings. This multi-volume work contains practical examples of implementation, emerging trends, case studies, and technological innovations essential for using imaging technologies for making medical decisions. This comprehensive publication is an essential resource for medical practitioners, digital imaging technologists, researchers, and medical students.

Encyclopedia of Biopharmaceutical Statistics - Four Volume Set - Shein-Chung Chow 2018-09-03

Since the publication of the first edition in 2000, there has been an explosive growth of literature in biopharmaceutical research and development of new medicines. This encyclopedia (1) provides a comprehensive and unified presentation of designs and analyses used at different stages of the drug development process, (2) gives a well-balanced summary of current regulatory requirements, and (3) describes recently developed statistical methods in the pharmaceutical sciences. Features of the Fourth Edition: 1. 78 new and revised entries have been added for a total of 308 chapters and a fourth volume has been added to encompass the increased number of chapters. 2. Revised and updated entries reflect changes and recent developments in regulatory requirements for the drug review/approval process and statistical designs and methodologies. 3. Additional topics include multiple-stage adaptive trial design in clinical research, translational medicine, design and analysis of biosimilar drug development, big data analytics, and real world evidence for clinical research and development. 4. A table of contents organized by stages of biopharmaceutical development provides easy access to relevant topics. About the Editor: Shein-Chung Chow, Ph.D. is currently an Associate Director, Office of Biostatistics, U.S. Food and Drug Administration (FDA). Dr. Chow is an Adjunct Professor at Duke University School of Medicine, as well as Adjunct Professor at Duke-NUS, Singapore and North Carolina State University. Dr. Chow is the Editor-in-Chief of the Journal of Biopharmaceutical Statistics and the Chapman & Hall/CRC Biostatistics Book Series and the author of 28 books and over 300 methodology papers. He was elected Fellow of the American Statistical Association in 1995.

Bayesian Analysis with Python - Osvaldo Martin 2018-12-26

Bayesian modeling with PyMC3 and exploratory analysis of Bayesian models with ArviZ Key FeaturesA step-by-step guide to conduct Bayesian data analyses using PyMC3 and ArviZA modern, practical and computational approach to Bayesian statistical modelingA tutorial for Bayesian analysis and best practices with the help of sample problems and practice exercises.Book Description The second edition of Bayesian Analysis with Python is an introduction to the main concepts of applied Bayesian inference and its practical implementation in Python using PyMC3, a state-of-the-art probabilistic programming library, and ArviZ, a new library for exploratory analysis of Bayesian models. The main concepts of Bayesian statistics are covered using a practical and computational approach. Synthetic and real data sets are used to introduce several types of models, such as generalized linear models for regression and classification, mixture models, hierarchical models, and Gaussian processes, among others. By the end of the book, you will have a working knowledge of probabilistic modeling and you will be able to design and implement Bayesian models for your own data science problems. After reading the book you will be better prepared to delve into more advanced material or specialized statistical modeling if you need to. What you will learnBuild probabilistic models using the Python library PyMC3 Analyze probabilistic models with the help of ArviZ Acquire the skills required to sanity check models and modify them if necessary Understand the advantages and caveats of hierarchical modelsFind out how different models can be used to answer different data analysis questionsCompare models and choose between alternative onesDiscover how different models are unified from a probabilistic perspective Think probabilistically and benefit from the flexibility of the Bayesian frameworkWho this book is for If you are a student, data scientist, researcher, or a developer looking to get started with Bayesian data analysis and probabilistic programming, this book is for you. The book is introductory so no previous statistical knowledge is required, although some experience in using Python and NumPy is expected.

Directional Estimation for Robotic Beating Heart Surgery - Kurz, Gerhard 2015-05-26

Case Studies in Bayesian Statistical Modelling and Analysis - Clair L. Alston 2012-10-10

Provides an accessible foundation to Bayesian analysis usingreal world models This book aims to present an introduction to Bayesian modellingand computation, by considering real case studies drawn fromdiverse fields spanning ecology, health, genetics and finance. Eachchapter comprises a description of the problem, the correspondingmodel, the computational method, results and inferences as well asthe issues that arise in the implementation of theseapproaches. Case Studies in Bayesian Statistical Modelling andAnalysis: Illustrates how to do Bayesian analysis in a clear and concisemanner using real-world problems. Each

chapter focuses on a real-world problem and describes the way in which the problem may be analysed using Bayesian methods. Features approaches that can be used in a wide area of application, such as, health, the environment, genetics,information science, medicine, biology, industry and remotesensing. Case Studies in Bayesian Statistical Modelling andAnalysis is aimed at statisticians, researchers andpractitioners who have some expertise in statistical modelling andanalysis, and some understanding of the basics of Bayesianstatistics, but little experience in its application. Graduatestudents of statistics and biostatistics will also find this bookbeneficial.

