Final Program and Abstracts

This conference is sponsored by the SIAM Activity Group on the Life Sciences.

The SIAM Activity Group on the Life Sciences was established to foster the application of mathematics to the life sciences and research in mathematics that leads to new methods and techniques useful in the life sciences.

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Monday, August 6
4:00 PM – 8:00 PM

Tuesday, August 7
7:30 AM – 4:00 PM

Wednesday, August 8
8:00 AM – 4:00 PM

Thursday, August 9
8:00 AM – 4:00 PM

Friday, August 10
8:00 AM – 4:00 PM

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Funding Agency

SIAM and the conference organizing committee wish to extend their thanks and appreciation to U.S. National Science Foundation for its support of this conference.

Funding Panel

Funding Agency Panel

1:00 pm - 2:00 pm

Emerald Ballroom - 2nd Floor

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- Coffee breaks daily
- Welcome Reception and Poster Sessions
- Room set-ups and audio/visual equipment

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The poster sessions are scheduled for Wednesday, August 8, 8:00 PM – 10:00 PM and Thursday, August 9, 8:00 PM – 10:00 PM. Presenters are requested to put up their posters no later than 8:00 PM, the official start time of both sessions. Boards and push pins will be available to Wednesday's presenters at 7:30 AM on Tuesday, August 7, and for Thursday's presenters the boards will be available on Thursday, August 9 at 8:00 AM. Please visit the speaker, organizer and co-author index to see in which session your poster has been scheduled.

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Table Top Display

SIAM

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Comments?

Comments about SIAM meetings are encouraged! Please send to:

Sven Leyffer, SIAM Vice President for Programs (*vpp@siam.org*)

Get-togethers

- Welcome Reception
  Monday, August 6
  6:00 PM – 8:00 PM
  Pool Terrace - 3rd Floor

- Poster Sessions
  Wednesday, August 8 and Thursday, August 9
  8:00 PM – 10:00 PM
  Foyer – 2nd Floor

- Business Meeting
  (open to SIAG/LS members)
  Wednesday, August 8
  5:30 PM – 6:00 PM
  Emerald Ballroom - 2nd Floor
  Complimentary beer and wine will be served.

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Minitutorials

Tuesday, August 7

MT1

Multiscale Modeling

10:00 AM - 12:00 PM

Room: Diamond I - 2nd Floor

There are a significant number of problems that exhibit a large range of physical scales, for example small vortex generators positioned on large scale aerofoils; but none so prominent in the 21st Century as that exemplified within the biological sciences and engineering. Biological Engineering problems have a multitude of physical scales. In the major arterial networks the blood flow dynamic scales are of the order of 1mm (cerebral vessels) up to 25mm (ascending aorta). Downstream of any major vessel exists a substantial network of arteries, arterioles and capillaries whose characteristic length scales reach the order of 10-20 microns. Within the walls of these cylindrical vessels lie ion channels consisting of proteins (100 nanometers and smaller) folded in such a way as to allow only certain molecules through the membrane.

Taking examples from cerebral perfusion and arterial coupled cell function this workshop will look at a range of ways in which multi-scale problems can be investigated. Our big question that has yet to be answered is in different models that highlight different scales do all the models provide essentially the same answer?

Organizer: Tim David, University of Canterbury, New Zealand

10:00-11:55 Multiscale Modeling

Tim David, University of Canterbury, New Zealand

Thursday, August 9

MT2

Numerical Methods for Studying Stochastic Models of Biological Systems

10:00 AM - 12:00 PM

Room: Diamond II - 2nd Floor

We will introduce several numerical methods for solving stochastic models of biological systems. The first half of the minitutorial will focus on numerical methods for simulating models involving continuous time Markov chains. Such models often arise in the study of chemical and population processes. The second half of the minitutorial will focus on particle-based models that incorporate explicit spatial transport due to random walks or drift-diffusion processes. Applications of these simulation methods to the study of problems in cell biology will be used to illustrate the methods developed.

Organizer: Samuel A. Isaacson, Boston University, USA

10:00-10:55 Stochastic Simulation of Models Arising in the Life Sciences

David Anderson, University of Wisconsin, Madison, USA

11:00-11:55 Stochastic Simulation of Spatially-Distributed Models Arising in the Life Sciences

Samuel A. Isaacson, Boston University, USA

SIAM Activity Group on Life Sciences (SIAG/LS)

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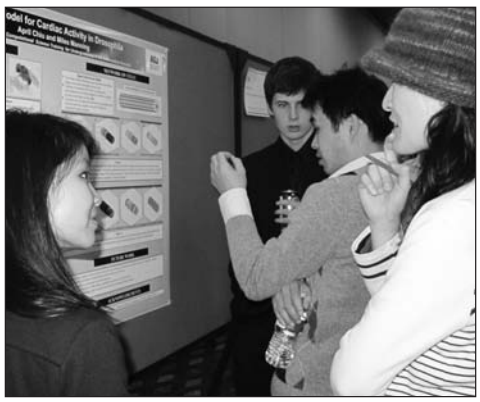

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Invited Plenary Speakers

All Invited Plenary Presentations will take place in Emerald Ballroom – 2nd Floor

Tuesday, August 7

8:45 AM – 9:30 AM

IP1 The Mysteries of Human Physiology (Can Only be Understood with Mathematics)

Michael C. Reed, *Duke University, USA*

2:00 PM – 2:45 PM

IP2 On Growth and Form: Geometry, Physics and Biology

L. Mahadevan, *Harvard University, USA*

Wednesday, August 8

8:45 AM – 9:30 AM

IP3 DNA Unknotting and Unlinking

Mariel Vazquez, *San Francisco State University, USA*

2:00 PM – 2:45 PM

IP4 Computational Physiology and the VPH/Physiome Project

Peter Hunter, *University of Auckland, New Zealand*

Invited Plenary Speakers

All Invited Plenary Presentations will take place in Emerald Ballroom – 2nd Floor

Thursday, August 9

8:45 AM – 9:30 AM

IP5 Patient-specific Computational Fluid Dynamics for Noninvasive Assessment of Heart Disease

Charles Taylor, *HeartFlow, Inc, USA*

2:00 PM – 2:45 PM

IP6 Complex Systems in Health and their Breakdown with Aging and Disease

Ary L. Goldberger, *Harvard Medical School, USA*

Friday, August 10

8:45 AM – 9:30 AM

IP7 Life at Stability's Edge: From the Fingertip to Seizure Onset

John Milton, *Claremont College, USA*

2:00 PM – 2:45 PM

IP8 Biological and Mathematical Perspectives on the Classification of Bursting Mechanisms

Arthur S. Sherman, *National Institutes of Health, USA*

LS12 Program

Notes

Monday, August 6

Registration
4:00 PM-8:00 PM

Room:Foyer - 2nd Floor

Welcome Reception
6:00 PM-8:00 PM

Room:Pool Terrace - 3rd Floor

Tuesday, August 7

Registration
7:30 AM-4:00 PM

Room:Foyer - 2nd Floor

Welcome Remarks
8:30 AM-8:45 AM

Room:Emerald Ballroom - 2nd Floor

IP1
The Mysteries of Human Physiology (Can Only be Understood with Mathematics)
8:45 AM-9:30 AM

Room:Emerald Ballroom - 2nd Floor

Chair: Robert Miura, New Jersey Institute of Technology, USA

Human physiological systems are difficult to understand because they involve regulatory mechanisms at the genomic, the cellular, and the physiological level and, of course, interactions between the levels. Only with mathematics can we discover the mechanisms underlying the bewildering collections of (variable) measurements at all three levels. Numerous examples, including maternal-fetal conflict, insulin signaling, and axonal transport, will be given illustrating both the difficulties and pleasures of investigating who we are and how we work. What fields of mathematics are necessary and useful for this endeavor, now and in the future? The answer is "almost all,'' but progress in dynamical systems and stochastic processes will be central.

Michael C. Reed
Duke University, USA

Coffee Break
9:30 AM-10:00 AM

Room:Foyer - 2nd Floor

Tuesday, August 7

MT1
Multiscale Modeling
10:00 AM-12:00 PM

Room:Diamond I - 2nd Floor

Chair: Tim David, University of Canterbury, New Zealand

There are a significant number of problems that exhibit a large range of physical scales, for example small vortex generators positioned on large scale aerofoils; but none so prominent in the 21st Century as that exemplified within the biological sciences and engineering. Biological Engineering problems have a multitude of physical scales.

10:00-11:55 Multiscale Modeling
Tim David, University of Canterbury, New Zealand

Tuesday, August 7

MS1

Model Reduction and Representation of Biochemical Reaction Networks

10:00 AM-12:00 PM

Room:Diamond II - 2nd Floor

Nonlinear, high-dimensional dynamical systems with many unknown parameters are usually used as models of biochemical networks. Therefore, simplifications of comprehensive models are typically necessary to facilitate the analysis of experimental data. However, it is not clear how properties (e.g., multistationarity) of a simplified/reduced model relate to those of the full model and, thus, whether the interpretation of data is transferrable across to the simplified model. This mini-symposium reports on new mathematical results in relation to model reduction, elimination of variables (e.g. using the quasi-steady state approximation), dynamically equivalent representations of networks (e.g conjugate networks) and parameter identifiability.

Organizer: Carsten Wiuf
University of Copenhagen, Denmark

10:00-10:25 Model Reduction and Elimination of Variables in Chemical Reaction Networks
Carsten Wiuf and Elisenda Feliu, University of Copenhagen, Denmark

10:30-10:55 Computing Linearly Conjugate Chemical Reaction Networks with Minimal Deficiency
Matthew D. Johnston and David Siegel, University of Waterloo, Canada; Gabor Szederkenyi, Hungarian Academy of Sciences, Hungary

11:00-11:25 Model Reduction and Parameter Identifiability for Biochemical Reaction Networks
Gheorghe Craciun, University of Wisconsin, Madison, USA

11:30-11:55 New Results and Methods for Computing Dynamically Equivalent and Linearly Conjugate Reaction Network Structures
Gabor Szederkenyi, Hungarian Academy of Sciences, Hungary; Zsolt Tuza, Alfréd Rényi Institute of Mathematics, Hungary; Tamas Peni, Hungarian Academy of Sciences, Hungary

Tuesday, August 7

MS2

Modelling Morphogensis in Plants at the Cellular and Subcellular Level

10:00 AM-12:00 PM

Room:Crystal Ballroom I - 2nd Floor

Plant morphogensis has been shown to be controlled by a small protein called auxin which is actively pumped through all cells. It is widely held that there is a feedback mechanism between the auxin concentration and the expression of auxin in- and out-pumps. In these talks mathematical and computer models are presented of auxin flow and the consequent cell response in terms of G-proteins that promote cell growth. Analyses of the consequent partial differential equations are shown to agree with laboratory experiments and large-scale computations via finite differences and agent based simulations.

Organizer: Alan R. Champneys
University of Bristol, United Kingdom

10:00-10:25 Modelling Root Hair Initiation Via Non-Homogeneous Reaction Diffusion Equations in 1D and 2D
Victor Brena and Alan R. Champneys, University of Bristol, United Kingdom; Michael Ward, University of British Columbia, Canada; Claire Grierson, University of Bristol, United Kingdom

10:30-10:55 Nonlocal Eigenvalue Problems and the Stability of Localized Biological Patterns in Reaction-Diffusion Systems
Michael Ward, University of British Columbia, Canada

11:00-11:25 From Cell Polarity to Morphomics
Veronica Grieneisen, Yara Sanchez-Corrales, Jop van Rooij, and Stan Marée, John Innes Research Centre, United Kingdom

11:30-11:55 Crossroads: Interplay Between Modelling and Experiments to Unravel Stem Cell Division in Arabidopsis
Stan Maree, John Innes Research Centre, United Kingdom; Alfredo Cruz-Ramirez, Sara Diaz-Trivino, and Ben Scheres, Utrecht University, The Netherlands; Veronica Grieneisen, John Innes Research Centre, United Kingdom

Tuesday, August 7

MS3

Converging Clinical Oncology with Physical Sciences Based Mathematical Modeling

10:00 AM-12:00 PM

Room:Emerald Ballroom - 2nd Floor

Cancer research has become increasingly quantitative in scope and content; however, a variety of challenges remain in the detection, treatment, management, and prevention of the disease. The convergence of physical sciences based mathematical modeling and simulations with clinical oncology will correspondingly play a critical role in synthesizing and comprehending some of the dynamics underlying the behavior of disease over various spatial and temporal scales. This minisymposium will present in the context of clinical oncology recent advances in physical sciences based, mathematical models and simulations that will explore the dynamics of cancer progression and therapeutic response treatment.

Organizer: Larry Nagahara
National Cancer Institute, USA

10:00-10:25 Dynamics in the Tissue State-Space: A Computational Environment
James Sethian, University of California, Berkeley, USA; Chris Rycroft, Lawrence Berkeley National Laboratory, USA; Robert Saye, University of California, Berkeley, USA

10:30-10:55 Optimizing Radiation Delivery Schedules for Gliomas
Kevin Leder, University of Minnesota, USA; Ken Pitter and Eric Holland, Memorial Sloan-Kettering Cancer Center, USA; Franziska Michor, Harvard University, USA

continued on next page

11:00-11:25 Phenotypic Transition Maps of 3D Breast Acini Obtained by Image-Guided Agent-Based Modeling
Jonathan Tang and Sabine Becker-Weimann, Lawrence Berkeley National Laboratory, USA; Heiko Enderling, Tufts University, USA; Mina Bissell and *Sylvain V. Costes*, Lawrence Berkeley National Laboratory, USA

11:30-11:55 A Novel, Patient-Specific Physical Pathology Approach for Prediction of Tumor Growth and Chemotherapy Outcome
Vittorio Cristini, University of New Mexico Cancer Center, USA

Tuesday, August 7

MS4

Cardiac Fluid Dynamics and Electromechanics

10:00 AM-12:00 PM

Room:Crystal Ballroom II - 2nd Floor

The heart is a coupled electro-fluid-mechanical system: the contractions of the cardiac muscle that drive the movement of blood are stimulated and coordinated by the electrophysiology of the heart; these contractions in turn affect the electrical function of the heart through the action of stretch-activated ion channels and by altering the macroscopic conductivity properties of the tissue. This minisymposium will present ongoing work to develop sophisticated computational models of cardiac fluid dynamics and electromechanics, and on the application of these models to study the dynamics of the embryonic, pediatric, and adult heart in health and disease.

Organizer: Laura A. Miller
University of North Carolina, Chapel Hill, USA

Organizer: Boyce Griffith
New York University, USA

10:00-10:25 Cardiac Fluid-structure and Electro-mechanical Interaction
Boyce E. Griffith, New York University, USA; David M. McQueen and Charles S. Peskin, Courant Institute of Mathematical Sciences, New York University, USA

10:30-10:55 Electromechanical Pumping in the Embryonic Tubular Heart
Laura A. Miller, University of North Carolina, Chapel Hill, USA; Austin Baird and Tiffany King, University of North Carolina, USA

11:00-11:25 Blood Flow Simulations in Coronary Artery Aneurysms in Children with Kawasaki Disease
Alison Marsden, Dibyendu Sengupta, Andrew Kahn, and Jane Burns, University of California, San Diego, USA

11:30-11:55 Multi-Scale Modeling of Electromechanics in the Failing Heart
Andrew D. McCulloch and Roy Kerckhoffs, University of California, San Diego, USA

Tuesday, August 7

MS5

Single Cell Systems Biology and Cytomics: The Future Has Just Begun

10:00 AM-12:00 PM

Room:Topaz - 2nd Floor

High-throughput high-content flow cytometry (HTFC) has made tremendous progress in the last ten years, and single-cell analyses of samples that can interrogate fifty intra-cellular processes are now feasible. HTFC experiments advance systems biology at the single cell level, leading to personalized medicine and new approaches to drug discovery. A single HTFC experiment can generate Terabytes of data, but the data processing and algorithmic infrastructure that can analyze this data in a reasonable amount of time is yet to be developed. Experts in flow cytometry and bioinformatics will present recent developments from this research area.

