

Computational Biology Of The Heart

In 1996, and with extraordinary prescience, Panfilov and Holden had highlighted in their seminal book 'Computational Biology of the Heart' that biology was, potentially, the most mathematical of all sciences. Fast-forward 20 years and we have seen an explosion of applications of mathematics in not only biology, but healthcare that has already produced significant breakthroughs not imaginable more than 20 years ago. Great strides have been made in explaining through quantitative methods the underlying mechanisms of human disease, not without considerable ingenuity and effort. Biological mechanisms are bewildering: complex, ever evolving, multi-scale, variable, difficult to fully access and understand. This poses immense challenges to the computational physiology community that, nevertheless, has developed an impressive arsenal of tools and methods in a vertiginous race to combat disease with the tall order of improving human healthcare. Mechanistic models are now contending with the advent of machine learning in healthcare and the hope is that both approaches will be used synergistically since the complexity of human pathophysiology and the difficulty of acquiring human datasets will require both, deductive and inductive methods. This Research Topic presents work that is currently at the frontier in computational physiology with a striking range of applications, from diabetes to graft failure and using a multitude of mathematical tools. This collection of articles represents a snapshot in a field that is moving a dizzying speed, bringing understanding of fundamental mechanism and solutions to healthcare problems experienced by healthcare systems all over the world.

This book constitutes the refereed proceedings of the First International Workshop on Functional Imaging and Modeling of the Heart, FIMH 2001, held in Helsinki, Finland, in November 2001. The 17 revised full papers presented together with four invited papers were carefully reviewed and selected for inclusion in the book. The papers are organized in topical sections on anatomical modeling, motion and deformation, functional imaging, and towards electromechanical modeling.

This book is devoted to computer-based modeling in cardiology, by taking an educational point of view, and by summarizing knowledge from several, commonly considered delimited areas of cardiac research in a consistent way. First, the foundations and numerical techniques from mathematics are provided, with a particular focus on the finite element and finite differences methods. Then, the theory of electric fields and continuum mechanics is introduced with respect to numerical calculations in anisotropic biological media. In addition to the presentation of digital image processing techniques, the following chapters deal with particular aspects of cardiac modeling: cardiac anatomy, cardiac electro physiology, cardiac mechanics, modeling of cardiac electro mechanics. This book was written for researchers in modeling and cardiology, for clinical cardiologists, and for advanced students.

This book constitutes the refereed proceedings of the 13th International Conference on Computational Methods in Systems Biology, CMSB 2015, held in Nantes, France, in September 2015. The 20 full papers and 2 short papers presented were carefully reviewed and selected from 43 full and 4 short paper submissions. The papers cover a wide range of topics in the analysis of biological systems, networks and data such as model checking, stochastic analysis, hybrid systems, circadian clock, time series data,

logic programming, and constraints solving ranging from intercellular to multiscale. The advent of genome sequencing and associated technologies has transformed biologists' ability to measure important classes of molecules and their interactions. This expanded cellular view has opened the field to thousands of interactions that previously were outside the researchers' reach. The processing and interpretation of these new vast quantities of interconnected data call for sophisticated mathematical models and computational methods. Systems biology meets this need by combining genomic knowledge with theoretical, experimental and computational approaches from a number of traditional scientific disciplines to create a mechanistic explanation of cellular systems and processes. *Systems Biology I: Genomics and Systems Biology II: Networks, Models, and Applications* offer a much-needed study of genomic principles and their associated networks and models. Written for a wide audience, each volume presents a timely compendium of essential information that is necessary for a comprehensive study of the subject. The chapters in the two volumes reflect the hierarchical nature of systems biology. Chapter authors-world-recognized experts in their fields-provide authoritative discussions on a wide range of topics along this hierarchy. Volume I explores issues pertaining to genomics that range from prebiotic chemistry to noncoding RNAs. Volume II covers an equally wide spectrum, from mass spectrometry to embryonic stem cells. The two volumes are meant to provide a reliable reference for students and researchers alike.

