Biotechnology And Bioinformatics Advances And Applications For Bioenergy Bioremediation And Biopharmaceutical Research

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.

This popular textbook has been revised and updated to provide a comprehensive overview and to reflect the latest developments in this rapidly developing area. Advances in basic research at the molecular level have provided many insights into biological processes and allowed the production of new developments across the fields of genome editing, proteomics, agriculture, microbial biotechnology, bioinformatics and therapeutics. This new edition provides the reader with a number of key areas in discrete chapters either updated from the previous edition or written as entirely new chapters concerning emerging fields. By presenting information in an easily assimilated form, this book makes an ideal undergraduate text for students of biology and chemistry, as well as appealing to postgraduates.

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Single-cell Omics, Volume 2: Advances in Applications provides the latest single-cell omics applications in the field of biomedicine. The advent of omics technologies have enabled us to identify the differences between cell types and subpopulations at the level of the genome, proteome, transcriptome, epigenome, and in several other fields of omics. The book is divided into two sections: the first is dedicated to biomedical applications, such as cell diagnostics, non-invasive prenatal testing (NIPT), circulating tumor cells, breast cancer, gliomas, nervous systems and autoimmune disorders, and more. The second focuses on cell omics in plants, discussing micro algal and single cell omics, and more. This book is a valuable source for bioinformaticians, molecular diagnostic researchers, clinicians and several members of biomedical field interested in understanding more about single-cell omics and its potential for research and diagnosis. Covers the diverse single cell omics applications in the biomedical field Summarizes the latest progress in single cell omics and discusses potential future developments for research and diagnosis Written by experts across the world, it brings different points-of-view and study cases to fully give a comprehensive overview of the topic

The convergence of biology and computer science was initially motivated by the need to organize and process a growing number of biological observations resulting from rapid advances in experimental techniques. Today, however, close collaboration between biologists, biochemists, medical researchers, and computer scientists has also generated remarkable benefits for the field of computer science. Systemic Approaches in Bioinformatics and Computational Systems Biology: Recent Advances presents new techniques that have resulted from the application of computer science methods to the organization and interpretation of biological data. The book covers three subject areas: bioinformatics, computational biology, and computational systems biology. It focuses on recent, systemic approaches in computer science and mathematics that have been used to model, simulate, and more generally, experiment with biological phenomena at any scale.

This book presents the latest developments in bioinformatics, highlighting the importance of bioinformatics in genomics, transcriptomics, metabolism and cheminformatics analysis, as well as in drug discovery and development. It covers tools, data mining and analysis, protein analysis, computational vaccine, and drug design. Covering cheminformatics, computational evolutionary biology and the role of next-generation sequencing and neural network analysis, it also discusses the use of bioinformatics tools in the development of precision medicine. This book offers a valuable source of information for not only beginners in bioinformatics, but also for students, researchers, scientists, clinicians, practitioners, policymakers, and stakeholders who are interested in harnessing the potential of bioinformatics in many areas.

Advances in Animal Genomics provides an outstanding collection of integrated strategies involving traditional and modern - omics (structural, functional, comparative and epigenomics) approaches and genomics-assisted breeding methods which animal biotechnologists can utilize to dissect and decode the molecular and gene regulatory networks involved in the complex quantitative yield and stress tolerance traits in livestock. Written by international experts on animal genomics, this book explores the recent advances in high-throughput, next-generation whole genome and transcriptome sequencing, array-based genotyping, and modern bioinformatics approaches which have enabled to produce huge genomic and transcriptomic resources globally on a genome-wide scale. This book is an important resource for researchers, students, educators and professionals in agriculture, veterinary and biotechnology sciences

that enables them to solve problems regarding sustainable development with the help of current innovative biotechnologies. Integrates basic and advanced concepts of animal biotechnology and presents future developments Describes current high-throughput next-generation whole genome and transcriptome sequencing, array-based genotyping, and modern bioinformatics approaches for sustainable livestock production Illustrates integrated strategies to dissect and decode the molecular and gene regulatory networks involved in complex quantitative yield and stress tolerance traits in livestock Ensures readers will gain a strong grasp of biotechnology for sustainable livestock production with its well-illustrated discussion

