

# Final Program and Abstracts



Art courtesy of Bourouiba, Gourley, Liu and Wu, SIAP 71-2

*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.

## **SIAM 2014 Events Mobile App**

Scan the QR code with any QR reader and download the TripBuilder® EventMobile app to your iPhone, iPad, iPod touch or Android mobile device. You can also visit [www.tripbuilder.com/siam/2014events](http://www.tripbuilder.com/siam/2014events)



Society for Industrial and Applied Mathematics  
3600 Market Street, 6th Floor  
Philadelphia, PA 19104-2688 USA

Telephone: +1-215-382-9800 Fax: +1-215-386-7999

Conference E-mail: [meetings@siam.org](mailto:meetings@siam.org)

Conference Web: [www.siam.org/meetings/](http://www.siam.org/meetings/)

Membership and Customer Service: (800) 447-7426 (US & Canada) or +1-215-382-9800 (worldwide)

**[www.siam.org/meetings/ls14](http://www.siam.org/meetings/ls14)**

## Table of Contents

Program-at-a-Glance... Separate handout	
General Information.....	2
Get-togethers.....	4
Minitutorial .....	7
Invited Plenary Presentations.....	8
Program Schedule.....	11
Poster Session .....	34
Abstracts .....	57
Speaker and Organizer Index.....	134
Conference Budget ... Inside Back Cover	
Hotel Meeting Room Map...Back Cover	

## Organizing Committee Co-Chairs

### Robert Guy

University of California, Davis, USA

### Mette Sofie Olufsen

North Carolina State University, USA

## Organizing Committee

### Dean Bottino

Takeda Pharmaceuticals, USA

### Paul C. Bressloff

University of Utah, USA

### Robert Stephen Cantrell

University of Miami, USA

### Gerardo Chowell-Puente

Arizona State University, USA

### Leah Edelstein-Keshet

University of British Columbia, Canada

### Nicholas A. Hill

University of Glasgow, Scotland

### Anita Layton

Duke University, USA

### Simon A. Levin

Princeton University, USA

### Eduardo D. Sontag

Rutgers University, USA

## SIAM Registration Desk

The SIAM registration desk is located in the Symphony Preconvene. It is open during the following hours:

Sunday, August 3  
4:00 PM – 8:00 PM

Monday, August 4  
7:00 AM – 5:00 PM

Tuesday, August 5  
7:30 AM – 5:00 PM

Wednesday, August 6  
7:30 AM – 5:00 PM

Thursday, August 7  
7:30 AM – 3:00 PM

## Hotel Address

### Sheraton Charlotte

555 South McDowell Street  
Charlotte, North Carolina, 28204  
Phone Number: +1-704-372-4100

Toll Free Reservations (USA and Canada): +1-800-325-3535

Fax: +1-704-348-4646

Hotel web address:

<http://www.sheratoncharlottehotel.com/>

## Hotel Telephone Number

To reach an attendee or leave a message, call +1-704-372-4100. If the attendee is a hotel guest, the hotel operator can connect you with the attendee's room.

## Hotel Check-in and Check-out Times

Check-in time is 3:00 PM and check-out time is 12:00 PM.

## Child Care

For local child care information, please contact the concierge at the Sheraton Charlotte, at +1-704-372-4100.

## Corporate Members and Affiliates

SIAM corporate members provide their employees with knowledge about, access to, and contacts in the applied mathematics and computational sciences community through their membership benefits. Corporate membership is more than just a bundle of tangible products and services; it is an expression of support for SIAM and its programs. SIAM is pleased to acknowledge its corporate members and sponsors. In recognition of their support, non-member attendees who are employed by the following organizations are entitled to the SIAM member registration rate.

## Corporate Institutional Members

The Aerospace Corporation  
Air Force Office of Scientific Research  
AT&T Laboratories - Research  
Bechtel Marine Propulsion Laboratory  
The Boeing Company  
CEA/DAM  
Department of National Defence (DND/CSEC)  
DSTO- Defence Science and Technology Organisation  
Hewlett-Packard  
IBM Corporation  
IDA Center for Communications Research, La Jolla  
IDA Center for Communications Research, Princeton  
Institute for Computational and Experimental Research in Mathematics (ICERM)  
Institute for Defense Analyses, Center for Computing Sciences  
Lawrence Berkeley National Laboratory

Lockheed Martin  
 Los Alamos National Laboratory  
 Mathematical Sciences Research  
 Institute  
 Max-Planck-Institute for Dynamics of  
 Complex Technical Systems  
 Mentor Graphics  
 National Institute of Standards and  
 Technology (NIST)  
 National Security Agency (DIRNSA)  
 Oak Ridge National Laboratory,  
 managed by UT-Battelle for the  
 Department of Energy  
 Sandia National Laboratories  
 Schlumberger-Doll Research  
 Tech X Corporation  
 U.S. Army Corps of Engineers, Engineer  
 Research and Development Center  
 United States Department of Energy

List current June 2014

## Funding Agency

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



## Funding Panel

Funding Agency Panel  
 Monday, August 4  
 8:45 PM - 9:30 PM  
*Symphony II*

## Leading the applied mathematics community . . .

### Join SIAM and save!

SIAM members save up to \$130 on full registration for the 2014 SIAM Conference on the Life Sciences! Join your peers in supporting the premier professional society for applied mathematicians and computational scientists. SIAM members receive subscriptions to *SIAM Review*, *SIAM News* and *Unwrapped*, and enjoy substantial discounts on SIAM books, journal subscriptions, and conference registrations.

If you are not a SIAM member and paid the Non-Member or Non-Member Mini Speaker/Organizer rate to attend the conference, you can apply the difference between what you paid and what a member would have paid (\$130 for a Non-Member and \$65 for a Non-Member Mini Speaker/Organizer) towards a SIAM membership. Contact SIAM Customer Service for details or join at the conference registration desk.

If you are a SIAM member, it only costs \$10 to join the SIAM Activity Group on the Life Sciences (SIAG/LS). As a SIAG/LS member, you are eligible for an additional \$10 discount on this conference, so if you paid the SIAM member rate to attend the conference, you might be eligible for a free SIAG/LS membership. Check at the registration desk.

Free Student Memberships are available to students who attend an institution that is an Academic Member of SIAM, are members of Student Chapters of SIAM, or are nominated by a Regular Member of SIAM.

Join onsite at the registration desk, go to [www.siam.org/joinsiam](http://www.siam.org/joinsiam) to join online or download an application form, or contact SIAM Customer Service:

Telephone: +1-215-382-9800  
(worldwide); or 800-447-7426 (U.S. and Canada only)

Fax: +1-215-386-7999

E-mail: [membership@siam.org](mailto:membership@siam.org)

Postal mail: Society for Industrial and Applied Mathematics, 3600 Market Street, 6th floor, Philadelphia, PA 19104-2688 USA

## Standard Audio/Visual Set-Up in Meeting Rooms

SIAM does not provide computers for any speaker. When giving an electronic presentation, speakers must provide their own computers. SIAM is not responsible for the safety and security of speakers' computers.

The Plenary Session Room will have two (2) screens, one (1) data projector and one (1) overhead projector. Cables or adaptors for Apple computers are not supplied, as they vary for each model. Please bring your own cable/adaptor if using an Apple computer.

All other concurrent/breakout rooms will have one (1) screen and one (1) data projector. Cables or adaptors for Apple computers are not supplied, as they vary for each model. Please bring your own cable/adaptor if using an Apple computer. Overhead projectors will be provided only if requested.

If you have questions regarding availability of equipment in the meeting room of your presentation, or to request an overhead projector for your session, please see a SIAM staff member at the registration desk.

## Internet Access

The Sheraton Charlotte offers wireless Internet access to hotel guests in the sleeping rooms at no additional charge.

Complimentary wireless Internet access in the meeting space is also available to SIAM attendees.

In addition, a limited number of computers with Internet access will be available during registration hours.

## Registration Fee Includes

- Admission to all technical sessions
- Business Meeting (*open to SIAG/LS members*)
- Coffee breaks daily
- Poster Session
- Room set-ups and audio/visual equipment
- Welcome Reception

## Job Postings

Please check with the SIAM registration desk regarding the availability of job postings or visit <http://jobs.siam.org>.

## Important Notice to Poster Presenters

The poster session is scheduled for Tuesday, August 5 at 8:00 PM. Poster presenters may set up their poster material on the provided poster boards in the Symphony IV Room beginning Monday, August 4 at 2:00 PM. All materials must be posted by 8:00 PM on Tuesday, August 5, the official start time of the session. Posters will remain on display through Thursday, August 7 and must be removed by 11:30 AM. Posters remaining after this time will be discarded. SIAM is not responsible for discarded posters.

## SIAM Books and Journals

Display copies of books and complimentary copies of journals are available on site. SIAM books are available at a discounted price during the conference. If a SIAM books representative is not available, completed order forms and payment (credit cards are preferred) may be taken to the SIAM registration desk. The books table will close at 9:30 AM on Thursday, August 7.

## Table Top Displays

Princeton University Press  
SIAM  
Springer

## Name Badges

A space for emergency contact information is provided on the back of your name badge. Help us help you in the event of an emergency!

## Comments?

Comments about SIAM meetings are encouraged! Please send to:

Cynthia Phillips, SIAM Vice President for Programs ([vpp@siam.org](mailto:vpp@siam.org)).

## Get-togethers

- Welcome Reception  
Sunday, August 3  
6:00 PM – 8:00 PM
- Poster Session  
Tuesday, August 5  
8:00 PM – 10:00 PM
- Business Meeting  
(open to SIAG/LS members)  
Wednesday, August 6  
8:00 PM – 8:45 PM  
*Complimentary beer and wine will be served.*



## Please Note

SIAM is not responsible for the safety and security of attendees' computers. Do not leave your laptop computers unattended. Please remember to turn off your cell phones, pagers, etc. during sessions.

## Recording of Presentations

Audio and video recording of presentations at SIAM meetings is prohibited without the written permission of the presenter and SIAM.

## Social Media

SIAM is promoting the use of social media, such as Facebook and Twitter, in order to enhance scientific discussion at its meetings and enable attendees to connect with each other prior to, during and after conferences. If you are tweeting about a conference, please use the designated hashtag to enable other attendees to keep up with the Twitter conversation and to allow better archiving of our conference discussions. The hashtag for this meeting is #SIAMLS14.

# SIAM Activity Group on Life Sciences (SIAG/LS)

[www.siam.org/activity/life-sciences](http://www.siam.org/activity/life-sciences)



## A GREAT WAY TO GET INVOLVED!

Collaborate and interact with mathematicians and applied scientists whose work involves the application of mathematics to the life sciences and research that leads to new methods and techniques useful in the life sciences.

### ACTIVITIES INCLUDE:

- Special sessions at SIAM Annual Meetings
- Biennial conference
- Talks about topics in the life sciences available online via "SIAM Presents"
- Website

### BENEFITS OF SIAG/LS membership:

- Free electronic subscription to *SIAM Journal on Applied Dynamical Systems*
- Listing in the SIAG's online membership directory
- Additional \$10 discount on registration at the SIAM Conference on Life Sciences (excludes student)
- Electronic communications about recent developments in your specialty
- Eligibility for candidacy for SIAG/LS office
- Participation in the selection of SIAG/LS officers

### ELIGIBILITY:

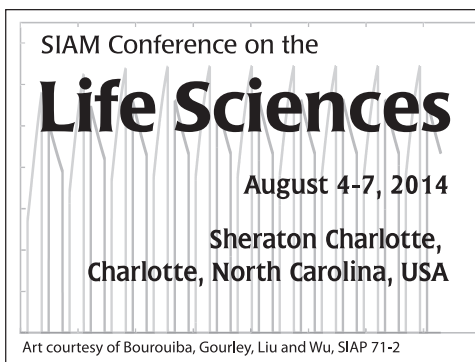
- Be a current SIAM member.

