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Prebiotics and ProbioticsThe Journal of Experimental BiologyBovine Viral Diarrhea Virus and Related PestivirusesThe Journal of ImmunologyGenetic Engineering & Biotechnology NewsToxicogenomics in non-mammalian speciesRoot Adaptations to Multiple Stress FactorsBig Mechanisms in Systems BiologyAlternative Splicing Regulation During Caenorhabditis Elegans Development and EvolutionImmunoparasitology: A Unique Interplay Between Host and PathogenBiochemical EcotoxicologyNew Aspects of Cancer Stem Cell Biology"Colourful Breeding and Genetics"Applying Next Generation Sequencing and Transgenic Models to Rare Disease ResearchCentral Nervous System Extracellular VesiclesMolecular Basis and Gene Therapies of Cystic FibrosisBiofuels and BioenergyPlant Organelle DNA MaintenanceIntegrative Genomics and Network Biology in Livestock and other Domestic AnimalsGene QuantificationSystems Immunology and Infection MicrobiologyDinophysis Toxins: Distribution, Fate in Shellfish and ImpactsInteractions Between Diets, Gut Microbiota and Host MetabolismIssues in Allied Fields of Medicine: 2011 EditionIssues in Pathology, Diagnostics, and Disease: 2011 EditionInnate Immune Response of Porcine Gut Associated Lymphoid Tissue to Salmonella Enterica Serovar Choleraesuis InfectionForbesGenetic Engineering NewsInternational Journal of OncologyResearch & DevelopmentPhysiological Adaptations of Insects Exposed to Different Stress ConditionsNatureThe Role of Mitochondria, Oxidative Stress and Altered Calcium Homeostasis in Amyotrophic Lateral Sclerosis: From Current Developments in the Laboratory to Clinical TreatmentsPituitary Adenylate Cyclase Activating Polypeptide — PACAPPseudomonas and Acinetobacter: From Drug Resistance to PathogenesisMicrobiome Interplay and ControlThe Human Microbiome and CancerBioinformaticsUsing Cereal Science and Technology for the Benefit of ConsumersInternational Journal of Radiation Biology

Big Mechanisms in Systems Biology: Big Data Mining, Network Modeling, and Genome-Wide Data Identification explains big mechanisms of systems biology by system identification and big data mining methods using models of biological systems. Systems biology is currently undergoing revolutionary changes in response to the integration of powerful technologies. Faced with a large volume of available literature, complicated mechanisms, small prior knowledge, few classes on the topics, and causal and mechanistic language, this is an ideal resource. This book addresses system immunity, regulation, infection, aging, evolution, and carcinogenesis, which are complicated biological systems with inconsistent findings in existing resources. These inconsistencies may reflect the underlying biology time-varying systems and signal transduction events that are often context-dependent, which raises a significant problem for mechanistic modeling since it is not clear which genes/proteins to include in models or experimental measurements. The book is a valuable resource for bioinformaticians and members of several areas of the biomedical field who are interested in an in-depth understanding on how to process and apply great amounts of biological data to improve research. Written in a didactic manner in order to explain how to investigate Big Mechanisms by big data mining and system identification Provides more than 140 diagrams to illustrate Big Mechanism in systems biology Presents worked examples in each chapterAmyotrophic lateral sclerosis (ALS) is a rapidly progressive, devastating and fatal disease characterized by selective loss of upper and lower motor neurons of the cerebral cortex, brainstem, spinal cord and muscle atrophy. In spite of many years of research, the pathogenesis of ALS is still not well understood. ALS is a multifaceted genetic disease, in which genetic susceptibility to motor neuron death interacts with environmental factors and there is still no cure for this deleterious disease. At present, there is only one FDA approved drug, Riluzole which according to past studies only modestly slows the progression of the disease, and improves survival by up to three months. The suffering of the ALS patients, and their families is enormous and the economic burden is colossal. There is therefore a pressing need for new therapies. Different molecular pathways and pathological mechanisms have been implicated in ALS. According to past studies, altered calcium homeostasis, abnormal mitochondrial function, protein misfolding, axonal transport defects, excessive production of extracellular superoxide radicals, glutamate-mediated excitotoxicity, inflammatory events, and activation of oxidative stress pathways within the mitochondria and endoplasmic reticulum can act as major contributor that eventually leads to loss of connection between muscle and nerve ultimately resulting to ALS. However, the detailed molecular and cellular pathophysiological mechanisms and origin and temporal progression of the disease still remained elusive. Ongoing research and future advances will likely advance our improve understanding about various involved pathological mechanism ultimately leading to discoveries of new therapeutic cures. Importantly, clinical biomarkers of disease onset and progression are thus also urgently needed to support the development of the new therapeutic agents and novel preventive and curative strategies. Effective translation from pre-clinical to clinical studies will