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

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)

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"In the last couple decades, we could see the combination of technology and biology taking large steps in science. As new fields, bioinformatics and biotechnology also led to important discussions between excited scientists and social thinkers. The divergent opinions argue about the amazing possibilities of human advances and the social issues that follow the progress. This paper discusses ethical matters of new developments and compares policy choices with respect to research and use of biotechnology and bioinformatics in different countries. Even though the world is increasingly globalized, the comparisons suggest that different cultures have different ethical responses and public policies are a reflection of divergent social economic scenarios. Yet in any modern society, the new biotechnological advances seem to change how we experience the life."--Abstract.

Biotechnology and BioinformaticsAdvances and Applications for Bioenergy, Bioremediation and Biopharmaceutical ResearchCRC Press

Every researcher in genomics and proteomics now has access to public domain databases containing literally billions of data entries. However, without the right analytical tools, and an understanding of the biological significance of the data, cataloging and interpreting the molecular evolutionary processes buried in those databases is difficult, if not impossible. The first editon of Bioinformatics Basics: Applications in Biological Science and Medicine answered the scientific community's need to learn about the bioinformatic tools available to them. That the book continues to be a best seller clearly demonstrates the authors' ability to provide scientists with the understanding to apply those tools to their research. Currently, it is being used as a reference text at MIT and other prestigious institutions. Recognizing the important advances in bioinformatices since their last edition, Buehler and

Rashidi have produced a completely revised and updated version of their pioneering work. To allow scientists to utilize significant databases from around the world, the authors consider some fresh approaches to data analysis while identifying computing techniques that will help them manage the massive flow of information their science requires. New to the second edition: Provides a more detailed view of the field while continuing to focus on the global concept approach that popularized the first edition. Offers the latest approaches to data analysis Introduces recent developments in genomics, microarrays, proteomics, genome mapping, and more. Adds two new sections offering insights from other experts in bioinformatics. Bioinformatics Basics is not intended to serve as a training manual for bioinformaticians. Instead, it's designed to help the general scientific community gain a thorough understanding of what bioinformatics tools are available to them and the best ways these tools can be utilized and adapted to meet the needs of their specific interests and projects.

Burgeoning world population, decreased water supply and land resources, coupled with climate change, result in severe stress conditions and a great threat to the global food supply. To meet these challenges, exploring Omics Technologies could lead to improved yields of cereals, tubers and grasses that may ensure food security. Improvement of yields through crop improvement and biotechnological means are the need-of-the-hour, and the current book "OMICS-Based Approaches in Plant Biotechnology", reviews the advanced concepts on breeding strategies, OMICS technologies (genomics, transcriptomics and metabolomics) and bioinformatics that help to glean the potential candidate genes/molecules to address unsolved problems related to plant and agricultural crops. The first six chapters of the book are focused on genomics and cover sequencing, functional genomics with examples on insecticide resistant genes, mutation breeding and miRNA technologies. Recent advances in metabolomics studies are elucidated in the next 3 chapters followed by 5 chapters on bioinformatics and advanced techniques in plant biotechnology and crop breeding. The information contained in the volume will help plant breeders, plant biotechnologists, plant biochemists, agriculture scientists and researchers in using this applied research to focus on better crop breeding and stress adaptation strategies.

The advances in biotechnology such as the next generation sequencing technologies are occurring at breathtaking speed. Advances and breakthroughs give competitive advantages to those who are prepared. However, the driving force behind the positive competition is not only limited to the technological advancement, but also to the companion data analytical skills and computational methods which are collectively called computational biology and bioinformatics. Without them, the biotechnology-output data by itself is raw and perhaps meaningless. To raise such awareness, we have collected the state-of-the-art research works in computational biology and bioinformatics with a thematic focus on gene regulation in this book. This book is designed to be self-contained and comprehensive, targeting senior undergraduates and junior graduate students in the related disciplines such as bioinformatics, computational biology, biostatistics, genome science, computer science, applied data mining, applied machine learning, life science, biomedical science, and genetics. In addition, we believe that this book will serve as a useful reference for both bioinformaticians and computational biologists in the post-genomic era.