### COST:

- \$10 per year
- Student members can join two activity groups for free!

### 2013-14 SIAG/LS OFFICERS

- Chair: Gregory Forest, University of North Carolina at Chapel Hill
- Vice Chair: Maia Martcheva-Drashanska, University of Florida
- Program Director: Robert Guy, University of California at Davis
- Secretary: Janet Best, Ohio State University



### TO JOIN:

SIAG/LS: [my.siam.org/forms/join\\_siag.htm](http://my.siam.org/forms/join_siag.htm)

SIAM: [www.siam.org/joinsiam](http://www.siam.org/joinsiam)

## The SIAM 2014 Events Mobile App Powered by TripBuilder®

To enhance your conference experience, we're providing a state-of-the-art mobile app to give you important conference information right at your fingertips. With this TripBuilder EventMobile™ app, you can:

- Create your own custom schedule
- View Sessions, Speakers, Exhibitors and more
- Take notes and export them to your email
- View Award-Winning TripBuilder Recommendations for the meeting location
- Get instant Alerts about important conference info



### SIAM 2014 Events Mobile App

Scan the QR code with any QR reader and download the TripBuilder EventMobile™ app to your iPhone, iPad, iPod touch or Android mobile device.

To access the app or the HTMLS version, visit [www.tripbuilder.com/siam2014events](http://www.tripbuilder.com/siam2014events)

## Minitutorials

**Monday, August 4**

**9:30 AM – 11:30 AM**

*Mecklenburg II*

### **MT1: Algebra in Life Sciences**

Algebra, in particular algebraic geometry, is playing an increasingly important role in many areas of biology, such as phylogenetics and biochemical reaction networks. Here, the modeling equations often form a polynomial or rational system of equations and might thus be studied using techniques from algebra and algebraic geometry. Recent years have seen much progress towards an algebraic understanding of reaction networks. In this tutorial it will be demonstrated how such techniques can be applied in concrete examples of reaction networks, backed by theoretical results.

Organizers and Speakers:

**Elisenda Feliu**, *University of Copenhagen, Denmark*

**Nicolette Meshkat**, *North Carolina State University, USA*

**Carsten Wiuf**, *University of Copenhagen, Denmark*

**Wednesday, August 6**

**9:30 AM – 11:30 AM**

*Symphony VI*

### **MT2: Modelling Arterial Wall Mechanics and Adaption using Structurally Based Constitutive Laws**

This minitutorial will introduce the four different aspects of modelling in arterial wall mechanics.

Organizers and Speakers:

**Yibin Fu**, *Keele University, United Kingdom*

**Nicholas A. Hill**, *University of Glasgow, Scotland, UK*

**Xiaoyu Luo**, *University of Glasgow, Scotland, United Kingdom*

**Leif Hellevik**, *Norwegian University of Science and Technology, Norway*

## Invited Plenary Speakers

*\*\* All Invited Plenary Presentations will take place in Symphony I, II & III\*\**

**Monday, August 4**

**8:15 AM – 9:00 AM**

**IP1** Perceptual Dynamics in an Ambiguous World

**John Rinzel**, *New York University, USA*

**1:00 PM – 1:45 PM**

**IP2** Patient-specific Mathematical Neuro-Oncology:  
Every Patient Deserves Their Own Equation

**Kristin Rae Swanson**, *Northwestern University, USA*

**Tuesday, August 5**

**8:15 AM – 9:00 AM**

**IP3** Modelling Plant Cell and Tissue Growth

**Oliver E. Jensen**, *University of Manchester, United Kingdom*

**1:00 PM – 1:45 PM**

**IP4** Robustness, Control and the Organization of Cell Lineages

**Arthur Lander**, *University of California, Irvine, USA*

**Wednesday, August 6**

**8:15 AM – 9:00 AM**

**IP5** Deterministic and Stochastic Thresholds  
for Disease Extinction in Infectious Disease Models

**Linda J. Allen**, *Texas Tech University, USA*

**1:00 PM – 1:45 PM**

**IP6** Is “Good Cholesterol” Always “Good”? New Insights about HDL from an In-Silico Model  
of Lipoprotein Metabolism and Kinetics

**Norman Mazer**, *F. Hoffmann-La Roche Ltd., Switzerland*

## Invited Plenary Speakers

*\*\* All Invited Plenary Presentations will take place in Symphony I, II & III\*\**

**Thursday, August 7**

**8:15 AM – 9:00 AM**

**IP7** Early Warning Signs and Critical Transitions in Ecology:  
Corals, Theory, Pitfalls, and Advances

**Alan M. Hastings**, *University of California, Davis, USA*

**1:00 PM – 1:45 PM**

**IP8** Synthetic Biology and Biocomputation: Life Redesigned

**James J. Collins**, *Boston University, USA*

## Notes

## LS14 Program



Art courtesy of Bourouiba, Gourley, Liu and Wu, SIAP 71-2

## Sunday, August 3

### Registration

4:00 PM-8:00 PM

Room: Symphony Preconvene Area

### Welcome Reception

6:00 PM-8:00 PM

Room: Mecklenburg I, II & III



## Monday, August 4

### Registration

7:00 AM-5:00 PM

Room: Symphony Preconvene Area

### Welcoming Remarks

8:00 AM-8:15 AM

Room: Symphony I, II & III

## IP1

### Perceptual Dynamics in an Ambiguous World

8:15 AM-9:00 AM

Room: Symphony I, II & III

Chair: Mette Olufsen, North Carolina State University, USA

When experiencing an ambiguous sensory stimulus (e.g., the vase-faces image), subjects may report haphazard alternations (time scale, seconds) between the possible interpretations. I will describe dynamical models for neuronal populations that compete through mutual inhibition for dominance - showing alternations, behaving as noisy oscillators or as multistable systems subject to noise-driven switching. In highly idealized formulations networks are percept specific without direct representation of stimulus features. Our recent work involves perception of ambiguous auditory stimuli (e.g., <http://auditoryneuroscience.com/topics/streaming-galloping-rhythm-paradigm>); the models incorporate feature specificity, tonotopy, so that perceptual selectivity is emergent rather than built-in.

John Rinzel  
New York University, USA

### Coffee Break

9:00 AM-9:30 AM

Room: Symphony Preconvene Area



## Monday, August 4

## MT1

### Algebra in Life Sciences

9:30 AM-11:30 AM

Room: Mecklenburg II

Chair: Carsten Wiuf, University of Copenhagen, Denmark

Algebra, in particular algebraic geometry, is playing an increasingly important role in many areas of biology, such as phylogenetics and biochemical reaction networks. Here, the modeling equations often form a polynomial or rational system of equations and might thus be studied using techniques from algebra and algebraic geometry. Recent years have seen much progress towards an algebraic understanding of reaction networks. In this tutorial it will be demonstrated how such techniques can be applied in concrete examples of reaction networks, backed by theoretical results.

### Algebra in Reaction Network Theory

Carsten Wiuf and Elisenda Feliu, University of Copenhagen, Denmark; Nicolette Meshkat, North Carolina State University, USA

### Determining the Steady States of Biochemical Reaction Networks

Elisenda Feliu, University of Copenhagen, Denmark

### Structural Identifiability of Reaction Networks using Differential Algebra

Nicolette Meshkat, North Carolina State University, USA

Monday, August 4

## MS1

### Recent Advances in Mathematical Epidemiology of Infectious Diseases - Part I of II

9:30 AM-11:30 AM

*Room: Symphony I*

**For Part 2 see MS9**

This minisymposium will bring researchers who are actively involved in development of mathematical approaches in mathematical biology. The purpose of the minisymposium is to address recent advances of mathematical methods used to study dynamics of infectious diseases and discuss a wide range of topics: computational, mathematical and statistical techniques to study the infectious diseases.

Organizer: Necibe Tuncer  
*University of Tulsa, USA*

Organizer: Maia Martcheva  
*University of Florida, USA*

#### 9:30-9:55 Modeling Avian Influenza and Implications for Control

*Maia Martcheva, University of Florida, USA*

#### 10:00-10:25 Mathematics of Anti-Hpv Vaccines

*Abba Gumel, University of Manitoba, Canada*

#### 10:30-10:55 Transient Periodic Oscillations and the Dynamics of CTL Response to Viral Infections

*Michael Li, University of Alberta, Canada*

#### 11:00-11:25 A Structured Model for the Transmission Dynamics of Mycobacterium Marinum Between Aquatic Animals

*Azmy S. Ackleh, University of Louisiana, Lafayette, USA*

Monday, August 4

## MS2

### Applications of Dynamical Systems to Biology and Medicine - Part I of II

9:30 AM-11:30 AM

*Room: Symphony II*

**For Part 2 see MS10**

Over the last decades mathematical models have been used to identify important features of immune responses during disease. In this minisymposium we bring together experts in modeling immune responses and infectious disease dynamics. Our sessions will focus on challenges and new directions in the study of viral kinetic dynamics, immune responses, drug and vaccine efficacy, and the best strategies to use the available biological data to identify parameters and propose new designs for experiments.

Organizer: Stanca Ciupe  
*Virginia Tech, USA*

Organizer: Matthias Chung  
*Virginia Tech, USA*

#### 9:30-9:55 Parameter Identifiability in Virus Infection Models

*Matthias Chung and Stanca Ciupe, Virginia Tech, USA*

#### 10:00-10:25 Coping with Model Uncertainty in the Analysis of Acute Hiv Infection Datasets

*Sivan Leviyang, Georgetown University, USA*

#### 10:30-10:55 Early {HIV} Infection Predictions: Role of Viral Replication Errors

*Jessica M. Conway and Alan S. Perelson, Los Alamos National Laboratory, USA*

#### 11:00-11:25 Multi-Scale Modeling of Immune Response to Influenza Infection

*Hulin Wu, University of Rochester, USA*

Monday, August 4

## MS3

### Physiological Modeling of Soft Tissues via Approach of Bio-mechanics

9:30 AM-11:30 AM

*Room: Symphony III*

Mechanical forces are significant factors for genesis of some diseases and physiological processes occurring in soft tissues. Several tubular organs are studied to demonstrate the power of bio-mechanical modeling for analyzing these alterations. Tracheal angioedema is modeled to see how swelling may hurt the tissue by forming stress concentration. Two another models show respectively the function of the stress of arterial wall in mediating arterial growth, and how the arterial residual stress is estimated via inverse spectral techniques. One last example is about the mechanical forces driving the embryonic tubular brain to twist and bend for brain morphogenesis.

Organizer: Kun Gou  
*Michigan State University, USA*

Organizer: Zi Chen  
*Washington University, USA*

#### 9:30-9:55 Bio-Mechanical Modeling of Tracheal Angioedema by Nonlinear Finite Elasticity

*Kun Gou and Thomas Pence, Michigan State University, USA*

#### 10:00-10:25 A Continuum Mechanics Model of Stress Mediated Arterial Growth During Hypertension Using An Eulerian Frame.