The Oxford Handbook of Applied Bayesian Analysis - Anthony O' Hagan 2010-03-18
Bayesian analysis has developed rapidly in applications in the last two decades and research in Bayesian methods remains dynamic and fast-growing. Dramatic advances in modelling concepts and computational technologies now enable routine application of Bayesian analysis using increasingly realistic stochastic models, and this drives the adoption of Bayesian approaches in many areas of science, technology, commerce, and industry. This Handbook explores contemporary Bayesian analysis across a variety of application areas. Chapters written by leading exponents of applied Bayesian analysis showcase the scientific ease and natural application of Bayesian modelling, and present solutions to real, engaging, societally important and demanding problems. The chapters are grouped into five general areas: Biomedical & Health Sciences; Industry, Economics & Finance; Environment & Ecology; Policy, Political & Social Sciences; and Natural & Engineering Sciences, and Appendix material in each touches on key concepts, models, and techniques of the chapter that are also of broader pedagogic and applied interest.

Classification and Data Mining - Antonio Giusti 2012-12-18
This volume contains both methodological papers showing new original methods, and papers on applications illustrating how new domain-specific knowledge can be made available from data by clever use of data analysis methods. The volume is subdivided in three parts: Classification and Data Analysis; Data Mining; and Applications. The selection of peer reviewed papers had been presented at a meeting of classification societies held in Florence, Italy, in the area of "Classification and Data Mining".

Bioinformatics in Human Health and Heredity - Ranajit Chakraborty 2012-10-03
The field of statistics not only affects all areas of scientific activity, but also many other matters such as public policy. It is branching rapidly into so many different subjects that a series of handbooks is the only way of comprehensively presenting the various aspects of statistical methodology, applications, and recent developments. The Handbook of Statistics, a series of self-contained reference books. Each volume is devoted to a particular topic in statistics with Volume 28 dealing with bioinformatics. Every chapter is written by prominent workers in the area to which the volume is devoted. The series is addressed to the entire community of statisticians and scientists in various disciplines who use statistical methodology in their work. At the same time, special emphasis is placed on applications-oriented techniques, with the applied statistician in mind as the primary audience. Comprehensively presents the various aspects of statistical methodology Discusses a wide variety of diverse applications and recent developments Contributors are internationally renowned experts in their respective areas

50 years of Statistical Physics in Mexico: Development, State of the Art and Perspectives - Ramon Castañeda-Priego 2021-09-13

Applied Directional Statistics - Christophe Ley 2018-09-03
This book collects important advances in methodology and data analysis for directional statistics. It is the companion book of the more theoretical treatment presented in Modern Directional Statistics (CRC Press, 2017). The field of directional statistics has received a lot of attention due to demands from disciplines such as life sciences or machine learning, the availability of massive data sets requiring adapted statistical techniques, and technological advances. This book covers important progress in bioinformatics, biology, astrophysics, oceanography, environmental sciences, earth sciences, machine learning and social sciences.

Bayesian Modeling in Bioinformatics - Dipak K. Dey 2019-10-17
Bayesian Modeling in Bioinformatics discusses the development and application of Bayesian statistical methods for the analysis of high-throughput bioinformatics data arising from problems in molecular and structural biology and disease-related medical research, such as cancer. It presents a broad overview of

statistical inference, clustering, and classification problems in two main high-throughput platforms: microarray gene expression and phylogenic analysis. The book explores Bayesian techniques and models for detecting differentially expressed genes, classifying differential gene expression, and identifying biomarkers. It develops novel Bayesian nonparametric approaches for bioinformatics problems, measurement error and survival models for cDNA microarrays, a Bayesian hidden Markov modeling approach for CGH array data, Bayesian approaches for phylogenic analysis, sparsity priors for protein-protein interaction predictions, and Bayesian networks for gene expression data. The text also describes applications of mode-oriented stochastic search algorithms, in vitro to in vivo factor profiling, proportional hazards regression using Bayesian kernel machines, and QTL mapping. Focusing on design, statistical inference, and data analysis from a Bayesian perspective, this volume explores statistical challenges in bioinformatics data analysis and modeling and offers solutions to these problems. It encourages readers to draw on the evolving technologies and promote statistical development in this area of bioinformatics.