Organizer: Alex Pothen
Purdue University, USA

10:00-10:25 An Overview of Data Analysis in High-throughput High-content Flow Cytometry
Ryan Brinkman, British Columbia Cancer Agency, United Kingdom

10:30-10:55 Quantitative Flow Cytometry Analysis using Domain Knowledge Constrained Spectral Unmixing
Bartek Rajwa, Purdue University, USA

11:00-11:25 Fingerprinting, Pattern Discovery and Mining Flow Cytometry Data
Wade Rogers, University of Pennsylvania, USA

11:30-11:55 Flowmatch: An Algorithm for Registering Cell Populations From high Throughput Flow Cytometry Data
Ariful Azad, Purdue University, USA; *Saumyadipta Pyne*, Dana Farber Cancer Institute and Harvard Medical School, USA; Alex Pothen, Purdue University, USA

Tuesday, August 7

MS6

Perceptual Rivalry and Mathematical Modeling - Part I of II

10:00 AM-12:00 PM

Room:Opal - 2nd Floor

For Part 2 see MS14

Binocular rivalry is a visual phenomenon in which perception alternates between dissimilar images presented to each eye. Binocular rivalry has been extensively studied, partly due to implications for conscious visual processing. Since the first systematic study of Charles Wheatstone back in 1830s, many beautiful experiments have been carried out and several interesting mathematical models have been proposed to address this phenomenon. This symposium aims to bring together experimentalists and mathematicians to discuss perceptual rivalry from different perspectives, give new insights for brain activities and inspire more collaboration.

Organizer: Yunjiao Wang
Rice University, USA

Organizer: Tyler McMillen
California State University, Fullerton, USA

10:00-10:25 The Role of Mutual Inhibition in Binocular Rivalry
Carson C. Chow, National Institutes of Health, USA

10:30-10:55 Neural Field Model of Binocular Rivalry waves
Paul C. Bressloff, University of Utah, USA and University of Oxford, United Kingdom; *Matthew Weber*, Oxford University, United Kingdom

11:00-11:25 Stochastic and Adaptive Switching in Competitive Neural Network Models of Perceptual Rivalry
Zachary Kilpatrick, University of Pittsburgh, USA

11:30-11:55 Explaining the Dynamics of Binocular Rivalry as Inference About Latent Images with Markov Chain Monte Carlo
Edward Vul, University of California, USA; Sam Gershman and Josh Tenenbaum, Massachusetts Institute of Technology, USA

Tuesday, August 7

MS7

Advanced Mathematical Models of Protein--Solvent Interactions - Part I of II

10:00 AM-12:00 PM

Room:Pearl - 3rd Floor

For Part 2 see MS15

Protein structure and function are determined in large part by interactions with the surrounding environment, usually a solvent that is mostly water with dissolved ions (e.g. sodium). Solvent influence can be modeled using all-atom molecular dynamics (MD), which require thousands of water molecules and ions, and are therefore computationally expensive; in contrast, continuum models can be hundreds or thousands of times faster, but sacrifice molecular detail for speed. A variety of promising multiscale modeling approaches have been proposed to bridge these two extremes, most of which face a common set of computational challenges (speed and scalability). This minisymposium will bring together mathematicians, chemists, and biophysicists to discuss the mathematical research that would have a broad, sustained impact on this important modeling problem.

Organizer: Jaydeep P. Bardhan
Rush University Medical Center, USA

Organizer: Bo Li
University of California, San Diego, USA

10:00-10:25 Progress and Ongoing Challenges in Protein-Solvent Modeling
Jaydeep P. Bardhan, Rush University Medical Center, USA

10:30-10:55 Continuum Electrostatics with Ionic Size Effects and Variational Solvation
Bo Li, University of Maryland, USA

11:00-11:25 Multi-scale Modeling of pH Dependent Viral Capsid Dynamics
Charles L. Brooks, University of Michigan, USA

11:30-11:55 Structured Continuum Free Energy Calculations
B.M. Pettitt, University of Houston, USA

Tuesday, August 7

Lunch Break

12:00 PM-2:00 PM

Attendees on their own

IP2

On Growth and Form: Geometry, Physics and Biology

2:00 PM-2:45 PM

Room:Emerald Ballroom - 2nd Floor

Chair: Carson Chow, National Institutes of Health, USA

The diversity of form in living beings led Darwin to state that it is “enough to drive the sanest man mad”. How can we describe this variety? How can we predict it? Motivated by biological observations on different scales from molecules to tissues, I will show how a combination of physical experiments, mathematical models and simple computations allow us to begin to unravel the physical basis for morphogenesis.

L Mahadevan
Harvard University, USA

Coffee Break

2:45 PM-3:15 PM

Room:Foyer - 2nd Floor

Tuesday, August 7

MS8

Understanding Multistationarity in Biochemical Reaction Networks

3:15 PM-5:15 PM

Room:Emerald Ballroom - 2nd Floor

Multistationarity in cellular systems provides a mechanism for switching between different responses and can be crucial for cellular decision making. It is in general difficult to decide whether a particular system has the capacity to exhibit multiple steady states. Typical systems are high-dimensional and contain many parameters that are unknown or poorly determined. In this session we will discuss recent theoretical and algorithmic results concerning the existence of multiple steady states in biochemical reaction networks, in the context of chemical reaction network theory. The focus will be on signaling events involving protein modifications (e.g. phosphorylation) for signal transmission.

Organizer: Elisenda Feliu
University of Copenhagen, Denmark

3:15-3:40 Preclusion of Switch Behavior in a Large Class of Reaction Networks
Elisenda Feliu and Carsten Wiuf, University of Copenhagen, Denmark

3:45-4:10 Switching in Multisite Phosphorylation Networks
Carsten Conradi, Max Planck Institute for Dynamics of Complex Systems, Germany

4:15-4:40 An Approach to Multistationarity via Elimination
Carsten Conradi, Max Planck Institute for Dynamics of Complex Systems, Germany; Alicia Dickenstein and *Mercedes Pérez Millán*, Universidad de Buenos Aires, Argentina; Anne Shiu, University of Chicago, USA

4:45-5:10 Steady States of Multisite Phosphorylation Systems
Anne Shiu, University of Chicago, USA; Carsten Conradi, Max Planck Institute for Dynamics of Complex Systems, Germany; Mercedes Perez Millan and Alicia Dickenstein, Universidad de Buenos Aires, Argentina

Tuesday, August 7

MS9

Models for Growth Hormone Transport in Plants

3:15 PM-5:15 PM

Room:Diamond II - 2nd Floor

The growth of plants is controlled by the action of growth hormones such as auxin and citokinin. Recently, various mathematical models have been developed that describe how these hormones are transported through a network of cells that make up a leaf or a root, how the hormones are synthesized, and how they signal and interact with the growth process. These models describe, amongst other phenomena, leaf vein patterns, tropic bending, root branching, and wound healing. This minisymposium gives an introduction to the biology, the mathematical models, and their dynamics.

Organizer: Wim I. Vanroose
University of Antwerp, Belgium

3:15-3:40 Numerical Bifurcation Analysis of Pattern Formed in a Leaf Growth Model
Delphine Draelants, Universiteit Antwerpen, Belgium

3:45-4:10 Cell-based Modeling of Plant Tissue Growth and Phytohormone Transport using VirtualLeaf
Roeland Merks, CWI, Amsterdam, Netherlands

4:15-4:40 Exploring the Dynamics of Stem Cell Maintenance in the Stem Cell Niche through Models of Inter and Intracellular Feedback Regulation
Vijay S. Chickarmane, California Institute of Technology, USA

4:45-5:10 Recent Developments in VirtualLeaf, a Framework for Cell-based Plant Tissue Simulations
Przemyslaw Klosiewicz, Universiteit Antwerpen, Belgium

Tuesday, August 7

MS10

Cancer Modeling in Clinical Practice

3:15 PM-5:15 PM

Room:Diamond I - 2nd Floor

Cancer Modeling in Clinical Practice New mathematical models on cancer treatment are developed to address the urgent clinical challenges. This minisymposium will present recent progress in cancer modeling using a variety of mathematical tools, including ODEs, PDEs, stochastic processes, and agent-based models. The speakers will address clinical questions in ovarian cancer, melanoma, and drug delivery in solid tumors. The results in these systems have direct translational applications to numerous cancer types and therapeutic regimens.

Organizer: Harsh Jain
Ohio State University, USA

Organizer: Chuan Xue
Ohio State University, USA

3:15-3:40 Guiding Ovarian Cancer Treatment with Mathematical Modeling
Harsh Jain, Ohio State University, USA

3:45-4:10 Energy Metabolism and Evolution of the Angiogenic Switch in Cancer: Novel Targets for Antiangiogenic Therapy
John D. Nagy, Arizona State University, USA

4:15-4:40 Temporal Dynamics of Cancer Recurrence
Jasmine Y. Foo, University of Minnesota, USA

4:45-5:10 Hypoxia Inducible Factors Mediate the Inhibition of Cancer by Gm-Csf: A Mathematical Model
Duan Chen, Mathematical Biosciences Institute, USA; Julie Roda, Clay Marsh, Timothy Eubank, and Avner Friedman, Ohio State University, USA

Tuesday, August 7

MS11

Mathematical Modeling of Cardiovascular Control - Part I of II

3:15 PM-5:15 PM

Room:Crystal Ballroom I - 2nd Floor

For Part 2 see MS19

Cardiovascular diseases are expensive for the society and are often vital for the diseased. Various control mechanisms of the cardiovascular system are involved in most dysfunctions leading to such cardiovascular diseases. In connection with this topic we pose the following question: How should mathematical modeling be approached and what can we learn from modeling? How does the various control mechanisms interact? Can mathematical models be used in the clinic for diagnosing and treatment planning? The speakers will present the state of the art in their field and address questions for future research. Thus we will try establish a consortium for grand applications with the field.

Organizer: Johnny T. Ottesen
Roskilde University, Denmark

Organizer: Mette S. Olufsen
North Carolina State University, USA

3:15-3:40 ATP, Adenosine and Coronary Regulation in Ischemia and Hypoxia
James B. Bassingthwaighte, University of Washington, USA

3:45-4:10 Theoretical Models for Regulation of Blood Flow in the Microcirculation
Timothy W. Secomb, University of Arizona, USA

4:15-4:40 Multiscale Blood Flow Regulation Models Incorporating Cellular Function of the Vessel Wall
Brian Carlson, Medical College of Wisconsin, USA

4:45-5:10 Modeling Firing of the Baroreceptor Nerves
Adam Mahdi, North Carolina State University, USA

Tuesday, August 7

MS12

Control of Cellular Processes: Computational and Experimental Approaches

3:15 PM-5:15 PM

Room:Topaz - 2nd Floor

Future advances in the biological sciences will be directed and accelerated by systems-level analysis of mathematical models of cellular processes. The inherent complexity of cellular systems limits the utility of intuition and exploratory experimental approaches and motivates the need for quantitative approaches to direct and control cell fate. However, controlling cellular processes involves unique challenges not encountered in the control of traditionally engineered systems. Robust computational strategies are needed for these systems, with laboratory validation being essential toward identifying successful strategies. This symposium will focus on efforts to design and experimentally validate control strategies for rationally engineering cell population behavior.

Organizer: Sarah L. Noble
United States Naval Academy, USA

3:15-3:40 Sparse-grid-based Adaptive Model Predictive Control of HL60 Cellular Differentiation
Sarah L. Noble, United States Naval Academy, USA; Lindsay Wendel, Johns Hopkins University, USA; Maia Donahue, Dow AgroSciences, USA; Gregery Buzzard and Ann Rundell, Purdue University, USA

3:45-4:10 A Dynamical Systems Perspective of Cytokine Signaling Responses by Human T Cells
Neda Bagheri, Northwestern University, USA

4:15-4:40 Interconnecting biochemical modules: propagation of oscillations as a case study
Elisa Franco, University of California, Riverside, USA

4:45-5:10 Quantification of the Interplay Between Growth and Stress Responses Using Automated Flow Cytometry
Ignacio A. Zuleta, Hao Li, and Hana El-Samad, University of California, San Francisco, USA

Tuesday, August 7

MS13

The Impact of Architecture on the Complexity of Neural Dynamics

3:15 PM-5:15 PM

Room:Crystal Ballroom II - 2nd Floor

Theoretical and experimental studies of neuronal networks have revealed a wide range of rich and complex activity. Over the past two decades the importance of network architecture has been increasingly recognized as being essential in shaping this behavior. Connectivity and other network characteristics generate the system's key dynamical properties -- both transient and stationary -- including stability, points of attraction, and correlation structure. The speakers in this mini-symposium will present recent results that show how dynamics and connectivity influence collective neuronal activity.

Organizer: James Trousdale
University of Houston, USA

Organizer: Natasha Cayco Gajic
University of Washington, USA

3:15-3:40 A Linear Response Theory of Correlations in Neuronal Networks
James Trousdale, University of Houston, USA; Yu Hu and Eric Shea-Brown, University of Washington, USA; Kresimir Josic, University of Houston, USA

3:45-4:10 Asynchronous States between Neural Populations
Jérémie Lefebvre, University of Geneva, Switzerland; Theodore J. Perkins, Ottawa Hospital Research Institute, Canada

4:15-4:40 Reliability of Spike Times in Sparsely Connected Networks
Guillaume Lajoie and Eric Shea-Brown, University of Washington, USA; Kevin K. Lin, University of Arizona, USA

4:45-5:10 Emergence of Nonuniform Connectivity in Spiking Neuronal Networks and Dynamical Consequences
Ashok L. Kumar, Carnegie Mellon University, USA; Brent Doiron, University of Pittsburgh, USA

Tuesday, August 7

MS14

Perceptual Rivalry and Mathematical Modeling - Part II of II

3:15 PM-5:15 PM

Room:Opal - 2nd Floor

For Part 1 see MS6

Binocular rivalry is a visual phenomenon in which perception alternates between dissimilar images presented to each eye. Binocular rivalry has been extensively studied, partly due to implications for conscious visual processing. Since the first systematic study of Charles Wheatstone back in 1830s, many beautiful experiments have been carried out and several interesting mathematical models have been proposed to address this phenomenon. This symposium aims to bring together experimentalists and mathematicians to discuss perceptual rivalry from different perspectives, give new insights for brain activities and inspire more collaboration.

Organizer: Yunjiao Wang
Rice University, USA

Organizer: Tyler McMillen
California State University, Fullerton, USA

3:15-3:40 Generalized Rivalry & Neural Decisions
Hugh R. Wilson, York University, Canada

3:45-4:10 On Wilson's Generalized Rivalry Network
Casey O. Diekman and *Martin Golubitsky*, The Ohio State University, USA; Tyler McMillen, California State University, USA; Yunjiao Wang, Ohio State University, USA

4:15-4:40 Percept Strength and Reaction Time at the Onset of Bistable Perception
Asya Shpiro, City University of New York, USA; Nava Rubin, New York University, USA; John M. Rinzel, Courant Institute of Mathematical Sciences, New York University, USA

4:45-5:10 Organizing Centers for Two Patterns and Preliminary Results for Multiple Patterns
Tyler McMillen, California State University, USA; Casey Diekman and Martin Golubitsky, The Ohio State University, USA; Yunjiao Wang, Rice University, USA

Tuesday, August 7

MS15

Advanced Mathematical Models of Protein--Solvent Interactions - Part II of II

3:15 PM-5:15 PM

Room:Pearl - 3rd Floor

For Part 1 see MS7

Protein structure and function are determined in large part by interactions with the surrounding environment, usually a solvent that is mostly water with dissolved ions (e.g. sodium). Solvent influence can be modeled using all-atom molecular dynamics (MD), which require thousands of water molecules and ions, and are therefore computationally expensive; in contrast, continuum models can be hundreds or thousands of times faster, but sacrifice molecular detail for speed. A variety of promising multiscale modeling approaches have been proposed to bridge these two extremes, most of which face a common set of computational challenges (speed and scalability). This minisymposium will bring together mathematicians, chemists, and biophysicists to discuss the mathematical research that would have a broad, sustained impact on this important modeling problem.

Organizer: Jaydeep P. Bardhan
Rush University Medical Center, USA

Organizer: Bo Li
University of California, San Diego, USA

3:15-3:40 Multiscale Modeling of Ion-protein Interactions with Density Functional Theory of Liquids
Dirk Gillespie, Rush University Medical Center, USA

3:45-4:10 Energetic Variational Approaches: General Diffusion, Stochastic Differential Equations and Optimal Transport
Chun Liu, Pennsylvania State University, USA

4:15-4:40 Conjunction of MD and DFT for Rapid Prediction of Solvation Free Energy with Atomic Details
Jianzhong Wu, University of California, Riverside, USA

4:45-5:10 Advances in Nonlocal Dielectric Modeling for Protein in Ionic Solvent
Dexuan Xie, University of Wisconsin, Milwaukee, USA

Tuesday, August 7

Intermission

5:15 PM-5:30 PM

Forward Looking Session

5:30 PM-6:30 PM

Room:Emerald Ballroom - 2nd Floor

The Forward Looking Session will consist of a panel-led discussion about areas that seem ripe for progress in quantitative life sciences research and developments that may have a large impact on research in this area in the near future.

