Maricel Kann Fran Lewitter Translational Bioinformatics

This text is designed for those who wish to study mathematics beyond linear algebra but are unready for abstract material. Rather than a theorem-proof-corollary exposition, it stresses geometry, intuition, and dynamical systems. 1996 edition.

The biological interactions of living organisms, and protein-protein interactions in particular, are astonishingly diverse. This comprehensive book provides a broad, thorough and multidisciplinary coverage of its field. It integrates different approaches from bioinformatics, biochemistry, computational analysis and systems biology to offer the reader a comprehensive global view of the diverse data on protein-protein interactions and protein interaction networks.

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 Gülsoy, 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 Salem)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 Syzmanski 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 Stankowski, 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 ImagesKey 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

The study of pharmacogenetics and pharmacogenomics focuses on how our genes and complex gene systems influence our response to drugs. Recent progress in clinical therapeutics has led to the discovery of new biomarkers that make it technically easier to identify groups of patients which are more or less likely to respond to individual therapies. The aim is to improve personalised medicine – not simply to prescribe the right medicine, but to deliver the right drug at the right dose at the right time. This textbook brings together leading experts to discuss the latest information on how human genetics impacts drug response phenotypes. It presents not only the basic principles of pharmacogenetics, but also clinically valuable examples that cover a broad range of specialties and therapeutic areas. This textbook is an invaluable introduction to pharmacogenetics and pharmacogenomics for health care professionals, medical students, pharmacy students, graduate students and researchers in the biosciences.

In this book, the latest tools available for functional metagenomics research are described.This research enables scientists to directly access the genomes from diverse microbial genomes at one time and study these "metagenomes". Using the modern tools of genome sequencing and cloning, researchers have now been able to harness this astounding metagenomic diversity to understand and exploit the diverse functions of microorganisms. Leading scientists from around the world demonstrate how these approaches have been applied in many different settings, including aquatic and terrestrial habitats, microbiomes, and many more environments. This is a highly informative and carefully presented book, providing microbiologists with a summary of the latest functional metagenomics literature on all specific habitats.

This edition provides a balanced presentation of theory and observation. It introduces the principles of genetics and statistics that are relevant to population studies, and examines the forces affecting genetic variation from the molecular to the organismic level. There is an increasing need throughout the biomedical sciences for a greater understanding of knowledge-based systems and their application to genomic and proteomic research. This book discusses knowledge-based and statistical approaches, along with applications in bioinformatics and systems biology. The text emphasizes the integration of different methods for analysing and interpreting biomedical data. This, in turn, can lead to breakthrough biomolecular discoveries, with applications in personalized medicine. Key Features: Explores the fundamentals and applications of knowledge-based and statistical approaches in

bioinformatics and systems biology. Helps readers to interpret genomic, proteomic, and metabolomic data in understanding complex biological molecules and their interactions. Provides useful guidance on dealing with large datasets in knowledge bases, a common issue in bioinformatics. Written by leading international experts in this field. Students, researchers, and industry professionals with a background in biomedical sciences, mathematics, statistics, or computer science will benefit from this book. It will also be useful for readers worldwide who want to master the application of bioinformatics to real-world situations and understand biological problems that motivate algorithms.

The formation and evolution of complex dynamical structures is one of the most exciting areas of nonlinear physics. Such pattern formation problems are common in practically all systems involving a large number of interacting components. Here, the basic problem is to understand how competing physical forces can shape stable geometries and to explain why nature prefers just these. Motivation for the intensive study of pattern formation phenomena during the past few years derives from an increasing appreciation of the remarkable diversity of behaviour encountered in nonlinear systems and of universal features shared by entire classes of nonlinear processes. As physics copes with ever more ambi tious problems in pattern formation, summarizing our present state of knowledge becomes a pressing issue. This volume presents an overview of selected topics in this field of current interest. It deals with theoretical models of pattern formation and with simulations that bridge the gap between theory and experiment. The book is a product of the International Symposium on the Physics of Structure Formation, held from October 27 through November 2, 1986, at the Institute for Information Sciences of the University of Tiibingen. The symposium brought together a group of distinguished scientists from various disciplines to exchange ideas about recent advances in pattern formation in the physical sciences, and also to introduce young scientists to the fi