further require extensive knowledge regarding drug activity, bioavailability and efficacy in both the pre-clinical and clinical setting, and proof of biological activity in the target tissue. During the last decades, the development of new therapeutic molecules, advance neuroimaging tools, patient derived induced stem cells and new precision medicine approaches to study ALS has significantly improved our understanding of disease. In particular, new genetic tools, neuroimaging methods, cellular probes, biomarker study and molecular techniques that achieve high spatiotemporal resolution have revealed new details about the disease onset and its progression. In our effort to provide the interested reader, clinician and researchers a comprehensive summaries and new findings in this field of ALS research, hereby we have created this electronic book which comprises of twenty seven chapters having various reviews, perspective and original research articles. All these chapters and articles in this book not only summarize the cutting-edge techniques, approaches, cell and animal models to study ALS but also provide unprecedented coverage of the current developments and new hypothesis emerging in ALS research. Some examples are novel genetic and cell culture based models, mitochondria-mediated therapy, oxidative stress and ROS mechanism, development of stem cells and mechanism-based therapies as well as novel biomarkers for designing and testing effective therapeutic strategies that can benefit ALS patients who are at the earlier stages in the disease. I am extremely grateful to all the contributors to this book and want to thank them for their phenomenal efforts. Manoj Kumar Jaiswal, Ph.D. February 5, 2017 New York, NYThe cancer stem cell (CSC) paradigm represents one of the most prominent breakthroughs of the last decades in tumor biology. CSCs are that subpopulation within a tumor that can survive conventional therapies and as a consequence are able to fuel tumor recurrence. Nevertheless, the biological characteristics of CSCs and even their existence, remain the main topic among tumor biologists debates. The difficulty in achieving a better definition of CSC biology may actually be explained by the plasticity of such a cell subpopulation. Indeed, the emerging view is that CSCs represent a dynamic “state” of tumor cells that can acquire stemness-related properties under specific circumstances, rather than referring to a well-defined group of cells. Regardless of their origin, it is clear that designing novel antitumor treatments based on the eradication of CSCs will only be possible upon unraveling the biological mechanisms that underlie their pathogenic role in tumor progression and therapy resistance. The Special Issue on “New aspects of cancer stem cell biology: implications for innovative therapies” aims at highlighting recent insights into CSC features that can make them an attractive target for novel therapeutic strategies.This book is a printed edition of the Special Issue "Prebiotics and Probiotics" that was published in NutrientsPseudomonas aeruginosa and Acinetobacter baumannii are among the most common non-lactose-fermenting Gram-negative pathogens responsible for hospital-acquired infections, especially in intensive care units (ICUs). The treatment of infections caused by these bacteria is complicated due to the emergence of multi-drug resistance as the two species are noted for their intrinsic resistance to antimicrobial agents and their ability to acquire genetic elements that encode for resistance determinants. In both species, resistance to multiple classes of antimicrobial agents can seriously compromise the ability to treat infected patients, especially the immunocompromised. Consequently, very few antimicrobials remain as treatment options. Mechanisms of resistance in both of these pathogens include the production of β-lactamases and aminoglycoside-modifying enzymes as well as reduced or lack of expression of outer membrane proteins, mutations in topoisomerases, and up-regulation of efflux pumps. To that purpose, the findings of the studies included in this book deal with the prevalence of resistant isolates to various antimicrobial agents in both P. aeruginosa and A. baumannii, their underlying mechanisms of resistance, their virulence factors, their pathogenesis, and prospective treatment options. Special thanks are due to Mr. Bassam El-Hafi for facilitating procedures involved in this publication.Systems Immunology and Infection Microbiology provides a large amount of biological system models, diagrams and flowcharts to illustrate development procedures and help users understand the results of systems immunology and infection microbiology. Chapters discuss systems immunology, systems infection microbiology, systematic inflammation and immune responses in restoration and regeneration process, systems' innate and adaptive immunity in infection process, systematic genetic and epigenetic pathogenic/defensive mechanism during bacterial infection on human cells is introduced, and the systematic genetic and epigenetic pathogenic/defensive mechanisms during viral infection on human cells. This book provides new big data-driven and systems-driven systems immunology and infection microbiology to researchers applying systems biology and bioinformatics in their work. It is also invaluable to several members of biomedical field who are interested in learning more about those approaches.