Proteins Biochemistry and Biotechnology 2e is a definitive source of information for all those interested in protein science, and particularly the commercial production and isolation of specific proteins, and their subsequent utilization for applied purposes in industry and medicine. Fully updated throughout with new or fundamentally revised sections on proteomics as, bioinformatics, protein glycosylation and engineering, well as sections detailing advances in upstream processing and newer protein applications such as enzyme-based biofuel production this new edition has an increased focus on biochemistry to ensure the balance between biochemisty and biotechnology, enhanced with numerous case studies. This second edition is an invaluable text for undergraduates of biochemistry and biotechnology but will also be relevant to students of microbiology, molecular biology, bioinformatics and any branch of the biomedical sciences who require a broad overview of the various medical, diagnostic and industrial uses of proteins. • Provides a comprehensive overview of all aspects of protein biochemisty and protein biotechnology • Includes numerous case studies • Increased focus on protein biochemistry to ensure balance between biochemisty and biotechnology • Includes new section focusing on proteomics as well as sections detailing protein function and enzyme-based biofuel production "With the potential of a standard reference source on the topic, any molecular biotechnologist will profit greatly from having this excellent book. " (Engineering in Life Sciences, 2004; Vol 5; No. 5) "Few texts would be considered competitors, and none compare favorably." (Biochemistry and Molecular Education, July/August 2002) "...The book is well written, making it informative and easy to read..." (The Biochemist, June 2002)

Single-Cell Omics: Volume 1: Technological Advances and Applications provides the latest technological developments and applications of single-cell technologies in the field of biomedicine. In the current era of precision medicine, the single-cell omics technology is highly promising due to its potential in diagnosis, prognosis and therapeutics. Sections in the book cover single-cell omics research and applications, diverse technologies applied in the topic, such as pangenomics, metabolomics, and multi-omics of single cells, data analysis, and several applications of single-cell omics within the biomedical field, for example in cancer, metabolic and neuro diseases, immunology, pharmacogenomics, personalized medicine and reproductive health. This book is a valuable source for bioinformaticians, molecular diagnostic researchers, clinicians and members of the biomedical field who are interested in understanding more about single-cell omics and its potential for research and diagnosis. Covers not only the technological aspects, but also the diverse applications of single cell omics in the biomedical field Summarizes the latest progress in single cell omics and discusses potential future developments for research and diagnosis Written by experts across the world, bringing different points-of-view and case studies to give a comprehensive overview on the topic

Bioinformatics, and by extension omic sciences – the collective disciplines that are dependent on the use of extensive datasets of biological information – present a challenge of data management for researchers all over the world. Big data collected as part of research projects and experiments can be complex, with several kinds of variables involved. Coupled with continuously changing bioinformatics and information technology tools, there is a need to bring a multidisciplinary approach into these fields. Advances in Bioinformatics, Biostatistics and Omic Sciences attempts to realize an integrated approach between all omic sciences, exploring innovative bioinformatics and biostatistical methodologies which enable researchers to unveil hidden sides of biological phenomena. This volume presents reviews on the following topics which give a glimpse of recent advances in the field: - New Integrated Mitochondrial DNA Bioinformatics Pipeline to Improve Quality Assessment of Putative Pathogenic Variants from NGS Experiments - Variant Calling on RNA Sequencing Data: State of Art and Future Perspectives - An innovative Gene Prioritization Pipeline for WES analyses - New Integrated Differential Expression Approach for RNA-Seq Data Analysis - Innovations in Data Visualization for Straightforward Interpretation of Nucleic Acid Omics Outcomes This volume serves as a guide for graduate

students in bioinformatics as well as researchers planning new projects as a part of their professional and academic activities. Over 500 prokaryotic genomes have been sequenced to date, and thousands more have been planned for the next few years. While these genomic sequence data provide unprecedented opportunities for biologists to study the world of prokaryotes, they also raise extremely challenging issues such as how to decode the rich information encoded in these genomes. This comprehensive volume includes a collection of cohesively written chapters on prokaryotic genomes, their organization and evolution, the information they encode, and the computational approaches needed to derive such information. A comparative view of bacterial and archaeal genomes, and how information is encoded differently in them, is also presented. Combining theoretical discussions and computational techniques, the book serves as a valuable introductory textbook for graduate-level microbial genomics and informatics courses.