A survey of current topics in computational molecular biology. Computational molecular biology, or bioinformatics, draws on the disciplines of biology, mathematics, statistics, physics, chemistry, computer science, and engineering. It provides the computational support for functional genomics, which links the behavior of cells, organisms, and populations to the information encoded in the genomes, as well as for structural genomics. At the heart of all large-scale and high-throughput biotechnologies, it has a growing impact on health and medicine. This survey of computational molecular biology covers traditional topics such as protein structure modeling and sequence alignment, and more recent ones such as expression data analysis and comparative genomics. It combines algorithmic, statistical, database, and AI-based methods for studying biological problems. The book also contains an introductory chapter, as well as one on general statistical modeling and computational techniques in molecular biology. Each chapter presents a self-contained review of a specific subject. Not for sale in China, including Hong Kong.

Second Edition features the latest tools for uncovering thegenetic basis of human disease The Second Edition of this landmark publication bringstogether a team of leading experts in the field to thoroughlyupdate the publication. Readers will discover the tremendousadvances made in human genetics in the seven years that haveelapsed since the First Edition. Once again, the editorshave assembled a comprehensive introduction to the strategies,designs, and methods of analysis for the discovery of genes incommon and genetically complex traits. The growing social, legal,and ethical issues surrounding the field are thoroughly examined aswell. Rather than focusing on technical details or particularmethodologies, the editors take a broader approach that emphasizesconcepts and experimental design. Readers familiar with theFirst Edition will find new and cutting-edge materialincorporated into the text: Updated presentations of bioinformatics, multiple comparisons,sample size requirements, parametric linkage analysis, case-controland family-based approaches, and genomic screening New methods for analysis of gene-gene and gene-environmentinteractions A completely rewritten and updated chapter on determininggenetic components of disease New chapters covering molecular genomic approaches such asmicroarray and SAGE analyses using single nucleotide polymorphism(SNP) and cDNA expression data, as well as quantitative trait loci(QTL) mapping The editors, two of the world's leading genetic epidemiologists,have ensured that each chapter adheres to a consistent and highstandard. Each one includes all-new discussion questions andpractical examples. Chapter summaries highlight key points, and alist of references for each chapter opens the door to furtherinvestigation of specific topics. Molecular biologists, human geneticists, geneticepidemiologists, and clinical and pharmaceutical researchers willfind the Second Edition a helpful guide to understanding thegenetic basis of human disease, with its new tools for detectingrisk factors and discovering treatment strategies.

This volume presents detailed laboratory procedures in an easy to follow format that can be carried out with success by investigators lacking previous exposure to a specific research method. Chapter guide readers through the application of molecular approaches to disease gene identification and overviews, and case studies are also presented. Written in the highly successful Methods in Molecular Biology series format, chapters include introductions to their respective topics, lists of the necessary materials and reagents, step-by-step, readily reproducible laboratory protocols, and tips on troubleshooting and avoiding known pitfalls. Authoritative and practical, Disease Gene Identification: Methods and Protocols, Second Edition aims to help with the identification and characterization of many more disease-related genes and provide novel, and effective strategies for disease treatment and prevention.

Providing information on the main approaches for the analysis of metabolites, this textbook: Covers basic methodologies in sample preparation and separation techniques, as well as the most recent techniques of mass spectrometry. Differentiates between primary and secondary metabolites. Includes four chapters discussing successful metabolome studies of different organisms. Highlights the analytical challenges of studying metabolites. Illustrates applications of metabolome analysis through the use of case studies.

This book constitutes the refereed proceedings of the 9th International Conference on Object-Oriented Information Systems, OOIS 2003, held in Geneva, Switzerland in September 2003. The 29 revised full papers and 11 revised short papers presented together with an invited paper and abstracts of 2 invited talks were carefully reviewed and selected from 80 submissions. The papers are organized in topical sections on evolution of OOIS, OOIS frameworks, patterns and components, object-oriented databases, XML on Web aspects, evolution, object-oriented design and architecture, and modeling of information systems.

