Probability Models For Dna Sequence Evolution Probability And Its Applications

A Mathematical Look at DNA Regulatory Sequence EvolutionMarkov Models for Pattern RecognitionMathematics of Genome AnalysisPlant Molecular Evolution2008 40th Southeastern Symposium on System TheoryBrazilian Journal of Probability and StatisticsHidden Markov Models for BioinformaticsMolecular Biology of the CellProbabilistic Modeling in Bioinformatics and Medical InformaticsDNA Technology in Forensic ScienceMarkov Processes for Stochastic ModelingCoalescent TheoryInvariant Probabilities of Transition FunctionsStochastic Models in Biological SciencesGenetics for SurgeonsMarkov Chains: Models, Algorithms and Applications2003 Data Compression ConferenceThe Evaluation of Forensic DNA EvidenceSequence — Evolution — FunctionBioinformaticsDiscrete Probability Models and MethodsStatistical Analysis of Next Generation Sequencing DataIntroduction to ProbabilityIt's in Your DNABulletin de L'Institut International de StatistiqueComputational Systems BioinformaticsBiological Sequence AnalysisIntroduction to Computational GenomicsProceedings of the National Academy of Sciences of the United States of AmericaSelected Works of Terry SpeedModels of DNA Sequence Evolution and Applications to Hypothesis TestingProbability Models for DNA Sequence EvolutionBioinformatics in the Era of Post Genomics and Big DataProbabilityGenetic Diversity and Disease SusceptibilityProbability Models for DNA Sequence EvolutionModern Statistics for Modern BiologyProbability Models for DNA Sequence EvolutionAmstat NewsStatistical Methods in Bioinformatics

A Mathematical Look at DNA Regulatory Sequence Evolution

Matching DNA samples from crime scenes and suspects is rapidly becoming a key source of evidence for use in our justice system. DNA Technology in Forensic Science offers recommendations for resolving crucial questions that are emerging as DNA typing becomes more widespread. The volume addresses key issues: Quality and reliability in DNA typing, including the introduction of new technologies, problems of standardization, and approaches to certification. DNA typing in the courtroom, including issues of population genetics, levels of understanding among judges and juries, and admissibility. Societal issues, such as privacy of DNA data, storage of samples and data, and the rights of defendants to quality testing technology. Combining this original volume with the new update--The Evaluation of Forensic DNA Evidence--provides the complete, up-to-date picture of this highly important and visible topic. This volume offers important guidance to anyone working with this emerging law enforcement tool: policymakers, specialists in criminal law, forensic scientists, geneticists, researchers, faculty, and students.

Markov Models for Pattern Recognition

"What underlying forces are responsible for the observed patterns of variability, given a collection of DNA sequences?" In approaching this question a number of probability models are introduced and anyalyzed.Throughout the book, the theory is developed in close connection with data from more than 60 experimental studies that illustrate the use of these results.

Mathematics of Genome Analysis

Markov processes are processes that have limited memory. In particular, their dependence on the past is only through the previous state. They are used to model the behavior of many systems including communications systems, transportation networks, image segmentation and analysis, biological systems and DNA sequence analysis, random atomic motion and diffusion in physics, social mobility, population studies, epidemiology, animal and insect migration, queueing systems, resource management, dams, financial engineering, actuarial science, and decision systems. Covering a wide range of areas of application of Markov processes, this second edition is revised to highlight the most important aspects as well as the most recent trends and applications of Markov processes. The author spent over 16 years in the industry before returning to academia, and he has applied many of the principles covered in this book in multiple research projects. Therefore, this is an applications-oriented book that also includes enough theory to provide a solid ground in the subject for the reader. Presents both the theory and applications of the different aspects of Markov processes Includes numerous solved examples as well as detailed diagrams that make it easier to understand the principle being presented Discusses different applications of hidden Markov models, such as DNA sequence analysis and speech analysis.