Encyclopedia of Bioinformatics and Computational Biology - 2018-08-21
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 BCB, 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

Bayesian Modeling in Bioinformatics - Dipak K. Dey 2010-09-03
Bayesian Modeling in Bioinformatics discusses the development and application of Bayesian statistical methods for the analysis of high-throughput bioinformatics data arising from problems in molecular and structural biology and disease-related medical research, such as cancer. It presents a broad overview of statistical inference, clustering, and c

Statistical Shape Analysis - Ian L. Dryden 2016-06-28
A thoroughly revised and updated edition of this introduction to modern statistical methods for shape analysis Shape analysis is an important tool in the many disciplines where objects are compared using geometrical features. Examples include comparing brain shape in schizophrenia; investigating protein molecules in bioinformatics; and describing growth of organisms in biology. This book is a significant update of the highly-regarded `Statistical Shape Analysis' by the same authors. The new edition lays the foundations of landmark shape analysis, including geometrical concepts and statistical techniques, and extends to include analysis of curves, surfaces, images and other types of object data. Key definitions and concepts are discussed throughout, and the relative merits of different approaches are presented. The authors have included substantial new material on recent statistical developments and offer numerous examples throughout the text. Concepts are introduced in an accessible manner, while retaining sufficient detail for more specialist statisticians to appreciate the challenges and opportunities of this new field. Computer code has been included for instructional use, along with exercises to enable readers to implement the applications themselves in R and to follow the key ideas by hands-on analysis. Statistical Shape Analysis: with Applications in R will offer a valuable introduction to this fast-moving research area for statisticians and other applied scientists working in diverse areas, including archaeology, bioinformatics, biology, chemistry, computer science, medicine, morphometics and image analysis .

Structural Bioinformatics - Zoltán Gáspári 2021-02-15
This volume looks at the latest techniques used to perform comparative structure analyses, and predict and

evaluate protein-ligand interactions. The chapters in this book cover tools and servers such as LiteMol; Bio3D-Web; DALI; CATH; HoTMuSiC, a contact-base protein structure analysis tool known as CAD-Score; PyDockSaxs and HADDOCK; CombDock and DockStar; the BioMagResBank database; as well as BME and CoNSEnsX+. Written in the highly successful Methods in Molecular Biology series format, chapters include introductions to their respective topics, step-by-step, readily reproducible computational protocols, and tips on troubleshooting and avoiding known pitfalls. Cutting-edge and comprehensive, Structural Bioinformatics: Methods and Protocols is a practical guide for researchers to learn more about the aforementioned tools to further enhance their studies in the growing field of structural bioinformatics. Chapter 13 is available open access under a CC-BY 4.0 license via link.springer.com.

Handbook of Statistics - 2012-12-31
The field of statistics not only affects all areas of scientific activity, but also many other matters such as public policy. It is branching rapidly into so many different subjects that a series of handbooks is the only way of comprehensively presenting the various aspects of statistical methodology, applications, and recent developments. The Handbook of Statistics, a series of self-contained reference books. Each volume is devoted to a particular topic in statistics with Volume 28 dealing with bioinformatics. Every chapter is written by prominent workers in the area to which the volume is devoted. The series is addressed to the entire community of statisticians and scientists in various disciplines who use statistical methodology in their work. At the same time, special emphasis is placed on applications-oriented techniques, with the applied statistician in mind as the primary audience. Comprehensively presents the various aspects of statistical methodology Discusses a wide variety of diverse applications and recent developments Contributors are internationally renowned experts in their respective areas