*Maya E. Johnson and Jay R. Walton, Texas A&M University, USA*

#### 10:30-10:55 Estimating Residual Stresses in Soft Tissues by An Inverse Spectral Technique

*Sunnie Joshi, Temple University, USA; Jay R. Walton, Texas A&M University, USA*

#### 11:00-11:25 Mechanical Forces Drive Morphogenesis: How the Embryonic Brain Twists

*Zi Chen, Washington University, USA; Qiaohang Guo, Fuzhou University, China; Eric Dai and Larry Taber, Washington University, USA*

Monday, August 4

## MS4

### Dynamics of Melanopsin and Collective Cell Migration: Two Collaborative Studies

9:30 AM-11:30 AM

Room:Symphony V

Two pairs of mathematics and biology faculty members present results from undergraduate teams formed in response to an NSF UBM grant awarded at UMBC. One team focuses on the dynamics of melanopsin, a light sensitive protein. They have modeled the activation and inactivation of the phototransduction cascade using both deterministic and stochastic models. A second team studies the acquisition and persistence of cell motility. They have modeled the intracellular signaling that triggers motility and, through force balance dynamics, the migration of cell clusters. Here they describe the extracellular signal that initiates the intracellular signaling cascade and newly discovered activation asymmetries.

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

#### 9:30-9:55 Phototransduction in Melanopsin Expressing Retinal Ganglion Cells

Phyllis R. Robinson, University of Maryland, Baltimore County, USA

#### 10:00-10:25 Modeling the Melanopsin Phototransduction Cascade

Kathleen A. Hoffman, University of Maryland, Baltimore County, USA

#### 10:30-10:55 Genetic Regulation of Cell Motility

Michelle Starz-Gaiano and Lathiena Manning, University of Maryland, Baltimore County, USA

#### 11:00-11:25 Collective Cell Migration: Modeling from Initiation to Destination

David Stonko, Bradford E. Peercy, and Michelle Starz-Gaiano, University of Maryland, Baltimore County, USA

Monday, August 4

## MS5

### Biofluids: Biological and Physical Complexity in Fluid Structure Interaction Problems - Part I of II

9:30 AM-11:30 AM

Room:Symphony VI

#### For Part 2 see MS13

Fluids are the natural environment of virtually every organism and fluid structure interaction problems are ubiquitous in biology. While Newtonian fluids and linearly elastic structures are found in nature, many important fluids and materials exhibit nonlinearities or other complex properties. The aim of this minisymposium is to present examples of such behavior in biological systems and the techniques used to address these problems. The first half focuses on complex fluids and other environmental considerations while the second half focuses on properties of the immersed structures. The systems vary across multiple scales and present a range of biofluids problems.

Organizer: Christina Hamlet  
Tulane University, USA

Organizer: Jacek K. Wrobel  
Tulane University, USA

#### 9:30-9:55 Sperm Altruism and Motility Near Surfaces

Julie Simons, Lisa J. Fauci, and Ricardo Cortez, Tulane University, USA

#### 10:00-10:25 Modeling Tumor and Microenvironment Interactions under Treatment: the Role of the Interstitial Fluid

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

#### 10:30-10:55 Swimming Through Highly Heterogeneous, Viscoelastic Media

Jacek K. Wrobel, Ricardo Cortez, and Lisa J. Fauci, Tulane University, USA

#### 11:00-11:25 Marine Invertebrate Sperm Chemotaxis: Search Trajectories

Sarah D. Olson, Worcester Polytechnic Institute, USA

Monday, August 4

## MS6

### Dynamics and Connectivity of Complex Networks in the Brain - Part I of II

9:30 AM-11:30 AM

Room:Symphony VII

#### For Part 2 see MS14

The dynamics of model neuronal networks have helped to explain many aspects of cognitive function. As more realism is incorporated into these models, novel dynamical features often arise which further enrich our understanding of the brain. This minisymposium explores this theme by discussing recent work in the modeling of both individual neuron dynamics and network topology, focusing upon implications on network behavior and information coding. The speakers will draw particular attention to new mathematical approaches in explaining sensory processing and information propagation.

Organizer: Victor Barranca  
New York University, USA

Organizer: Douglas Zhou  
Shanghai Jiao Tong University, China

#### 9:30-9:55 Improved Estimation of Neural Correlations Suggests Detailed Interactions in Visual Cortex

Kresimir Josic, University of Houston, USA; Yu Hu, University of Washington, USA; James Trousdale, University of Houston, USA; Eric Shea-Brown, University of Washington, USA

#### 10:00-10:25 Sparsity and Compressed Coding in Sensory Systems

Gregor Kovacic, Rensselaer Polytechnic Institute, USA; Victor Barranca, New York University, USA; Douglas Zhou, Shanghai Jiao Tong University, China; David Cai, Shanghai Jiao Tong University, China and Courant Institute of Mathematical Sciences, New York University, USA

*continued on next page*

**10:30-10:55 Spatiotemporal Dynamics of Neuronal Population Response in the Primary Visual Cortex**

*Douglas Zhou*, Shanghai Jiao Tong University, China; Aaditya Rangan, David McLaughlin, and David Cai, Courant Institute of Mathematical Sciences, New York University, USA

**11:00-11:25 Novel Characterization of Brain Networks Through Low-Rank Network Decomposition**

*Victor Barranca*, New York University, USA; Douglas Zhou, Shanghai Jiao Tong University, China; David Cai, Courant Institute of Mathematical Sciences, New York University, USA

Monday, August 4

**MS7**

**Convergence of Applied Mathematics and Oncology**

9:30 AM-11:30 AM

*Room: Mecklenburg I*

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 interface of applied mathematical modeling and simulations with clinical oncology are beginning to play a critical role in synthesizing and comprehending some of the dynamics underlying the behavior of disease and simultaneously integrating across different spatial and temporal scales. This minisymposium will present in the context of clinical oncology recent advances in applied mathematical models and simulations that will explore the dynamics of cancer progression and therapeutic response treatment.

Organizer: Larry Nagahara  
*National Cancer Institute, USA*

**9:30-9:55 Random Walks, Markov Chains, and Cancer Progression Models from Longitudinal and Autopsy Data**

*Paul Newton*, University of Southern California, USA

**10:00-10:25 Bayesian Support Vector Machines and Supervised Factor Modeling for General Omic Data**

*Larry Carin*, Duke University, USA

**10:30-10:55 Perfusion Heterogeneity in Tumors As a Challenge for Optimal Nanotherapeutics Delivery**

*Hermann Frieboes*, University of Louisville, USA

**11:00-11:25 Dynamics of Living Systems: Wave-Based Mechanisms for Contact Guidance and Collective Migration**

*Wolfgang Losert*, University of Maryland, College Park, USA; John Fourkas, Meghan Driscoll, Xiaoyu Sun, Can Guven, and Chenlu Wang, University of Maryland, USA; Carole Parent, National Cancer Institute, USA

Monday, August 4

**MS8**

**Structured Population Dynamics: Modeling, Estimation, and Validation - Part I of II**

9:30 AM-11:30 AM

*Room: Mecklenburg III*

**For Part 2 see MS16**

Structured population models are ubiquitous in many areas of mathematical biology including microbial bioreactors, amyloid diseases, and cellular proliferation assays. In these populations, individual aggregates can combine, fragment, and/or grow. Each of these phenomena impact the model in substantially different ways. Accordingly, significant research has focused on the development of correct models as well as accurate estimation of kernels and rates. This minisymposium will showcase current directions of research in advanced simulation, estimation, and validation techniques to better understand structured populations.

Organizer: David M. Bortz  
*University of Colorado Boulder, USA*

Organizer: John G. Younger  
*University of Michigan, USA*

**9:30-9:55 Applied Particle Aggregation for Cell Isolation in the Life Sciences**

*John G. Younger*, University of Michigan, USA

**10:00-10:25 Flocculation Dynamics and Cell Sorting**

*David M. Bortz*, University of Colorado Boulder, USA

**10:30-10:55 Modeling and Inverse Problems in Environmental Toxicity**

*H. Thomas Banks* and Kevin Flores, North Carolina State University, USA

**11:00-11:25 Estimating the Division Rate for a Growth-fragmentation Equation with Self-similar Kernel**

*Thibault Bourgeron*, UPMC and Inria Paris-Rocquencourt, France

**Lunch Break**

11:30 AM-1:00 PM

*Attendees on their own*

Monday, August 4

**IP2****Patient-Specific Mathematical Neuro-Oncology: Every Patient Deserves Their Own Equation**

1:00 PM-1:45 PM

*Room: Symphony I, II & III**Chair: Katarzyna Rejniak, H. Lee Moffit Cancer Center Research Institute, USA*

Glioblastoma are notoriously aggressive, malignant brain tumors that have variable response to treatment. Mathematical neuro-oncology (MNO) is a young and burgeoning field that leverages mathematical models to predict and quantify response to therapies. These mathematical models can form the basis of modern “precision medicine” approaches to tailor therapy in a patient-specific manner. Patient-specific models (PSMs) can be used to overcome imaging limitations, improve prognostic predictions, stratify patients, and assess treatment response in silico. The information gleaned from such models can aid in the construction and efficacy of clinical trials and treatment protocols, accelerating the pace of clinical research in the war on cancer. This talk will focus on the growing translation of PSM to clinical neuro-oncology. It will also provide a forward-looking view on a new era of patient-specific MNO.

Kristin Rae Swanson  
Northwestern University, USA

**Intermission**

1:45 PM-2:00 PM

Monday, August 4

**MS9****Recent Advances in Mathematical Epidemiology of Infectious Diseases - Part II of II**

2:00 PM-4:00 PM

*Room: Symphony I***For Part 1 see MS1**

This minisymposium will bring researchers who are actively involved in development of mathematical approaches in mathematical biology. The purpose of the minisymposium is to address recent advances of mathematical methods used to study dynamics of infectious diseases and discuss a wide range of topics: computational, mathematical and statistical techniques to study the infectious diseases.

Organizer: Necibe Tuncer  
University of Tulsa, USA

Organizer: Maia Martcheva  
University of Florida, USA

**2:00-2:25 Dynamics of Low and High Pathogenic Avian Influenza in Wild and Domestic Bird Populations***Necibe Tuncer, University of Tulsa, USA***2:30-2:55 Modeling Hiv Latency and Viral Blips***Libin Rong, Oakland University, USA***3:00-3:25 A Model for the Spatial Transmission of Dengue with Daily Movement between Villages and a City**

*Andrew Nevai, University of Central Florida, USA; Edy Soewono, Institut Teknologi Bandung, Indonesia*

**3:30-3:55 Disease Invasion of Community Networks with Environmental Pathogen Movement**

*Joseph Tien, The Ohio State University, USA; Zhisheng Shuai, University of Central Florida, USA; Marisa Eisenberg, University of Michigan, USA; P. van Den Driessche, University of Victoria, Canada*

Monday, August 4

**MS10****Applications of Dynamical Systems to Biology and Medicine - Part II of II**

2:00 PM-4:00 PM

*Room: Symphony II***For Part 1 see MS2**

Over the last decades mathematical models have been used to identify important features of immune responses during disease. In this minisymposium we bring together experts in modeling immune responses and infectious disease dynamics. Our sessions will focus on challenges and new directions in the study of viral kinetic dynamics, immune responses, drug and vaccine efficacy, and the best strategies to use the available biological data to identify parameters and propose new designs for experiments.