Plant Molecular Evolution

2008 40th Southeastern Symposium on System Theory

Brazilian Journal of Probability and Statistics

Plant molecular biology has produced an ever-increasing flood of data about genes and genomes. Evolutionary biology and systematics provides the context for synthesizing this information. This book brings together contributions from evolutionary biologists, systematists, developmental geneticists, biochemists, and others working on diverse aspects of plant biology whose work touches to varying degrees on plant molecular evolution. The book is organized in three parts, the first of which introduces broad topics in evolutionary biology and summarizes advances in plant molecular phylogenetics, with emphasis on model plant systems. The second segment presents a series of case studies of gene family evolution,

while the third gives overviews of the evolution of important plant processes such as disease resistance, nodulation, hybridization, transposable elements and genome evolution, and polyploidy.

Hidden Markov Models for Bioinformatics

In 1992 the National Research Council issued DNA Technology in Forensic Science, a book that documented the state of the art in this emerging field. Recently, this volume was brought to worldwide attention in the murder trial of celebrity O. J. Simpson. The Evaluation of Forensic DNA Evidence reports on developments in population genetics and statistics since the original volume was published. The committee comments on statements in the original book that proved controversial or that have been misapplied in the courts. This volume offers recommendations for handling DNA samples, performing calculations, and other aspects of using DNA as a forensic tool--modifying some recommendations presented in the 1992 volume. The update addresses two major areas: Determination of DNA profiles. The committee considers how laboratory errors (particularly false matches) can arise, how errors might be reduced, and how to take into account the fact that the error rate can never be reduced to zero. Interpretation of a finding that the DNA profile of a suspect or victim matches the evidence DNA. The committee addresses controversies in population genetics, exploring the problems that arise from the mixture of groups and subgroups in the American population and how this substructure can be accounted for in calculating frequencies. This volume examines statistical issues in interpreting frequencies as probabilities, including adjustments when a suspect is found through a database search. The committee includes a detailed discussion of what its recommendations would mean in the courtroom, with numerous case citations. By resolving several remaining issues in the evaluation of this increasingly important area of forensic evidence, this technical update will be important to forensic scientists and population geneticists--and helpful to attorneys, judges, and others who need to understand DNA and the law. Anyone working in laboratories and in the courts or anyone studying this issue should own this book.

Molecular Biology of the Cell

Probabilistic Modeling in Bioinformatics and Medical Informatics

This classic introduction to probability theory for beginning graduate students covers laws of large numbers, central limit theorems, random walks, martingales, Markov chains, ergodic theorems, and Brownian motion. It is a comprehensive treatment concentrating on the results that are the most useful for applications. Its philosophy is that the best way to learn probability is to see it in action, so there are 200 examples and 450 problems. The fourth edition begins with a short chapter on measure theory to orient readers new to the subject.

DNA Technology in Forensic Science

Advances in computers and biotechnology have had a profound impact on biomedical research, and as a result complex data sets can now be generated to address extremely complex biological questions. Correspondingly, advances in the statistical methods necessary to analyze such data are following closely behind the advances in data generation methods. The statistical methods required by bioinformatics present many new and difficult problems for the research community. This book provides an introduction to some of these new methods. The main biological topics treated include sequence analysis, BLAST, microarray analysis, gene finding, and the analysis of evolutionary processes. The main statistical techniques covered include hypothesis testing and estimation, Poisson processes, Markov models and Hidden Markov models, and multiple testing methods. The second edition features new chapters on microarray analysis and on statistical inference, including a discussion of ANOVA, and discussions of the statistical theory of motifs and methods based on the hypergeometric distribution. Much material has been clarified and reorganized. The book is written so as to appeal to biologists and computer scientists who wish to know more about the statistical methods of the field, as well as to trained statisticians who wish to become involved with bioinformatics. The earlier chapters introduce the concepts of probability and statistics at an elementary level, but with an emphasis on material relevant to later chapters and often not covered in standard introductory texts. Later chapters should be immediately accessible to the trained statistician. Sufficient mathematical background consists of introductory courses in calculus and linear algebra. The basic biological concepts that are used are explained, or can be understood from the context, and standard mathematical concepts are summarized in an Appendix. Problems are provided at the end of each chapter allowing the reader to develop aspects of the theory outlined in the main text. Warren J. Ewens holds the Christopher H. Brown Distinguished Professorship at the University of Pennsylvania. He is the author of two books, Population Genetics and Mathematical Population Genetics. He is a senior editor of Annals of Human Genetics and has served on the editorial boards of Theoretical Population Biology, GENETICS, Proceedings of the Royal Society B and SIAM Journal in Mathematical Biology. He is a fellow of the Royal Society and the Australian Academy of Science. Gregory R. Grant is a senior bioinformatics researcher in the University of Pennsylvania Computational Biology and Informatics Laboratory. He obtained his Ph.D. in number theory from the University of Maryland in 1995 and his Masters in Computer Science from the University of Pennsylvania in 1999. Comments on the first edition: "This book would be an ideal text for a postgraduate course[and] is equally well suited to individual study. I would recommend the book highly." (Biometrics) "Ewens and Grant have given us a very welcome introduction to what is behind those pretty [graphical user] interfaces." (Naturwissenschaften) "The authors do an excellent job of presenting the essence of the material without getting bogged down in mathematical details." (Journal American Statistical Association) "The authors have restructured classical material to a great extent and the new organization of the different topics is one of the outstanding services of the book." (Metrika)