Love is a little word with a universe of meanings and has engaged people's interest throughout human history. The need to give and receive love lies deep within human nature. Philosophers, poets, theologians, sociologists, and scientists have all attempted to explain its exact origin, but is it an evolutionary adaptation, or a social construct? Walsh discusses that the nature of and need for love has biological origins. He draws upon Darwin's sexual selection theory to define the perceptions of love by infants through the process of experience-dependent brain wiring. He observes that mother love makes a child capable of loving and that father love makes a child feel worthy of love. He appraises the origin and purpose of romantic love in his discussions on sexual reproduction by looking at chemical and neurological responses to love and the influence of love on one's physical and mental health. With frequent quotes from literary masters like Shakespeare to orient one's scientific and humanistic understanding of love, Walsh goes on to explore various styles of romantic love, including monogamy, promiscuity, bartering love, and betrayed love; the effects of a skewed sex ratio on dating and mating practices; and the age-old quest for a perfect society populated by perfect people obeying the biblical command to "love one another."

This comprehensively revised second edition of *Computational Systems Biology* discusses the experimental and theoretical foundations of the function of biological systems at the molecular, cellular or organismal level over temporal and spatial scales, as systems biology advances to provide clinical solutions to complex medical problems. In particular the work focuses on the engineering of biological systems and network modeling. Logical information flow aids understanding of basic building blocks of life through disease phenotypes Evolved principles gives insight into underlying organizational principles of biological organizations, and systems processes, governing functions such as adaptation or response patterns Coverage of technical tools and

systems helps researchers to understand and resolve specific systems biology problems using advanced computation Multi-scale modeling on disparate scales aids researchers understanding of dependencies and constraints of spatio-temporal relationships fundamental to biological organization and function.

Computational Cardiovascular Mechanics provides a cohesive guide to creating mathematical models for the mechanics of diseased hearts to simulate the effects of current treatments for heart failure. Clearly organized in a two part structure, this volume discusses various areas of computational modeling of cardiovascular mechanics (finite element modeling of ventricular mechanics, fluid dynamics) in addition to a description an analysis of the current applications used (solid FE modeling, CFD).

Edited by experts in the field, researchers involved with biomedical and mechanical engineering will find Computational Cardiovascular Mechanics a valuable reference. For decades biology has focused on decoding cellular processes one gene at a time, but many of the most pressing biological questions, as well as diseases such as cancer and heart disease, are related to complex systems involving the interaction of hundreds, or even thousands, of gene products and other factors. How do we begin to understand this complexity? Fundamentals of Systems Biology: From Synthetic Circuits to Whole-cell Models introduces students to methods they can use to tackle complex systems head-on, carefully walking them through studies that comprise the foundation and frontier of systems biology. The first section of the book focuses on bringing students quickly up to speed with a variety of modeling methods in the context of a synthetic biological circuit. This innovative approach builds intuition about the strengths and weaknesses of each method and becomes critical in the book's second half, where much more complicated network models are addressed—including transcriptional, signaling, metabolic, and even integrated multi-network models. The approach makes the work much more accessible to novices (undergraduates, medical students, and biologists new to mathematical modeling) while still having much to offer experienced modelers--whether their interests are microbes, organs, whole organisms, diseases, synthetic biology, or just about any field that investigates living systems.

The book comprises contributions by some of the most respected scientists in the field of mathematical modeling and numerical simulation of the human cardiocirculatory system. The contributions cover a wide range of topics, from the preprocessing of clinical data to the development of mathematical equations, their numerical solution, and both in-vivo and in-vitro validation. They discuss the flow in the systemic arterial tree and the complex electro-fluid-mechanical coupling in the human heart. Many examples of patient-specific simulations are presented. This book is addressed to all scientists interested in the mathematical modeling and numerical simulation of the human cardiocirculatory system.

The book presents the proceedings of four conferences: The 24th International Conference on Image Processing, Computer Vision, & Pattern Recognition (IPCV'20), The 6th International Conference on Health Informatics and Medical Systems (HIMS'20), The 21st International Conference on Bioinformatics & Computational Biology (BIOCOMP'20), and The 6th International Conference on Biomedical Engineering and Sciences (BIOENG'20). The conferences took place in Las Vegas, NV, USA, July 27-30, 2020, and are part of the larger 2020 World Congress in Computer Science, Computer Engineering, & Applied Computing (CSCE'20), which features 20 major tracks. Authors include academics, researchers, professionals, and students. Presents the proceedings of four conferences as part of the 2020 World Congress in Computer Science, Computer Engineering, & Applied Computing (CSCE'20); Includes the tracks on Image Processing, Computer Vision, & Pattern Recognition, Health Informatics & Medical Systems, Bioinformatics, Computational Biology & Biomedical Engineering; Features papers from IPCV'20, HIMS'20, BIOCOMP'20, and BIOENG'20.