Organizer: Stanca Ciupe  
Virginia Tech, USA

Organizer: Matthias Chung  
Virginia Tech, USA

**2:00-2:25 Within-Host Virus Model with Immune Response and Infected Cell Age Structure***Cameron Browne, Vanderbilt University, USA***2:30-2:55 Modeling Human Papilloma Virus and the Onset of Cervical Cancer***Jonathan Forde, Hobart and William Smith Colleges, USA***3:00-3:25 A Basic Model for In-Host TB Infection***Jane Heffernan, Yimin Du, and Jianhong Wu, York University, Canada***3:30-3:55 Mechanism Elucidation in Intracellular Signaling Models Via Sensitivity Functions***Karyn L. Sutton, University of Louisiana, USA*

Monday, August 4

**MS11****Biomechanics in Medicine**

2:00 PM-4:00 PM

*Room:Symphony III*

Mathematics and biomechanics can bring a quantitative understanding to many questions that arise in medicine. This minisymposium brings together a diverse group of researchers that use mathematical and engineering perspectives to better understand medical questions pertaining to atherosclerosis, tumor growth and aortic valve disease. A range of topics will be presented, from basic theoretical issues to more experimentally-driven approaches.

Organizer: Rebecca Vandiver  
*St. Olaf College, USA*

Organizer: Pak-Wing Fok  
*University of Delaware, USA*

**2:00-2:25 A Mechanical and Biochemical Model of Intimal Hyperplastic Lesions**

Rebecca Vandiver, St. Olaf College, USA;  
Pak-Wing Fok, University of Delaware, USA

**2:30-2:55 Understanding the Role of Cell-substrate Interaction in Cell and Focal Adhesion Shapes**

Magdalena Stolarska, University of St. Thomas, USA

**3:00-3:25 Quantification of Iliac Artery Tortuosity and Its Implication for Rotation of Fenestrated Aortic Stent Grafts**

Matthew G. Doyle and Cristina Amon, University of Toronto, Canada; Leonard Tse, Toronto General Hospital, Canada

**3:30-3:55 Modeling the Growth of an Atherosclerotic Lesion**

Jay R. Walton, Texas A&M University, USA

Monday, August 4

**MS12**

**Recent Developments in Modeling and Analysis of Bacterial Motion and Chemotaxis**

2:00 PM-4:00 PM

*Room:Symphony V*

Chemotaxis is the active movement of cells or organisms in response to external chemical signals. It is critical in many multicellular processes such as wound healing, cancer metastasis, and embryonic development. In this minisymposium, we bring together experts in modeling and analysis of chemotactic movement of cells and present recent developments in this area. The topics of this minisymposium include new mathematical modeling and analytical methods of chemotaxis at both single cell and cell population levels, and methods that bridge these two scales.

Organizer: Chuan Xue  
*The Ohio State University, USA*

**2:00-2:25 Remarks on Modeling and Identification in Bacterial Chemotaxis**

Zahra Aminzare, Maja Skataric, and Eduardo Sontag, Rutgers University, USA

**2:30-2:55 Global Asymptotic Stability of Constant Equilibrium States of a Repulsive Chemotaxis Model with Logarithmic Sensitivity**

Kun Zhao, Tulane University, USA

**3:00-3:25 Collective Effects and Correlations in Semidilute Bacterial Suspensions**

Shawn Ryan, Pennsylvania State University, USA; Igor Aranson, Argonne National Laboratory, USA; Leonid Berlyand, Pennsylvania State University, USA; Andrey Sokolov, Argonne National Laboratory, USA

**3:30-3:55 Relating the Chemotactic Sensitivity with Intracellular Signaling and Cell Movement**

Chuan Xue, The Ohio State University, USA

Monday, August 4

**MS13**

**Biofluids: Biological and Physical Complexity in Fluid Structure Interaction Problems - Part II of II**

2:00 PM-4:00 PM

*Room:Symphony VI*

**For Part 1 see MS5**

Fluids are the natural environment of virtually every organism and fluid structure interaction problems are ubiquitous in biology. While Newtonian fluids and linearly elastic structures are found in nature, many important fluids and materials exhibit nonlinearities or other complex properties. The aim of this minisymposium is to present examples of such behavior in biological systems and the techniques used to address these problems. The first half focuses on complex fluids and other environmental considerations while the second half focuses on properties of the immersed structures. The systems vary across multiple scales and present a range of biofluids problems.

Organizer: Christina Hamlet  
*Tulane University, USA*

Organizer: Jacek K. Wrobel  
*Tulane University, USA*

**2:00-2:25 Hydrodynamic Contributions to Amoeboid Cell Motility**

Owen Lewis and Robert D. Guy, University of California, Davis, USA; Juan Carlos del Alamo and Shun Zhang, University of California, San Diego, USA

**2:30-2:55 Flow Through a Two-Chambered Zebrafish Heart with Trabeculae**

Nicholas A. Battista, Andrea Lane, and Laura A. Miller, University of North Carolina, Chapel Hill, USA

**3:00-3:25 The Effects of Perturbations on Lamprey Swimming**

Christina Hamlet, Tulane University, USA; Eric Tytell, Tufts University, USA; Lisa J. Fauci, Tulane University, USA

**3:30-3:55 Population Scale Effects of Macrophytes on Plankton Mobility**

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

Monday, August 4

## MS14

### Dynamics and Connectivity of Complex Networks in the Brain - Part II of II

2:00 PM-4:00 PM

Room: *Symphony VII*

#### For Part 1 see MS6

The dynamics of model neuronal networks have helped to explain many aspects of cognitive function. As more realism is incorporated into these models, novel dynamical features often arise which further enrich our understanding of the brain. This minisymposium explores this theme by discussing recent work in the modeling of both individual neuron dynamics and network topology, focusing upon implications on network behavior and information coding. The speakers will draw particular attention to new mathematical approaches in explaining sensory processing and information propagation.

Organizer: Victor Barranca  
*New York University, USA*

Organizer: Douglas Zhou  
*Shanghai Jiao Tong University, China*

#### 2:00-2:25 Path-integrals and Large Deviations in a Stochastic Hybrid Neural Network

*Paul C. Bressloff*, University of Utah, USA and University of Oxford, United Kingdom; *Jay Newby*, The Ohio State University, USA

#### 2:30-2:55 Theoretical Modeling of Nonlinear Dendritic Integration

*Songting Li* and *Douglas Zhou*, Shanghai Jiao Tong University, China; *David Cai*, Shanghai Jiao Tong University, China and Courant Institute of Mathematical Sciences, New York University, USA

#### 3:00-3:25 Analytical Evaluation of Targeting Performances at Short and Long Distances in a Stochastic Model for Neural Arborization

*Remus Osan* and *Jun Xia*, Georgia State University, USA; *Emily Su*, Rutgers University, USA

#### 3:30-3:55 Vasculature Adaptation and Optimization in Embryonic Zebrafish Brain

*Dan Hu*, Shanghai Jiao Tong University, China

Monday, August 4

## MS15

### Algebraic Aspects of Biochemical Reaction Networks - Part I of II

2:00 PM-4:00 PM

Room: *Mecklenburg II*

#### For Part 2 see MS22

Nonlinear, high-dimensional dynamical systems with many unknown parameters are usually used as models of biochemical reaction networks. The nonlinearities and the high number of parameters and variables make the direct mathematical analysis of the networks' behavior difficult. This minisymposium focuses on recent progress towards understanding the mathematical aspects of reaction networks using techniques from algebraic geometry and computational algebra. The progress bypasses the need for simulation and highlights the rich algebraic structure that underlies reaction networks. Topics that will be covered include multistationarity, qualitative properties, model comparison, and identifiability, with special focus on mass-action kinetics.

Organizer: Elisenda Feliu  
*University of Copenhagen, Denmark*

Organizer: Carsten Wiuf  
*University of Copenhagen, Denmark*

#### 2:00-2:25 A Global Convergence Result for Processive Multisite Phosphorylation Systems

*Anne Shiu*, University of Chicago, USA; *Carsten Conradi*, Max Planck Institute for Dynamics of Complex Systems, Germany

#### 2:30-2:55 Structural Identifiability of Biological Models

*Nicolette Meshkat* and *Seth Sullivant*, North Carolina State University, USA

#### 3:00-3:25 Degree Two Polynomials for Saddle Node Bifurcations in Mass Action Networks

*Carsten Conradi*, Max Planck Institute for Dynamics of Complex Systems, Germany

#### 3:30-3:55 The Dependence of the Existence of Positive Steady States on the Rate Coefficients for Deficiency-One Mass Action Systems

*Balázs Boros*, Eötvös Loránd University, Hungary

Monday, August 4

## MS16

### Structured Population Dynamics: Modeling, Estimation, and Validation - Part II of II

2:00 PM-4:00 PM

Room: *Mecklenburg III*

#### For Part 1 see MS8

Structured population models are ubiquitous in many areas of mathematical biology including microbial bioreactors, amyloid diseases, and cellular proliferation assays. In these populations, individual aggregates can combine, fragment, and/or grow. Each of these phenomena impact the model in substantially different ways. Accordingly, significant research has focused on the development of correct models as well as accurate estimation of kernels and rates. This minisymposium will showcase current directions of research in advanced simulation, estimation, and validation techniques to better understand structured populations.

Organizer: David M. Bortz  
*University of Colorado Boulder, USA*

Organizer: John G. Younger  
*University of Michigan, USA*

#### 2:00-2:25 Limited Measurement Domains: Robustness of Parameter Estimation in Flocculation Dynamics

*Dustin Keck*, University of Colorado, Boulder & US Air Force, USA

#### 2:30-2:55 A General Structured Population Model with the Application to Amphibians Infected with Chytridiomycosis

*Baoling Ma* and *Azmy S. Ackleh*, University of Louisiana, Lafayette, USA; *Jacoby Carter*, USGS National Wetlands Research Center, USA; *Vinodh Challamuthu*, University of Louisiana, Lafayette, USA

#### 3:00-3:25 Data Assimilation Methods and Inverse Problem for Protein Polymerization

*Aurora Armiento* and *Marie Doumic*, INRIA Rocquencourt, France

#### 3:30-3:55 Impact of Ellipsoid Geometry and Deformation on Flocculation Dynamics

*Eric Kightley*, University of Colorado, USA

Monday, August 4

## CP1

### Cancer

2:00 PM-4:00 PM

Room: Mecklenburg I

Chair: Hermann Frieboes, University of Louisville, USA

#### 2:00-2:25 A Mathematical Model of Intermittent Androgen Suppression Therapy for Treatment of Advanced Prostate Cancer

John G. Alford, Edward Swim, and Alacia M. Voth, Sam Houston State University, USA

#### 2:30-2:55 Can Mathematical Models Predict the Outcomes of Prostate Cancer Patients Undergoing Intermittent Androgen Suppression Therapy?

Rebecca A. Everett, Aaron Packer, and Yang Kuang, Arizona State University, USA

#### 3:00-3:25 Variance Reduced Model for Tumor Growth

Annelies Lejon, Giovanni Samaey, and Dirk Roose, Katholieke Universiteit Leuven, Belgium

#### 3:30-3:55 On the Accumulation of Mutations in Cancer

Cristian Tomasetti, Johns Hopkins University, USA

## Coffee Break

4:00 PM-4:30 PM



Room: Symphony Preconvene Area

Monday, August 4

## MS17

### New Interventions and Recent Progress on Modeling Malaria

4:30 PM-6:30 PM

Room: Symphony I

New intervention techniques are being considered or currently being employed as tools to control malaria in endemic malaria regions. Some of these include the use of Intermittent Preventive Treatment (IPT), where at risk individuals receive a full curative dose of an antimalarial medication, or the use/consideration of genetically modified mosquitoes. The benefits and/or impact of these intervention methods are still emerging and not fully understood, and it will require some time to be fully evaluated in the field. Mathematical models can shed some light on these. This minisymposium aims to do that.