Markov Processes for Stochastic Modeling

Sequence - Evolution - Function is an introduction to the computational approaches that play a critical role in the emerging new branch of biology known as functional genomics. The book provides the reader with an understanding of the principles and approaches of functional genomics and of the potential and limitations of computational and experimental approaches to genome analysis. Sequence - Evolution - Function should help bridge the "digital divide" between biologists and computer scientists, allowing biologists to better grasp the peculiarities of the emerging field of Genome Biology and to learn how to benefit from the enormous amount of sequence data available in the public databases. The book is non-technical with respect to the computer methods for genome analysis and discusses these methods from the user's viewpoint, without addressing mathematical and algorithmic details. Prior practical familiarity with the basic methods for sequence analysis is a major advantage, but a reader without such experience will be able to use the book as an introduction to these methods. This book is perfect for introductory level courses in computational methods for comparative and functional genomics.

Coalescent Theory

A far-reaching course in practical advanced statistics for biologists using R/Bioconductor, data exploration, and simulation.

Invariant Probabilities of Transition Functions

Where did SARS come from? Have we inherited genes from Neanderthals? How do plants use their internal clock? The genomic revolution in biology enables us to answer such questions. But the revolution would have been impossible without the support of powerful computational and statistical methods that enable us to exploit genomic data. Many universities are introducing courses to train the next generation of bioinformaticians: biologists fluent in mathematics and computer science, and data analysts familiar with biology. This readable and entertaining book, based on successful taught courses, provides a roadmap to navigate entry to this field. It guides the reader through key achievements of bioinformatics, using a hands-on approach. Statistical sequence analysis, sequence alignment, hidden Markov models, gene and motif finding and more, are introduced in a rigorous yet accessible way. A companion website provides the reader with Matlab-related software tools for reproducing the steps demonstrated in the book.

Stochastic Models in Biological Sciences

Next Generation Sequencing (NGS) is the latest high throughput technology to revolutionize genomic research. NGS

generates massive genomic datasets that play a key role in the big data phenomenon that surrounds us today. To extract signals from high-dimensional NGS data and make valid statistical inferences and predictions, novel data analytic and statistical techniques are needed. This book contains 20 chapters written by prominent statisticians working with NGS data. The topics range from basic preprocessing and analysis with NGS data to more complex genomic applications such as copy number variation and isoform expression detection. Research statisticians who want to learn about this growing and exciting area will find this book useful. In addition, many chapters from this book could be included in graduate-level classes in statistical bioinformatics for training future biostatisticians who will be expected to deal with genomic data in basic biomedical research, genomic clinical trials and personalized medicine. About the editors: Somnath Datta is Professor and Vice Chair of Bioinformatics and Biostatistics at the University of Louisville. He is Fellow of the American Statistical Association, Fellow of the Institute of Mathematical Statistics and Elected Member of the International Statistical Institute. He has contributed to numerous research areas in Statistics, Biostatistics and Bioinformatics. Dan Nettleton is Professor and Laurence H. Baker Endowed Chair of Biological Statistics in the Department of Statistics at Iowa State University. He is Fellow of the American Statistical Association and has published research on a variety of topics in statistics, biology and bioinformatics.