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.

Nonlinear dynamics has become an important field of research in recent years in many areas of the natural sciences. In particular, it has potential applications in biology and medicine; nonlinear data analysis has helped to detect the progress of cardiac disease, physiological disorders, for example episodes of epilepsy, and others. This book focuses on the current trends of research concerning the prediction of sudden cardiac death and the onset of epileptic seizures, using the nonlinear analysis based on ECG and EEG data. Topics covered include the analysis of cardiac models and neural models. The book is a collection of recent research papers by leading physicists, mathematicians, cardiologists and neurobiologists who are actively involved in using the concepts of nonlinear dynamics to explore the functional behaviours of heart and brain under normal and pathological conditions. This collection is intended for students in physics, mathematics and medical sciences, and researchers in interdisciplinary areas of physics and biology.

Emerging imaging techniques have opened new fronts to investigate tissues, cells, and proteins. Transformative technologies such as microCT scans, super-resolution microscopy, fluorescence-based tools, and other methods now allow us to study the mechanics of cancer, dissect the origins of cellular force regulation, and examine biological specimens

Encyclopedia of Bioinformatics and Computational Biology: ABC of Bioinformatics combines elements of computer science, information technology, mathematics, statistics and biotechnology, providing the methodology and in silico solutions to mine biological data and processes. The book covers Theory, Topics and Applications, with a special focus on Integrative –omics and Systems Biology. The theoretical, methodological underpinnings of BCB, including phylogeny are covered, as are more current areas of focus, such as translational bioinformatics, cheminformatics, and environmental informatics. Finally, Applications provide guidance for commonly asked questions. This major reference work spans basic and cutting-edge methodologies authored by leaders in the field, providing an invaluable resource for students, scientists, professionals in research institutes, and a broad swath of researchers in biotechnology and the biomedical and pharmaceutical industries. Brings together information from computer science, information technology, mathematics, statistics and biotechnology Written and reviewed by leading experts in the field, providing a unique and authoritative resource Focuses on the main theoretical and methodological concepts before expanding on specific topics and applications Includes interactive images, multimedia tools and crosslinking to further resources and databases

This book highlights the latest research on practical applications of computational biology and bioinformatics, and addresses emerging experimental and sequencing techniques that are posing new challenges for bioinformatics and computational biology. Successfully applying these techniques calls for new algorithms and approaches from fields such as statistics, data mining, machine learning, optimization, computer science, and artificial intelligence. In

response to these challenges, we have seen the rise of a new generation of interdisciplinary scientists with a strong background in the biological and computational sciences. These proceedings include 21 papers covering many different subfields of bioinformatics and computational biology. Focusing on interdisciplinary applications that combine e.g. bioinformatics, chemoinformatics, and system biology, they are intended to promote the collaboration of scientists from different research groups and with different backgrounds (computer scientists, mathematicians, biologists) to reach breakthrough solutions and overcome the challenges outlined above.

The difficulty in achieving effective translation of basic mechanistic biomedical knowledge into effective therapeutics, is the greatest challenge in biomedical research. Nowhere is this more apparent than in the reductionist approaches to understanding and manipulating the acute inflammatory response in the settings of sepsis, trauma/hemorrhage, wound healing, and related processes. This book discusses complex systems and computational biology methods and approaches that have advanced sufficiently to allow for knowledge generation, knowledge integration, and clinical translation in the settings of complex diseases related to the inflammatory response. Well-regulated, self-resolving inflammation is necessary for the appropriate communication and resolution of infection and trauma, and for maintenance of proper physiology and homeostasis. In contrast, self-sustaining inflammation drives the pathobiology of the aforementioned diseases. It is now increasingly recognized that controlling and reprogramming inflammation in order to reap the benefits of this evolutionarily-conserved process is preferred to simply abolishing indiscriminately.

This book constitutes the refereed proceedings of the Third International Workshop on Functional Imaging and Modeling of the Heart, FIMH 2005, held in Barcelona, Spain in June 2005. The 47 revised full papers presented were carefully reviewed and selected from numerous submissions. The papers are organized in topical sections on modeling of the heart: anatomy extraction and description; electro-physiology and electro- and magnetography; modeling of the cardiac mechanisms and functions; and cardiac motion estimation.