Covering topics from individual molecules to systemic diseases, from basic concepts to advanced technologies, Pharmacogenomics in Drug Discovery and Development , Second Edition provides a practical, state-of-the-art and integrative view of the application of pharmacogenomics in drug discovery and development. A wide range of theoretical and experimental approaches are introduced to meet the problem-solving objectives for understanding the complexity in health and diseases, from laboratory tests to computational analysis. The development of pharmacogenomics represents the evolution of biomedicine from treating the disease itself to treating the malfunction of an individual person, the "root" of diseases. With the change of focus from

disease-centered to human-centric medicine, pharmacogenomics brings hope for the transformation from simple disease treatment to accurate prediction and effective prevention. Written in the successful Methods in Molecular Biology series format, chapters include introductions to their respective topics, lists of the necessary materials and reagents, step-by-step, readily reproducible protocols, and notes on troubleshooting and avoiding known pitfalls. Authoritative and easily accessible, Pharmacogenomics in Drug Discovery and Development, Second Edition seeks to serve both professionals and novices with comprehensive resources and a holistic view for the translation of pharmacogenomics into better preventive and personalized medical care.

An engaging introduction to vectors and matrices and the algorithms that operate on them, intended for the student who knows how to program. Mathematical concepts and computational problems are motivated by applications in computer science. The reader learns by "doing," writing programs to implement the mathematical concepts and using them to carry out tasks and explore the applications. Examples include: error-correcting codes, transformations in graphics, face detection, encryption and secret-sharing, integer factoring, removing perspective from an image, PageRank (Google's ranking algorithm), and cancer detection from cell features. A companion web site, codingthematrix.com provides data and support code. Most of the assignments can be auto-graded online. Over two hundred illustrations, including a selection of relevant "xkcd" comics. Chapters: "The Function," "The Field," "The Vector," "The Vector Space," "The Matrix," "The Basis," "Dimension," "Gaussian Elimination," "The Inner Product," "Special Bases," "The Singular Value Decomposition," "The Eigenvector," "The Linear Program" A new edition of this text, incorporating corrections and an expanded index, has been issued as of September 4, 2013, and will soon be available on Amazon.

BACKGROUND Sir Isaac Newton hrought to the world the idea of modeling the motion of physical systems with equations. It was necessary to invent calculus along the way, since fundamental equations of motion involve velocities and accelerations, of position. His greatest single success was his discovery that which are derivatives the motion of the planets and moons of the solar system resulted from a single fundamental source: the gravitational attraction of the hodies. He demonstrated that the ohserved motion of the planets could he explained hy assuming that there is a gravitational attraction he tween any two ohjects, a force that is proportional to the product of masses and inversely proportional to the square of the distance between them. The circular, elliptical, and parabolic orhits of astronomy were v INTRODUCTION no longer fundamental determinants of motion, but were approximations of laws specified with differential equations. His methods are now used in modeling motion and change in all areas of science. Subsequent generations of scientists extended the method of using differ ential equations to describe how physical systems evolve. But the method had a limitation. While the differential equations were sufficient to determine the behavior-in the sense that solutions of the equations did exist-it was frequently difficult to figure out what that behavior would be. It was often impossible to write down solutions in relatively simple algebraic expressions using a finite number of terms. Series solutions involving infinite sums often would not converge beyond some finite time.

Disease-relevant intracellular protein-protein interactions occurring at defined cellular sites possess great potential as drug targets. They permit highly specific pharmacological interference with defined cellular functions. Drugs targeting such interactions are likely to act with fewer side effects than conventional medication influencing whole cell functions. This book discusses therapeutically relevant protein-protein interactions with a major focus on scaffolding proteins tethering signal transduction processes to defined cellular compartments by direct protein-protein interactions. Recent advances in the development of pharmacological agents interfering with protein-protein interactions are highlighted.

This book outlines 11 courses and 15 research topics in bioinformatics, based on curriculums and talks in a graduate summer school on bioinformatics that was held in Tsinghua University. The courses include: Basics for Bioinformatics, Basic Statistics for Bioinformatics, Topics in Computational Genomics, Statistical Methods in Bioinformatics, Algorithms in Computational Biology, Multivariate Statistical Methods in Bioinformatics Research, Association Analysis for Human Diseases: Methods and Examples, Data Mining and Knowledge Discovery Methods with Case Examples, Applied Bioinformatics Tools, Foundations for the Study of Structure and Function of Proteins, Computational Systems Biology Approaches for Deciphering Traditional Chinese Medicine, and Advanced Topics in Bioinformatics and Computational Biology. This book can serve as not only a primer for beginners in bioinformatics, but also a highly summarized yet systematic reference book for researchers in this field. Rui Jiang and Xuegong Zhang are both professors at the Department of Automation, Tsinghua University, China. Professor Michael Q. Zhang works at the Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, USA.