Genetics for Surgeons

"An introduction to coalescent theory, which provides the foundation for molecular population genetics and genomics. Coalescent theory is the conceptual framework for studies of DNA sequence variation within species, and is the source of essential tools for making inferences about mutation, recombination, population structure and natural selection from DNA sequence data"--Provided by publisher.

Markov Chains: Models, Algorithms and Applications

Summary: "This volume contains papers presented at the workshop 'Stochastic Models in Biological Sciences' held at the Stefan Banach International Mathematical Center in Warsaw, 29 May-2 June 2006."--Preface (p. 5).

2003 Data Compression Conference

Developed from celebrated Harvard statistics lectures, Introduction to Probability provides essential language and tools for understanding statistics, randomness, and uncertainty. The book explores a wide variety of applications and examples, ranging from coincidences and paradoxes to Google PageRank and Markov chain Monte Carlo (MCMC). Additional

The Evaluation of Forensic DNA Evidence

The emphasis in this book is placed on general models (Markov chains, random fields, random graphs), universal methods (the probabilistic method, the coupling method, the Stein-Chen method, martingale methods, the method of types) and versatile tools (Chernoff's bound, Hoeffding's inequality, Holley's inequality) whose domain of application extends far beyond the present text. Although the examples treated in the book relate to the possible applications, in the communication and computing sciences, in operations research and in physics, this book is in the first instance concerned with theory. The level of the book is that of a beginning graduate course. It is self-contained, the prerequisites consisting merely of basic calculus (series) and basic linear algebra (matrices). The reader is not assumed to be trained in probability since the first chapters give in considerable detail the background necessary to understand the rest of the book.

Sequence — Evolution — Function

Polymorphism or variation in DNA sequence can affect individual phenotypes such as color of skin or eyes, susceptibility to diseases, and response to drugs, vaccines, chemicals, and pathogens. Especially, the interfaces between genetics, disease susceptibility, and pharmacogenomics have recently been the subject of intense research activity. This book is a self-contained collection of valuable scholarly papers related to genetic diversity and disease susceptibility, pharmacogenomics, ongoing advances in technology, and analytic methods in this field. The book contains nine chapters that cover the three main topics of genetic polymorphism, genetic diversity, and disease susceptibility and pharmacogenomics. Hence, this book is particularly useful to academics, scientists, physicians, pharmacists, practicing researchers, and postgraduate students whose work relates to genetic polymorphisms.

Bioinformatics

Discrete Probability Models and Methods

The purpose of this volume is to provide an overview of Terry Speed's contributions to statistics and beyond. Each of the fifteen chapters concerns a particular area of research and consists of a commentary by a subject-matter expert and selection of representative papers. The chapters, organized more or less chronologically in terms of Terry's career, encompass a wide variety of mathematical and statistical domains, along with their application to biology and medicine. Accordingly, earlier chapters tend to be more theoretical, covering some algebra and probability theory, while later chapters concern more recent work in genetics and genomics. The chapters also span continents and generations, as they

present research done over four decades, while crisscrossing the globe. The commentaries provide insight into Terry's contributions to a particular area of research, by summarizing his work and describing its historical and scientific context, motivation, and impact. In addition to shedding light on Terry's scientific achievements, the commentaries reveal endearing aspects of his personality, such as his intellectual curiosity, energy, humor, and generosity.

Statistical Analysis of Next Generation Sequencing Data

The massive research effort known as the Human Genome Project is an attempt to record the sequence of the three trillion nucleotides that make up the human genome and to identify individual genes within this sequence. While the basic effort is of course a biological one, the description and classification of sequences also lend themselves naturally to mathematical and statistical modeling. This short textbook on the mathematics of genome analysis presents a brief description of several ways in which mathematics and statistics are being used in genome analysis and sequencing. It will be of interest not only to students but also to professional mathematicians curious about the subject.