Over recent decades vast amounts of biological data have been accumulated. However, it is becoming increasingly difficult to apply traditional theoretical methods to the formulation of coherent pictures of cell and organ function because it is no longer possible for a human theorist to integrate all of the available information. Instead, computer technologies must now be used to perform this integration. This book brings together contributions from many different fields to summarize the current status of computer-assisted modelling of biological processes. The initial chapters deal with fundamental developments in hardware, software and mathematics that underlie current approaches to biological modelling. Next, different approaches to collating data on gene structure and function are presented. These databases form a vital resource for any investigator trying to construct an integrated picture of particular biological systems. Cell signalling systems form a particularly complicated aspect of all cellular function and are important both in the understanding of basic cellular

processes and in selecting targets for drugs. Recent approaches to integrating data on cell signalling into computer models are covered. Further chapters build on these approaches to show how computerized models of intact cells can be developed. Finally, approaches to the computer modelling of whole organs such as the heart are presented. The role of computer modelling in drug design is the subject of the final chapter and is also touched on throughout the discussions. This thesis describes the development of Beatbox - a simulation environment for computational biology of the heart. Beatbox aims to provide an adaptable, approachable simulation tool and an extensible framework with which High Performance Computing may be harnessed by researchers. Beatbox is built upon the QUI software package, which is studied in Chapter 2. The chapter discusses QUI's functionality and common patterns of use, and describes its underlying software architecture, in particular its extensibility through the addition of new software modules called 'devices'. The chapter summarises good practice for device developers in the Laws of Devices. Chapter 3 discusses the parallel architecture of Beatbox and its implementation for distributed memory clusters. The chapter discusses strategies for domain decomposition, halo swapping and introduces an efficient method for exchange of data with diagonal neighbours called Magic Corners. The development of Beatbox's parallel Input/Output facilities is detailed, and its impact on scaling performance discussed. The chapter discusses the way in which parallelism can be hidden from the user, even while permitting the runtime execution user-defined functions. The chapter goes on to show how QUI's extensibility can be continued in a parallel environment by providing implicit parallelism for devices and defining Laws of Parallel Devices to guide third-party developers. Beatbox's parallel performance is evaluated and discussed. Chapter 4 describes the extension of Beatbox to simulate anatomically realistic tissue geometry. Representation of irregular geometries is described, along with associated user controls. A technique to compute no-flux boundary conditions on irregular boundaries is introduced. The Laws of Devices are further developed to include irregular geometries. Finally, parallel performance of anatomically realistic meshes is evaluated.

“A fascinating look at how scientists are working to help doctors treat not just one disease at a time, but the aging process itself.” —Dr. Sanjay Gupta A startling chronicle by a brilliant young scientist takes us onto the frontiers of the science of aging, and reveals how close we are to an astonishing extension of our life spans and a vastly improved quality of life in our later years. Aging--not cancer, not heart disease--is the true underlying cause of most human death and suffering. We accept as inevitable that as we advance in years our bodies and minds begin to deteriorate and that we are ever more likely to be felled by dementia or disease. But we never really ask--is aging necessary? Biologists, on the other hand, have been investigating that question for years. After all, there are tortoises and salamanders whose risk of dying is the same no matter how old they are. With the help of science, could humans find a way to become old without getting

frail, a phenomenon known as "biological immortality"? In *Ageless*, Andrew Steele, a computational biologist and science writer, takes us on a journey through the laboratories where scientists are studying every bodily system that declines with age--DNA, mitochondria, stem cells, our immune systems--and developing therapies to reverse the trend. With bell-clear writing and intellectual passion, Steele shines a spotlight on a little-known revolution already underway. This book constitutes the proceedings of the 11th International Conference on Computational Methods in Systems Biology, CMSB 2013, held in Klosterneuburg, Austria, in September 2013. The 15 regular papers included in this volume were carefully reviewed and selected from 27 submissions. They deal with computational models for all levels, from molecular and cellular, to organs and entire organisms.