Handbook of Research on Trends in the Diagnosis and Treatment of Chronic Conditions - Fotiadis, Dimitrios I. 2015-08-26
Stemming from environmental, genetic, and situational factors, chronic disease is a critical concern in modern medicine. Managing treatment and controlling symptoms is imperative to the longevity and quality of life of patients with such diseases. The Handbook of Research on Trends in the Diagnosis and Treatment of Chronic Conditions features current research on the diagnosis, monitoring, management, and treatment of recurring diseases such as diabetes, Parkinson's disease, autoimmune disorders, and others. This handbook is intended for practitioners and researchers across various disciplines including, but not limited to, biology, biomedical engineering, computer science, and information and communication technologies. Aimed at identifying new disease determinants and the way in which new technologies can contribute to improved health outcomes, this handbook covers a variety of topics, including wearable and mobile technologies, capillaroscopy imaging, diagnostic and monitoring methods, and disease prediction modeling, among others.

Encyclopedia of Evolutionary Biology - 2016-04-14
Encyclopedia of Evolutionary Biology is the definitive go-to reference in the field of evolutionary biology. It provides a fully comprehensive review of the field in an easy to search structure. Under the collective leadership of fifteen distinguished section editors, it is comprised of articles written by leading experts in the field, providing a full review of the current status of each topic. The articles are up-to-date and fully illustrated with in-text references that allow readers to easily access primary literature. While all entries are authoritative and valuable to those with advanced understanding of evolutionary biology, they are also intended to be accessible to both advanced undergraduate and graduate students. Broad topics include the history of evolutionary biology, population genetics, quantitative genetics; speciation, life history evolution, evolution of sex and mating systems, evolutionary biogeography, evolutionary developmental biology, molecular and genome evolution, coevolution, phylogenetic methods, microbial evolution, diversification of plants and fungi, diversification of animals, and applied evolution. Presents fully comprehensive content, allowing easy access to fundamental information and links to primary research Contains concise articles by leading experts in the field that ensures current coverage of each topic Provides ancillary learning tools like tables, illustrations, and multimedia features to assist with the comprehension process

Computational Methods for Protein Structure Prediction and Modeling - Ying Xu 2007-08-24
Volume One of this two-volume sequence focuses on the basic characterization of known protein structures,

and structure prediction from protein sequence information. Eleven chapters survey of the field, covering key topics in modeling, force fields, classification, computational methods, and structure prediction. Each chapter is a self contained review covering definition of the problem and historical perspective; mathematical formulation; computational methods and algorithms; performance results; existing software; strengths, pitfalls, challenges, and future research.

Bayesian Inference for Gene Expression and Proteomics - Marina Vannucci 2012-04-30
The interdisciplinary nature of bioinformatics presents a research challenge in integrating concepts, methods, software and multiplatform data. Although there have been rapid developments in new technology and an inundation of statistical methods for addressing other types of high-throughput data, such as proteomic profiles that arise from mass spectrometry experiments. This book discusses the development and application of Bayesian methods in the analysis of high-throughput bioinformatics data that arise from medical, in particular, cancer research, as well as molecular and structural biology. The Bayesian approach has the advantage that evidence can be easily and flexibly incorporated into statistical methods. A basic overview of the biological and technical principles behind multi-platform high-throughput experimentation is followed by expert reviews of Bayesian methodology, tools and software for single group inference, group comparisons, classification and clustering, motif discovery and regulatory networks, and Bayesian networks and gene interactions.