Organizer: Miranda I. Teboh-Ewungkem

Lehigh University, USA

Organizer: Zhilan Feng

Purdue University, USA

#### 4:30-4:55 Ipt and the Spread of Drug Resistant Malaria

Zhilan Feng, Purdue University, USA; Miranda Teboh-Ewungkem, Lehigh University, USA; Katharine Gurski, Howard University, USA; Carrie A. Manore, Tulane University, USA; Angela Peace, Arizona State University, USA; Olivia Prosper, Dartmouth College, USA

#### 5:00-5:25 The Effect of IPT on the Spread of Drug Resistant Malaria Parasite When Regions are Connected

Scott Duke-Sylvester, University of Louisiana, Lafayette, USA; Jemal Mohammed-Awel, Valdosta State University, USA; Frederick Baliraine, LeTourneau University, USA; Miranda Teboh-Ewungkem, Lehigh University, USA

*continued in next column*

#### 5:30-5:55 Merging Population Genetics, Mosquito Behaviour and Epidemiology to Predicting the Success of the Use of GM Mosquitoes for Malaria Control

Christophe Boëte, Aix-Marseille Université, France

#### 6:00-6:25 Application of P. Falciparum Gametocyte Sex Ratios Via Competitive and Non-Competitive Strategies: The Evolutionary Implications

Miranda I. Teboh-Ewungkem, Lehigh University, USA; Thomas Yuster, Lafayette College, USA

Monday, August 4

## MS18

### Modeling Biological Phenomena Through the Use of Diffusion Models

4:30 PM-6:30 PM

*Room: Symphony III*

The role of mathematical diffusion has become an increasingly important tool as developing an understanding of diffusion will help us explain natural processes. Diffusion is imperative in modeling processes where spatial factors are essential. In addition to the standard heat equation, recent studies consider nonlinear reaction-diffusion models that give rise to traveling wave solutions while investigating heterogeneous environments. This session will highlight a variety of biological phenomena that can be modeled with diffusion ranging from epidemiology, physiology and inflammation, and population ecology utilizing theoretical and simulation results.

Organizer: Kamuela E. Yong  
*Arizona State University, USA*

Organizer: Tracy L. Stepien  
*Arizona State University, USA*

#### 4:30-4:55 Modeling and Analysis of Glioma Tumor Growth

*Tracy L. Stepien, Erica Rutter, and Yang Kuang, Arizona State University, USA*

#### 5:00-5:25 An Application of Mathematics to Osteoarthritis Related Inflammation

*Jason Graham, University of Scranton, USA*

#### 5:30-5:55 The Effects of Cross-diffusion on an SIR Model

*Kamuela E. Yong, Arizona State University, USA*

#### 6:00-6:25 Success, Failure, and Spreading Speeds for Invasions on Spatial Gradients

*Bingtuan Li, University of Louisville, USA*

Monday, August 4

## MS19

### Cell Mechanics and Motility

4:30 PM-6:30 PM

*Room: Symphony V*

Cell migration is important in many processes, such as embryonic development, tissue repair, obtaining nutrients, and cancer metastasis. Intracellular forces necessary for migration are generated by cytoskeletal rearrangement, which is a dynamic process that effects the mechanical properties of the cell. The appropriate rheological description of the cell is generally unknown and depends on the timescale, cell type, environment, and migration mode. This minisymposium will present recent work on modeling the cytoplasm in migrating cells and elucidating the role of mechanics in single and collective cell migration.

Organizer: Wanda Strychalski  
*Case Western Reserve University, USA*

#### 4:30-4:55 The Physics of Collective Cell Migration in Wound Healing and Cancer Metastasis

*Charles Wolgemuth, University of Arizona, USA*

#### 5:00-5:25 Exploring Motility of Breast Cancer Cells Using a 3D Individual Cell Based Model

*Hildur Knutsdottir, University of British Columbia, Canada*

#### 5:30-5:55 Insights into Cytoplasmic Rheology Gained from Modeling Cellular Blebbing

*Wanda Strychalski, Case Western Reserve University, USA*

#### 6:00-6:25 Actin-myosin Spatial Patterns from a Simplified Isotropic Viscoelastic Model

*Jun Allard, Owen Lewis, and Robert D. Guy, University of California, Davis, USA*

Monday, August 4

## MS20

### Mechanisms and Computation in Neuronal Networks

4:30 PM-6:30 PM

*Room: Symphony VII*

Our speakers address a range of neural networks mechanisms in order to understand their impact on specific computations.

Organizer: Andrea K. Barreiro  
*Southern Methodist University, USA*

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

#### 4:30-4:55 Impact of Single-Neuron Dynamics on Transfer of Correlations from Common Input

*Andrea K. Barreiro, Southern Methodist University, USA*

#### 5:00-5:25 Reduction Methods for Spiking Networks

*Cheng Ly, Virginia Commonwealth University, USA; Wilten Nicola and Sue Ann Campbell, University of Waterloo, Canada*

#### 5:30-5:55 Integrate-and-Fire Model of Insect Olfaction

*Pamela B. Fuller, Rensselaer Polytechnic Institute, USA*

#### 6:00-6:25 The Essential Role of Phase Delayed Inhibition in Decoding Synchronized Oscillations within the Brain

*Mainak Patel, Duke University, USA; Badal Joshi, California State University, San Marcos, USA*

Monday, August 4

**MS21****Modeling Endocrine Regulation of Female Reproduction**

4:30 PM-6:30 PM

*Room: Mecklenburg I*

The complex interplay between hormones produced by the brain and the ovaries is a key ingredient for regulating and maintaining the female reproductive system. Abnormal levels of these hormones often result in cycle irregularities and infertility in humans and animals. Minisymposium speakers will describe physiological mechanisms and mathematical models of various aspects of cycle regulation. Data analysis, modeling and simulation may be helpful in understanding the roles of the many components of the sexual endocrine system, in predicting successful hormone therapies for young and aging women, and in studying methods of contraception.

Organizer: James F. Selgrade  
*North Carolina State University, USA*

**4:30-4:55 Multiple Cycles and Bifurcation in Models of Hormonal Control of the Menstrual Cycle**

*James F. Selgrade, North Carolina State University, USA*

**5:00-5:25 A Differential Equation Model for the Bovine Estrous Cycle**

*Claudia Stoetzel, Julia Ploentzke, and Susanna Roebnitz, Zuse Institute Berlin, Germany*

**5:30-5:55 The Use of Physiological Model of Menstrual Cycle Regulation in Women's Health: Fertility and Contraception**

*Anna Kondic and Craig Fancourt, Merck & Co., Inc., USA*

**6:00-6:25 The Role of Insulin and Androgen Dynamics in Female Hormone Dysregulation**

*Erica J. Graham and James Selgrade, North Carolina State University, USA*

Monday, August 4

**MS22****Algebraic Aspects of Biochemical Reaction Networks - Part II of II**

4:30 PM-6:30 PM

*Room: Mecklenburg II***For Part 1 see MS15**

Nonlinear, high-dimensional dynamical systems with many unknown parameters are usually used as models of biochemical reaction networks. The nonlinearities and the high number of parameters and variables make the direct mathematical analysis of the networks' behavior difficult. This minisymposium focuses on recent progress towards understanding the mathematical aspects of reaction networks using techniques from algebraic geometry and computational algebra. The progress bypasses the need for simulation and highlights the rich algebraic structure that underlies reaction networks. Topics that will be covered include multistationarity, qualitative properties, model comparison, and identifiability, with special focus on mass-action kinetics.

Organizer: Elisenda Feliu  
*University of Copenhagen, Denmark*

Organizer: Carsten Wiuf  
*University of Copenhagen, Denmark*

**4:30-4:55 Atoms of Multistationarity in Chemical Reaction Networks**

*Badal Joshi, California State University, San Marcos, USA; Anne Shiu, University of Chicago, USA*

**5:00-5:25 An Algebraic Framework for Describing and Studying Binary Enzymatic Networks**

*Gilles Gnacadja, Amgen Inc., USA*

**5:30-5:55 Exploiting Reaction Network Structure for Parameter Identification of Biochemical Switches**

*Irene Otero-Muras, IIM-CSIC, Vigo, Spain; Pencho Yordanov, ETH Zürich, Switzerland; Attila Gabor, CSIC, Madrid, Spain; Julio R. Banga, IIM-CSIC, Vigo, Spain*

**6:00-6:25 Correspondence of Regular and Generalized Mass Action Systems**

*Matthew Johnston, University of Wisconsin, Madison, USA*

Monday, August 4

**MS23****Heterogeneity in Electrically Excitable Cells and Networks - Part I of II**

4:30 PM-6:30 PM

*Room: Mecklenburg III***For Part 2 see MS31**

Electrically excitable cells include neurons, muscle and cardiac cells, and many endocrine cells. Such cells typically exhibit a great deal of heterogeneity, both among interacting cell types and within populations of single cell types. In this minisymposium we focus on examples in which heterogeneity is a crucial element of the system, ways in which one can use mathematical models to understand the basis of heterogeneity and overcome the challenges it presents, and methods for extracting network connectivity using data on a heterogeneous cellular population.

Organizer: Richard Bertram  
*Florida State University, USA*

Organizer: Duncan J. MacGregor  
*University of Edinburgh, United Kingdom*

**4:30-4:55 Paracrine Regulation of Glucagon and Somatostatin Secretion**

*Margaret A. Watts, National Institutes of Health, USA; Ofer Kimchi, Princeton University, USA; Arthur Sherman, National Institutes of Health, USA*

**5:00-5:25 Hypothalamic Vasopressin Neurons: Signal Processing in An Asynchronous Bursting Population**

*Duncan J. MacGregor and Gareth Leng, University of Edinburgh, United Kingdom*

**5:30-5:55 Real-Time Model Calibration and Prediction Testing with the GPU and Dynamic Clamp**

*Patrick A. Fletcher, Joël Tabak, and Richard Bertram, Florida State University, USA*

**6:00-6:25 Leveraging Mathematical Models to Understand Population Variability in Response to Cardiac Drugs**

*Eric Sobie, Icahn School of Medicine at Mount Sinai, USA*

Monday, August 4

## CP2

### Epidemiology I

4:30 PM-6:00 PM

Room: Symphony II

Chair: Andrew Nevai, University of Central Florida, USA

#### 4:30-4:55 An SIRS Epidemic Model with Non-Exponential Probability for Temporary Immunity

Thomas W. Carr, Southern Methodist University, USA

#### 5:00-5:25 A Simple Model Incorporating Demographic and Epidemiological Processes in a Spatially Heterogeneous

Yongli Cai and Shangbin Cui, Sun Yat-Sen University, China; Weiming Wang, Wenzhou University, China

### Dinner Break

6:30 PM-8:00 PM

Attendees on their own

## PD1

### Forward Looking Session

8:00 PM – 8:45 PM

Room: Symphony II

Chair: Mette Sofie Olufsen, North Carolina State University, USA

#### Panelists:

##### Martin Golubitsky

Mathematical Biosciences Institute, Ohio State University, USA

##### Nicholas Hill

University of Glasgow, United Kingdom

##### Norman A. Mazer

F. Hoffmann-La Roche Ltd, Switzerland

##### John Rinzel

New York University, USA

##### Timothy W. Secomb

University of Arizona, USA

##### Kristin Rae Swanson

Northwestern University, USA

Monday, August 4

### Funding Agency Panel

8:45 PM-9:30 PM

Room: Symphony II

Chair: Mette Sofie Olufsen, North Carolina State University, USA

#### Panelists:

##### Mary Ann Horn,

National Science Foundation, USA

##### Larry Nagahara,

National Cancer Institute, USA

##### Virginia Pasour,

U.S. Army Research Office, USA

## Tuesday, August 5

### Registration

7:30 AM-5:00 PM

Room: Symphony Preconvene Area

### Remarks

8:10 AM-8:15 AM

Room: Symphony I, II & III

## IP3

### Modelling Plant Cell and Tissue Growth

8:15 AM-9:00 AM

Room: Symphony I, II & III

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

Plant growth typically occurs through the coordinated anisotropic expansion of plant cells. Growth is regulated by hormones and is driven by high intracellular pressures generated by osmosis. This machinery allows a plant primary root, for example, to penetrate soil in a direction guided by gravity, while seeking out nutrients and avoiding obstacles. I will describe the biomechanical aspects of a multiscale model for root gravitropism recently developed with colleagues at the Centre for Plant Integrative Biology at the University of Nottingham, UK. This incorporates descriptions of cell walls as fibre-reinforced viscoelastic polymer networks and adopts upscaling approaches to efficiently describe the growth of multicellular tissues.