The book Bioinformatics and Human Genomics Research provides up to date and comprehensive information about multiple approaches of bioinformatic tools in research in human genomics. Experts, from around the worlds of the applications in bioinformatics and human genomics have contributed chapters in the book.

Crop Improvement: Biotechnological Advances – Biomedical Science The field of biotechnology is advancing at a fast pace. The availability of low-cost DNA/genome sequencing technologies has led to the discovery and functional characterization of myriad of genes imparting stress tolerance and quality traits. The 'omics' group of technologies including genomics, proteomics, transcriptomics and metabolomics has revolutionized the agricultural biotechnology sector. The Nobel Prize-winning technology, such as the genome editing technique, is being employed to edit various gene functions in plants aiding in crop improvement. This technology may be adopted very quickly by consumers compared with the transgenic technique because the genome-edited plants have no adverse effects on the genome of the plant itself and on the environment and related species/non-target organisms. In this book, authors have attempted to compile the latest techniques of agricultural biotechnology and their applications in crop improvement. Certain chapters have been dedicated to describe the use of nanotechnology, a fast emerging new technique in the agriculture sector. Features Development, potential and safety issues in biotechnology Advances in genomics, proteomics and transcriptomics in agriculture Protein bioinformatics and its applications Genetically modified (GM) technology and its implications Genome editing in crop improvement Marker-assisted selection (MAS) in crop improvement Mutation breeding Cryobiotechnology Nanotechnology and biosensors This book includes real-world examples and applications making it accessible to a broader interdisciplinary readership. We hope that it will serve as a reference book for researchers engaged in molecular biology and biotechnology and will act as a ready reckoner for postgraduate (PG) students in the biotechnology discipline.

Over the past few decades, major advances in the field of molecular biology, coupled with advances in genomic technologies, have led to an explosive growth in the biological information generated by the scientific community. This surge of genomic information has, in turn, led to an absolute requirement for computerized databases to store, organize, and index the data and for specialized tools to view and analyze the data. There are many tools in bioinformatics, with many functions to suit the needs and expertise of the scientists using them. Gene and protein databases are constantly being updated with information that aid scientists all around the world, in whatever field of the life sciences they are working. Bioinformatics carries benefits for plant researchers: it can aid in plant breeding and genetic engineering, and allow plant scientists to produce better crops for the future. By knowing which plants are closely related, scientists can figure out which sexually compatible species have desirable characteristics (such as longer stalks for rice plants, or larger grains for barley, corn, or wheat). The wild relatives of today's plants may be sources of crop improvement genes. This information, in conjunction with appropriate technology, may provide predictive measures of plant health and quality and become part of future breeding decision management systems. Next-generation sequencing coupled with high-performance computing methods have revolutionized the field of plant breeding and genetics. The volume Biotechnology and Bioinformatics contains recent advances in certain biotechnological applications. It presents some of the key concepts, methods, software packages, and databases used in bioinformatics, with an emphasis on those relevant to plant science. It also cover some fundamental issues related to biological sequence analyses, transcriptome analyses, computational proteomics, computational metabolomics, bio-ontologies, and biological databases. A focus on a few emerging research topics in bioinformatics is given. This book will be very helpful to the undergraduate and postgraduate students, researchers, teachers of microbiology, biotechnology, agriculture and horticulture.

Bioinformatics is a platform between the biology and information technology. The book covers a broad spectrum of the bioinformatics fields starting from the basic principles, concepts, and multidisciplinary application areas. It comprises a collection of chapters describing the role of bioinformatics in drug design and discovery including the molecular modeling aspects; chapters detailing topics such as silico design, protein modeling, DNA Microarray Analysis, DNA-RNA barcoding, gene sequencing; specialized topics such as bioinformatics in cancer detection, genomics, proteomics, machine learning, covalent approaches in drug design

"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.