This title is part of the Pearson Modern Classics series. Pearson Modern Classics are acclaimed titles at a value price. Please visit www.pearsonhighered.com/math-classics-series for a complete list of titles. For courses in Multivariate Statistics, Marketing Research, Intermediate Business Statistics, Statistics in Education, and graduate-level courses in Experimental Design and Statistics. Appropriate for experimental scientists in a variety of disciplines, this market-leading text offers a readable introduction to the statistical analysis of multivariate observations. Its primary goal is to impart the knowledge necessary to make proper interpretations and select appropriate techniques for analyzing multivariate data. Ideal for a junior/senior or graduate level course that explores the statistical methods for describing and analyzing multivariate data, the text assumes two or more statistics courses as a prerequisite.

A molecular understanding of electron transfer is crucial to understanding the molecular basis of metabolic processes in which electron transfer is essential, diseases involving these processes, and drug design targeting these processes. This book provides a cohesive and comprehensive discussion of computational methods used for electron transfer proteins and what has been learned from such studies for the first time in a book. It also gives an overview of results from theory, computation, and experiment about electron transfer proteins. This resource also includes strategies for studying metal sites that have not been examined computationally.

Guiding readers from the elucidation and analysis of a genomic sequence to the prediction of a protein structure and the identification of the molecular function, Introduction to Bioinformatics describes the rationale and limitations of the bioinformatics methods and tools that can help solve biological problems. Requiring only a limited mathematical and statistical background, the book shows how to efficiently apply these approaches to biological data and evaluate the resulting information. The author, an expert bioinformatics researcher, first addresses the ways of storing and retrieving the enormous amount of biological data produced every day and the methods of decrypting the information encoded by a genome. She then covers the tools that can detect and exploit the evolutionary and functional relationships among biological elements. Subsequent chapters illustrate how to predict the three-dimensional structure of a protein. The book concludes with a discussion of the future of bioinformatics. Even though the future will undoubtedly offer new tools for tackling problems, most of the fundamental aspects of bioinformatics will not change. This resource provides the essential information to understand bioinformatics methods, ultimately facilitating in the solution of biological problems. Bioinformatics is an amalgamation of mathematics, engineering, computer sciences and statistics. It refers to the practice of using software tools to understand biological data. This book explores all the important aspects of bioinformatics in the present day scenario. It elaborates the different branches related to the subject and their applications. While understanding the long-term perspectives of the topics, the book makes an effort in highlighting their impact as a modern tool for the growth of bioinformatics. This text, with its detailed analyses and data, will prove immensely beneficial to students involved in this area at various levels. It will be of great help to those in the fields of genetics, forensic science and evolutionary biology.

Historically, the study of infection has focused on acute illnesses and their treatment. Infection, however, is not simply an acute process; microbial agents thrive in the human body throughout life. The unrecognized, intimate relationship we share with microorganisms is a critical factor in longevity and health. In recent years, it has become apparent that some cancers may be attributable to underlying chronic infection. Fortunately, infectious diseases are often treatable or preventable. Also, the composition of infectious agents is far less complex than that of humans. Thus the link between infection and cancer may offer insight into the pathogenesis and prevention of all cancers. This book, authored by some of the world's leaders in microbiology, virology, biochemistry, and pathology, provides an overview of oncogenic mechanisms imputed to infection. Individual chapters examine the epidemiologic, clinical and molecular links between specific infectious agents and cancer, and address methods of disease prevention. Microbiologists, cancer biologists, pathologists, oncologists, and infectious disease specialists interested in the etiology of malignancy will find this book an indispensable addition to their libraries.