Oliver E. Jensen

University of Manchester, United Kingdom

### Coffee Break

9:00 AM-9:30 AM

Room: Symphony Preconvene Area



Tuesday, August 5

**MS24****Mathematical Modeling of Infectious Diseases - Part I of II**

9:30 AM-11:30 AM

*Room: Symphony I***For Part 2 see MS32**

Mathematical modeling has played an important role in understanding the spread and control of infectious diseases in populations. Mathematical models have been increasingly used to guide public health policy decisions and explore questions in infectious disease control. This minisymposium will gather researchers employing a variety of mathematical techniques to study relevant phenomena of infectious diseases.

Organizer: Zhisheng Shuai  
*University of Central Florida, USA*

Organizer: Isaac Chun-Hai Fung  
*Georgia Southern University, USA*

**9:30-9:55 A Simple Epidemic Model with Nosocomial Transmission**

*Fred Brauer, University of British Columbia, Canada*

**10:00-10:25 Epidemiological and Economic Benefits of Targeted Tuberculosis Screening in a Correctional Facility of New River Health District**

*Kaja Abbas, Virginia Polytechnic Institute and State University, USA*

**10:30-10:55 Demographic Transition and the Dynamics of Measles in China**

*Sheng Li, Pennsylvania State University, USA*

**11:00-11:25 Modeling SIS Disease Dynamics on Random Contact Networks**

*Junling Ma, University of Victoria, Canada*

Tuesday, August 5

**MS25****Mathematical Modeling of Oxygen Transport in Various Tissues - Part I of II**

9:30 AM-11:30 AM

*Room: Symphony III***For Part 2 see MS34**

The efficient transport of oxygen along the entire vascular pathway is essential to maintaining homeostasis, as improper oxygen transport is a leading cause of disease in many tissues. This session presents theoretical models that are used to quantitatively assess solute transport processes for which experiments can merely provide qualitative observations. These modeling studies integrate structural and functional experimental data about oxygen-consuming tissues and the non-uniform vasculature that delivers oxygen to them, providing insights into the behavior and regulation of a variety of tissues, including the kidney, skeletal muscle, eye, and brain.

Organizer: Brendan C. Fry  
*Duke University, USA*

**9:30-9:55 Assessing the Impact of Structural Organization of the Renal Medulla on Oxygen Distribution Using a Mathematical Model**

*Brendan C. Fry, Duke University, USA*

**10:00-10:25 Can Pre-Glomerular Oxygen Transport Be Used to Investigate Renal Anatomy?**

*Bruce S. Gardiner, Saptarshi Kar, and David Smith, University of Western Australia, Australia; Roger Evans, Monash University, Australia*

**10:30-10:55 Development of Hypoxia in a Model of Renal Blood Flow Control and Oxygen Consumption**

*Ioannis Sgouralis, Duke University, USA*

**11:00-11:25 Models of Neurovascular Coupling and Cerebral Autoregulation**

*Tim David, University of Canterbury, New Zealand*

Tuesday, August 5

**MS26****Molecular Biosciences: Macromolecular Structures and Interactions - Part I of II**

9:30 AM-11:30 AM

*Room: Symphony V***For Part 2 see MS35**

Molecular based mathematical biology has been emerging as one of the most promising interdisciplinary research areas in the interface of mathematics and biology, driven by the fact that most experimental researches in life sciences are based on molecular biology or molecular level understanding. This minisymposium will focus on recent advances on a variety of modeling and computation developments for studying macromolecular structures and interactions. Example topics include molecular mechanics and dynamics, implicit solvent models, molecular docking, protein folding, protein-protein interaction, biomolecular solvation, membrane, ion-channels, etc. Emphasis will be placed not only on mathematical theories and methods, but also on biomolecular simulations and software developments.

Organizer: Shan Zhao  
*University of Alabama, USA*

Organizer: Benzhuo Lu  
*Institute of Computational Mathematics, China*

**9:30-9:55 Computational Design of Megadalton-Scale Nucleic Acid Nanoassemblies**

*Mark Bathe, Massachusetts Institute of Technology, USA*

**10:00-10:25 The Structural Glycobiology of HIV: Insights from Molecular Simulations and Implications for the Design of Virucidal Lectins**

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

*continued on next page*

Tuesday, August 5

## MS26

### Molecular Biosciences: Macromolecular Structures and Interactions - Part I of II

9:30 AM-11:30 AM

continued

#### 10:30-10:55 3D Continuum Modeling of Ion Permeation in Ion Channel Systems

*Benzhuo Lu*, Bin Tu, and Yan Xie, Institute  
of Computational Mathematics, China;  
Linbo Zhang, Chinese Academy of  
Sciences, China

#### 11:00-11:25 Monte Carlo Solution of Biochemical Electrostatics Problems

*Michael Mascagni*, Florida State  
University, USA

Tuesday, August 5

## MS27

### Low Reynolds Number Locomotion in Viscoelastic and Heterogeneous Fluids - Part I of II

9:30 AM-11:30 AM

*Room: Symphony VI*

#### For Part 2 see MS36

Locomotion at low Reynolds number in Newtonian fluids is a classical well-studied problem. Many biological systems involve heterogeneous viscoelastic materials, such as the mucus in the reproductive, digestive, and respiratory systems. The basic physics of viscoelastic fluids is not fully understood, and different modeling assumptions have led to conflicting predictions about the effect of viscoelasticity on swimming speed. Simulations of these types of complex systems must address the nonlinear coupling between elastic stresses from the fluid and active complex structures. In this session we present recent work on locomotion in low Reynolds number viscoelastic fluids and in heterogeneous media.

Organizer: Becca Thomases  
*University of California, Davis, USA*

Organizer: Robert D. Guy  
*University of California, Davis, USA*

#### 9:30-9:55 Finite Length Undulatory Swimmers: Whether to Kick or to Burrow in a Viscoelastic Fluid

*Becca Thomases* and Robert D. Guy,  
University of California, Davis, USA

#### 10:00-10:25 Flagellar Kinematics in Complex Fluids: Viscous and Elastic Effects

*Arvind Gopinath*, Max Planck Institute  
for Dynamics and Self-Organization,  
Germany; Boyang Qin, University of  
Pennsylvania, USA; Jing Yang and Jerry P.  
Gollub, Haverford College, USA; Paulo E.  
Arratia, University of Pennsylvania, USA

#### 10:30-10:55 Near Wall Motion of a Model Swimmer in a Viscoelastic Fluid

Gaojin Li, Alireza Karimi, and *Arezo*  
*Ardekani*, University of Notre Dame, USA

#### 11:00-11:25 Lyme Disease and Microorganism Swimming in Complex Fluids

*Charles Wolgemuth*, University of Arizona,  
USA

*continued in next column*

Tuesday, August 5

**MS28****Modeling and Analysis of Rhythm Generation and Control: CPGs - Part I of II**

9:30 AM-11:30 AM

*Room:Symphony VII***For Part 2 see MS37**

Neural circuits produce rhythmic outputs that underlie a variety of behaviors. How these activity patterns arise and are modulated represent fundamental questions in neuronal dynamics. An ideal setting in which to study these issues of rhythm generation and control is provided by central pattern generators (CPGs), relatively accessible circuits that produce the repetitive, multi-phasic outputs critical to fundamental rhythmic behaviors such as breathing, chewing, swimming, and walking. This minisymposium will explore a variety of interesting topics that arise in the theoretical study of CPGs, including the nonlinear dynamics of emergent rhythmicity, dynamics involving multiple time scales and stochasticity, and closed loop feedback control of neural systems.

Organizer: Jonathan E. Rubin  
*University of Pittsburgh, USA*

Organizer: Lucy Spardy  
*University of Pittsburgh, USA*

**9:30-9:55 Multiple Rhythms from One Network: Phase Plane and Stochastic Analyses of Rhythmic Activity in Turtle Motor Circuits**

*Abigail Snyder and Jon Rubin, University of Pittsburgh, USA*

**10:00-10:25 Using Experimental Phase Response Curves to Characterize Inter-Leg Coupling**

*Silvia Daum-Gruhn, Nils Rosjat, and Tibor I. Toth, University of Cologne, Germany*

**10:30-10:55 Shilnikov Cornerstone Bifurcation Generates a Family of Mechanisms Governing Dynamics of Central Pattern Generators**

*William H. Barnett, Georgia State University, USA*

**11:00-11:25 Dynamical Architectures for Control of Rhythmic Behavior**

*Peter J. Thomas, Hillel Chiel, and Jeffrey Gill, Case Western Reserve University, USA; David Lyttle, University of Arizona, USA; Kendrick Shaw, Case Western Reserve University, USA*

Tuesday, August 5

**MS29****Dynamics of Thrombus Development: Formation, Degradation, and Therapeutic Design**

9:30 AM-11:30 AM

*Room:Mecklenburg I*

Blood clot (thrombus) regulation is a complex process coordinated by biochemistry, biomechanics, and fluid flow. Thrombus dysregulation can result in severe medical problems. Current research explores various aspects of thrombus development (structural formation of fibrin, interaction of blood components and flow, clot dissolution) and employs a wide range of mathematical tools (differential equations, stochastic processes, numerics, multiscale modeling). This minisymposium will highlight advances in thrombus modeling and discuss implications for designing effective therapies for clotting defects.

Organizer: Erica J. Graham  
*North Carolina State University, USA*

Organizer: Brittany Bannish  
*University of Central Oklahoma, USA*

**9:30-9:55 A Model-Based Comparison of Clinical and Biological Determinants for Anticoagulation Therapy**

*Lisette G. dePillis, Harvey Mudd College, USA; Erica J. Graham, North Carolina State University, USA; Yanping Ma, Loyola Marymount University, USA; Ami Radunskaya, Pomona College, USA; Julie Simons, Tulane University, USA*

**10:00-10:25 Structural Hierarchy Governs Nonlinear Mechanics of Fibrin Networks and Transport of Blood Clotting Factors**

*Oleg Kim, University of Notre Dame, USA*

**10:30-10:55 Fibrin Polymerization in Flow: Gelation and Post Gelation Dynamics**

*Cheryl Zapata-Allegro, North Carolina State University, USA*

**11:00-11:25 Therapeutic Implications from a Multiscale Model of Blood Clot Degradation**

*Brittany Bannish, University of Central Oklahoma, USA; Aaron L. Fogelson and James P. Keener, University of Utah, USA*

Tuesday, August 5

**MS30****Developments in the Mathematics of Biochemical Reaction Networks - Part I of II**

9:30 AM-11:30 AM

*Room:Mecklenburg II***For Part 2 see MS39**

Mathematical models of biochemical networks usually consist of intricate systems of deterministic or stochastic nonlinear differential equations. 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. In this minisymposium, speakers will describe current efforts to (1) relate dynamical properties of these models (e.g. existence and uniqueness of equilibria, stability, long-term behavior) with the topology of the underlying network; (2) identify functional modules of biochemical networks; and (3) use recently obtained theoretical advances in modeling specific biochemical networks.