This textbook has been conceptualized to provide a detailed description of the various aspects of Systems and Synthetic Biology, keeping the

requirements of M.Sc. and Ph.D. students in mind. Also, it is hoped that this book will mentor young scientists who are willing to contribute to this area but do not know from where to begin. The book has been divided into two sections. The first section will deal with systems biology – in terms of the foundational understanding, highlighting issues in biological complexity, methods of analysis and various aspects of modelling. The second section deals with the engineering concepts, design strategies of the biological systems ranging from simple DNA/RNA fragments, switches and oscillators, molecular pathways to a complete synthetic cell will be described. Finally, the book will offer expert opinions in legal, safety, security and social issues to present a well-balanced information both for students and scientists.

This volume contains the papers selected for presentation at the 4th Brazilian Sym- sium on Bioinformatics, BSB 2009, which was held in Porto Alegre, Brazil, during August 29–31, 2009. The BSB symposium had its origins in the Brazilian Workshop on Bioinformatics (WOB). WOB had three editions, in 2002 (Gramado, RS), in 2003 (Macaé, RJ), and in 2004 (Brasília, DF). The change in the designation from wo- shop to symposium reflects the increase in the quality of the contributions and also in the interest of the scientific community for the meeting. The previous editions of BSB took place in São Leopoldo, RS, in 2005, in Angra dos Reis, RJ, in 2007, and in Santo André, SP, in 2008. As evidence of the internationalization of the event, BSB 2009 had 55 submissions from seven countries. Of the 55 papers submitted, 36 were full papers, with up to 12 pages each, and 19 were extended abstracts, with up to 4 pages each. The articles submitted were carefully reviewed and selected by an international Program Comm- tee, comprising three chairs and 45 members from around the world, with the help of 21 additional reviewers. The Program Committee Chairs are very thankful to the - thors of all submitted papers, and especially to the Program Committee members and the additional reviewers, who helped select the 12 full papers and the six extended abstracts that make up this book.

Biomedical advances have made it possible to identify and manipulate features of living organisms in useful ways--leading to improvements in public health, agriculture, and other areas. The globalization of scientific and technical expertise also means that many scientists and other individuals around the world are generating breakthroughs in the life sciences and related technologies. The risks posed by bioterrorism and the proliferation of biological weapons capabilities have increased concern about how the rapid advances in genetic engineering and biotechnology could enable the production of biological weapons with unique and unpredictable characteristics. Globalization, Biosecurity, and the Future of Life Sciences examines current trends and future objectives of research in public health, life sciences, and biomedical science that contain applications relevant to developments in biological weapons 5 to 10 years into the future and ways to anticipate, identify, and mitigate these dangers.

The recent discovery of small and long non-coding RNAs (ncRNAs) has represented a major breakthrough in the life sciences. These molecules add a new layer of complexity to biological processes and pathways by revealing a sophisticated and dynamic interconnected system whose structure is just beginning to be uncovered. Genetic and epigenetic aberrations affecting ncRNA gene sequences and their expression have been linked to a variety of pathological conditions, including cancer, cardiovascular and neurological diseases. Latest advances in the development of high throughput analysis techniques may help to shed light on the complex regulatory mechanisms in which ncRNA molecules are involved. Bioinformatics tools constitute a unique and essential resource for non-coding RNA studies, providing a powerful technology to organize, integrate and analyze the huge amount of data produced daily by wet biology experiments in order to discover patterns, identify relationships among heterogeneous biological elements and formulate functional hypotheses. This Research Topic reviews current knowledge, introduces novel methods, and discusses open challenges of this exciting and innovative field in connection with the most important biomedical applications. It consists of four reviews and six original research and methods articles, spanning the full scope of the Research Topic.