Introduction to Probability

DCC is international conference for current work on data compression for text, images, video, audio, and related areas. The proceedings cover topics such as lossless and lossy compression algorithms for specific types of data, source coding, joint source-channel coding, multiple description coding, quantization theory, vector quantization, encoding with wavelets, bi-level image compression, video compression, source coding in multiple access networks, parallel compression algorithms and hardware, and fractal based methods.

It's in Your DNA

Hidden Markov Models for Bioinformatics

Bulletin de L'Institut International de Statistique

Probabilistic models are becoming increasingly important in analysing the huge amount of data being produced by large-scale DNA-sequencing efforts such as the Human Genome Project. For example, hidden Markov models are used for analysing biological sequences, linguistic-grammar-based probabilistic models for identifying RNA secondary structure, and probabilistic evolutionary models for inferring phylogenies of sequences from different organisms. This book gives a unified, up-to-date and self-contained account, with a Bayesian slant, of such methods, and more generally to probabilistic methods

of sequence analysis. Written by an interdisciplinary team of authors, it aims to be accessible to molecular biologists, computer scientists, and mathematicians with no formal knowledge of the other fields, and at the same time present the state-of-the-art in this new and highly important field.

Computational Systems Bioinformatics

The structure of the set of all the invariant probabilities and the structure of various types of individual invariant probabilities of a transition function are two topics of significant interest in the theory of transition functions, and are studied in this book. The results obtained are useful in ergodic theory and the theory of dynamical systems, which, in turn, can be applied in various other areas (like number theory). They are illustrated using transition functions defined by flows, semiflows, and one-parameter convolution semigroups of probability measures. In this book, all results on transition probabilities that have been published by the author between 2004 and 2008 are extended to transition functions. The proofs of the results obtained are new. For transition functions that satisfy very general conditions the book describes an ergodic decomposition that provides relevant information on the structure of the corresponding set of invariant probabilities. Ergodic decomposition means a splitting of the state space, where the invariant ergodic probability measures play a significant role. Other topics covered include: characterizations of the supports of various types of invariant probability measures and the use of these to obtain criteria for unique ergodicity, and the proofs of two mean ergodic theorems for a certain type of transition functions. The book will be of interest to mathematicians working in ergodic theory, dynamical systems, or the theory of Markov processes. Biologists, physicists and economists interested in interacting particle systems and rigorous mathematics will also find this book a valuable resource. Parts of it are suitable for advanced graduate courses. Prerequisites are basic notions and results on functional analysis, general topology, measure theory, the Bochner integral and some of its applications.

Biological Sequence Analysis

Probabilistic Modelling in Bioinformatics and Medical Informatics has been written for researchers and students in statistics, machine learning, and the biological sciences. The first part of this book provides a self-contained introduction to the methodology of Bayesian networks. The following parts demonstrate how these methods are applied in bioinformatics and medical informatics. All three fields - the methodology of probabilistic modeling, bioinformatics, and medical informatics - are evolving very quickly. The text should therefore be seen as an introduction, offering both elementary tutorials as well as more advanced applications and case studies.

Introduction to Computational Genomics

This proceedings volume contains 29 papers covering many of the latest developments in the fast-growing field of bioinformatics. The contributions span a wide range of topics, including computational genomics and genetics, protein function and computational proteomics, the transcriptome, structural bioinformatics, microarray data analysis, motif identification, biological pathways and systems, and biomedical applications. The papers not only cover theoretical aspects of bioinformatics but also delve into the application of new methods, with input from computation, engineering and biology disciplines. This multidisciplinary approach to bioinformatics gives these proceedings a unique viewpoint of the field. Contents: Voting Algorithms for the Motif Finding Problem (X-W Liu et al.)MSDash: Mass Spectrometry Database and Search (Z Wu et al.)GaborLocal: Peak Detection in Mass Spectrum by Gabor Filters and Gaussian Local Maxima (N Nguyen et al.)Designing Secondary Structure Profiles for Fast ncRNA Identification (Y Sun & J Buhler)Iterative Non-sequential Protein Structural Alignment (S Salem & M J Zaki)Consistent Alignment of Metabolic Pathways Without Abstraction (F Ay et al.)On the Accurate Construction of Consensus Genetic Maps (Y-H Wu et al.)Graph Wavelet Alignment Kernels for Drug Virtual Screening (A Smalter et al.)and other papers Readership: Graduate students, postdoctoral fellows, researchers, and practitioners in the field of bioinformatics and systems biology; biotech and pharmaceutical companies; computational scientists and engineers interested in biology. Keywords:Bioinformatics;Computational Systems Biology;Computational Techniques;Systems Biology ProblemsKey Features:The CSB meetings accept only the highest-quality research papers, with a paper-acceptance rate of below 20%The CSB meetings represent a unique bioinformatics conference in which papers blend bioinformatic tool development with in silico biologyCSB meetings have become one of the most well-attended bioinformatics conferencesCSB proceedings are indexed by Medline