From the spontaneous rapid firing of cortical neurons to the spatial diffusion of disease epidemics, biological systems exhibit rich dynamic behaviour over a vast range of time and space scales. Unifying many of these diverse phenomena, *Dynamics of Biological Systems* provides the computational and mathematical platform from which to understand the underlying processes of the phenomena. Through an extensive tour of various biological systems, the text introduces computational methods for simulating spatial diffusion processes in excitable media, such as the human heart, as well as mathematical tools for dealing with systems of nonlinear ordinary and partial differential equations, such as neuronal activation and disease diffusion. The mathematical models and computer simulations offer insight into the dynamics of temporal and spatial biological systems, including cardiac pacemakers, artificial electrical defibrillation, pandemics, pattern formation, flocking behaviour, the interaction of autonomous agents, and hierarchical and structured network topologies. Tools from complex systems and complex networks are also presented for dealing with real phenomenological systems. With exercises and projects in each chapter, this classroom-tested text shows students how to apply a variety of mathematical and computational techniques to model and analyze the temporal and spatial phenomena of biological systems. MATLAB® implementations of algorithms and case studies are available on the author's website.

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.

This second edition expands upon and updates the vital research covered in its predecessor, by presenting state-of-the-art multidisciplinary and systems-oriented approaches to complex diseases arising from and driven by the acute inflammatory response. The chapters in this volume provide an introduction to different types of computational modeling, and how these methods can be applied to specific inflammatory diseases, with a focus on providing readers a roadmap for integrating advanced mathematical and computational techniques with traditional experimental methods. In this second edition, we cover both well-established and emerging modeling methods, especially state-of-the-art machine learning approaches and the integration of data-driven and mechanistic modeling. This volume introduces the concept of Model-based Precision Medicine as an alternative approach to the current view of Precision Medicine, based on leveraging mechanistic computational modeling to decrease cost while increasing the information value of the data being obtained. By presenting the role of computational modeling as an integrated component of the research process, *Complex Systems and Computational Biology Approaches to Acute Inflammation: A Framework for Model-based Precision Medicine* offers a window into the recent past, the present, and the future of computationally-augmented biomedical research.

This is a book of an international series on interdisciplinary topics of the Mathematical and Biological Sciences. The chapters are related to selected papers on the research themes presented at BIOMAT 2015 International Symposium on Mathematical and Computational Biology which was held in the Roorkee Institute of Technology, in Roorkee, Uttarakhand, India, on November 02–06, 2015. The treatment is both pedagogical and advanced in order to motivate research students to fulfill the requirements of professional practitioners. As in other volumes of this series, there are new important results on the interdisciplinary fields of mathematical and biological sciences and comprehensive reviews written by prominent scientific leaders of famous research groups. There are new results based on the state of art research in Population Dynamics, on Pattern Recognition of Biological Phenomena, the Mathematical Modelling of Infectious Diseases, Computational Biology, the Dynamic and Geometric Modelling of Biological Phenomena, the Modelling of Physiological Disorders, the Optimal Control Techniques in Mathematical Modelling of Biological Phenomena, the Hydrodynamics and Elasticity of Cell Tissues and Bacterial Growth and the Mathematical Morphology of Biological Structures. All these contributions are also strongly recommended to professionals from other scientific areas aiming to work on these interdisciplinary fields.

Contents: Mathematical Modelling of Infectious Diseases: Network Structure and Enzymatic Evolution in *Leishmania* Metabolism: A Computational Study (A Subramanian & R R Sarkar) Long-Term Potential of Imperfect Seasonal Flu Vaccine in Presence of Natural Immunity (S Ghosh & J M Heffernan) Impact of Non-Markovian Recovery on Network Epidemics (G Röst, Z Vizi & I Z Kiss) A Modelling Framework for Serotype Replacement in Vaccine-Preventable Diseases (M Kang, A L Espindola, M Laskowski & S M Moghadas) Pattern Recognition of Biological Phenomena: An Integrative Approach for Model Driven Computation of Treatments in Reproductive Medicine (R Ehrig, T Dierkes, S Schäfer, S Röblitz, E Tronci, T Mancini, I Salvo, V Alimguzhin, F Mari, I Melatti, A Massini, B Leeners, T H C Krüger, M Egli, F Ille & B Leeners) The Network Route to Biological Complexity (S J Banerjee, R K Grewal, S Sinha & S Roy) A Systems Biology Approach to Bovine Fertility and Metabolism: Introduction of a Glucose Insulin Model (Julia Plöntzke, M Berg, C Stötzel & S