Chair: Mette S. Olufsen
North Carolina State University, USA

Panelists:

L. Mahadevan
Harvard University, USA

Michael Reed
Duke University, USA

Jonathan Rubin
University of Pittsburgh, USA

Timothy Secomb
University of Arizona, USA

Mariel Vazquez
San Francisco State University, USA

Wednesday, August 8

Registration
8:00 AM-4:00 PM

Room:Foyer - 2nd Floor

Remarks
8:40 AM-8:45 AM

Room:Emerald Ballroom - 2nd Floor

IP3
DNA Unknotting and Unlinking
8:45 AM-9:30 AM

Room:Emerald Ballroom - 2nd Floor

Chair: To Be Determined

Multiple cellular processes such as replication, recombination, and packing change the topology of DNA. Controlling these changes is key to ensuring stability inside the cell. The cell uses enzymes to simplify DNA topology. In Escherichia coli, DNA unlinking is typically mediated by the type II topoisomerase topoIV. In the absence of topo IV, the site-specific recombination system XerCD mediates sister chromosome unlinking. We here focus on DNA unknotting and unlinking by Xer recombination. We use topological methods, aided by computational tools, to unveil unlinking pathways and study the topological mechanism of action of these enzymes.

Mariel Vazquez
San Francisco State University, USA

Coffee Break
9:30 AM-10:00 AM

Room:Foyer - 2nd Floor

Wednesday, August 8

MS16
Stochastic Dynamics in Cell Biology: Simulation, Analysis, and Experiment - Part I of II
10:00 AM-12:00 PM

Room:Emerald Ballroom - 2nd Floor

For Part 2 see MS23

It is well established that stochastic phenomena have nontrivial effects in many biological systems, particularly at the cellular and subcellular levels. Understanding the structure and function of such systems requires continual elaboration of numerical, analytical and experimental methods. Numerical challenges include finding computationally efficient methods, spatially resolved systems, and systems with multiple time scales. Recent analytical advances include Markov chain aggregation techniques, formulation of asymptotic results in the stochastic setting, and stochastic analogs of deterministic limit cycles. This minisymposium will include applications to networks of protein-protein interactions, engineered gene networks, molecular motor-cargo complexes, and ion channel fluctuations.

Organizer: Peter J. Thomas
Case Western Reserve University, USA

Organizer: David Anderson
University of Wisconsin, Madison, USA

10:00-10:25 Numerical Methods for Stochastic Bio-chemical Reacting Networks with Multiple Time Scales
Di Liu, Michigan State University, USA

10:30-10:55 Stochastic Reaction-drift-diffusion Methods for Studying the Influence of Subcellular Structure on Biochemical Processes
Samuel A. Isaacson, Boston University, USA

11:00-11:25 Computational Methods for Stochastic Models Arising in the Biosciences
David Anderson, University of Wisconsin, Madison, USA

11:30-11:55 Markov Chain Aggregation, with Application to Protein-protein Interaction
Arnab Ganguly, ETH Zürich, Switzerland

Wednesday, August 8

MS17
Dynamics, Regulation and Function of the Actin Cytoskeleton - Part I of II
10:00 AM-12:00 PM

Room:Opal - 2nd Floor

For Part 2 see MS24

The actin cytoskeleton polymerizes and organizes into various structures including acto-myosin contractile networks, a dynamic cell cortex and lamella/lamellipodia, which perform vital cell functions including motility, signaling, endocytosis, cell division and embryogenesis. Mathematics continues to contribute to understanding these dynamic structures with techniques including reaction-diffusion and stochastic PDEs, equations from fluid dynamics and liquid crystal theory, networks of ODEs, and agent-based Monte Carlo simulation. In this session we discuss recent models which address self-organization, cell mechanics, and biochemical regulation. Several talks will discuss the many recent reports of actin traveling waves.

Organizer: Jun Allard
University of California, Davis, USA

Organizer: Nessy Tania
Smith College, USA

10:00-10:25 Quantitative Analysis of Actin Dynamics during Clathrin-mediated Endocytosis
Julien Berro, Yale University, USA

10:30-10:55 Steady State Patterning and Remodeling Dynamics of Actin Asters
Kripa Gowrishankar, University of California, Davis, USA

11:00-11:25 Formation of Regular Actin Bundle Networks Driven by Entropic Forces
Florian Huber, University of Leipzig, Germany

11:30-11:55 Role of the SCAR/WAVE-mediated, Dendritic F-actin Polymerization in the Chemotactic Migration of Amoeboid Cells
Juan Lasheras, Effie Bastounis, Ruedi Meili, Juan C. del Alamo, and Richard Firtel, University of California, San Diego, USA

Wednesday, August 8

MS18

Mathematical Methods in Oncology: from Prognostic Screening to Therapeutic Treatment - Part I of II

10:00 AM-12:00 PM

Room:Diamond I - 2nd Floor

For Part 2 see MS25

A better prognostic screening and an improvement in anticancer treatment are among the most important current challenges in oncology. In this minisymposium we will showcase several mathematical approaches that directly address these two issues by providing data-based multiscale models and robust simulation platforms, quantitative data analysis methods and experimentally testable predictions. Models of several different tumor types (such as brain, breast, lung and prostate cancers) will be discussed, as well as various anticancer treatments, including chemo-, radio- and immuno-therapies.

Organizer: Katarzyna A. Rejniak
H. Lee Moffitt Cancer Center & Research Institute, USA

10:00-10:25 The Role of Tissue Architecture in Anticancer Drug Penetration and Efficacy
Katarzyna A. Rejniak, H. Lee Moffitt Cancer Center & Research Institute, USA

10:30-10:55 Impact of Improved Intracellular Fluid and Calcification Dynamics on Patient-Calibrated Simulation of Dcis and Comedonecrosis
Paul Macklin and Shannon Mumenthaler, University of Southern California, USA; Lee Jordan, Colin Purdie, and Andrew Evans, University of Dundee, Scotland; David Agus, University of Southern California, USA; Alastair Thompson, University of Dundee, Scotland

continued in next column

11:00-11:25 How Does miR451 (microRNA) Regulate the Proliferation and Migration of Glioblastoma Cells: A Mathematical Model
Yangjin Kim, University of Michigan, USA; Avner Friedman, Ohio State University, USA; Sean Lawler, University of Leeds, United Kingdom; Soyeon Roh, University of Michigan, USA

11:30-11:55 Assessing Breast Tumor Aggressiveness Using Histopathology-based Computational Modeling
Banu Baydil, H. Lee Moffitt Cancer Center & Research Institute, USA

Wednesday, August 8

MS19

Mathematical Modeling of Cardiovascular Control - Part II of II

10:00 AM-12:00 PM

Room:Crystal Ballroom I - 2nd Floor

For Part 1 see MS11

Cardiovascular diseases are expensive for the society and are often vital for the diseased. Various control mechanisms of the cardiovascular system are involved in most dysfunctions leading to such cardiovascular diseases. In connection with this topic we pose the following question: How should mathematical modeling be approached and what can we learn from modeling? How does the various control mechanisms interact? Can mathematical models be used in the clinic for diagnosing and treatment planning? The speakers will present the state of the art in their field and address questions for future research. Thus we will try establish a consortium for grand applications with the field.

Organizer: Johnny T. Ottesen
Roskilde University, Denmark

Organizer: Mette S. Olufsen
North Carolina State University, USA

10:00-10:25 Neural and Cardiovascular Alterations During Changes in Posture: A Dynamic Example of Physiological Regulation
Jesper Mehlsen, Frederiksberg Hospital, Denmark

10:30-10:55 Modeling Blood Pressure Dynamics during Head-up Tilt
Johnny T. Ottesen, Roskilde University, Denmark; Mette Olufsen, North Carolina State University, USA

11:00-11:25 Control of the Cardiovascular System on the Basis of the Arterial CO2 Concentration
Franz Kappel, University of Graz, Austria

11:30-11:55 Theoretical Models of Blood Flow Autoregulation in Skeletal Muscle and the Retina
Julia Arciero, Indiana University - Purdue University Indianapolis, USA

Wednesday, August 8

MS20

Spatiotemporal Dynamics in Networks of the Brain - Part I of II

10:00 AM-12:00 PM

Room:Diamond II - 2nd Floor

For Part 2 see MS28

Spatially structured activity in networks of the brain subserves various sensory, motor, and memory related functions. Advances in optogenetics, voltage sensitive dyes, and multi-electrode recording are expanding our ability to study such patterns of activity both in vivo and in vitro slice preparations. These data sets offer a plethora of new opportunities for theoretical modeling to complement experimental observation. Resulting models are spatially extended dynamical systems whose analyses reveal diverse coherent activity patterns like spiral waves, oscillatory pulses, and wandering bumps. This minisymposium brings together several leading researchers to discuss results at the forefront of this multi-disciplinary field.

Organizer: Zachary Kilpatrick
University of Pittsburgh, USA

Organizer: Stefanos Folias
University of Pittsburgh, USA

10:00-10:25 Associative Memory in Bump Attractor Networks
Vladimir Itskov, University of Nebraska, Lincoln, USA

10:30-10:55 Phase Locking of Brainstem Nuclei Coordinate Orofacial Behaviors
Martin Deschenes, Université Laval, Canada; *David Kleinfeld* and Jeffrey Moore, University of California, San Diego, USA

11:00-11:25 A Model for the Origin and Properties of Flicker-induced Geometric Phosphenes
Michael Rule, Brown University, USA; Matthew Stoffregen and Bard Ermentrout, University of Pittsburgh, USA

11:30-11:55 Effective Stochastic Equations and Fluctuations in Neural Networks
Michael Buice, University of Texas at Austin, USA

Wednesday, August 8

MS21

Model Analysis for Neural Dynamics

10:00 AM-12:00 PM

Room:Topaz - 2nd Floor

Phase plane and fast/slow analysis methods of simple neuron models have greatly advanced our understanding of spiking and bursting behaviors in neuronal dynamics. However, understanding the dynamics of models with more than three variables is more challenging. This minisymposium will present some recent methods that can be used to reduce complex models and simplify their dynamics while retaining the original system's behavior.

Organizer: Robert Clewley
Georgia State University, USA

Organizer: Joel Tabak
Florida State University, USA

10:00-10:25 Contributions of the Two Negative Feedback Variables in the Hodgkin-Huxley Model
Joël Tabak, Richard Bertram, and Sevgi Sengul, Florida State University, USA

10:30-10:55 Analysis of Soft Thresholds and the Consequences for Parameter Estimation in Spiking Dynamics
Robert Clewley, Bryce Chung, and Ricky Tolefree, Georgia State University, USA

11:00-11:25 Coarse-graining and Simplification of the Dynamics Seen in Bursting Neurons
Alona Ben-Tal and Joshua Duley, Massey University, New Zealand; Yannis Kevrekidis, Princeton University, USA

11:30-11:55 A Dynamical Systems Analysis of a Neuromechanical Locomotor System: Model Reduction and Extensions
Lucy Spardy and Jonathan Rubin, University of Pittsburgh, USA

Wednesday, August 8

MS22

Advancements in Biomolecular Design: Accurate Models and Efficient Algorithms

10:00 AM-12:00 PM

Room:Crystal Ballroom II - 2nd Floor

Throughout engineering, computer-aided design (CAD) tools must balance the computational costs of accurate device models (the forward problem) and efficient pruning of the design space (the inverse problem). Progress in both forward and inverse modeling methods drives the evolution of this balance, as this minisymposium will illustrate using the emerging area of biomolecular design---including drug design and protein engineering---as a case study. Speakers from disciplines ranging from applied math to physiology will showcase advances in design capabilities from a variety of advances including statistical methods, boundary-integral equation analysis, high-performance computing, and optimization theory.

Organizer: David F. Green
State University of New York, Stony Brook, USA

Organizer: Jaydeep P. Bardhan
Rush University Medical Center, USA

10:00-10:25 Boundary-Integral Formulations for Fast Solutions of the Poisson-Boltzmann Equation in Ligand Optimization
Jaydeep P. Bardhan, Rush University Medical Center, USA

10:30-10:55 Understanding the Designability of Proteins with Generalized Models
Gevorg Grigoryan, Dartmouth College, USA

11:00-11:25 Adapting Computational Protein Design Algorithms to Define the Space of Functional Protein Sequences
Loretta Au, State University of New York, Stony Brook, USA

11:30-11:55 Understanding Molecular Evolution through Computational Protein Design
Corey Wilson, Yale University, USA

Wednesday, August 8

Lunch Break

12:00 PM-2:00 PM

Attendees on their own

Funding Agency Panel

1:00 PM-2:00 PM

Room:Emerald Ballroom - 2nd Floor

Wednesday, August 8

IP4

Computational Physiology and the VPH/Physiome Project

2:00 PM-2:45 PM

Room:Emerald Ballroom - 2nd Floor

Chair: Tim David, University of Canterbury, New Zealand

Multi-scale models of organs and organ systems are being developed under the umbrella of the Physiome Project of the International Union of Physiological Sciences (IUPS) and the Virtual Physiological Human (VPH) project funded by the European Commission. These computational physiology models deal with multiple physical processes (coupled tissue mechanics, electrical activity, fluid flow, etc) and multiple spatial and temporal scales. They are intended both to help understand physiological function and to provide a basis for diagnosing and treating pathologies in a clinical setting. A long term goal of the project is to use computational modeling to analyze integrative biological function in terms of underlying structure and molecular mechanisms. It is also establishing web-accessible physiological databases dealing with model-related data at the cell, tissue, organ and organ system levels. This talk will provide an update on the current state of the standards, databases and software being developed to support robust and reproducible multi-scale models for the VPH/Physiome project. These standards include CellML and FieldML for encoding models and BioSignalML for encoding time-varying signal data, together with model repositories and software tools for creating, visualizing and executing the models based on these standards.

Peter Hunter
University of Auckland, New Zealand

Coffee Break

2:45 PM-3:15 PM

Room:Foyer - 2nd Floor

Wednesday, August 8

MS23

Stochastic Dynamics in Cell Biology: Simulation, Analysis, and Experiment - Part II of II

3:15 PM-5:15 PM

Room:Emerald Ballroom - 2nd Floor

For Part 1 see MS16

It is well established that stochastic phenomena have nontrivial effects in many biological systems, particularly at the cellular and subcellular levels. Understanding the structure and function of such systems requires continual elaboration of numerical, analytical and experimental methods. Numerical challenges include finding computationally efficient methods, spatially resolved systems, and systems with multiple time scales. Recent analytical advances include Markov chain aggregation techniques, formulation of asymptotic results in the stochastic setting, and stochastic analogs of deterministic limit cycles. This minisymposium will include applications to networks of protein-protein interactions, engineered gene networks, molecular motor-cargo complexes, and ion channel fluctuations.

Organizer: Peter J. Thomas
Case Western Reserve University, USA

Organizer: David Anderson
University of Wisconsin, Madison, USA

3:15-3:40 Stochastic Limits for Molecular Motor-Cargo Complexes
John Fricks, Pennsylvania State University, USA

3:45-4:10 Noise Induced Stochastic Cell Fate Determination in Engineered Gene Networks
Xiao Wang, Arizona State University, USA

4:15-4:40 Connection between Microscopic Stochastic and Macroscopic Nonlinear Diffusion Models of Reversing Bacteria
Mark S. Alber, University of Notre Dame, USA

4:45-5:10 Stochastic Limit Cycles for Conductance-Based Neural Models: A Master Equation Approach
Peter J. Thomas, Case Western Reserve University, USA

Wednesday, August 8

MS24

Dynamics, Regulation and Function of the Actin Cytoskeleton - Part II of II

3:15 PM-5:15 PM

Room:Opal - 2nd Floor

For Part 1 see MS17

The actin cytoskeleton polymerizes and organizes into various structures including acto-myosin contractile networks, a dynamic cell cortex and lamella/lamellipodia, which perform vital cell functions including motility, signaling, endocytosis, cell division and embryogenesis. Mathematics continues to contribute to understanding these dynamic structures with techniques including reaction-diffusion and stochastic PDEs, equations from fluid dynamics and liquid crystal theory, networks of ODEs, and agent-based Monte Carlo simulation. In this session we discuss recent models which address self-organization, cell mechanics, and biochemical regulation. Several talks will discuss the many recent reports of actin traveling waves.