Proceedings of the National Academy of Sciences of the United States of America

Bioinformatics has evolved significantly in the era of post genomics and big data. Huge advancements were made toward storing, handling, mining, comparing, extracting, clustering and analysis as well as visualization of big macromolecular data using novel computational approaches, machine and deep learning methods, and web-based server tools. There are extensively ongoing world-wide efforts to build the resources for regional hosting, organized and structured access and improving the pre-existing bioinformatics tools to efficiently and meaningfully analyze day-to-day increasing big data. This book intends to provide the reader with updates and progress on genomic data analysis, data modeling and network-based system tools.

Selected Works of Terry Speed

This thoroughly revised and expanded new edition now includes a more detailed treatment of the EM algorithm, a description of an efficient approximate Viterbi-training procedure, a theoretical derivation of the perplexity measure and

coverage of multi-pass decoding based on n-best search. Supporting the discussion of the theoretical foundations of Markov modeling, special emphasis is also placed on practical algorithmic solutions. Features: introduces the formal framework for Markov models; covers the robust handling of probability quantities; presents methods for the configuration of hidden Markov models for specific application areas; describes important methods for efficient processing of Markov models, and the adaptation of the models to different tasks; examines algorithms for searching within the complex solution spaces that result from the joint application of Markov chain and hidden Markov models; reviews key applications of Markov models.

Models of DNA Sequence Evolution and Applications to Hypothesis Testing

Probability Models for DNA Sequence Evolution

Annotation Surgeons, medical geneticists, genetics counselors Review of leading medical and surgical journals shows that the most frequent area of publication is papers with a genetic or molecular biology component. Some of these papers will involve childhood or prenatal diagnostic issues, while an increasing proportion involve adult-onset single disorders such as neurological disease or familial cancers. In the future, complex multifactorial for polygenicl diseases such as cardiovascular and respiratory diseases will become more prevalent, and already the ethical issues involved are complex and widely discussed. Surgeons need to know about genetics and how it interacts with modern surgical practice. Inherited diseases contribute to a substantial proportion of the surgical workload. Recognition of a positive history of disease in a family will allow genetic testing and precise diagnosis, leading to the ability to presymptomatically screen at-risk members of a family and allow screening and prevention strategies to be implemented.

Bioinformatics in the Era of Post Genomics and Big Data

Probability

"What underlying forces are responsible for the observed patterns of variability, given a collection of DNA sequences?" In approaching this question a number of probability models are introduced and anyalyzed.Throughout the book, the theory is developed in close connection with data from more than 60 experimental studies that illustrate the use of these results.

Genetic Diversity and Disease Susceptibility

Markov chains are a particularly powerful and widely used tool for analyzing a variety of stochastic (probabilistic) systems over time. This monograph will present a series of Markov models, starting from the basic models and then building up to higher-order models. Included in the higher-order discussions are multivariate models, higher-order multivariate models, and higher-order hidden models. In each case, the focus is on the important kinds of applications that can be made with the class of models being considered in the current chapter. Special attention is given to numerical algorithms that can efficiently solve the models. Therefore, Markov Chains: Models, Algorithms and Applications outlines recent developments of Markov chain models for modeling queueing sequences, Internet, re-manufacturing systems, reverse logistics, inventory systems, bio-informatics, DNA sequences, genetic networks, data mining, and many other practical systems.