Encompasses one applicable example in every chapter to illustrate the solution procedure from big data mining, network modeling, host/pathogen cross-talk detection, drug target identification and systems drug design Presents flowcharts to represent the development procedure of systematic immunology and infection in a very clear format Contains 100 color diagrams to help readers understand the related biological networks, their corresponding mechanisms, and significant network biomarkers for therapeutic drug designSummary of Genes. Thirty years ago, the gene responsible for cystic fibrosis (CF), a recessive genetic disease caused by mutations in the cystic fibrosis transmembrane conductance regulator gene, was identified. This progress has considerably changed our understanding of the pathophysiology of CF and has paved the way for the development of novel and specific therapies for the disease. The CFTR gene contains 27 exons and is characterized by a frequent three base pair deletion of the p.Phe508del. As a result of collaborative work, today more than 2000 mutations have been reported in the gene, and their impact on protein function is now more evident and useful in designing new strategies to correct the gene defect. The field of gene therapy, as illustrated by Ziying Yan in this book, has worked on identifying an efficient vector system for the delivery of the wild-type CFTR gene to the lung. At the same time, animal models have been developed in mice, rats, rabbits, zebrafish, ferrets, and pigs to establish the efficacy of gene delivery. These animals are also of the utmost importance in testing new molecules as modulators or correctors to improve the CFTR lung function. During the last three decades, the epidemiology of CF has dramatically changed, as today cystic fibrosis is now a chronic adult pulmonary disease.The pestiviruses encompass some of the most economically important viral infections in the cattle, swine, and sheep industries worldwide. Discovered more than 70 years ago, bovine viral diarrhea virus (BVDV) and classical swine fever virus (CSFV) were long the main concern, but many new pestiviruses have emerged in recent years, which may also present additional threats to biosecurity and food safety. This issue brings together contributions from multiple disciplines – virology, immunology, veterinary clinical medicine, epidemiology, and pathology – on the subject of BVDV and related pestiviruses, and cover host–virus interactions, virus–cell interactions, cross-species transmission as well as the role of wildlife species as reservoirs of some of the pestiviruses.Issues in Allied Fields of Medicine / 2011 Edition is a ScholarlyEditions™ eBook that delivers timely, authoritative, and comprehensive information about Allied Fields of Medicine. The editors have built Issues in Allied Fields of Medicine: 2011 Edition on the vast information databases of ScholarlyNews.™ You can expect the information about Allied Fields of Medicine in this eBook to be deeper than what you can access anywhere else, as well as consistently reliable, authoritative, informed, and relevant. The content of Issues in Allied Fields of Medicine: 2011 Edition has been produced by the world's leading scientists, engineers, analysts, research institutions, and companies. All of the content is from peer-reviewed sources, and all of it is written, assembled, and edited by the editors at ScholarlyEditions™ and available exclusively from us. You now have a source you can cite with authority, confidence, and credibility. More information is available at http://www.ScholarlyEditions.com/.Biochemical Ecotoxicology: Principles and Methods presents practical approaches to biochemical ecotoxicology experiments for environmental protection and conservation. With its methodical, stepped approach this essential reference introduces readers to current techniques for toxicity endpoint testing, suitable for laboratories of any size and budget. Each chapter presents a state-of-the-art principle, a quick and inexpensive procedure (including appropriate reagents), case studies, and demonstrations on how to analyze your results. Generic techniques are covered, suitable for a variety of organisms, as well as high-throughput techniques like quantitative polymerase chain reactions and enzyme-linked immunoassays. Cutting-edge approaches, including gPCR arrays and lipidomic techniques, are also included, making this is an essential reference for anyone who needs to assess environmental toxicity. Practical, cost-effective approaches to assess environmental toxicity endpoints for all types of organism Presents theory, methods, case studies and information on how to analyze results State-of-the-art techniques, such as 'omics' approaches to toxicology"Bioinformatics: Concepts, Methodologies, Tools, and Applications highlights the area of bioinformatics and its impact over the medical community with its innovations that change how we recognize and care for illnesses"--Provided by publisher.A rare disease is a disease that occurs infrequently in the general population, typically affecting fewer than 200,000 Americans at any given time. More than 30 million people in the United States of America (USA) and 350 million people globally suffer from rare diseases. Out of the 7000+ known rare diseases, less than 5% have approved treatments. Rare diseases are frequently chronic, progressive, degenerative, and life-threatening, compromising the lives of patients by loss of autonomy. In the USA, it can take years for a rare disease patient to receive a correct diagnosis. The socioeconomic burden for rare disease is huge. For those living with