Organizer: Jun Allard
University of California, Davis, USA

Organizer: Nessy Tania
Smith College, USA

3:15-3:40 Coupling Actin Flow, Adhesion, and Morphology in a Computational Cell Motility Model
Wouter-Jan Rappel, Danying Shao, and Herber Levine, University of California, San Diego, USA

3:45-4:10 Understanding Actomyosin Contractions with Simulations, and Continuum Analysis
Callie Miller, Lance Davidson, and Bard Ermentrout, University of Pittsburgh, USA

4:15-4:40 A Model of Excitable Actin Dynamics Underlying Leading Edge Protrusion and Retraction in XTC Cells
Gillian L. Ryan, Lehigh University, USA; Naoki Watanabe, Tohoku University, Japan; Dimitrios Vavylonis, Lehigh University, USA

4:45-5:10 The Nonlinear Dynamics of F-actin at Cell Membranes
A. E. Carlsson, Washington University, St. Louis, USA

Wednesday, August 8

MS25

Mathematical Methods in Oncology: from Prognostic Screening to Therapeutic Treatment - Part II of II

3:15 PM-5:15 PM

Room:Diamond I - 2nd Floor

For Part 1 see MS18

A better prognostic screening and an improvement in anticancer treatment are among the most important current challenges in oncology. In this minisymposium we will showcase several mathematical approaches that directly address these two issues by providing data-based multiscale models and robust simulation platforms, quantitative data analysis methods and experimentally testable predictions. Models of several different tumor types (such as brain, breast, lung and prostate cancers) will be discussed, as well as various anticancer treatments, including chemo-, radio- and immuno-therapies.

Organizer: Katarzyna A. Rejniak
H. Lee Moffitt Cancer Center & Research Institute, USA

3:15-3:40 Multiscale Modeling of Breast Cancer Angiogenesis with Therapeutic Applications
Stacey D. Finley and Aleksander S. Popel, Johns Hopkins University, USA

3:45-4:10 Using Mathematical Models to Plan Dendritic Cell Vaccine Strategies
Ami Radunskaya, Pomona College, USA; *Angela Gallegos*, Loyola Marymount University and Occidental College, USA

4:15-4:40 Microtubule Bundling as an Indicator of Cancer Cell Response to Chemotherapy
MunJu Kim, H. Lee Moffitt Cancer Center & Research Institute, USA

4:45-5:10 Patient-specific Spatial and Temporal Variation of Treatment Resistance Mechanisms in Radiation Therapy
Russell Rockne, Andrew Trister, Maxwell L. Neal, Maciej Mrugala, Jason Rockhill, and Kristin R. Swanson, University of Washington, USA

Wednesday, August 8

MS26

Applications of Mathematics in Atherosclerosis: Diagnosis, Modeling and Prediction

3:15 PM-5:15 PM

Room:Topaz - 2nd Floor

Atherosclerosis, an inflammatory disease of large and medium-sized arteries, is one of the most common causes of death in Western nations. However, the main mechanisms of this disease are only beginning to be elucidated. This minisymposium brings together a young and diverse group of researchers who use mathematics to better understand this disease. Current directions of research include: the use free boundary problems to predict growth, interpretation of ultrasound images for diagnosis, and the coupling of growth and deformation in arteries. A range of topics will be presented, from basic theoretical issues to more application-driven approaches.

Organizer: Pak-Wing Fok
University of Delaware, USA

3:15-3:40 A Mathematical Model for Intimal Thickening
Pak-Wing Fok, University of Delaware, USA

3:45-4:10 Coronary Morphology Quantification for Bifurcating Stent Design
Laura M. Ellwein, Marquette University, USA; Raymond Migrino, VA Health Care System, Phoenix, AZ, USA; David Marks, Medical College of Wisconsin, USA; John LaDisa, Marquette University and Medical College of Wisconsin, USA

4:15-4:40 On the Mechanical Stability of Growing Arteries
Rebecca Vandiver, St. Olaf College, USA; Alain Goriely, University of Oxford, United Kingdom

4:45-5:10 Parameter Identification for Atherosclerotic Plaques from its Material Spectrum gained by Intravascular Ultrasound Imaging
Kun Gou, Sunnie Joshi, and Walton Jay, Texas A&M University, USA

Wednesday, August 8

MS27

Modeling Biological Thin Filaments in Fluid Flow

3:15 PM-5:15 PM

Room:Crystal Ballroom I - 2nd Floor

In the past forty years, there has been an ever-increasing interest in thin filament dynamics in applications to biology, in particular with regard to the shape, dynamics, or biomaterial parameters, flagellated swimming organisms, and filament growth. In many of these applications, hydrodynamic interactions have been of the utmost importance. We bring together a diverse group of mathematicians and physicists whose work has included the modeling of thin biological structures coupled to a fluid environment, each having different approaches. This minisymposium will disseminate recent advances and help bridge the gap between disparate perspectives on the modeling of thin filaments in fluids.

Organizer: Bree Cummins
Tulane University, USA

Organizer: Eva M. Strawbridge
University of Chicago, USA

3:15-3:40 An Overview of Modeling Thin Filaments in Fluid
Eva M. Strawbridge, University of Chicago, USA

3:45-4:10 Simulating Elastic Filaments with Bend and Twist by the Generalized Immersed Boundary Method
Sookkyung Lim, University of Cincinnati, USA

4:15-4:40 Helices, Waves, and Kinks: Geometric Optimization of Prokaryotic and Eukaryotic Flagella
Saverio E. Spagnolie, Brown University, USA

4:45-5:10 The Morphology and Motility of the Lyme Disease Spirochete
Charles Wolgemuth, University of Connecticut Health Center, USA

Wednesday, August 8

MS28

Spatiotemporal Dynamics in Networks of the Brain - Part II of II

3:15 PM-5:15 PM

Room:Diamond II - 2nd Floor

For Part 1 see MS20

Spatially structured activity in networks of the brain subserves various sensory, motor, and memory related functions. Advances in optogenetics, voltage sensitive dyes, and multi-electrode recording are expanding our ability to study such patterns of activity both in vivo and in vitro slice preparations. These data sets offer a plethora of new opportunities for theoretical modeling to complement experimental observation. Resulting models are spatially extended dynamical systems whose analyses reveal diverse coherent activity patterns like spiral waves, oscillatory pulses, and wandering bumps. This minisymposium brings together several leading researchers to discuss results at the forefront of this multi-disciplinary field.

Organizer: Zachary Kilpatrick
University of Pittsburgh, USA

Organizer: Stefanos Folias
University of Pittsburgh, USA

3:15-3:40 Dynamics of Transitions Between Depth Perception and Binocular Rivalry
Hugh R. Wilson, York University, Canada

3:45-4:10 Front Propagation in Stochastic Neural Fields
Paul C. Bressloff, University of Utah, USA and University of Oxford, United Kingdom

4:15-4:40 Observing and Controlling Spatiotemporal Brain Dynamics
Steven J. Schiff, Pennsylvania State University, USA

4:45-5:10 Bifurcations of Smooth and Lurching Waves in a One-dimensional Thalamic Neuronal Network
Carlo R. Laing, Massey University, New Zealand

Wednesday, August 8

MS29

Dynamics in Transition Regimes between Different Neural Activity States

3:15 PM-5:15 PM

Room:Crystal Ballroom II - 2nd Floor

Over the past 50 years, mathematical and computational modeling has helped to improve our understanding of neural activity states, and of the dynamics in the transitions and bifurcations between states. The minisymposium speakers will present a number of recently-discovered transition phenomena between tonic spiking and bursting in models of single neurons and networks of neurons, including elliptic, Hopf/fold-cycle, fold/fold cycle, and circle/fold-cycle bursting. Transitions to MMOs and other complex activity states will also be studied. Diverse methods are used to study the dynamics, including interval mappings, isochron portraits, advanced numerical continuation, and the geometric theory of slow invariant manifolds.

Organizer: John Burke
Boston University, USA

Organizer: Mathieu Desroches
INRIA, France

Organizer: Tasso J. Kaper
Boston University, USA

Organizer: Mark Kramer
Boston University, USA

3:15-3:40 Dynamics in Models of Individual and Networked Neurons
Jeremy Wojcik and *Andrey Shilnikov*, Georgia State University, USA

3:45-4:10 Torus Canards in the Transitions from Spiking to Bursting
John Burke, Boston University, USA; Mathieu Desroches, University of Bristol, United Kingdom; Anna Barry, Tasso J. Kaper, and *Mark Kramer*, Boston University, USA

4:15-4:40 Isochron Portraits at Transitions between Bursting and Spiking Modes
Erik Sherwood, University of Utah, USA

4:45-5:10 When Transitions Between Bursting Modes Induce Network Synchrony
Igor Belykh, Georgia State University, USA

Wednesday, August 8

MS30

Computational Biological Modeling at the Interface of Molecular Simulation and Continuum Diffusion - Part I of II

3:15 PM-5:15 PM

Room:Pearl - 3rd Floor

For Part 2 see MS38

The integration of molecular simulations and numerical approximation of partial differential equations presents a promising approach for describing diffusion-based biological phenomena, including protein-substrate association, electrodiffusion, and protein-protein signaling. The modeling of these phenomena offer novel insights into critical factors governing system behavior at both molecular and mesoscopic scales. These models would naturally benefit from a rigorous examination of the mathematics interfacing these scales, as well as the choice of simplifying assumptions. This minisymposium will bring together researchers from a variety of fields within computational biology to discuss common threads in the interaction between molecular domain and biological function.

Organizer: Andrew Gillette
University of California, San Diego, USA

Organizer: Peter Kekenes-Huskey
University of California, San Diego, USA

3:15-3:40 Binding Kinetics of Proteins with Small-Molecule Ligands and Macromolecular Targets: Influence of Conformational Switch
Huan-Xiang Zhou, Florida State University, USA

3:45-4:10 Energetic Variational Approaches for Ionic Fluids: Diffusion and Transport
Chun Liu, Pennsylvania State University, USA

4:15-4:40 Ion Channels: Nanovalves that use Atomic Structures to Control Macroscopic Flows
Bob Eisenberg, Rush University Medical Center, USA

4:45-5:10 Pump-Leak Models of Cell Volume Control and Electrolyte Balance
Yoichiro Mori, University of Minnesota, USA

Wednesday, August 8

Intermission

5:15 PM-5:30 PM

SIAG/LS Business Meeting

5:30 PM-6:00 PM

Room:Emerald Ballroom - 2nd Floor

Complimentary wine and beer witll be served.

Dinner Break

6:00 PM-8:00 PM

Attendees on their own

Wednesday, August 8

PP1

Poster Session I

8:00 PM-10:00 PM

Room:Foyer - 2nd Floor

Bridging Cell and Tissue Scale Models for Nutrient Diffusion and Uptake in Articular Cartilage
Andreas Aristotelous, Duke University, USA; Mansoor Haider, North Carolina State University, USA

Modeling Hepatitis C Viral Dynamics: Sensitivity, Identifiability, and Parameter Estimation
Joseph Arthur and Hien Tran, North Carolina State University, USA

Detecting and Measuring the Influence of Functional Coupling on Protein Fitness
Loretta Au and David F. Green, State University of New York, Stony Brook, USA

Sensitivity Analysis of a Mathematical Model of Antibody Mediated Immune Responses
Sandip Banerjee, Indian Institute of Technology Roorkee, India

Neuronal Transmission of Timing Precision: Dependence on Intrinsic and Synaptic Properties
Heather A. Brooks and Alla Borisyuk, University of Utah, USA

3D Improved Mathematical Model for Lumbar Intervertebral Ligaments (lils)
Francisco Casesnoves, American Mathematical Society

The Effect of Antibody Attachment on the Infectivity of Virus Invasion
Alex Chen, SAMSI and UNC at Chapel Hill; Scott McKinley, University of Florida, USA; Sam Lai, Greg Forest, and Peter J. Mucha, University of North Carolina, Chapel Hill, USA

A Mathematical Spatiotemporal Model of Gnrh Neurons
Xingjiang Chen, University of Auckland, New Zealand

Hopf Bifurcation and Oscillatory Solutions in Gene Regulatory Networks with Delays
ChangYuan Cheng, National Pingtung University of Education, Taiwan; Shyan-Shiou Chen, National Taiwan Normal University, Taiwan

continued on next page

A Stochastic Multiscale Model of Esophageal Adenocarcinoma
Kit Curtius, University of Washington, USA

Quantifying the Influence of Drug Resistance Mechanisms Used in Mathematical Models When Assessing the Public Health Impact of PrEP Interventions
Dobromir Dimitrov, Fred Hutchinson Cancer Research Center, USA; Marie-Claude Boily, Imperial College London, United Kingdom; Elizabeth Brown, Fred Hutchinson Cancer Research Center, USA

Modeling the Role of the Bacterium Xylella Fastidiosa in the Development of Plant Diseases
Matthew Donahue, Florida State University, USA

Random and Regular Dynamics of Stochastically Driven Neuronal Networks
Pamela B. Fuller, Rensselaer Polytechnic Institute, USA

A Gene Set Analysis of Acute Lymphocytic Leukemia
Jacob A. Gagnon, Worcester Polytechnic Institute, USA; Anna Liu, University of Massachusetts, Amherst, USA

Robust Dorsal-Ventral Patterning Across Organisms
Heather D. Hardway, Cynthia Bradham, and Tasso J. Kaper, Boston University, USA

Model of the Immune System with An Inflammatory Host Response to a Bacterial Infection
Angela M. Jarrett and Nicholas Cogan, Florida State University, USA

Global Parametric Analysis of Heterotrimeric G-Protein Signaling
Tao Jiang and David F. Green, State University of New York, Stony Brook, USA

Amplification of Synaptic Inputs by Dendritic Spines
William Kath, Northwestern University, USA

Qualitatively Stable Numerical Methods for Dynamical Systems in Ecology
Hristo Kojouharov, University of Texas at Arlington, USA

Inflammation and Cholesterol: Friend Or Foe in Alzheimer's Disease
Christina Rose Kyrtsos, University of Maryland, USA; John Baras, University of Maryland, College Park, USA

continued in next column

Stochastic Simulation of Biochemical Systems with Randomly Fluctuating Rate Constants
Chia Ying Lee, University of North Carolina, USA

Structural Adaptation of Microvessels in Disease States
Larissa Little, Elizabeth Threlkeld, Jea Young Park, Patrick Varin, Alisha Sarang-Sieminski, and John B. Geddes, Franklin W. Olin College of Engineering, USA

Spatial Scale and Field Stability in a Modular Grid Cell to Place Cell Model
David Lyttle, Kevin K. Lin, and Jean-Marc Fellous, University of Arizona, USA

A Model for Hormonal Regulation of the Menstrual Cycle Applying to Women from Ages 20 to 51 Years
Alison Margolskee and James Selgrade, North Carolina State University, USA

Mathematical Modeling of Bone Remodeling in Response to Osteoporosis Treatments
Khamir Mehta, Merck & Co., Inc., USA; David S. Ross, Rochester Institute of Technology, USA; Antonio Cabal, Merck & Co., Inc., USA

Zip Bifurcation in Non-Smooth Population Models
Gerard Olivar, Universidad Nacional de Colombia, Colombia; Jocirei Ferreira, Federal University of Mato Grosso, Brazil; Carlos Escobar, University of Pereira, Colombia

Interior-Point Methods for An Optimal Control Influenza Model
Paula A. Gonzalez Parra and Leticia Velazquez, University of Texas at El Paso, USA; Sunmi Lee and Carlos Castillo-Chavez, Arizona State University, USA

Thermodynamically Compatible Model of Yield Stress Polymeric Fluids
Ilya Peshkov, École Polytechnique de Montréal, Canada; Evgeniy Romenski, Sobolev Institute of Mathematics, Russia; Miroslav Grmela, École Polytechnique de Montréal, Canada

A Mathematical Model for Protein Oscillations in Bacteria
Peter Rashkov and Bernhard Schmitt, Philipps-Universität Marburg, Germany; Stephan Dahlke, University of Marburg, Germany; Peter Lenz, Philipps-Universität Marburg, Germany; Lotte Sogaard-Andersen, Max Planck Institute for Terrestrial Microbiology, Germany

continued in next column

Mathematical Model to Quantify Dosing and Evaluate Effects of Modifications of Cancer Virotherapy
Brent Rogers, University of Missouri, Kansas City, USA