Röblitz)Biographer: Visualization of Graph Theoretical Patterns, Measurements, and Analysis in Mathematical Biology (R Viswanathan, S Liang, Y Yang & J R Jungck)Hydrodynamics and Elasticity of Cell Tissues and Bacterial Growth:Modelling the Early Growth of Stem Cell Tissues (R A Barrio, S Orozco-Fuentes & R Romero-Arias)Non-local Hydrodynamics of Swimming Bacteria and Self-Activated Process (S Roy & R Llinás)Dynamic and Geometric Modelling of Biomolecular Structures:Geometric Analysis of the Conformational features of Protein Structures (M Datt)Computational Biology:Prediction of System States, Robustness and Stability of the Human Wnt Signal Transduction Pathway using Boolean Logic (L Nayak, R K De & A Datta)Entropy Measures and the Statistical Analysis of Protein Family Classification (R P Mondaini & S C de Albuquerque Neto)Clustering Neuraminidase Influenza Protein Sequences (X Li, H Jankowski, S Boonpatcharanon, V Tran, X Wang & J M Heffernan)Optimal Control Techniques in Mathematical Modelling of Biological Phenomena:Optimal Control for Therapeutic Drug Treatment on a Delayed Model Incorporating Immune Response (P Dubey, B Dubey & U S Dubey)Population Dynamics:Bifurcations and Oscillatory Dynamics in a Tumor Immune Interaction Model (S Khajanchi)On a Nonlinear System Modelling Darwinian Dynamics and the Immune Response to Cancer Evolution (A Bellouquid, M Ch-Chaoui & E de Angelis)Sexual Selection is Not Required: A Mathematical Model of Species with Sexually Differentiated Death Rates (D Wallace, E Dauson, C Pinion & K Hayashi)Models for Two Strains of the Caprine Arthritis Encephalitis Virus Disease (S Collino, E Venturino, L Ferreri, L Bertolotti, S Rosati & M Giacobini)Conservation of Forestry Biomass Introducing Variable Taxation for Harvesting: A Mathematical Model (M Chaudhary, J Dhar & O P Misra)Stability Analysis of a Two Species Competition Model with Fuzzy Initial Conditions: Fuzzy Differential Equation Approach Environment (S Paul, P Bhattacharya & K S Chaudhuri)Modelling Physiological Disorders:Magnetic Resonance Guided High Intensity Focused Ultrasound — Mathematical Modeling of an Innovative, State of the Art Technology for Cancer Therapy (J Murley, J Thangaraj, J Drake, A Waspe & S Sivaloganathan)The Effects of Fibroblasts on Wave Dynamics in a Mathematical Model for Human Ventricular Tissue (A R Nayak & R Pandit)A Simple Logistic Sigmoidal Model Predicts Oxidative Stress Thresholds in Newly Diagnosed Diabetics on Glucose Control Therapy (R Kulkarni) Readership: Undergraduates, graduates, researchers and all practitioners in the interdisciplinary fields of Mathematical Biology, Biological Physics and Mathematical Modelling of Biosystems.

Development of powerful new high- throughput technologies for probing the transcriptome, proteome and metabolome is driving the rapid acquisition of information on the function of molecular systems. The importance of these achievements cannot be understated – they have transformed the nature of both biology and medicine. Despite this dramatic progress, one of the greatest challenges that continues to confront modern biology is to understand how behavior at the level of genome, proteome and metabolome determines physiological function at the level of cell, tissue and organ in both health and disease. Because of the inherent complexity of biological systems, the development, analysis, and validation of integrative computational models based directly on experimental data is necessary to achieve this understanding. This approach, known as systems biology, integrates computational and experimental approaches through iterative development of mathematical models and experimental validation and testing. The combination of these approaches allows for a mechanistic understanding of the function of complex biological systems in health and their dysfunction in disease. The National Heart, Lung, and Blood Institute (NHLBI) has recognized the importance of the systems biology approach for understanding normal physiology and perturbations associated with heart, lung, blood, and sleep diseases and disorders. In 2006, NHLBI announced the Exploratory Program in Systems Biology, followed in 2010 by the NHLBI Systems Biology Collaborations. The goal of these programs is to support collaborative teams of investigators in using experimental and computational strategies to integrate the component

parts of biological networks and pathways into computational models that are based firmly on and validated using experimental data. These validated models are then applied to gain insights into the mechanisms of altered system function in disease, to generate novel hypotheses regarding these mechanisms that can be tested experimentally, and to then use the results of experiments to refine the models. The purpose of this Research Topic is to present the range of innovative, new approaches being developed by investigators working in areas of systems biology that couple experimental and modeling studies to understand the cause and possible treatment of heart, lung, blood and sleep diseases and disorders. This Research Topic will be of great interest to the cardiovascular research community as well as to the general community of systems biologists.