This book is Part II of the fourth edition of Robert Sedgewick and Kevin Wayne's Algorithms , the leading textbook on algorithms today, widely used in colleges and universities worldwide. Part II contains Chapters 4 through 6 of the book. The fourth edition of Algorithms surveys the most important computer algorithms currently in use and provides a full treatment of data structures and algorithms for sorting, searching, graph processing, and string processing -- including fifty algorithms every programmer should know. In this edition, new Java implementations are written in an accessible modular programming style, where all of the code is exposed to the reader and ready to use. The algorithms in this book represent a body of knowledge developed over the last 50 years that has become indispensable, not just for professional programmers and computer science students but for any student with interests in science, mathematics, and engineering, not to mention students who use computation in the liberal arts. The companion web site, algs4.cs.princeton.edu contains An online synopsis Full Java implementations Test data Exercises and answers Dynamic visualizations Lecture slides Programming assignments with checklists Links to related material The MOOC related to this book is accessible via the "Online Course" link at algs4.cs.princeton.edu. The course offers more than 100 video lecture segments that are integrated with the text, extensive online assessments, and the large-scale discussion forums that have proven so valuable. Offered each fall and spring, this course regularly attracts tens of thousands of registrants. Robert Sedgewick and Kevin Wayne are developing a modern approach to disseminating knowledge that fully embraces technology, enabling people all around the world to discover new ways of learning and teaching. By integrating their textbook, online content, and MOOC, all at the state of the art, they have built a unique resource that greatly expands the breadth and depth of the educational experience. Often considered the workhorse of the cellular machinery, proteins are responsible for functions ranging from molecular motors to signaling. The broad recognition of their involvement in all cellular processes has led to focused efforts to predict their functions from sequences, and if available, from their structures. An overview of current research directions, Computational Protein-Protein Interactions examines topics in the prediction of protein-protein interactions, including interference with protein-protein interactions and their design. Explores Computational Approaches to Understanding Protein-Protein Interactions Outlining fundamental and applied aspects of the usefulness of computations when approaching protein-protein interactions, this book incorporates different views of the same biochemical problem from sequence to structure to energetics. It covers protein-protein interaction prediction and dynamics, design, drug design for inhibition, and uses for the prediction of function. The text provides general chapters that overview the topic and also includes advanced material. The chapters detail the complexity of protein interaction studies and discuss potential caveats. Addresses the Next Big Problem in Molecular Biology While it is important to predict protein associations, this is a daunting task. Edited by two experts in the field and containing contributions from those at the forefront of research, the book provides a basic outline of major directions in computational protein-protein interactions research at the heart of functional genomics and crucial for drug discovery. It addresses the next big problem in molecular biology: how to create links between all the pieces of the cell jigsaw puzzle.

The Handbook of Natural Language Processing, Second Edition presents practical tools and techniques for implementing natural language processing in computer systems. Along with removing outdated material, this edition updates every chapter and expands the content to include emerging areas, such as sentiment analysis.New to the Second EditionGreater

First published in 1986. Routledge is an imprint of Taylor & Francis, an informa company.

This textbook teaches introductory data structures.

Bioinformatics for Systems Biology bridges and unifies many disciplines. It presents the life scientist, computational biologist, and mathematician with a common framework. Only by linking the groups together may the true life sciences revolution move forward. Identifying causal genes underlying susceptibility to human disease is a problem of primary importance in the post-genomic era and in current biomedical research. Recently, there has been a paradigm shift of such gene-discovery efforts from rare, monogenic conditions to common "oligogenic" or "multifactorial" conditions such as asthma, diabetes, cancers and neurological

disorders. These conditions are referred to as multifactorial because, susceptibility to these diseases is attributed to the combinatorial effects of genetic variation at a number of different genes and their interaction with relevant environmental exposures. The goal of this book is to introduce gene prioritization aspects and the candidate gene prioritization algorithms to give readers a comprehensive view on the subject.

A brief and accessible introduction to molecular biology for students and professionals who want to understand this rapidly expanding field. Recent research in molecular biology has produced a remarkably detailed understanding of how living things operate. Becoming conversant with the intricacies of molecular biology and its extensive technical vocabulary can be a challenge, though, as introductory materials often seem more like a barrier than an invitation to the study of life. This text offers a concise and accessible introduction to molecular biology, requiring no previous background in science, aimed at students and professionals in fields ranging from engineering to journalism—anyone who wants to get a foothold in this rapidly expanding field. It will be particularly useful for computer scientists exploring computational biology. A reader who has mastered the information in The Processes of Life is ready to move on to more complex material in almost any area of contemporary biology.