Probability Models for DNA Sequence Evolution

"In this book, Andy Baxevanis and Francis Ouellette . . . haveundertaken the difficult task of organizing the knowledge in thisfield in a logical progression and presenting it in a digestibleform. And they have done an excellent job. This fine text will makea major impact on biological research and, in turn, on progress inbiomedicine. We are all in their debt." —Eric Lander from the Foreword Reviews from the First Edition "provides a broad overview of the basic tools for sequenceanalysis For biologists approaching this subject for the firsttime, it will be a very useful handbook to keep on the shelf afterthe first reading, close to the computer." —Nature Structural Biology "should be in the personal library of any biologist who usesthe Internet for the analysis of DNA and protein sequencedata." —Science "a wonderful primer designed to navigate the novice throughthe intricacies of in scripto analysis The accomplished genesearcher will also find this book a useful addition to theirlibrary an excellent reference to the principles ofbioinformatics." —Trends in Biochemical Sciences This new edition of the highly successful Bioinformatics:A Practical Guide to the Analysis of Genes and Proteinsprovides a sound foundation of basic concepts, with practicaldiscussions and comparisons of both computational tools anddatabases relevant to biological research. Equipping biologists with the modern tools necessary to solvepractical problems in sequence data analysis, the Second Editioncovers the broad spectrum of topics in bioinformatics, ranging fromInternet concepts to predictive algorithms used on sequence,structure, and expression data. With chapters written by experts inthe field, this up-to-date reference thoroughly covers vitalconcepts and is appropriate for both the novice and the experiencedpractitioner. Written in clear, simple language, the book isaccessible to users without an advanced mathematical or computerscience background. This new edition includes: All new end-of-chapter Web resources, bibliographies, andproblem sets Accompanying Web site containing the answers to the problems,as well as links to relevant Web resources New coverage of comparative genomics, large-scale genomeanalysis, sequence assembly, and expressed sequence tags A glossary of commonly used terms in bioinformatics andgenomics Bioinformatics: A Practical Guide to the Analysis of Genesand Proteins, Second Edition is essential reading forresearchers, instructors, and students of all levels in molecularbiology and bioinformatics, as well as for investigators involvedin genomics, positional cloning, clinical research, andcomputational biology.

Modern Statistics for Modern Biology

V. 1-5, v. 7-10 include "Bulletin bibliographique."

Probability Models for DNA Sequence Evolution

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Amstat News

It's in Your DNA: From Discovery to Structure, Function and Role in Evolution, Cancer and Aging describes, in a clear, approachable manner, the progression of the experiments that eventually led to our current understanding of DNA. This fascinating work tells the whole story from the discovery of DNA and its structure, how it replicates, codes for proteins, and our current ability to analyze and manipulate it in genetic engineering to begin to understand the central role of DNA in evolution, cancer, and aging. While telling the scientific story of DNA, this captivating treatise is further enhanced by brief sketches of the colorful lives and personalities of the key scientists and pioneers of DNA research. Major discoveries by Meischer, Darwin, and Mendel and their impacts are discussed, including the merging of the disciplines of genetics, evolutionary biology, and nucleic acid biochemistry, giving rise to molecular genetics. After tracing development of the gene concept, critical experiments are described and a new biological paradigm, the hologenome concept of evolution, is introduced and described. The final two chapters of the work focus on DNA as it relates to cancer and gerontology. This book provides readers with much-needed knowledge to help advance their understanding of the subject and stimulate further research. It will appeal to researchers, students, and others with diverse backgrounds within or beyond the life sciences, including those in biochemistry, genetics/molecular genetics, evolutionary biology, epidemiology, oncology, gerontology, cell biology, microbiology, and anyone interested in these mechanisms in life. Highlights the importance of DNA research to science and medicine Explains in a simple but scientifically correct manner the key experiments and concepts that led to the current knowledge of what DNA is, how it works, and the increasing impact it has on our lives Emphasizes the observations and reasoning behind each novel idea and the critical experiments that were performed to test them

Statistical Methods in Bioinformatics

ROMANCE ACTION & ADVENTURE MYSTERY & THRILLER BIOGRAPHIES & HISTORY CHILDREN'S YOUNG ADULT FANTASY HISTORICAL FICTION HORROR LITERARY FICTION NON-FICTION SCIENCE FICTION