Handbook of Statistical Genomics - David J. Balding 2019-09-10
A timely update of a highly popular handbook on statistical genomics This new, two-volume edition of a classic text provides a thorough introduction to statistical genomics, a vital resource for advanced graduate students, early-career researchers and new entrants to the field. It introduces new and updated information on developments that have occurred since the 3rd edition. Widely regarded as the reference work in the field, it features new chapters focusing on statistical aspects of data generated by new sequencing technologies, including sequence-based functional assays. It expands on previous coverage of the many processes between genotype and phenotype, including gene expression and epigenetics, as well as metabolomics. It also examines population genetics and evolutionary models and inference, with new chapters on the multi-species coalescent, admixture and ancient DNA, as well as genetic association studies including causal analyses and variant interpretation. The Handbook of Statistical Genomics focuses on explaining the main ideas, analysis methods and algorithms, citing key recent and historic literature for further details and references. It also includes a glossary of terms, acronyms and abbreviations, and features extensive cross-referencing between chapters, tying the different areas together. With heavy use of up-to-date examples and references to web-based resources, this continues to be a must-have reference in a vital area of research. Provides much-needed, timely coverage of new developments in this expanding area of study Numerous, brand new chapters, for example covering bacterial genomics, microbiome and metagenomics Detailed coverage of application areas, with chapters on plant breeding, conservation and forensic genetics Extensive coverage of human genetic epidemiology, including ethical aspects Edited by one of the leading experts in the field along with rising stars as his co-editors Chapter authors are world-renowned experts in the field, and newly emerging leaders. The Handbook of Statistical Genomics is an excellent introductory text for advanced graduate students and early-career researchers involved in statistical genetics.

Modern Directional Statistics - Christophe Ley 2017-08-03
Modern Directional Statistics collects important advances in methodology and theory for directional statistics over the last two decades. It provides a detailed overview and analysis of recent results that can help both researchers and practitioners. Knowledge of multivariate statistics eases the reading but is not mandatory. The field of directional statistics has received a lot of attention over the past two decades, due to new demands from domains such as life sciences or machine learning, to the availability of massive data sets requiring adapted statistical techniques, and to technological advances. This book covers important progresses in distribution theory,high-dimensional statistics, kernel density estimation, efficient inference on directional supports, and computational and graphical methods. Christophe Ley is professor of mathematical statistics at Ghent University. His research interests include semi-parametrically efficient inference, flexible modeling, directional statistics and the study of asymptotic approximations via Stein's

Method. His achievements include the Marie-Jeanne Laurent-Duhamel prize of the Société Française de Statistique and an elected membership at the International Statistical Institute. He is associate editor for the journals Computational Statistics & Data Analysis and Econometrics and Statistics. Thomas Verdebout is professor of mathematical statistics at Université libre de Bruxelles (ULB). His main research interests are semi-parametric statistics, high- dimensional statistics, directional statistics and rank-based procedures. He has won an annual prize of the Belgian Academy of Sciences and is an elected member of the International Statistical Institute. He is associate editor for the journals Statistics and Probability Letters and Journal of Multivariate Analysis.

Bayesian Analysis with Python - Osvaldo Martin 2016-11-25

Unleash the power and flexibility of the Bayesian frameworkAbout This Book- Simplify the Bayes process for solving complex statistical problems using Python; - Tutorial guide that will take the you through the journey of Bayesian analysis with the help of sample problems and practice exercises; - Learn how and when to use Bayesian analysis in your applications with this guide.Who This Book Is ForStudents, researchers and data scientists who wish to learn Bayesian data analysis with Python and implement probabilistic models in their day to day projects. Programming experience with Python is essential. No previous statistical knowledge is assumed.What You Will Learn- Understand the essentials Bayesian concepts from a practical point of view- Learn how to build probabilistic models using the Python library PyMC3- Acquire the skills to sanity-check your models and modify them if necessary- Add structure to your models and get the advantages of hierarchical models- Find out how different models can be used to answer different data analysis questions - When in doubt, learn to choose between alternative models.- Predict continuous target outcomes using regression analysis or assign classes using logistic and softmax regression.- Learn how to think probabilistically and unleash the power and flexibility of the Bayesian frameworkIn DetailThe purpose of this book is to teach the main concepts of Bayesian data analysis. We will learn how to effectively use PyMC3, a Python library for probabilistic programming, to perform Bayesian parameter estimation, to check models and validate them. This book begins presenting the key concepts of the Bayesian framework and the main advantages of this approach from a practical point of view. Moving on, we will explore the power and flexibility of generalized linear models and how to adapt them to a wide array of problems, including regression and classification. We will also look into mixture models and clustering data, and we will finish with advanced topics like non-parametrics models and Gaussian processes. With the help of Python and PyMC3 you will learn to implement, check and expand Bayesian models to solve data analysis problems.Style and approachBayes algorithms are widely used in statistics, machine learning, artificial intelligence, and data mining. This will be a practical guide allowing the readers to use Bayesian methods for statistical modelling and analysis using Python.