A Framework for Exploring Dynamics of Genetic Diversity of Hiv Population in Hiv-Infected Patients
Ori Sargsyan, Los Alamos National Laboratory, USA

A Shortest Path Tree Approach for Inferring and Exploring Gene Networks.
Michael Schnabel and Daniel Grady, Northwestern University, USA; Christian Thiemann, University of Goettingen, Germany; Adilson E. Motter, William Kath, and Dirk Brockmann, Northwestern University, USA

Deformation of a Single Red Blood Cell in Bounded Poiseuille Flows
Tsorng-Whay Pan, *Lingling Shi*, and Roland Glowinski, University of Houston, USA

Modeling Blood Pressure Dynamics
Alberto Soto, California Polytechnic State University, Pomona, USA; Bridget Stichnot, Murray State University, USA; Jairus Cuffie, Albany State University, USA; Christiana Sabett, St. Mary's College of Maryland, USA; Andrea Brown, Spelman College, USA; Ou Lu, Zhejiang University, China

Modeling the Cofilin Pathway and Actin Dynamics in Cell Motility Activity of Mammary Carcinomas
Nessy Tania, Smith College, USA

Noise-Induced Transitions in Stochastic Neural Fields
Jonathan D. Touboul, INRIA, France

Simplifying the Testing of Models of Flow-Cell Optical Biosensor Experiments for Global a Priori Identifiability
Jason M. Whyte, University of Adelaide, Australia

Phase Locking in Chains of Half-Center Oscillators: Mechanisms Underlying the Metachronal Rhythm in the Crayfish Swimmeret System
Jiawei Zhang and Tim Lewis, University of California, Davis, USA

Title: The Effects of Limb Coordination on the Swimming Efficiency of Crayfish
Qinghai Zhang, Jiawei Zhang, Robert Guy, and Timothy Lewis, University of California, Davis, USA

continued on next page

Stochastic Trojan Y-chromosome Models for Eradication of an Invasive Fish Species

Xueying Wang and Jay R. Walton, Texas A&M University, USA; Rana Pashad, King Abdullah University of Science & Technology (KAUST), Saudi Arabia; Katie Storey, Carleton College, USA

Thursday, August 9

Registration

8:00 AM-4:00 PM

Room:Foyer - 2nd Floor

Remarks

8:40 AM-8:45 AM

Room:Emerald Ballroom - 2nd Floor

IP5

Patient-specific Computational Fluid Dynamics for Noninvasive Assessment of Heart Disease

8:45 AM-9:30 AM

Room:Emerald Ballroom - 2nd Floor

Chair: Allison Marsden, University of California, San Diego, USA

Heart disease is the number one killer worldwide. Each year in the U.S. more than 6 million patients go to the Emergency room and there are 9 million physician's office visits for patients with symptoms of heart disease. Restrictions in the coronary arteries resulting from atherosclerosis are the principal cause of heart disease. The severity of these restrictions and their effect on blood flow to the heart are difficult to measure, yet this information is critical for treating patients. Currently, only invasive diagnostic cardiac catheterization can provide critical flow information through coronary arteries, but this procedure is expensive and poses risk to the patient. A recent breakthrough in imaging technologies with CT scanners and software from HeartFlow, Inc is enabling an inexpensive and far safer diagnostic tool to emerge. Broad application of CT Scans and HeartFlow software could potentially reduce annual health care costs nationally by over 10 billion dollars and save thousands of lives

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each year. Based on over 15 years of research, HeartFlow is able to analyze a patient's coronary CT scan images and, using high performance computing and computational fluid dynamics, to solve for coronary blood flow and pressure. Initial clinical data has demonstrated significant improvements in diagnostic accuracy as compared to other noninvasive technologies. HeartFlow employs a service model whereby patient data is uploaded through a secure web browser, processed on-site using custom software and High Performance Computing platforms and transmitted back to the ordering physician through a secure web browser. This analysis enables the physician to quickly determine the best treatment without invasive diagnostic cardiac catheterization. Worldwide, tens of millions of patients could benefit from this technology each year.

Charles Taylor
HeartFlow, Inc, USA

Coffee Break

9:30 AM-10:00 AM

Room:Foyer - 2nd Floor

Thursday, August 9

MT2

Numerical Methods for Studying Stochastic Models of Biological Systems

10:00 AM-12:00 PM

Room:Diamond II - 2nd Floor

Chair: Samuel A. Isaacson, Boston University, USA

We will introduce several numerical methods for solving stochastic models of biological systems. The first half of the minitutorial will focus on numerical methods for simulating models involving continuous time Markov chains. Such models often arise in the study of chemical and population processes. The second half of the minitutorial will focus on particle-based models that incorporate explicit spatial transport due to random walks or drift-diffusion processes. Applications of these simulation methods to the study of problems in cell biology will be used to illustrate the methods developed.

10:00-10:55 Stochastic Simulation of Models Arising in the Life Sciences
David Anderson, University of Wisconsin, Madison, USA

11:00-11:55 Stochastic Simulation of Spatially-Distributed Models Arising in the Life Sciences
Samuel A. Isaacson, Boston University, USA

Thursday, August 9

MS31

Long-term Dynamical Properties of Biochemical Reaction Networks - Part I of II

10:00 AM-12:00 PM

Room:Emerald Ballroom - 2nd Floor

For Part 2 see MS39

Analyzing biochemical network models is generally a difficult task, since the corresponding dynamical systems are usually nonlinear, high-dimensional, and contain many unknown parameters. Despite this great level of complexity, important properties of biochemical network models may depend only on the structure of the network and not on the specific values of the parameters involved. Since parameter uncertainty is widespread in biology, relating dynamical properties to network topology has become an important area of research. This minisymposium will focus on recent results on the long-term dynamical properties of biochemical network models (e.g. persistence, global stability, oscillatory behavior) and their connection to the network structure.

Organizer: Casian Pantea
Imperial College London, United Kingdom

Organizer: Maya Mincheva
Northern Illinois University, USA

10:00-10:25 Turing-Hopf Instability in Biochemical Reaction Networks
Maya Mincheva, Northern Illinois University, USA

10:30-10:55 Ultrasensitivity for Graded Multisite Activation Networks
German Enciso and *Shane Ryerson*, University of California, Irvine, USA

11:00-11:25 Oscillatory Patterns in Cell Signaling Networks
Maria Leite, University of Toledo, USA; Yunjiao Wang, Ohio State University, USA

11:30-11:55 Some Results on Chemical Reaction Networks without the Assumption of Mass Action
Murad Banaji, University of Portsmouth, United Kingdom

Thursday, August 9

MS32

Understanding Failure of Cell Signalling

10:00 AM-12:00 PM

Room:Opal - 2nd Floor

Signals in cells are due to a complex interaction of feedback loops, each displaying a characteristic time scale. Resulting oscillations, spikes and bursts trigger hormone secretion, insulin production and many other vital regulatory systems. From a physiological point of view, the signalling appears to be extremely cell specific, but the respective mathematical cell models are amazingly similar. This suggests unifying fundamental mechanisms for cell signalling and its failure, which are investigated in this mini-symposium with tools from dynamical systems.

Organizer: Hinke M. Osinga
University of Auckland, New Zealand

Organizer: Bernd Krauskopf
University of Auckland, New Zealand

10:00-10:25 Dynamical Systems Tools for the Investigation of Cell Signalling
Hinke M. Osinga, University of Auckland, New Zealand

10:30-10:55 Negative Feedback for Oscillations, Negative Feedback for Robustness
Arthur S. Sherman and Joon Ha, National Institutes of Health, USA

11:00-11:25 Modelling Electrical Activity and Calcium Signalling in Developing Inner Hair Cells
Krasimira Tsaneva-Atanasova, University of Bristol, United Kingdom; Daniele Avitabile, University of Surrey, United Kingdom; Helen Kennedy, University of Bristol, United Kingdom

11:30-11:55 Effects of Multiple Time Scales in Cell Dynamics
Martin Wechselberger, University of Sydney, Australia

Thursday, August 9

MS33

Recent Advances of Mathematical Modeling for Cell and Developmental Biology - Part I of II

10:00 AM-12:00 PM

Room:Diamond I - 2nd Floor

For Part 2 see MS41

This minisymposium aims to bring researchers to address recent advances of mathematical modeling for complex biological systems, and many such systems usually consist of multiple interacting components that exhibit complicated temporal and spatial dynamics with multiple scales, which are extremely difficult to describe, model or predict. In this minisymposium, researchers will discuss a wide range of complex biological systems which include but not limited to cell polarization, cell signaling pathways, cancer stem cells, to developmental biology and tumor growth. The challenges of modeling these complex systems will be discussed, and more beyond, the new computational techniques to simulate these models will also be presented.

Organizer: Xinfeng Liu
University of South Carolina, USA

Organizer: Ching-Shan Chou
The Ohio State University, USA

10:00-10:25 Adaptation in a Eukaryotic Pathway: Combining Experiments with Modeling
Wouter Rappel and Herbert Levine, University of California, San Diego, USA

10:30-10:55 The Conflicting Influence of Spatial Stochastic Dynamics on Cell Polarity
Tau-Mu Yi, University of Santa Barbara, USA

11:00-11:25 Changes in Domain Thickness Halt Par Protein Travelling Wave Solutions in a Model of the Early C. Elegans Embryo
Adriana Dawes, Ohio State University, USA; David Iron, Dalhousie University, Canada

Thursday, August 9

MS33

Recent Advances of Mathematical Modeling for Cell and Developmental Biology - Part I of II

10:00 AM-12:00 PM

continued

11:30-11:55 Signaling Regulated Endocytosis and Exocytosis Lead to Mating Pheromone Concentration Dependent Morphologies in Yeast
Ching-Shan Chou, The Ohio State University, USA; Travis Moore, Seoul National University, Korea; Qing Nie, University of California, Irvine, USA; Tau-Mu Yi, University of California, Santa Barbara, USA

Thursday, August 9

MS34

Biological Locomotion

10:00 AM-12:00 PM

Room:Crystal Ballroom I - 2nd Floor

Organisms have evolved various forms of motility to move effectively and efficiently in a given fluid environment. Understanding the mechanism of biological locomotion is one of the challenging areas in the life sciences. In this minisymposium, the focus will be on aquatic locomotion over a wide range of Reynolds number, including motility of microorganisms to the swimming of fish. The movement of different organisms will be presented, with emphasis on the links to mechanics, hydrodynamics, and biology. This minisymposium on biological locomotion will highlight recent developments and current challenges through simulation, analysis, and experiments.

Organizer: Sookkyung Lim
University of Cincinnati, USA

Organizer: Sarah D. Olson
Worcester Polytechnic Institute, USA

10:00-10:25 Following Hydrodynamic Signals in Underwater Locomotion
Eva Kanso and Andrew Tchieu, University of Southern California, USA

10:30-10:55 Helical Swimming in Viscoelastic and Porous Media
Bin Liu, Thomas R Powers, and Kenneth S Breuer, Brown University, USA

11:00-11:25 Modeling the Undulatory Swimming of Sperm: Mechanics, Biochemistry, and Hydrodynamics
Sarah D. Olson, Worcester Polytechnic Institute, USA

11:30-11:55 Locomotion at Low Reynolds Number: Some Theoretical Topics
Hirofumi Wada, Ritsumeikan University, Japan

Thursday, August 9

MS35

Modeling and Inverse Problems of Complex Biological Systems - Part I of II

10:00 AM-12:00 PM

Room:Topaz - 2nd Floor

For Part 2 see MS43

The analysis of complex hierarchical biological systems, which are at the core of genetics, neurobiology, immunology and developmental biology, represents one of the most important open areas in biology. At the molecular and cellular levels, detailed components of biological systems are being uncovered by powerful and modern experimental methodologies. The coordination and integration of these details into a functional biological systems require insights that come from mathematical abstraction as well as experimental data from biologists. In this minisymposium, invited speakers will discuss mathematical development and methodologies that provide biological insights into a wide spectrum of life science applications.

Organizer: Hien Tran
North Carolina State University, USA

Organizer: Mette S. Olufsen
North Carolina State University, USA

10:00-10:25 Mathematical Problems in the Diagnosis and Treatment of Breast Cancer
David Isaacson, Rensselaer Polytechnic Institute, USA

10:30-10:55 Mathematical Modeling of Cancer Immunotherapy
L G. dePillis, Harvey Mudd College, USA

11:00-11:25 Patient Specific Subset Selection and Parameter Estimation of an HIV-1 Model with Censored Observations
Adam Attarian, North Carolina State University, USA

11:30-11:55 Modeling Patient Response to HIV Using Artificial Neural Networks
John David, Virginia Military Institute, USA

Thursday, August 9

MS36

CANCELLED

10:00 AM-12:00 PM

Thursday, August 9

MS37

Issues in Modeling Biological Excitable Systems

10:00 AM-12:00 PM

Room:Crystal Ballroom II - 2nd Floor

Developing robust models of biological excitable systems and analyzing their dynamics pose particular difficulties. Biological variability and experimental limitations lead to large ranges of plausible parameter values. Difficulties in accessing system components experimentally can result in sparse data that inadequately constrain model functions. Integration across subcellular, cellular, and tissue scales presents additional challenges. As a result of these issues, the level of uncertainty in mathematical models is often quite high, which makes model analysis problematic and model predictions of questionable value. This minisymposium will discuss issues surrounding the modeling and analysis of biological excitable systems and their implications.

Organizer: Elizabeth M. Cherry
Rochester Institute of Technology, USA

10:00-10:25 Discrepant Predictions Among Models of Cardiac Cells
Elizabeth M. Cherry, Rochester Institute of Technology, USA

10:30-10:55 Curve Fitting to Sparse Experimental data: Implications for the Dynamics of Cardiac Electrophysiology Models
Benjamin Liu and Elizabeth M. Cherry, Rochester Institute of Technology, USA

11:00-11:25 The Statistics of Calcium-mediated Focal Excitations in Cardiac Tissue
Yohannes Shiferaw, Mesfin Asfaw, and Wei Chen, California State University, Northridge, USA

11:30-11:55 Meta-bifurcation Analysis of a Mean-field Model of the Human Cortex
Lennaert van Veen, University of Ontario Institute of Technology, Canada; Federico Frascoli, University of Melbourne, Australia; Bojak Ingo, University of Birmingham, United Kingdom; Liley David, Swinburne University of Technology, Australia; Kevin R. Green, University of Ontario Institute of Technology, Canada

Thursday, August 9

MS38

Computational Biological Modeling at the Interface of Molecular Simulation and Continuum Diffusion - Part II of II

10:00 AM-12:00 PM

Room:Pearl - 3rd Floor

For Part 1 see MS30

The integration of molecular simulations and numerical approximation of partial differential equations presents a promising approach for describing diffusion-based biological phenomena, including protein-substrate association, electrodiffusion, and protein-protein signaling. The modeling of these phenomena offer novel insights into critical factors governing system behavior at both molecular and mesoscopic scales. These models would naturally benefit from a rigorous examination of the mathematics interfacing these scales, as well as the choice of simplifying assumptions. This minisymposium will bring together researchers from a variety of fields within computational biology to discuss common threads in the interaction between molecular domain and biological function.

Organizer: Andrew Gillette
University of California, San Diego, USA

Organizer: Peter Kekenes-Huskey
University of California, San Diego, USA

10:00-10:25 Molecular and Subcellular Modeling of Cardiac Troponin C Calcium Handling
Pete Kekenes-Huskey, University of California, San Diego, USA

10:30-10:55 Boundary Integral Methods for Biomolecule Diffusion and Association: Challenges and Progress
Jaydeep P. Bardhan, Rush University Medical Center, USA

continued in next column

continued

11:00-11:25 Spatially Adaptive Stochastic Numerical Methods for Intrinsic Fluctuations in Reaction-Diffusion Systems
Paul J. Atzberger, University of California, Santa Barbara, USA

11:30-11:55 Level-set Variational Implicit-Solvent Approach to Biomolecular Interactions
Bo Li, University of California, San Diego, USA

Lunch Break

12:00 PM-2:00 PM

Attendees on their own

Thursday, August 9

IP6

Complex Systems in Health and their Breakdown with Aging and Disease

2:00 PM-2:45 PM

Room:Emerald Ballroom - 2nd Floor

Chair: James Bassingthwaite, University of Washington, USA

The output of human physiologic control systems, exemplified by the heartbeat at rest or during modest activity, shows complex dynamics, characterized by fractality, multiscale time irreversibility, nonstationarity and nonlinearity. In contrast, the frailty syndrome, and a wide variety of prevalent disease states, are associated with a loss of complexity. The collapse of complexity may serve as the basis of a new class of dynamical biomarkers, with potential applications to drug safety testing, disease detection and clinical monitoring. Restoration of complexity (incorporating multiscale plasticity and resilience) as a therapeutic goal invites consideration of new treatment modalities. Biologic complexity also poses challenges to those involved in efforts to create and test mathematical models of biologic dynamics in health and disease.