This important new book covers recent advancements, innovations, and technologies in industrial biotechnology, specifically addressing the application of various biomolecules in industrial production and in cleaning and environmental remediation sectors. The goal of industrial biotechnology is to develop new techniques and technologies to transform renewable raw materials into chemicals, materials, and fuels by the substitution of fossil fuels. With the increase in the world's population and the resultant growing energy demand, the need for more energy can be successfully met with the advancements in industrial biotechnology. Currently across the globe significant research has been undertaken in the production of cleaner fuels, materials, and semi-synthetic chemicals, with environmental benefits. Developing countries have huge agricultural resources that could be utilized for production of value-added byproducts for the sustainable development of bio-based economy. The book opens with the chapter on the production of exopolysaccharides from halophilic microorganisms, a polymer that is normally very useful in various production sectors of the food, pharmaceutical, and petroleum industries. The book goes on to cover: The production of antimicrobial compounds from alkaliphilic bacteria Thermophilic actinomycetes Food, agro, and pharmaceutical potential and biotechnological applications of biosurfactants, halophiles, cyclodextrin glycosyl transferease, fungal chitinase, proteases, yeasts and yeast products Also covered in the book are the environmental aspects of industrial biotechnology such as the genetic enhancement for biofuel production, the production of biodegradable thermoplastics, advancements in the synthesis of bio-oil, ecofriendly treatment of agro-based lignocelluloses, and anaerobic bio reactors for hydrocarbon remediation. The international roster of chapter authors have been chosen for their renowned expertise and contribution to the various fields of industrial biotechnology. This book is suitable to chemists, biotechnologists from research institutes, academia, and students as well as for industry professionals

The advances in genomic technologies, such as microarrays and high throughput sequencing, have expanded the realm of possibilities for capturing data and analyzing it using automated computer driven bioinformatics tools. With the completion of the sequencing of genomes of human and several model organisms, a quest for scientific discoveries being fueled by integrative and multidimensional techniques in mathematics and computational sciences. In this volume, leading researchers and experts have provided an overview of significant concepts from biological, mathematical, and computational perspectives. It provides a high level view of fungal genomic data integration and annotation, classification of proteins and identification of vaccine targets, identification of secretome or secreted proteins in fungal genomes, as well as tools for analyzing microarray expression profiles. Provides a survey of theoretical underpinnings on the technological tools and applications Discusses the tools utilized for the annotation of fungal genomes and addresses issues related to automated annotation generation in a high throughput biotechnology environment Describes the applications of the concepts and methodologies presented throughout the book

Reflecting the interdisciplinary nature of biotechnology, this book covers the role of targeted delivery of polymeric nanodrugs to cancer cells, microbial detoxifying enzymes in bioremediation and bacterial plasmids in antimicrobial resistance. It addresses modern trends such as pharmacogenomics, evaluation of gene expression, recombinant proteins from methylotrophic yeast, identification of novel fermentation inhibitors of bioethanol production, and polyhydroxyalkanoate based biomaterials. The book highlights the practical utility of biotechnology and bioinformatics for bioenergy, production of high value biochemicals, modeling molecular interactions, drug discovery, and personalized medicine.

The Most Comprehensive and Cutting-Edge Guide to Statistical Applications in Biomedical Research With the increasing use of

biotechnology in medical research and the sophisticated advances in computing, it has become essential for practitioners in the biomedical sciences to be fully educated on the role statistics plays in ensuring the accurate analysis of research findings. Statistical Advances in the Biomedical Sciences explores the growing value of statistical knowledge in the management and comprehension of medical research and, more specifically, provides an accessible introduction to the contemporary methodologies used to understand complex problems in the four major areas of modern-day biomedical science: clinical trials, epidemiology, survival analysis, and bioinformatics. Composed of contributions from eminent researchers in the field, this volume discusses the application of statistical techniques to various aspects of modern medical research and illustrates how these methods ultimately prove to be an indispensable part of proper data collection and analysis. A structural uniformity is maintained across all chapters, each beginning with an introduction that discusses general concepts and the biomedical problem under focus and is followed by specific details on the associated methods, algorithms, and applications. In addition, each chapter provides a summary of the main ideas and offers a concluding remarks section that presents novel ideas, approaches, and challenges for future research. Complete with detailed references and insight on the future directions of biomedical research, Statistical Advances in the Biomedical Sciences provides vital statistical guidance to practitioners in the biomedical sciences while also introducing statisticians to new, multidisciplinary frontiers of application. This text is an excellent reference for graduate- and PhD-level courses in various areas of biostatistics and the medical sciences and also serves as a valuable tool for medical researchers, statisticians, public health professionals, and biostatisticians.

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