Modelling the genesis and propagation of electrical activity in the heart in quantitative terms is one of the most important recent applications of mathematical modelling in biology. The main research direction, and the most important for biological and medical applications, is the development of realistic models of electrical activity in cardiac tissue and the whole mammalian heart. Recent progress in nonlinear dynamics, advances in computer technology and experiments on cardiac tissue have made feasible the construction of such models. *Computational Biology of the Heart* is the first book to provide a comprehensive survey of recent research together with a systematic overview of the subject. The contributions, all written by experts in the different areas of the subject, cover all main aspects of whole heart modelling: from excitation in single cells, to two and three dimensional models of cardiac tissue and the whole heart. Various computational models and techniques are described and then applied to reconstruct and visualise modelled activity in both normal and pathological heart tissues. The models are nonlinear and use techniques of ordinary differential equations, partial differential equations and eikonal equations. The book also provides a review of modelling cardiac contraction, mapping electrical activity from electrocardiograms, and recent experimental observations of wave propagation in the whole heart. Graduate students and researchers in such areas as applied mathematical biology, clinical physiology and cardiology will find this book to be an invaluable resource for their work.

Computational Biology of the Heart Wiley-Blackwell

Peter Hunter Computational physiology for the cardiovascular system is entering a new and exciting phase of clinical application. Biophysically based models of the human heart and circulation, based on patient-specific anatomy but also informed by population atlases and incorporating a great deal of mechanistic understanding at the cell, tissue, and organ levels, offer the prospect of evidence-based diagnosis and treatment of cardiovascular disease. The clinical value of patient-specific modeling is well illustrated in application areas where model-based interpretation of clinical images allows a more precise analysis of disease processes than can otherwise be achieved. For example, Chap. 6 in this volume, by Speelman et al., deals with the very difficult problem of trying to predict whether and when an abdominal aortic aneurysm might burst. This requires automated segmentation of the vascular geometry from magnetic resonance images and finite element analysis of wall stress using large deformation elasticity theory applied to the geometric model created from the segmentation. The time-varying normal and shear stress acting on the arterial wall is estimated from the arterial pressure and flow distributions. Thrombus formation is identified as a potentially important contributor to changed material properties of the arterial wall. Understanding how the wall adapts and remodels its material properties in the face of changes in both the stress loading and blood constituents associated with inflammatory processes (IL6, CRP, MMPs, etc). This volume compiles accepted contributions for the 2nd Edition of the Colombian Computational Biology and Bioinformatics Congress CCBCOL, after a rigorous review process in which 54 papers were accepted for publication from 119 submitted contributions. Bioinformatics and Computational Biology are areas of knowledge that have emerged due to

advances that have taken place in the Biological Sciences and its integration with Information Sciences. The expansion of projects involving the study of genomes has led the way in the production of vast amounts of sequence data which needs to be organized, analyzed and stored to understand phenomena associated with living organisms related to their evolution, behavior in different ecosystems, and the development of applications that can be derived from this analysis.

Readership: Academics, researchers, industrialists, postgraduate and graduate students in databases, fuzzy logic, machine vision/pattern recognition, neural networks, bioengineering, electrical & electronic engineering, and bioinformatics. Key Features: Provides a significant and uniquely comprehensive reference source for research workers and practitioners Features 130 contributors from 27 countries, among the foremost authorities in industry, government and academia Institutions, laboratories and individuals involved in the area of medical imaging should possess this set Keywords: Medical Imaging; Systems Technology; Cardiovascular Systems; Brain Systems; General Anatomy; Modalities; Diagnosis Optimization Methods; Computational Methods

This book describes mathematical models and numerical techniques for simulating the electrical activity in the heart. It gives an introduction to the most important models, followed by a detailed description of numerical techniques. Particular focus is on efficient numerical methods for large scale simulations on both scalar and parallel computers. The results presented in the book will be of particular interest to researchers in bioengineering and computational biology.