Ary L. Goldberger
Harvard Medical School, USA

Coffee Break

2:45 PM-3:15 PM

Room:Foyer - 2nd Floor

Thursday, August 9

MS39

Long-term Dynamical Properties of Biochemical Reaction Networks - Part II of II

3:15 PM-5:15 PM

Room:Emerald Ballroom - 2nd Floor

For Part 1 see MS31

Analyzing biochemical network models is generally a difficult task, since the corresponding dynamical systems are usually nonlinear, high-dimensional, and contain many unknown parameters. Despite this great level of complexity, important properties of biochemical network models may depend only on the structure of the network and not on the specific values of the parameters involved. Since parameter uncertainty is widespread in biology, relating dynamical properties to network topology has become an important area of research. This minisymposium will focus on recent results on the long-term dynamical properties of biochemical network models (e.g. persistence, global stability, oscillatory behavior) and their connection to the network structure.

Organizer: Maya Mincheva
Northern Illinois University, USA

Organizer: Casian Pantea
Imperial College London, United Kingdom

3:15-3:40 Persistence and Global stability in Biochemical Interaction Networks
Casian Pantea, Imperial College London, United Kingdom; Gheorghe Craciun, University of Wisconsin, Madison, USA; Fedor Nazarov, Kent State University, USA

3:45-4:10 Uniqueness and Asymptotic Stability of Equilibria in a Reversible, Non-Complex-Balanced Reaction Network
Gilles Gnacadja, Amgen Inc., USA

4:15-4:40 Non-persistent Reaction Networks with Regular Dynamics
David Siegel, University of Waterloo, Canada

4:45-5:10 Perspectives on the Global Attractor Conjecture
Manoj Gopalkrishnan, Tata Institute of Fundamental Research, India; Ezra Miller, Duke University, USA; Anne Shiu, University of Chicago, USA

Thursday, August 9

MS40

Signaling: Vitamin D in Monocytes and Receptor Clustering in Mast Cells

3:15 PM-5:15 PM

Room:Crystal Ballroom I - 2nd Floor

Understanding through experiment and modeling activation of immune response from ligand binding to transcription factors is critical to improving health and wellness. Vitamin D acts primarily in bone health, but also acts to boost immune responses in the presence of microbial invaders. Upregulation of anti-microbial proteins in vitro is modeled and used to address in vivo concerns of sufficiency and individual variation. FceRI oligomerization activates signaling pathways leading to release of inflammatory mediators. Single particle tracking and computational analysis indicate receptor diffusion is restricted by transient residency in membrane domains. High-resolution microscopy, biochemical methods, and mathematical modeling provide insight into initiation and regulation of signaling.

Organizer: Bradford E. Peercy
University of Maryland, Baltimore County, USA

3:15-3:40 Monocyte Innate Immune Response to Vitamin D
Rene F. Chun, University of California, Los Angeles, USA

3:45-4:10 Modeling Vitamin D Regulation in Monocytes
Bradford E. Peercy, University of Maryland, Baltimore County, USA

4:15-4:40 Initiation and Regulation of Mast Cell Signaling through the FceRI Pathway
Avanika Mahajan, University of New Mexico, USA; Dipak Barua and William S. Hlavacek, Los Alamos National Laboratory, USA; Bridget Wilson, University of New Mexico, USA

continued on next page

Thursday, August 9

MS40

Signaling: Vitamin D in Monocytes and Receptor Clustering in Mast Cells

3:15 PM-5:15 PM

continued

4:45-5:10 Insights Into Cell Membrane Microdomain Organization from Live Cell Single Particle Tracking of the IgE High Affinity Receptor FceRI of Mast Cells
Flor A. Espinoza, Michael Wester, and Janet Oliver, University of New Mexico, USA; Bridget Wilson, University of New Mexico School of Medicine, USA; Nicholas Andrews, Diane Lidke, and Stanly Steinberg, University of New Mexico, USA

Thursday, August 9

MS41

Recent Advances of Mathematical Modeling for Cell and Developmental Biology - Part II of II

3:15 PM-5:15 PM

Room:Diamond I - 2nd Floor

For Part 1 see MS33

This minisymposium aims to bring researchers to address recent advances of mathematical modeling for complex biological systems, and many such systems usually consist of multiple interacting components that exhibit complicated temporal and spatial dynamics with multiple scales, which are extremely difficult to describe, model or predict. In this minisymposium, researchers will discuss a wide range of complex biological systems which include but not limited to cell polarization, cell signaling pathways, cancer stem cells, to developmental biology and tumor growth. The challenges of modeling these complex systems will be discussed, and more beyond, the new computational techniques to simulate these models will also be presented.

Organizer: Xinfeng Liu
University of South Carolina, USA

Organizer: Ching-Shan Chou
The Ohio State University, USA

3:15-3:40 A Computational Study of Cell Population Heterogeneity
Liming Wang, California State University, Los Angeles, USA

3:45-4:10 A Multi-scale Approach to Spatially Distributed Regulatory Networks
Bill Holmes, University of British Columbia, Canada

4:15-4:40 External Noise Control in Auto-regulated Biological Networks
Likun Zheng, Meng Chen, and Qing Nie, University of California, Irvine, USA

4:45-5:10 Mathematical Modeling of Tumor Heterogeneity and the Role of HER2 in Breast Cancer Stem Cells
Xinfeng Liu and Hexin Chen, University of South Carolina, USA

Thursday, August 9

MS42

Fluid/Structure Interactions in Biology - Part I of II

3:15 PM-5:15 PM

Room:Diamond II - 2nd Floor

For Part 2 see MS49

In a wide range of biological applications, the behavior of the system depends on the coupled dynamics of fluids and structures. In some situations, such as swimming of organisms, the structure initially drives the fluid which then feeds back and influences the motility. In other situations, such as blood clotting, fluid initiates the growth of a cellular mass which feeds back and influences the fluid. Unfolding the driving mechanism for swelling/de-swelling of gels is much less straightforward. This session will collect several examples of fluid/structure interactions with a variety of spatial and temporal scales and a variety of mathematical treatments.

Organizer: Nick Cogan
Florida State University, USA

Organizer: Karin Leiderman
Duke University, USA

3:15-3:40 The Influence of Hindered Transport on the Development of Platelet Thrombi Under Flow
Karin Leiderman, Duke University, USA

3:45-4:10 Multiscale Modeling of Tumor Dynamics
John Lowengrub, University of California, Irvine, USA

4:15-4:40 Modeling Hydrodynamic Contributions to Ameboid Cell Motility
Owen Lewis and Robert D. Guy, University of California, Davis, USA

4:45-5:10 Modeling the Role of the Bacterium *Xylella fastidiosa* in the Development of Plant Diseases
Matt Donahue, Florida State University, USA

Thursday, August 9

MS43

Modeling and Inverse Problems of Complex Biological Systems - Part II of II

3:15 PM-5:15 PM

Room:Topaz - 2nd Floor

For Part 1 see MS35

The analysis of complex hierarchical biological systems, which are at the core of genetics, neurobiology, immunology and developmental biology, represents one of the most important open areas in biology. At the molecular and cellular levels, detailed components of biological systems are being uncovered by powerful and modern experimental methodologies. The coordination and integration of these details into a functional biological systems require insights that come from mathematical abstraction as well as experimental data from biologists. In this minisymposium, invited speakers will discuss mathematical development and methodologies that provide biological insights into a wide spectrum of life science applications.

Organizer: Hien Tran
North Carolina State University, USA

Organizer: Mette S. Olufsen
North Carolina State University, USA

3:15-3:40 The Impact of Gravity during Head-up Tilt
Mette S. Olufsen, North Carolina State University, USA; Johnny Ottesen, Roskilde University, Denmark

3:45-4:10 A Spatially Distributed Model of the Inverse Problem of the Energetic of Consciousness
Daniela Calvetti, Case Western Reserve University, USA

4:15-4:40 Modeling of Hyaluronan Clearance: Application to Estimation of Lymph Flow
Jerry Batzel, University of Graz, Austria

4:45-5:10 Scalability and Dimension Reduction in Multiscale Models of Physiological Systems
Scott M. Bugenhagen and Daniel Beard, Medical College of Wisconsin, USA

Thursday, August 9

MS44

Coherent Dynamics of Neuronal Networks - Part I of III

3:15 PM-5:15 PM

Room:Opal - 2nd Floor

For Part 2 see MS51

A fundamental component of understanding brain function is determining the collective behavior of a neuronal network in terms of the well-defined dynamics of individual neurons and the properties of their connections to each other. The speakers in this three-part minisymposium will provide their perspectives on this question, spanning the spectrum from theoretical to experimental techniques. The use of relatively simple models allows deeper mathematical studies of how the interactions of individual neurons produce coherent dynamics, leading to a better understanding of brain function.

Organizer: Katherine Newhall
Courant Institute of Mathematical Sciences, New York University, USA

Organizer: Andrea K. Barreiro
University of Washington, USA

Organizer: Gregor Kovacic
Rensselaer Polytechnic Institute, USA

3:15-3:40 Synchronous Firing Events in Stochastic Model Neuron Systems
Katherine Newhall, Courant Institute of Mathematical Sciences, New York University, USA

3:45-4:10 The Structure of Network Activity in the Neocortex
Andreas Tolias, Baylor College of Medicine, USA

4:15-4:40 Reliability and Modular Decompositions of Oscillator Networks
Kevin K. Lin, University of Arizona, USA; Eric Shea-Brown, University of Washington, USA; Lai-Sang Young, Courant Institute of Mathematical Sciences, New York University, USA

4:45-5:10 Stochastic Neuronal Dynamics on Complex Networks
Lee DeVille, University of Illinois at Urbana-Champaign, USA

Thursday, August 9

MS45

Current Topics in Pharmacometrics

3:15 PM-5:15 PM

Room:Crystal Ballroom II - 2nd Floor

The needs of the pharmaceutical industry for new methods of drug development have lead to an explosion in the use of Modeling and Simulation techniques. Statistical descriptions of pharmacokinetic variables are thus now coupled with the use of numerical solutions of dynamical equations. This merging of approaches has benefitted from recent incorporations of dynamics techniques, but the full benefits are yet to be reached. The goal of this minisymposium is to attract modelers and pharmacometricians from both academia and industry to exchange on the underlying mathematical ideas in this emerging discipline.

Organizer: Jacques Belair
Universite de Montreal, Canada

3:15-3:40 What is Pharmacometrics - How Can Modeling Help ?
Fahima Nekka and Jun Li, Universite de Montreal, Canada

3:45-4:10 Pharmacodynamic Models of Delayed Drug Effects
Wojciech Krzyzanski, State University of New York, Buffalo, USA

4:15-4:40 Predicting the Drug Release Kinetics of Matrix Tablets
Ami Radunskaya, Pomona College, USA; Peter Hinow, University of Wisconsin, Milwaukee, USA

4:45-5:10 A Model for Myelosuppression and the Influence of Timing in Drug Administration
Jacques Belair, Universite de Montreal, Canada

Intermission

5:15 PM-5:30 PM

Thursday, August 9

Lee Segel Forum

Mathematics in Mediciine

5:30 PM-6:30 PM

Room:Emerald Ballroom - 2nd Floor

The focus of this year's Lee Segel Forum will focus on the impact of mathematics and computational modeling on diagnosing, treating, and preventing disease. The Forum will start with brief presentations by panelists, which will be followed by an open question and answer session. The audience for the Forum will likely include many students seeking advice for career directions as well as faculty interested in updating the training that their own institutions provide. This Forum is in memory of Lee Segel.

Chair: Tim Lewis
University of California, Davis, USA

Panelists:

Anna Georgieva
Novartis Pharmaceuticals Corporation, USA

Ary Goldberger
Harvard Medical School, USA

Jesper Mehlsen
Frederiksberg Hospital, Denmark

John Milton
Claremont College, USA

Charles Taylor
Heartflow, Inc. USA

Dinner Break

6:30 PM-8:00 PM

Attendees on their own

Thursday, August 9

PP2

Poster Session II

8:00 PM-10:00 PM

Room:Foyer - 2nd Floor

Polymerization-Driven, Adhesion-Mediated Actin Traveling Waves in Motile Cells
Jun Allard, University of California, Davis, USA; Erin Barnhart, Stanford University, USA; Alex Mogilner, University of California, Davis, USA; Julie Theriot, Stanford University, USA

Mathematical Modelling of Dna Base Excision Repair
Philip J. Aston, Ruan Elliott, and Lisi Meira, University of Surrey, United Kingdom

Compressed Sensing in Retinal Image Processing
Victor Barranca, Rensselaer Polytechnic Institute, USA

Mathematical Investigation of Calcium Dynamics in Human Airway Smooth Muscle
Pengxing Cao, University of Auckland, New Zealand

Initiation of Spiral Calcium Waves in a 3-D Cardiac Cell Based on Analysis of a 1-D Deterministic Model
Zana A. Coulibaly, Bradford E. Peercy, and Matthias K. Gobbert, University of Maryland, Baltimore County, USA

A Transient Structured Tree Boundary Condition for Hemodynamic Modeling
William Cousins and Pierre Gremaud, North Carolina State University, USA

A Multiscale Examination of Nonlinear Waves in the Cochlea
Kimberly Fessel and Mark Holmes, Rensselaer Polytechnic Institute, USA

Computational Modeling of Tumor Response to Vascular-Targeting Therapies
Jana Gevertz, The College of New Jersey, USA

continued in next column

Modelling Foot-and-Mouth Disease Virus Infection in Bovine Epithelial Tissues Potential Determinants of Cell Lysis
Kyriaki Giorgakoudi, Loughborough University, United Kingdom; Simon Gubbins, Pirbright Laboratory, United Kingdom; John P. Ward, Loughborough University, United Kingdom; Nicholas Juleff and David Schley, Pirbright Laboratory, United Kingdom

Mathematical Modeling and Data Analysis for Cerebral Blood Flow
Rachael K. Gordon-Wright, North Carolina State University, USA

Multiple Attractors of Intraguild Predation Models with Generalist Or Specialist Predator
Yun Kang and Lauren Wedekin, Arizona State University, USA

Wandering and Transitions of Pulses in Stochastic Neural Fields
Zachary Kilpatrick and Bard Ermentrout, University of Pittsburgh, USA

A Mechanism for Robust Circadian Timekeeping: Stoichiometric Balance Through Double Negative Feedback Loop Structure
Jae Kyoung Kim, University of Michigan, Ann Arbor, USA; Daniel Forger, University of Michigan, USA

Molecular Network Structure Detection based on Oscilating Timecourses
Jae Kyoung Kim, University of Michigan, Ann Arbor, USA; Daniel Forger, University of Michigan, USA

From Discrete to Continuous Models of Cell Movement: An Application to Medical Implants
Alicia Prieto Langarica, Hristo Kojouharov, and Bentio Chen-Charpentier, University of Texas at Arlington, USA

High Performance Simulations of Platelets in Flow
Joshua Lioi, Charles Maggio, and Mark S. Alber, University of Notre Dame, USA; Scott Christley, University of Chicago, USA

Ensemble Modeling of Symptoms to Human Immune Response of Influenza A Virus Infection
Sarah R. Lukens, David Swigon, and Gilles Clermont, University of Pittsburgh, USA

continued on next page

Multiscale Population Dynamics Study of Heterotypic Cell Aggregation in a Shear Flow and Related Parameter Identification Problem
Yanping Ma, Loyola Marymount University, USA; Qiang Du and Cheng Dong, Pennsylvania State University, USA

Effect of Parity on Boundedness of Orbits in Lotka-Volterra Food Chains
Nicole Massarelli and Kathleen Hoffman, University of Maryland, Baltimore County, USA; Joseph Previte, Pennsylvania State University,Erie Campus, USA

Incorporating Drift into the First-Passage Kinetic Monte Carlo Method
Ava J. Mauro, Boston University, USA; Paul J. Atzberger, University of California, Santa Barbara, USA; Samuel A. Isaacson, Boston University, USA; Justin Shrake, University of California, Santa Barbara, USA