This book is a gentle but rigorous introduction to formal logic. It is intended primarily for use at the college level. However, it can also be used for advanced secondary school students, and it can be used at the start of graduate school for those who have not yet seen the material. The approach to teaching logic used here emerged from more than 20 years of teaching logic to students at Stanford University and from teaching logic to tens of thousands of others via online courses on the World Wide Web. The approach differs from that taken by other books in logic in two essential ways, one having to do with content, the other with form. Like many other books on logic, this one covers logical syntax and semantics and proof theory plus induction. However, unlike other books, this book begins with Herbrand semantics rather than the more traditional Tarskian semantics. This approach makes the material considerably easier for students to understand and leaves them with a deeper understanding of what logic is all about. The primary content difference concerns the semantics of the logic that is taught. In addition to this text, there are online exercises (with automated grading), online logic tools and applications, online videos of lectures, and an online forum for discussion. They are available at logic.stanford.edu/intrologic/.

Bioinformatics is a relatively new field of research. It evolved from the requirement to process, characterize, and apply the information being produced by DNA sequencing technology. The production of DNA sequence data continues to grow exponentially. At the same time, improved bioinformatics such as faster DNA sequence search methods have been combined with increasingly powerful computer systems to process this information. Methods are being developed for the ever more detailed quantification of gene expression, providing an insight into the function of the newly discovered genes, while molecular genetic tools provide a link between these genes and heritable traits. Genetic tests are now available to determine the likelihood of suffering specific ailments and can predict how plant cultivars may respond to the environment. The steps in the translation of the genetic blueprint to the observed phenotype is being increasingly understood through proteome, metabolome and phenome analysis, all underpinned by advances in bioinformatics. Bioinformatics is becoming increasingly central to the study of biology, and a day at a computer can often save a year or more in the laboratory. The volume is intended for graduate-level biology students as well as researchers who wish to gain a better understanding of applied bioinformatics and who wish to use bioinformatics technologies to assist in their research. The volume would also be of value to bioinformatics developers, particularly those from a computing background, who would like to understand the application of computational tools for biological research. Each chapter would include a comprehensive introduction giving an overview of the fundamentals, aimed at introducing graduate students and researchers from diverse backgrounds to the field and bring them up-to-date on the current state of knowledge. To accommodate the broad range of topics in applied bioinformatics, chapters have been grouped into themes: gene and genome analysis, molecular genetic analysis, gene expression analysis, protein and proteome analysis, metabolome analysis, phenome data analysis, literature mining and bioinformatics tool development. Each chapter and theme provides an introduction to the biology behind the data describes the requirements for data processing and details some of the methods applied to the data to enhance biological understanding.

Stochastic processes are found in probabilistic systems that evolve with time. Discrete stochastic processes change by only integer time steps (for some time scale), or are characterized by discrete occurrences at arbitrary times. Discrete Stochastic Processes helps the reader develop the understanding and intuition necessary to apply stochastic process theory in engineering, science and operations research. The book approaches the subject via many simple examples which build insight into the structure of stochastic processes and the general effect of these phenomena in real systems. The book presents mathematical ideas without recourse to measure theory, using only minimal mathematical analysis. In the proofs and explanations, clarity is favored over formal rigor, and simplicity over generality. Numerous examples are given to show how results fail to hold when all the conditions are not satisfied. Audience: An excellent textbook for a graduate level course in engineering and operations research. Also an invaluable reference for all those requiring a deeper understanding of the subject.

This book presents current advances in the emerging interdisciplinary field of microRNA research of human cancers from a unique perspective of quantitative sciences: bioinformatics, computational and systems biology, and mathematical modeling. This volume contains adaptations and critical reviews of recent state-of-the-art studies, ranging from technological advances in microRNA detection and profiling, clinically oriented microRNA profiling in several human cancers, to a systems biology analysis of global patterns of microRNA regulation of signaling and metabolic pathways. Interactions with transcription factor regulatory networks and mathematical modeling of microRNA regulation are also discussed.

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