Organizer: Casian Pantea  
*West Virginia University, USA*

Organizer: Maya Mincheva  
*Northern Illinois University, USA*

**9:30-9:55 Recent Developments, Connections and Open Problems in Chemical Reaction Network Theory**

*Murad Banaji, University of Portsmouth, United Kingdom*

**10:00-10:25 Monotonicity of Chemical Reaction Networks with Respect to Non-Simplicial Cones**

*Pete Donnell and Murad Banaji, University of Portsmouth, United Kingdom*

**10:30-10:55 Sign Vectors in Chemical Reaction Network Theory**

*Stefan Mueller, RICAM, Austrian Academy of Sciences, Austria*

**11:00-11:25 Persistence and the Global Attractor Conjecture**

*Gheorghe Craciun, University of Wisconsin, Madison, USA*

Tuesday, August 5

## MS31

### Heterogeneity in Electrically Excitable Cells and Networks - Part II of II

9:30 AM-11:30 AM

Room: Mecklenburg III

#### For Part 1 see MS23

Electrically excitable cells include neurons, muscle and cardiac cells, and many endocrine cells. Such cells typically exhibit a great deal of heterogeneity, both among interacting cell types and within populations of single cell types. In this minisymposium we focus on examples in which heterogeneity is a crucial element of the system, ways in which one can use mathematical models to understand the basis of heterogeneity and overcome the challenges it presents, and methods for extracting network connectivity using data on a heterogeneous cellular population.

Organizer: Richard Bertram  
*Florida State University, USA*

Organizer: Duncan J. MacGregor  
*University of Edinburgh, United Kingdom*

#### 9:30-9:55 Estimating the Functional Connectivity in Networks of Neurons

*Henry D. Abarbanel, University of California, San Diego, USA*

#### 10:00-10:25 Inference of Network Structure from Spikes and Time Series

*Timothy Sauer, George Mason University, USA*

#### 10:30-10:55 Using Mathematical Models to Determine the Source of Heterogeneity in Cellular Calcium Dynamics

*Richard Bertram, Florida State University, USA; Maurizio Tomaiuolo, University of Pennsylvania, USA; Arturo Gonzalez-Iglesias and Joël Tabak, Florida State University, USA; Henry D. Abarbanel, University of California, San Diego, USA*

#### 11:00-11:25 Heterogeneity As a Consequence of Homeostasis

*Timothy O'Leary, Brandeis University, USA*

Tuesday, August 5

## CP3

### Epidemiology II

9:30 AM-11:30 AM

Room: Symphony II

Chair: Yun Kang, Arizona State University, USA

#### 9:30-9:55 Comparison of a Deterministic and Stochastic Model for the Transmission Dynamics of Influenza

*Adnan Khan, Lahore University of Management Sciences (Pakistan)*

#### 10:00-10:25 Analysis of Labour Productivity in the Presence of Substance Abuse

*Isaac Takaidza, Vaal University of Technology, South Africa*

#### 10:30-10:55 A Mixed-Strategy Game Theoretical Approach for Infectious Disease Prevention by Social Distancing

*Jing Li, California State University, Northridge, USA; Timothy Reluga, Pennsylvania State University, USA*

#### 11:00-11:25 Abms for Infectious Diseases Spreading and Ill-Posed Problems

*Valeriy D. Perminov, BioTeckFarm Ltd., Russia*

## Lunch Break

11:30 AM-1:00 PM

*Attendees on their own*

Tuesday, August 5

## IP4

### Robustness, Control, and the Organization of Cell Lineages

1:00 PM-1:45 PM

Room: Symphony I, II & III

Chair: Qing Nie, University of California, Irvine, USA

In the wake of a deluge of phenotypic, molecular, genomic and genetic data, biologists are increasingly returning to questions of biological organization: Why are biological systems built the way they are? Why are they so complex? How much is chance, and how much is necessity? Systems Biologists maintain that “design principles” are drivers of biological organization, but given a biological system, how does one identify the design principles that (presumably) shaped it? The study of embryonic development—especially the elaboration of spatial pattern, the determination of organ size, and the control of tissue growth—provides fertile ground for investigating such questions, in part because developmental systems are highly complex, highly conserved, and likely to have been selected for high performance. In this talk, I will discuss how requirements for stability, speed and robustness can be used to understand some of the complex intra- and intercellular interactions that take place within animal cell lineage pathways.

Arthur Lander  
*University of California, Irvine, USA*

## Intermission

1:45 PM-2:00 PM

Tuesday, August 5

**MS32****Mathematical Modeling of Infectious Diseases - Part II of II**

2:00 PM-4:00 PM

*Room: Symphony I***For Part 1 see MS24**

Mathematical modeling has played an important role in understanding the spread and control of infectious diseases in populations. Mathematical models have been increasingly used to guide public health policy decisions and explore questions in infectious disease control. This minisymposium will gather researchers employing a variety of mathematical techniques to study relevant phenomena of infectious diseases.

Organizer: Zhisheng Shuai  
*University of Central Florida, USA*

Organizer: Isaac Chun-Hai Fung  
*Georgia Southern University, USA*

**2:00-2:25 Economic Evaluation of the Fungal Meningitis Outbreak Response in New River Valley: Local Health Department and Clinical Perspectives**

*Nargesalsadat Dorratoltaj and Kaja Abbas, Virginia Tech, USA*

**2:30-2:55 Contact and Transmission in Epidemiological Models**

*Lydia Bourouiba, Massachusetts Institute of Technology, USA*

**3:00-3:25 Modeling Cholera in Heterogeneous Environments**

*Jin Wang, Old Dominion University, USA*

**3:30-3:55 Mathematical Modeling of Cholera**

*Zhisheng Shuai, University of Central Florida, USA*

Tuesday, August 5

**MS33****Parameter Estimation for Biological Systems**

2:00 PM-4:00 PM

*Room: Symphony II*

Parameter estimation techniques are a key tool to analyze biological systems by comparing mathematical models with available data. With these methods researchers are able to validate models and predict the behavior of the underlying system. Parameter estimation faces various challenges, such as robustness of the estimates, ill-posedness of the problem, and efficiency of the numerical methods. Without properly addressing these questions results of the parameter estimation problem may be meaningless. In this minisymposium we will discuss these challenges and provide new directions and results for parameter estimation techniques for biological systems.

Organizer: Matthias Chung  
*Virginia Tech, USA*

**2:00-2:25 Parameter Estimation for Large-Scale Biological Systems**

*Justin Krueger, Virginia Tech, USA*

**2:30-2:55 Beyond Acceptable Parameter Fits**

*Eberhard O. Voit, Georgia Institute of Technology, USA*

**3:00-3:25 Removing Irrelevant Parameters from Complex Biological Models**

*Mark K. Transtrum, Brigham Young University, USA*

**3:30-3:55 Convergence Properties of Gauss-Newton Methods, Well-Posedness of Parameter Estimation Problems and the Reliability of Parameter Estimates**

*Ekaterina Kostina, Fachbereich Mathematik und Informatik, Philipps-Universität Marburg, Germany*

Tuesday, August 5

**MS34****Mathematical Modeling of Oxygen Transport in Various Tissues - Part II of II**

2:00 PM-3:30 PM

*Room: Symphony III***For Part 1 see MS25**

The efficient transport of oxygen along the entire vascular pathway is essential to maintaining homeostasis, as improper oxygen transport is a leading cause of disease in many tissues. This session presents theoretical models that are used to quantitatively assess solute transport processes for which experiments can merely provide qualitative observations. These modeling studies integrate structural and functional experimental data about oxygen-consuming tissues and the non-uniform vasculature that delivers oxygen to them, providing insights into the behavior and regulation of a variety of tissues, including the kidney, skeletal muscle, eye, and brain.

Organizer: Brendan C. Fry  
*Duke University, USA*

**2:00-2:25 Effect of Intraocular Pressure and Arterial Blood Pressure on Oxygen Saturation Levels in the Retina: a Theoretical Model**

*Julia Arciero and Giovanna Guidoboni, Indiana University - Purdue University Indianapolis, USA; Brent Siesky and Alon Harris, Indiana University School of Medicine, USA*

**2:30-2:55 Computational Modeling of Oxygen and ATP Transport in Skeletal Muscle Capillary Networks of Normal and Pre-Diabetic Rats**

*Daniel Goldman, University of Western Ontario, Canada*

**3:00-3:25 Green's Function Methods for Simulating Solute Transport in the Microcirculation**

*Timothy W. Secomb, University of Arizona, USA*

Tuesday, August 5

## MS35

### Molecular Biosciences: Macromolecular Structures and Interactions - Part II of II

2:00 PM-4:00 PM

Room:Symphony V

#### For Part 1 see MS26

Molecular based mathematical biology has been emerging as one of the most promising interdisciplinary research areas in the interface of mathematics and biology, driven by the fact that most experimental researches in life sciences are based on molecular biology or molecular level understanding. This minisymposium will focus on recent advances on a variety of modeling and computation developments for studying macromolecular structures and interactions. Example topics include molecular mechanics and dynamics, implicit solvent models, molecular docking, protein folding, protein-protein interaction, biomolecular solvation, membrane, ion-channels, etc. Emphasis will be placed not only on mathematical theories and methods, but also on biomolecular simulations and software developments.

Organizer: Shan Zhao  
University of Alabama, USA

Organizer: Benzhao Lu  
Institute of Computational Mathematics,  
China

#### 2:00-2:25 Nonlinear Poisson-Nernst-Planck Equations for Ion Flux Through Confined Geometries

Marie-Therese Wolfram, Johann Radon  
Institute for Computational and Applied  
Mathematics, Austria

#### 2:30-2:55 New Effective Finite Element Algorithms for Solving Local and Nonlocal Poisson-Boltzmann Equations for Biomolecules in Ionic Solvent

Dexuan Xie, University of Wisconsin,  
Milwaukee, USA

#### 3:00-3:25 Fluctuation and Fidelity Control of Single Transcriptional Machine

Jin Yu, Beijing Computational Science  
Research Center, China

#### 3:30-3:55 Fast Pseudo-Time Simulations of the Nonlinear Poisson-Boltzmann (NPB) Equation

Shan Zhao, University of Alabama, USA

Tuesday, August 5

## MS36

### Low Reynolds Number Locomotion in Viscoelastic and Heterogeneous Fluids - Part II of II

2:00 PM-4:00 PM

Room:Symphony VI

#### For Part 1 see MS27

Locomotion at low Reynolds number in Newtonian fluids is a classical well-studied problem. Many biological systems involve heterogeneous viscoelastic materials, such as the mucus in the reproductive, digestive, and respiratory systems. The basic physics of viscoelastic fluids is not fully understood, and different modeling assumptions have led to conflicting predictions about the effect of viscoelasticity on swimming speed. Simulations of these types of complex systems must address the nonlinear coupling between elastic stresses from the fluid and active complex structures. In this session we present recent work on locomotion in low Reynolds number viscoelastic fluids and in heterogeneous media.