diagnosed rare diseases, there is no support system or resource bank for navigating financial, educational, or other aspects of having a rare disease. The purpose of this Research Topic is to bring together leading researchers, non-profit organizations, healthcare providers/diagnostic companies, and pharma/biotech/CROs in the field to provide a broad perspective on the latest advances, challenges, and opportunities in rare disease research. A genomic approach to rare disease research is becoming the key to discovering unknown causes behind these syndromes. Genomic rare disease research has attracted not only academic researchers but also researchers from the biotech/pharma and non-profit organizations. The breadth and depth of current genomic approaches in rare disease is largely unexplored. While the creation of novel CRISPR mouse models and the use of NGS (ChIP Seq, RNA Seq, etc) have become more routine for fields such as oncology, rare disease researchers are now making advances in modifying and applying these approaches for rare diseases. This Research Topic provides a fruitful platform for rare disease researchers to share their findings and advance the field of genomics research in the rare disease space.Issues in Pathology, Diagnostics, and Disease: 2011 Edition is a ScholarlyEditions™ eBook that delivers timely, authoritative, and comprehensive information about Pathology, Diagnostics, and Disease. The editors have built Issues in Pathology, Diagnostics, and Disease: 2011 Edition on the vast information databases of ScholarlyNews.™ You can expect the information about Pathology, Diagnostics, and Disease in this eBook to be deeper than what you can access anywhere else, as well as consistently reliable, authoritative, informed, and relevant. The content of Issues in Pathology, Diagnostics, and Disease: 2011 Edition has been produced by the world's leading scientists, engineers, analysts, research institutions, and companies. All of the content is from peer-reviewed sources, and all of it is written, assembled, and edited by the editors at ScholarlyEditions™ and available exclusively from us. You now have a source you can cite with authority, confidence, and credibility. More information is available at http://www.ScholarlyEditions.com/.This book provides reviews and primary research articles that discuss the replication, repair, maintenance, and structures of plant organelle genomes. Rearrangements of these genomes are common and provide a way to distinguish closely related plant species. Some articles in the book discuss recent advances in identifying specific proteins and potential mechanisms involved in DNA replication, recombination, and repair in plant mitochondria and chloroplasts.The Proceedings of the 12th International Cereal and Bread Congress provide a wide-ranging, comprehensive and up-to-date review of the latest advances in cereal science and technology with contributions from leading cereals institutes and individuals from around the world. They bring together all elements of the 'grain chain' from breeding of new wheat varieties through the milling processes and on to the conversion of flour into baked products ready for the consumer at large. Evaluating and predicting wheat flour properties require new equipment and new techniques and these are covered in depth. Cereals other than wheat are given due consideration. The versatility of wheat flour and its conversion into food is reviewed across a whole spectrum of products. There is a strong emphasis on the use of wheat flour for bread making but with consideration of applications in the manufacture of cakes, cookies, pastries, extruded foods, pasta and noodles. The development process and the benefits to consumers are also addressed. The Editors and the Organising Committee have assembled a collection of high-quality papers which provide a showpiece for the latest developments in cereal science and technology. Extensive collection of proceedings from the 12th International Cereal and Bread Congress High-quality papers highlighting the most recent developments in cereal science and technology Benefits for the industry and consumers are discussedSeveral species of Dinophysis produce one or two groups of lipophilic toxins: okadaic acid (OA) and its derivatives; or the dinophysistoxins (DTXs) (also known as diarrhetic shellfish poisons or DSP toxins) and pectenotoxins (PTXs). DSP toxins are potent inhibitors of protein phosphatases, causing gastrointestinal intoxication in consumers of contaminated seafood. Forty years after the identification of Dinophysis as the causative agent of DSP in Japan, contamination of filter feeding shellfish exposed to Dinophysis blooms is recognized as a problem worldwide. DSP events affect public health and cause considerable losses to the shellfish industry. Costly monitoring programs are implemented in regions with relevant shellfish production to prevent these socioeconomic impacts. Harvest closures are enforced whenever toxin levels exceed regulatory limits (RLs). Dinophysis species are kleptoplastidic dinoflagellates; they feed on ciliates (Mesodinium genus) that have previously acquired plastids from cryptophycean (genera Teleaulax, Plagioselmis, and Geminigera) nanoflagellates. The interactions of Dinophysis with different prey regulate their growth and toxin production. When Dinophysis cells are ingested by shellfish, their toxins are partially biotransformed and bioaccumulated, rendering the shellfish unsuitable for human consumption. DSP toxins may also affect shellfish metabolism. This book covers diverse aspects of the abovementioned topics—from the laboratory culture of Dinophysis and the kinetics of uptake, transformation, and depuration of DSP toxins in shellfish to Dinophysis population dynamics, the monitoring and regulation of DSP toxins, and their impact on the shellfish industry in some of the aquaculture regions that are traditionally most affected, namely, northeastern Japan, western Europe, southern Chile, and New Zealand.In complex systems, such as our body or a plant, the host is living together with thousands of microbes, which support the entire system in function and health. The stability of a microbiome is influenced by environmental changes, introduction of microbes and microbial communities, or other factors. As learned in the past,