An Adjoint-Based Method for Automatically Identifying Key Processes in a Nonlinear Mixed-Type Pde Model of Cell Motility
Philip Maybank, Jonathan Whiteley, and David Gavaghan, University of Oxford, United Kingdom

Neurovascular Coupling During Cortical Spreading Depression: A Mathematical Model
K.C. Brennan, University of Utah, USA; Joshua Chang and Thomas Chou, University of California, Los Angeles, USA; Dongdong He and Huaxiong Huang, York University, Canada; *Robert M. Miura*, New Jersey Institute of Technology, USA; Phillip Wilson, University of Canterbury, New Zealand; Jonathan J. Wylie, City University of Hong Kong, Hong Kong

Evaluation of Diagnostic Test for Lymphatic Filariasis in Papua New Guinea Using a Mathematical Model
Anuj Mubayi, Northeastern Illinois University, USA

The Effect of Intramitochondrial Stochasticity on the Tricarboxylic Acid Cycle
John D. Nagy, Arizona State University, USA

continued in next column

Understanding Physiological Systems with Three Time Scales
Pingyu Nan, University of Auckland, New Zealand

Modelling Contractility and Antiparallel Flows in Actomyosin Bundles
Dietmar B. Oelz, Radon Institute for Computational and Applied Mathematics, Austria

Optimal Control of Dengue with Periodicity
Gerard Olivar and Luis Lopez, Universidad Nacional de Colombia, Colombia; Anibal Muñoz, Universidad del Quindio, Colombia

Beta Oscillations in the Basal Ganglia Circuit
Alex Pavlides, S. John Hogan, and Rafal Bogacz, University of Bristol, United Kingdom

Models of Plankton Dynamics
Sofia Piltz, Mason A. Porter, and Philip K. Maini, University of Oxford, United Kingdom

Spatio-Temporal Modelling of Cell Cycle Control
Jana Hutter, *Alexander Prechtel*, and Peter Knabner, Friedrich-Alexander-Universität Erlangen-Nürnberg, Germany

Data Mining and Machine Learning Methods to Improve Serodetection in the Mouse Model of Infectious Diseases
Resmi Ravindran, University of California, Davis, USA; Imran Khan, University of California, Davis Health System; S Mannepalli, California State University, Fresno, USA; Michael Hogarth, University of California, Davis Health System; Paul Luciw, University of California, Davis, USA; Krish Krishnan, University of California, Davis and California State University, Fresno

Mathematical Modeling of Chromosome Segregation in Bacteria
Blerta Shtylla, Mathematical Biosciences Institute, USA; James P. Keener, University of Utah, USA

Posterior Distributions in Parameter Estimation
Shelby R. Stanhope, Jonathan E. Rubin, and David Swigon, University of Pittsburgh, USA

continued in next column

Modelling of Endocrinological Networks
Claudia Stoetzel, Susanna Roeblitz, Julia Ploentzke, and Peter Deuflhard, Zuse Institute Berlin, Germany

Prediction of Effective Elastic Properties of Osteons by Means of Multiscale Models and Homogenization Methods
Sara Tiburtius, Technische Universität Darmstadt, Germany; Peter Varga, Susanne Schrof, and Kay Raum, Charité - Universitätsmedizin Berlin, Germany; Alf Gerisch, Technische Universität Darmstadt, Germany

Formation of Anti-Waves in Gap Junction Coupled Chains of Neurons
Alexander Urban, U.S. Army Research Laboratory, USA; Bard Ermentrout, University of Pittsburgh, USA

Modeling of Controlled-Release Drug Delivery from Polymer Microspheres Using Reaction-Diffusion Equations with Hindered Diffusion
Ashlee N. Ford Versypt and Daniel Pack, University of Illinois at Urbana-Champaign, USA; Richard Braatz, Massachusetts Institute of Technology, USA

Numerical Computations of Multiphase Systems
Mark E. Whidden, Florida State University, USA

An Optimal Control Approach for Modeling the Response to Head-Up Tilt
Nakeya D. Williams, North Carolina State University, USA

A Model of Self-Destructive Bacteria
Glenn S. Young, University of Pittsburgh, USA; Christian Woods, University of California, San Diego, USA; Bard Ermentrout and Jon Rubin, University of Pittsburgh, USA

Friday, August 10

Registration

8:00 AM-4:00 PM

Room:Foyer - 2nd Floor

Closing Remarks

8:40 AM-8:45 AM

Room:Emerald Ballroom - 2nd Floor

IP7

Life at Stability's Edge: From the Fingertip to Seizure Onset

8:45 AM-9:30 AM

Room:Emerald Ballroom - 2nd Floor

Chair: Jacques Bélgin, Université de Montreal, Canada

Mathematical models of bistability arise in discussions of seizure onset, balance control and decision making. In the presence of random perturbations and time delay, the unstable fixed point ('separatrix') that separates basins of attraction can have unexpected effects on dynamics, including transient stabilizations and oscillations not seen when the delay is zero. Thus when trajectories travel sufficiently close to the separatrix, the nervous system becomes vulnerable to the generation of novel dynamical behaviors not seen when the delay is zero. This mechanism may explain phenomena ranging from the increased risk of seizures as sleep stages change to the beneficial effects of vibration on human balance to the indecisiveness in decision making that occurs when athletes 'choke'.

John Milton
Claremont College, USA

Coffee Break

9:30 AM-10:00 AM

Room:Foyer - 2nd Floor

Friday, August 10

MS46

Stochastic Modeling of Gene Expression

10:00 AM-12:00 PM

Room:Emerald Ballroom - 2nd Floor

Understanding the effect of stochasticity is key to understanding the underlying dynamics of gene expression. Due to the low copy number of some of the chemical species involved in these systems, random fluctuations can have a big effect. Deterministic descriptions of these systems do not always take this into account. In this minisymposium, we aim to consider a range of new methods and applications for stochastic modeling of gene expression.

Organizer: Jay M. Newby
Oxford University, United Kingdom

Organizer: Simon Cotter
University of Oxford, United Kingdom

10:00-10:25 Isolating Intrinsic Noise Sources in a Stochastic Genetic Switch
Jay M. Newby, Oxford University, United Kingdom

10:30-10:55 Solution of the Effective Fokker-Planck Equation for High Dimensional Chemical Systems
Simon Cotter, University of Oxford, United Kingdom

11:00-11:25 Modeling Intrinsic Noise in Gene Expression Circuits
Rahul Kulkarni, Virginia Polytechnic Institute & State University, USA

11:30-11:55 Rigorous Relationship between Two Stochastic-reaction Diffusion Models for the Time Required to First Find a Binding Site
Ikemefuna Agbanusi, Boston University, USA

Friday, August 10

MS47

Modeling Cell Migration Using Theory and Experiment

10:00 AM-12:00 PM

Room:Topaz - 2nd Floor

Cell migration plays a critical role in biological processes such as wound healing, angiogenesis, development, and cancer metastasis. The migration of single cells or collections of cells has been defined using reaction-diffusion equations, continuum mechanics descriptions, and the cellular Potts model. Such models are developed alongside experimental data in order to provide realistic insight into the mechanisms and behavior of cell migration under normal or disease conditions. This minisymposium will introduce new cell migration modeling approaches that are used to understand important aspects of multiple biological problems.

Organizer: Julia Arciero
Indiana University - Purdue University Indianapolis, USA

Organizer: Tracy L. Stepien
University of Pittsburgh, USA

10:00-10:25 Effect of Stretch-dependent Proliferation on Collective Cell Migration
Tracy L. Stepien and David Swigon, University of Pittsburgh, USA

10:30-10:55 Multiscale Modeling of Bacterial Chemotaxis
Chuan Xue, Ohio State University, USA

11:00-11:25 Modeling Cancer Progression Due to Somatic Evolution
James A. Glazier, Indiana University, USA

11:30-11:55 Modeling Collective Cell Migration: Wound Healing and Cancer Metastasis
Pilhwa Lee and Charles Wolgemuth, University of Connecticut Health Center, USA

Friday, August 10

MS48

Mathematical Modeling and Simulations of Angiogenesis - Part I of II

10:00 AM-12:00 PM

Room:Diamond I - 2nd Floor

For Part 2 see MS56

Angiogenesis is a crucial component of many physiological and pathological processes, including cancer, and ocular diseases. The angiogenic cascade is extremely complex, spanning from the genetic and subcellular level all the way to the cellular, tissue, and organ levels. Cutting across multiple scales, angiogenesis involves interactions between large amount of molecules, various cell types, extracellular matrix, and blood flow. Areas represented by the speakers include mathematical modeling of the initiation, extension, maturation of blood vessels, and the role of angiogenesis in a variety of physiological and pathological processes. The modeling techniques include stochastic models; cell-based and agent-based approaches; and discrete, continuous, and hybrid models.

Organizer: Xiaoming Zheng
Central Michigan University, USA

Organizer: Trachette Jackson
University of Michigan, Ann Arbor, USA

10:00-10:25 A Viscoelastic Model of Blood Capillary Extension and Regression: Derivation, Analysis, and Simulation
Xiaoming Zheng, Central Michigan University, USA; Chunjing Xie, Shanghai Jiaotong University, China

10:30-10:55 Using Computer Simulation Combined with Experimentation to Explore Notch Dynamics During Angiogenesis
Katie Bentley, Vascular Biology Laboratory Cancer Research, United Kingdom

11:00-11:25 Cell Behavior Patterns During Neurovascular Formation: A Rule-Oriented Modeling Study
Amina Qutub, Byron Long, and Rahul Rekhi, Rice University, USA

11:30-11:55 Vascular Patterning by Matrix-Mediated Paracrine Signalling
Alvaro Köhn-Luque, Technische Universität Dresden, Germany

Friday, August 10

MS49

Fluid/Structure Interactions in Biology - Part II of II

10:00 AM-12:00 PM

Room:Diamond II - 2nd Floor

For Part 1 see MS42

In a wide range of biological applications, the behavior of the system depends on the coupled dynamics of fluids and structures. In some situations, such as swimming of organisms, the structure initially drives the fluid which then feeds back and influences the motility. In other situations, such as blood clotting, fluid initiates the growth of a cellular mass which feeds back and influences the fluid. Unfolding the driving mechanism for swelling/de-swelling of gels is much less straightforward. This session will collect several examples of fluid/structure interactions with a variety of spatial and temporal scales and a variety of mathematical treatments.

Organizer: Nick Cogan
Florida State University, USA

Organizer: Karin Leiderman
Duke University, USA

10:00-10:25 Fluid Dynamics and Bacterial Disinfection
Nick Cogan, Florida State University, USA

10:30-10:55 A Langrangian Technique for Modeling Moving Structures in a Viscoelastic Fluid
Bree Cummins, Tulane University, USA

11:00-11:25 Computational Explorations of Cellular Blebbing
Wanda Strychalski, University of California, Davis, USA

11:30-11:55 The Motility Analysis of the Lyme Disease Spirochete through Viscous Fluids
Mike W. Harman, University of Connecticut Health Center, USA

Friday, August 10

MS50

Contemporary Approaches in Mathematical Epidemiology, Ecology and Population Dynamics - Part I of II

10:00 AM-12:00 PM

Room:Crystal Ballroom I - 2nd Floor

For Part 2 see MS58

Using applied mathematical tools and techniques in understanding and finding answers of problems in epidemiology, ecology and immunology has become increasingly important. This mini-symposium focuses on recent advances in these areas of population dynamics. The mini symposium brings together young researchers to discuss and share ideas on current research trends. Talks will be given on recent mathematical models developed for problems in epidemiology and immunology. Some example talk subjects are immune response to influenza and Hepatitis C virus, and optimal control of treatments for HIV, AIDS and Malaria.

Organizer: Necibe Tuncer
University of Tulsa, USA

Organizer: Maia Martcheva
University of Florida, USA

10:00-10:25 Seasonality in Avian Influenza H5N1
Necibe Tuncer, University of Tulsa, USA; Maia Martcheva, University of Florida, USA

10:30-10:55 Impact of Malaria Control on the Competition between Plasmodium falciparum and Plasmodium vivax
Olivia Prosper and Maia Martcheva, University of Florida, USA

11:00-11:25 Optimal Control of Treatments and Prevention in a Two Strain Malaria-HIV/AIDS Co-infection Model
Folashade Augusto, Austin Peay State University, USA

11:30-11:55 Bistability and Long-term Cure in a Within-host Model of Hepatitis C
Swati Debroy, University of Missouri, Kansas City, USA

Friday, August 10

MS51

Coherent Dynamics of Neuronal Networks - Part II of III

10:00 AM-12:00 PM

Room:Opal - 2nd Floor

For Part 1 see MS44
For Part 3 see MS59

A fundamental component of understanding brain function is determining the collective behavior of a neuronal network in terms of the well-defined dynamics of individual neurons and the properties of their connections to each other. The speakers in this three-part minisymposium will provide their perspectives on this question, spanning the spectrum from theoretical to experimental techniques. The use of relatively simple models allows deeper mathematical studies of how the interactions of individual neurons produce coherent dynamics, leading to a better understanding of brain function.

Organizer: Katherine Newhall
Courant Institute of Mathematical Sciences, New York University, USA

Organizer: Andrea K. Barreiro
University of Washington, USA

Organizer: Gregor Kovacic
Rensselaer Polytechnic Institute, USA

10:00-10:25 Higher Order Interactions in Microcircuits: A Mechanistic View
Andrea K. Barreiro, University of Washington, USA

10:30-10:55 Dynamical Sensitivity and Stability: Suprathreshold Conditional Bursting Induced by Transient Potassium Promotes Information Transfer
Aushra Abouzeid, University of Pittsburgh, USA

11:00-11:25 On Tiling and Noise Correlations
Tatyana Sharpee, Salk Institute for Biological Studies, USA

11:30-11:55 The Influence of Network Structure on Neuronal Network Dynamics
Duane Nykamp, University of Minnesota, USA

Friday, August 10

MS52

Multi-timescale Dynamics in Neural Control Systems

10:00 AM-12:00 PM

Room:Crystal Ballroom II- 2nd Floor

Many activities within the body require an appropriate balance of reactants and fuels, such as hormones, oxygen, and glucose. Various subcortical neurons play key roles in regulating these substances, through control of the endocrine, respiratory, and cardiovascular systems, for example. This minisymposium will survey work on some models of such neuronal control units. Often the dynamics of these units involves features evolving on multiple timescales, and this temporal complexity will be a focus of the session.

Organizer: Jonathan E. Rubin
University of Pittsburgh, USA

Organizer: Martin Wechselberger
University of Sydney, Australia

10:00-10:25 Why Fast Negative Feedback is Necessary for Electrical Bursting in Pituitary Cells
Richard Bertram, Wondimu W. Teka, and Joel Tabak, Florida State University, USA

10:30-10:55 Canard-Induced Mixed Mode Oscillations In Pituitary Lactotrophs
Theodore Vo and Martin Wechselberger, University of Sydney, Australia; Wondimu W. Teka, Richard Bertram, and Joel Tabak, Florida State University, USA

11:00-11:25 A Minimal Model for a Slow Pacemaking Neuron
Alexey Kuznetsov, Indiana University - Purdue University Indianapolis, USA

11:30-11:55 Interaction of Multiple Respiratory Rhythm Generation Mechanisms
Choongseok Park and Jonathan Rubin, University of Pittsburgh, USA

Friday, August 10

MS53

Mathematics of Drug Delivery from Polymeric Matrices and Related Topics

10:00 AM-12:00 PM

Room:Pearl - 3rd Floor

In this minisymposium we would like to bring together researchers from different fields to discuss drug delivery from polymeric matrices. We will investigate this topic from an experimental, analytical, numerical and also computational point of view. Special emphasis will be layed on the interplay between physicochemical and mechanical phenomena also on different scales, including diffusive and reactive processes. The well founded consideration of polymer degradation and erosion and drug delivery will lead to a better understanding of this important biotechnological application.