The tenth Henry Goldberg Workshop is an excellent occasion to recall our goals and celebrate some of our humble achievements. Vision and love of our fellow man are combined here to: 1) Foster interdisciplinary interaction between leading world scientists and clinical cardiologists so as to identify missing knowledge and catalyze new research ideas; 2) relate basic microscale, molecular and subcellular phenomena to the global clinically manifested cardiac performance; 3) apply conceptual modelling and quantitative analysis to better explore, describe, and understand cardiac physiology; 4) interpret available clinical data and design new revealing experiments; and 5) enhance international cooperation in the endless search for the secrets of life and their implication on cardiac pathophysiology. The first Goldberg Workshop, held in Haifa, in 1984, explored the interaction of mechanics, electrical activation, perfusion and metabolism, emphasizing imaging in the clinical environment. The second Workshop, in 1985, discussed the same parameters with a slant towards the control aspects. The third Goldberg Workshop, held in the USA at Rutgers University, in 1986, highlighted the transformation of the microscale activation phenomena to macro scale activity and performance, relating electrophysiology, energy metabolism and cardiac mechanics. The fourth Goldberg Workshop continued the effort to elucidate the various parameters affecting cardiac performance, with emphasis on the ischemic heart. The fifth Workshop concentrated on the effect of the inhomogeneity of the cardiac muscle on its performance. The sixth Workshop highlighted new imaging techniques which allow insight into the local and global cardiac performance.

Computational biology, mathematical biology, biology and biomedicine are currently undergoing spectacular progresses due to a synergy between technological advances and inputs from physics, chemistry, mathematics, statistics and computer science. The goal of this book is to evidence this synergy by describing selected developments in the following fields: bioinformatics, biomedicine and neuroscience. This work is unique in

two respects - first, by the variety and scales of systems studied and second, by its presentation: Each chapter provides the biological or medical context, follows up with mathematical or algorithmic developments triggered by a specific problem and concludes with one or two success stories, namely new insights gained thanks to these methodological developments. It also highlights some unsolved and outstanding theoretical questions, with a potentially high impact on these disciplines. Two communities will be particularly interested in this book. The first one is the vast community of applied mathematicians and computer scientists, whose interests should be captured by the added value generated by the application of advanced concepts and algorithms to challenging biological or medical problems. The second is the equally vast community of biologists. Whether scientists or engineers, they will find in this book a clear and self-contained account of concepts and techniques from mathematics and computer science, together with success stories on their favorite systems. The variety of systems described represents a panoply of complementary conceptual tools. On a practical level, the resources listed at the end of each chapter (databases, software) offer invaluable support for getting started on a specific topic in the fields of biomedicine, bioinformatics and neuroscience.

Out of all non-communicable diseases, heart diseases have become the leading cause of death and disease burden worldwide. Heart diseases describe a variety of circumstances that affect your heart. One common condition is the heart rhythm problem often called an arrhythmia. The rhythmic beating of the human heart can be altered due to various reasons. This inconsistency in beating can lead to a lethal form of arrhythmia that we call ventricular fibrillation. We treat fibrillation by applying an electrical shock to the heart using a unipolar electrode or bipolar electrodes. To build better pace makers and defibrillators, we must understand how the heart responds to an electrical shock. One way to study cardiac arrhythmias is using a mathematical model. The computational biology of the heart is one of the most important recent applications of mathematical modeling in biology. By using mathematical models, we can understand the mechanisms responsible of the heart's electrical behavior. We investigate if the time-independent, inwardly rectifying potassium current through the cell membrane inhibits the hyperpolarization after a stimulus electrical pulse is applied to the resting heart tissue. The inhibition of hyperpolarization is due to long duration stimulus pulses, but not short duration pulses. We also investigate the minimum conditions required for the dip in strength-interval curves using a simple but not so simple parsimonious ionic current model coupled with the bidomain model. Unipolar anodal stimulations still results in the dip in the strength-interval curves and this explains the minimum conditions for this phenomenon to occur. Bipolar stimulation of cardiac tissue using the parsimonious ionic current model reveals (sic) that the strength-interval curves are sensitive to the separation between electrodes and the electrode orientation relative to the fiber direction. One of the ionic currents in the parsimonious ionic current model mimics the time-independent inwardly rectifying potassium current and this study examines the importance of this current in mathematical models that describe cardiac electrical behavior.

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