microbial diversity is the key and low-diverse microbiomes often mirror out-of-control situations or disease. It is now our task to understand the molecular principles behind the complex interaction of microbes in, on and around us in order to optimize and control the function of the microbial community – by changing the environment or the addition of the right microorganisms. This Research Topic focuses on studies (including e.g. original research, perspectives, mini reviews, and opinion papers) that investigate and discuss: 1) The role of the microbiome for the host/environmental system 2) The exchange and change of microbes and microbial communities (interplay) 3) The influence of external factors toward the stability of a microbiome 4) Methods, possibilities and approaches to change and control a system's microbiome (e.g. in human or plant disease) 5) Experimental systems and approaches in microbiome research. The articles span the areas: human health and disease, animal and plant microbiomes, microbial interplay and control, methodology and the built environment microbiome.Some molecules or conditions are exclusively toxic to biological systems and classified as being non-essential; others are essential for life. Nevertheless, above certain threshold even the essential will become toxic. Tightly controlled homeostatic control mechanisms are thus vital drivers of well being, longevity and survival. The identification and characterization of these intricate pathways form the foundations of Toxicogenomics. The initiation, and indeed completion, of numerous non-mammalian genome-sequencing projects, has driven the exponential growth of available genetic sequences. Collating this vast amount of data into functional and mechanistically meaningful units will provide novel insights into pathogenesis, new methods of risk assessment, genetic risk-modifications in preventative medicine and new therapeutic targets for pharmaceutical and biological medicines. This Research Topic issue will explore the current knowledgebase pertaining to the multitude of genomic and toxicological tools within non-mammalian organisms. The encyclopaedic coverage will span the full taxonomic breadth ranging from simple unicellular bacteria and yeast to complex creatures such as birds and fish. The resulting collection of unique, complimentary or indeed contrasting approaches, tools and technologies (which are defined by the availability and feasibility for each organism to study genomics of xenobiotic or stress biology) will not only foster cross-phyla awareness but expand the horizon of Toxicogenomics.Geneticists and molecular biologists have been interested in quantifying genes and their products for many years and for various reasons (Bishop, 1974). Early molecular methods were based on molecular hybridization, and were devised shortly after Marmur and Doty (1961) first showed that denaturation of the double helix could be reversed - that the process of molecular reassociation was exquisitely sequence dependent. Gillespie and Spiegelman (1965) developed a way of using the method to titrate the number of copies of a probe within a target sequence in which the target sequence was fixed to a membrane support prior to hybridization with the probe - typically a RNA. Thus, this was a precursor to many of the methods still in use, and indeed under development, today. Early examples of the application of these methods included the measurement of the copy numbers in gene families such as the ribosomal genes and the immunoglo bulin family. Amplification of genes in tumors and in response to drug treatment was discovered by this method. In the same period, methods were invented for estimating gene num bers based on the kinetics of the reassociation process - the so-called Cot analysis. This method, which exploits the dependence of the rate of reassociation on the concentration of the two strands, revealed the presence of repeated sequences in the DNA of higher eukaryotes (Britten and Kohne, 1968). An adaptation to RNA, Rot analysis (Melli and Bishop, 1969), was used to measure the abundance of RNAs in a mixed population.The first comprehensive book to cover all aspects of the last 25 years of PACAP (pituitary adenylate cyclase activating polypeptide) research, this book contains contributions from virtually all the leading researchers in the field, and addresses some of the following topics: evolutionary aspects of PACAP, distribution and occurrence of PACAP and its receptors, hormonal effects of PACAP, intracellular signaling, effects on cellular proliferation and differentiation, protective effects of PACAP, behavioral effects of PACAP, developmental aspects of PACAP, other physiological effects of PACAP (cardiovascular, thermoregulatory), human studies, drug design, metabolism and transport. This compendium can serve as an important reference for researchers and students in PACAP research and can also be a thorough introduction for those in related fields.