Organizer: Alexander Prechtel
Friedrich-Alexander-Universität Erlangen-Nürnberg, Germany

Organizer: Peter Knabner
Friedrich-Alexander-Universität Erlangen-Nürnberg, Germany

Organizer: Paula de Oliveira
University of Coimbra, Portugal

10:00-10:25 Modeling of Drug Delivery from Collagen Matrices Including Different Spatial Scales
Nadja Ray, Peter Knabner, and Tycho van Noorden, Friedrich-Alexander-Universität Erlangen-Nürnberg, Germany; Florin Radu, University of Bergen, Norway

10:30-10:55 Drug Delivery into the Anterior Camera of the Eye: From Drops to Therapeutic Lens
Pascoal M. Silva, José A. Ferreira, and Paula de Oliveira, University of Coimbra, Portugal

11:00-11:25 Memory Effects in Diffusion Processes
José A. Ferreira, Elias Gudino, Paula de Oliveira, and Pascoal M. Silva, University of Coimbra, Portugal

11:30-11:55 Use of Population Balances in Modelling and Simulation of Drug Release from Collagen Matrices
Oleh Krehel and Peter Knabner, Friedrich-Alexander-Universität Erlangen-Nürnberg, Germany

Friday, August 10

Lunch Break

12:00 PM-2:00 PM

Attendees on their own

IP8

Biological and Mathematical Perspectives on the Classification of Bursting Mechanisms

2:00 PM-2:45 PM

Room:Emerald Ballroom - 2nd Floor

Chair: Richard Bertram, Florida State University, USA

One of the success stories in mathematical physiology has been the classification of mechanisms for bursting oscillations, episodes of active spiking phases alternating with silent phases. This work has produced persuasive models for diverse neurons and endocrine cells. Further, bifurcation analysis has classified these mechanisms as exemplars of a broad family of systems based on the bifurcations that mediate switching between active and silent phases. This approach can, however, combine systems that are actually different. I will discuss classification based on unfolding of normal forms, learning from models of pituitary cells and pancreatic beta cells, as well as the duality of biology and mathematics: models corresponding to different cell types are related evolutionarily and developmentally, and different cell types sample nearby regions of parameter space.

Arthur S. Sherman
National Institutes of Health, USA

Coffee Break

2:45 PM-3:15 PM

Room:Foyer - 2nd Floor

Friday, August 10

MS54

Statistical Inference for Biochemical Reaction Networks

3:15 PM-5:15 PM

Room:Emerald Ballroom - 2nd Floor

Biochemical reaction networks are modeled both deterministically and stochastically, depending on the abundance of the reactant species and other factors. Technological advances in molecular biology are producing vast amounts of data describing cellular processes at all levels. A detailed understanding of such processes will require use of the generated data for parameter identification, model selection, model refinement, testing appropriate hypotheses, etc. Recent researches in the area involve applications of diverse statistical techniques including Bayesian methods, latest MCMC schemes, particle filtering, variational methods. The mini symposium will bring together different experts to discuss state-of-the-art tools for statistical inference for biochemical reaction networks.

Organizer: Arnab Ganguly
ETH Zürich, Switzerland

Organizer: Heinz Koeppl
ETH Zürich, Switzerland

3:15-3:40 Accounting for Extrinsic Variability in the Estimation of Stochastic Rate Constants
Heinz Koeppl, ETH Zürich, Switzerland

3:45-4:10 Statistical Inference for Biochemical Reaction Network Models
Grzegorz Rempala, Medical College of Georgia, USA

4:15-4:40 Parameter Estimation in Subdiffusion Model with Proteins for Nanoscale Biophysics
Bishwal Jaya, University of North Carolina, Charlotte, USA

4:45-5:10 Joint High-dimensional Bayesian Variable and Covariance Selection with an Application to eQTL Analysis
Anindya Bhadra, Texas A&M University, USA

Friday, August 10

MS55

CANCELLED

3:15 PM-5:15 PM

Friday, August 10

MS56

Mathematical Modeling and Simulations of Angiogenesis - Part II of II

3:15 PM-5:15 PM

Room:Diamond I - 2nd Floor

For Part 1 see MS48

Angiogenesis is a crucial component of many physiological and pathological processes, including wound healing, embryogenesis, vascular diseases, cancer, and ocular diseases. The angiogenic cascade is extremely complex, spanning from the genetic and subcellular level all the way to the cellular, tissue, and organ levels. Cutting across multiple scales, angiogenesis involves interactions between a large amount of molecules, chemokines, various cell types, extracellular matrix, and blood flow. Areas represented by the speakers include mathematical modeling of the initiation, extension, maturation of blood vessels, and the role of angiogenesis in a variety of physiological and pathological processes. The modeling techniques include stochastic models; cell-based and agent-based approaches; and discrete, continuous, and hybrid models.

Organizer: Xiaoming Zheng
Central Michigan University, USA

Organizer: Trachette Jackson
University of Michigan, Ann Arbor, USA

3:15-3:40 Growing Capillaries with the Phase-field Model

Rui Travasso, Susete Neiva, and Antonio Correia, Universidade de Coimbra, Portugal; Eugenia Corvera, UNAM, Mexico; Mario Castro, Universidad Pontificia Comillas de Madrid, Spain; Juan Carlos Rodriguez-Manzaneque, GENYO, Spain; Aurora Hernandez-Machado, Universitat Politecnica de Barcelona, Spain

continued in next column

3:45-4:10 Statistical Quantification of Vascular Patterning During Developmental Angiogenesis in the Retina of the Mouse

Florian Milde, ETH Zürich, Switzerland

4:15-4:40 Cell-based Computational Models of Collective Cell Behavior and Cell-ECM Interactions During Angiogenesis

Roeland Merks, CWI, Amsterdam, Netherlands

4:45-5:10 A Particle-Based Modeling Framework for Migration, Growth and Juxtacrine Signaling

Florian Milde and Petros Koumoutsakos, ETH Zürich, Switzerland

Friday, August 10

MS57

Marine Fluid-Structure Interactions: Organs to Ecosystems

3:15 PM-5:15 PM

Room:Diamond II - 2nd Floor

Fluid-structure interactions are important in most, if not all, biological systems and across all scales, from the organ level to the ecosystem level. The talks in this minisymposium range from driving fluid through the open circulatory systems of sea squirts to the interaction of water with large aquatic plants. The approaches used combine computational, analytic and experimental results.

Organizer: Virginia B. Pasour
U.S. Army Research Office, USA

3:15-3:40 Efficient Power Strokes in Jellyfish Swimming

Silas Alben, Georgia Institute of Technology, USA; Jifeng Peng, University of Alaska, Fairbanks, USA

3:45-4:10 Feeding Currents Generated by Upside Down Jellyfish in the Presence of Background Flow

Christina L. Hamlet, North Carolina State University, USA; Laura Millller, University of North Carolina at Chapel Hill, USA

4:15-4:40 Pumping Mechanism of the Tubular Sea Squirt Heart

Austin Baird, University of North Carolina, USA; Laura Miller and Tiffany King, University of North Carolina, Chapel Hill, USA

4:45-5:10 Flow through Flexible, Deforming Macrophytes

Virginia B. Pasour, U.S. Army Research Office, USA; Laura Miller, University of North Carolina, Chapel Hill, USA

Friday, August 10

MS58

Contemporary Approaches in Mathematical Epidemiology, Ecology and Population Dynamics - Part II of II

3:15 PM-5:15 PM

Room:Crystal Ballroom I - 2nd Floor

For Part 1 see MS50

Using applied mathematical tools and techniques in understanding and finding answers of problems in epidemiology, ecology and immunology has become increasingly important. This mini-symposium focuses on recent advances in the areas of population dynamics. The minisymposium brings together young researchers to discuss and share ideas on current research trends. Talks will be given on recent mathematical models developed for problems in epidemiology and immunology. Some example talk subjects are immune response to influenza and Hepatitis C virus, and optimal control of treatments for HIV, AIDS and Malaria.

Organizer: Necibe Tuncer
University of Tulsa, USA

Organizer: Maia Martcheva
University of Florida, USA

3:15-3:40 Avian Influenza: Modeling and Implications for Control
Maia Martcheva, University of Florida, USA

3:45-4:10 Evaluation of Diagnostic Test for Lymphatic Filariasis in Papua New Guinea using a Mathematical Model'
Anuj Mubayi, Northeastern Illinois University, USA; Daniel Tisch, Case Western Reserve University, USA; Marian Gidea, Northeastern Illinois University, USA; Carlos Castillo-Chavez, Arizona State University, USA

4:15-4:40 Dynamics of Influenza Virus Infection with Immune Responses'
Libin Rong, Oakland University, USA

4:45-5:10 An HIV Model: Theoretical Analysis and Experimental Verification
Souvik Bhattacharya, North Dakota State University, USA

Friday, August 10

MS59

Coherent Dynamics of Neuronal Networks - Part III of III

3:15 PM-5:15 PM

Room:Opal - 2nd Floor

For Part 2 see MS51

A fundamental component of understanding brain function is determining the collective behavior of a neuronal network in terms of the well-defined dynamics of individual neurons and the properties of their connections to each other. The speakers in this three-part minisymposium will provide their perspectives on this question, spanning the spectrum from theoretical to experimental techniques. The use of relatively simple models allows deeper mathematical studies of how the interactions of individual neurons produce coherent dynamics, leading to a better understanding of brain function.

Organizer: Katherine Newhall
Courant Institute of Mathematical Sciences, New York University, USA

Organizer: Andrea K. Barreiro
University of Washington, USA

Organizer: Gregor Kovacic
Rensselaer Polytechnic Institute, USA

3:15-3:40 How Firing Rate is Reflected in Network Topology
Gregor Kovacic, Rensselaer Polytechnic Institute, USA; Maxim Shkarayev, College of William & Mary, USA; David Cai, Shanghai Jiaotong University, China

3:45-4:10 The Essential Role of Phase-Delayed Inhibition in the Decoding of Synchronized Neural Oscillations
Mainak Patel and Badal Joshi, Duke University, USA

4:15-4:40 Transient Propagation and Traveling Waves of Activity in Integrate-and-fire Neural Networks
Remus Osan, Georgia State University, USA

4:45-5:10 Steps Towards Coarse-Graining Inhomogeous Neuronal Network Dynamics
Jiwei Zhang and Aaditya Rangan, Courant Institute of Mathematical Sciences, New York University, USA; David Cai and David McLaughlin, New York University, USA

Friday, August 10

MS60

Hysteresis in Neuroscience: Bursting and Beyond

3:15 PM-5:15 PM

Room:Crystal Ballroom - 2nd Floor

In single neuron models, bursting behavior provides a classical example of hysteresis. Different kinds of bursting have been identified, both mathematically and in experimental preparations, and a formal classification based on the bifurcation structure of the system has been proposed. Recent work has extended analysis of bursting mechanisms to the network level and applied these analytic techniques to other systems exhibiting hysteresis. This session will present current results in the analysis of hysteresis at multiple spatial and temporal scales arising in neuroscience.

Organizer: Cecilia Diniz Behn
Gettysburg College, USA

Organizer: Justin Dunmyre
University of Michigan, USA

3:15-3:40 Using Maps to Predict Activation Order in Multiphase Rhythms
Jonathan E. Rubin, University of Pittsburgh, USA; David H. Terman, Ohio State University, USA

3:45-4:10 Markov State Kinetic Model for P2X2 Receptor-Channel Gating: Bistability and Desensitization
Anmar Khadra, McGill University, Canada; Zonghe Yan, Arthur S. Sherman, and Stanko S. Stojilkovic, National Institutes of Health, USA

4:15-4:40 Hysteresis and a Mechanism for REM Sleep Generation
Cecilia Diniz Behn, Gettysburg College, USA; Victoria Booth, University of Michigan, USA

4:45-5:10 Coupled Flip-flops: Noise and Analysis for a Sleep-wake Cycle Model
Justin Dunmyre and Victoria Booth, University of Michigan, USA

Friday, August 10

MS61

CANCELLED

3:15 PM-5:15 PM

LS12 Abstracts

Abstracts are printed as submitted by the author.

Notes

LS12 Speaker and Organizer Index

Italicized names indicate session organizers.

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Notes

LS12 Budget

August 7-10, 2012
San Diego, California, USA

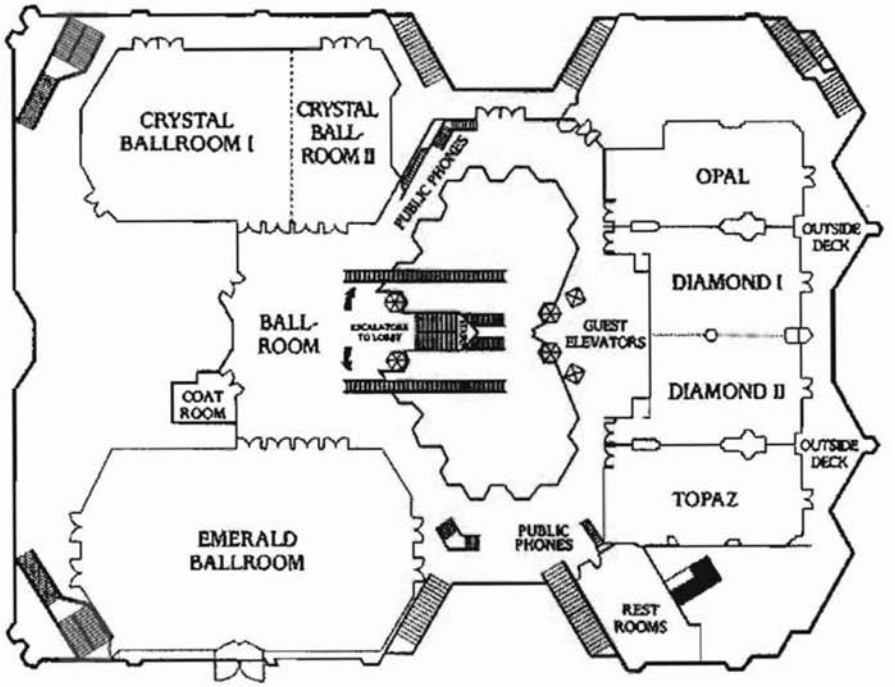
Expected Paid Attendance 375

Revenue	
Registration	$118,790
Total	$118,790
Direct Expenses	
Printing	$2,700
Organizing Committee	$2,800
Invited Speaker	$9,800
Food and Beverage	$21,750
Telecomm	$2,000
AV and Equipment (rental)	$16,000
Room (rental)	$0
Advertising	$7,700
Conference Staff Labor	$25,700
Other (supplies, staff travel, freight, exhibits, misc.)	$4,200
Total Direct Expenses:	$92,650
Support Services: *	
Services covered by Revenue	$26,140
Services covered by SIAM	$54,963
Total Support Services:	$81,103
Total Expenses:	$173,753

* Support services includes customer service (who handle registration), accounting, computer support, shipping, marketing and other SIAM support staff. It also includes a share of the computer systems and general items (building expenses in the SIAM HQ).

Westin San Diego Map

CONFERENCE/ MEETING ROOMS



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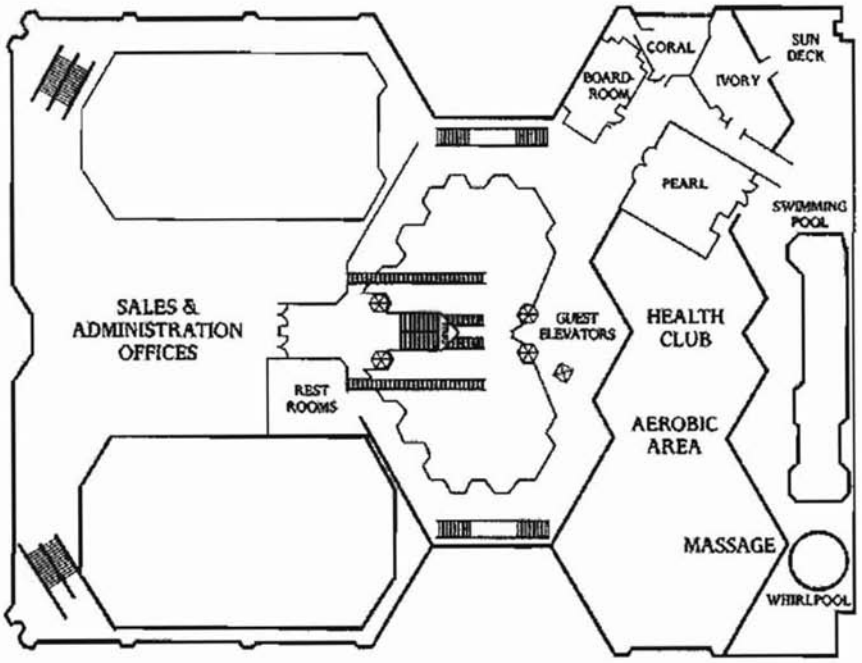

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