Organizer: Becca Thomases  
University of California, Davis, USA

Organizer: Robert D. Guy  
University of California, Davis, USA

#### 2:00-2:25 Computational Models of Cilia and Flagella in a Brinkman Fluid

Karin Leiderman, University of California,  
Merced, USA; Sarah D. Olson, Worcester  
Polytechnic Institute, USA

#### 2:30-2:55 An Immersed Boundary Method for Two-fluid Mixtures

Robert D. Guy, University of California,  
Davis, USA; Jian Du, Florida Institute of  
Technology, USA; Aaron L. Fogelson,  
University of Utah, USA

#### 3:00-3:25 Swimming Through Heterogeneous Networks

Henry Fu, University of Nevada, Reno, USA

#### 3:30-3:55 An Active Polar Nematic Model of Microtubule/motor-Protein Assemblies

Tony Gao and Michael J. Shelley, Courant  
Institute of Mathematical Sciences, New  
York University, USA; Robert Blackwell,  
Matthew Glaser, and Meredith Betterton,  
University of Colorado, USA

*continued in next column*

Tuesday, August 5

**MS37****Modeling and Analysis of Rhythm Generation and Control: CPGs - Part II of II**

2:00 PM-4:00 PM

*Room: Symphony VII***For Part 1 see MS28**

Neural circuits produce rhythmic outputs that underlie a variety of behaviors. How these activity patterns arise and are modulated represent fundamental questions in neuronal dynamics. An ideal setting in which to study these issues of rhythm generation and control is provided by central pattern generators (CPGs), relatively accessible circuits that produce the repetitive, multi-phasic outputs critical to fundamental rhythmic behaviors such as breathing, chewing, swimming, and walking. This minisymposium will explore a variety of interesting topics that arise in the theoretical study of CPGs, including the nonlinear dynamics of emergent rhythmicity, dynamics involving multiple time scales and stochasticity, and closed loop feedback control of neural systems.

Organizer: Jonathan E. Rubin  
*University of Pittsburgh, USA*

Organizer: Lucy Spardy  
*University of Pittsburgh, USA*

**2:00-2:25 Identifying and Explaining Three Time Scale Oscillations**

*Yangyang Wang* and Jon Rubin, University of Pittsburgh, USA; Vivien Kirk and Pingyu Nan, University of Auckland, New Zealand

**2:30-2:55 Robustness and Multifunctionality of Reduced CPG Models**

Aaron Kelley, Justus T. Schwabedal, and *Andrey Shilnikov*, Georgia State University, USA

**3:00-3:25 Differential Effects of Conductances on Pyloric CPG Output**

*Wafa Soofi*, Georgia Institute of Technology, USA

**3:30-3:55 Linear Currents Can Be Pacemaker Currents**

*Jorge Golowasch*, New Jersey Institute of Technology and Rutgers University, USA

Tuesday, August 5

**MS38****Mathematical Problems in Pharmacology: Perspectives and Challenges**

2:00 PM-4:00 PM

*Room: Mecklenburg I*

Pharmacology has recently been submitted to increasing mathematical influences, to the extent that “quantitative pharmacology” and “systems pharmacology” are shaping identities of their own. In this minisymposium, we present some of the central topics in these developing fields, emphasizing where mathematical challenges arise. Mathematical analysis and closed forms of newly reported pharmacokinetics phenomena, identification of drug disposition characteristics in clinical conditions, knowledge translation from in vitro to in vivo conditions for drug design, as well as signal transduction modeling in hematopoietic diseases are some of the examples that will be highlighted.

Organizer: Fahima Nekka  
*Universite de Montreal, Canada*

Organizer: Jacques Belair  
*Université de Montréal, Canada*

Organizer: Jun Li  
*Université de Montréal, Canada*

**2:00-2:25 Old Problems, New Solutions: Variability and Nonlinearity in Biopharmaceutical Processes and Mathematical Model-Based Problem Solving**

*Fahima Nekka*, Université de Montreal, Canada

**2:30-2:55 Translational Modeling and Optimal Concurrent Treatment in Oncology**

*Morgan Craig*, Université de Montréal, Canada; Anthony Humphries, McGill University, Canada; Jacques Bélair and Jun Li, Université de Montréal, Canada; Michael Mackey, McGill University, Canada; Fahima Nekka, Université de Montreal, Canada

**3:00-3:25 Systems Pharmacology: Revolutionizing Health Care One Equation at a Time**

*Angelean O. Hendrix*, North Carolina State University, USA

**3:30-3:55 Nonlinear Pharmacokinetic-Modeling: A Real Example**

*Carolyn Cho*, Merck & Co., Inc., USA

*continued in next column*

Tuesday, August 5

## MS39

### Developments in the Mathematics of Biochemical Reaction Networks - Part II of II

2:00 PM-4:00 PM

Room: Mecklenburg II

#### For Part 1 see MS30

Mathematical models of biochemical networks usually consist of intricate systems of deterministic or stochastic nonlinear differential equations. 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. In this minisymposium, speakers will describe current efforts to (1) relate dynamical properties of these models (e.g. existence and uniqueness of equilibria, stability, long-term behavior) with the topology of the underlying network; (2) identify functional modules of biochemical networks; and (3) use recently obtained theoretical advances in modeling specific biochemical networks.

Organizer: Casian Pantea  
West Virginia University, USA

Organizer: Maya Mincheva  
Northern Illinois University, USA

#### 2:00-2:25 Perturbations of the Lotka-Volterra System

Manoj Gopalkrishnan, Tata Institute of Fundamental Research, India; Gheorghe Craciun, University of Wisconsin, Madison, USA

#### 2:30-2:55 Reaction-Diffusion Equations With Periodic Behavior

David Siegel, University of Waterloo, Canada; Blair Davey, University of Minnesota, USA

#### 3:00-3:25 Elimination of Intermediate Species in the Stochastic Reaction Networks

Daniele Cappelletti and Carsten Wiuf, University of Copenhagen, Denmark

#### 3:30-3:55 Bistability in the Dual Futile Cycle

Alan Rendall, Johannes Gutenberg-Universität, Mainz, Germany

Tuesday, August 5

## CP4

### Neuroscience I

2:00 PM-4:00 PM

Room: Mecklenburg III

Chair: To Be Determined

#### 2:00-2:25 Fast-Slow Analysis of Neural Excitability with Synaptic Noise

Xueying Wang, Washington State University, USA; James P. Keener, University of Utah, USA

#### 2:30-2:55 Nonlinear Stochastic Dynamics of Sensory Hair Cells

Rami M. Amro and Alexander Neiman, Ohio University, USA

#### 3:00-3:25 Large Deviations of An Ergodic System of Hebbian Neurons

James Maclaurin and Olivier Faugeras, INRIA Sophia Antipolis, France

#### 3:30-3:55 Stationary Solutions for Neural Field Equations with Periodic Microstructures

Elena Malyuting, Arcady Ponomov and John Wyller, Norwegian University of Life Sciences

## Coffee Break

4:00 PM-4:30 PM

Room: Symphony Preconvene Area



Tuesday, August 5

## MS40

### Mathematical Models in Biology and Epidemiology - Part I of II

4:30 PM-6:30 PM

Room: Symphony I

#### For Part 2 see MS46

Mathematical modeling and analysis are powerful tools to gain important insights on the complicated biological and epidemiological processes by formulating, analyzing, simulating, and interpreting mathematical models. In the proposed minisymposium, we bring together a group of distinguished researchers who have particular expertise in applying mathematical models and theory to study the challenging problems arising from the field of biology and epidemiology. The invited speakers will present the most cutting-edge studies in the field, which may provide valuable opportunities for future modeling improvement and practical applications. The diversity of our speakers may spur new interests and promote participation among underrepresented groups including women in this exciting field.

Organizer: Yun Kang  
Arizona State University, USA

Organizer: Sophia Jang  
Texas Tech University, USA

#### 4:30-4:55 On a Diffusive Predator-prey Model with Nonlinear Harvesting

Peng Feng, Florida Gulf Coast University, USA

#### 5:00-5:25 Qualitative Behavior of Tumor—CD4+ Cytokine System

Sophia Jang, Texas Tech University, USA

#### 5:30-5:55 An Application of Optimal Control Theory to a Simple Age-of-Infection Sir Model

Sunmi Lee, KyungHee University, South Korea

#### 6:00-6:25 Evolutionary Dynamics of a Population Model with Component Allee Effects

Yun Kang, Arizona State University, USA

Tuesday, August 5

**MS41****Probability Inverse Problems in Biophysics**

4:30 PM-6:30 PM

*Room:Symphony II*

Data collected across biology is noisy and incomplete. This is especially true of data collected on small systems such as single molecules where conformational and dynamical fluctuations are strong. Inferring models from such data poses fundamental challenges. What physical models are consistent with data? How should the model search be refined? What level of model detail is appropriate given data? A quantitative understanding of biology and biomedicine critically depends on how these questions are answered. This minisymposium will illustrate inference methods used to answer such questions across biophysics.

Organizer: Steve Presse

*Indiana University - Purdue University Indianapolis, USA***4:30-4:55 Estimating Velocity for Processive Motor Proteins with Random Detachment***John Hughes, University of Minnesota, USA***5:00-5:25 From Single Molecule Experiments to Coupled Molecules***John Fricks, Pennsylvania State University, USA***5:30-5:55 Superresolution Microscopy As a Quantitative Tool***Steve Presse, Indiana University - Purdue University Indianapolis, USA***6:00-6:25 Form-Function Relationship in E. coli Chemotaxis***Jayajit Das, The Ohio State University, USA*

Tuesday, August 5

**MS42****Molecular Biosciences: Boundary Elements Computing and Applications**

4:30 PM-6:30 PM

*Room:Symphony V*

Electrostatics, as long range interactions with abundant presence, are critical in determining biological functions and structures at both the molecular and cellular levels. Structural biologists inevitably consider the effect of electrostatics in studying protein folding, protein-protein interactions, ion-channels, cell-cell interactions, etc. Meanwhile, attracted by electrostatics related scientific significances and computational challenges, numerical analysts actively seek numerical methods for accurate and efficient computing. Among these methods, boundary integral methods together with N-body fast algorithms stand themselves out at the combination of both accuracy and efficiency. We bring together experts in addressing different aspects of these problems, methods, and applications.

Organizer: Weihua Geng

*Southern Methodist University, USA***4:30-4:55 A Computational Method for Nearly Singular Integrals***J. Thomas Beale, Duke University, USA***5:00-5:25 On a Parallel Adaptive Fast Multipole Poisson-Boltzmann Solver**

Bo Zhang, Duke University, USA; Xiaolin Cheng, Oak Ridge National Laboratory, USA; *Jingfang Huang*, University of North Carolina at Chapel Hill, USA; Benzhuo Lu, Institute of Computational Mathematics, China; J Andrew McCammon, University of California, San Diego, USA; Nikos Pitsianis, Aristotle University of Thessaloniki, Greece; Xiaobai Sun, Duke University, USA

**5:30-5:55 Surface-Tension Molecular Surfaces for Deployment in Boundary Element Electrostatic Calculations***Randy Zauhar, University of the Sciences, USA***6:00-6:25 A Treecode-Accelerated Boundary Integral Poisson-Boltzmann Solver for Electrostatics of Solvated Biomolecules**

*Weihua Geng*, Southern Methodist University, USA; Robert Krasny, University of Michigan, Ann Arbor, USA

*continued in next column*

Tuesday, August 5

## MS43

### Blood Flow Propagation in Vessel Networks

4:30 PM-6:30 PM

Room: Symphony VI

During the last decades numerous models have been put forward analyzing wave propagation in cardiovascular networks, yet numerous questions still remain, in particular related to model validation. This minisymposium addresses new developments in cardiovascular modeling and methodologies for validation of these models, in particular seen in the light of sparse data available for rendering models patient specific. Another question is that of fluid dynamics models coupled with system level models enabling analysis of the complete system, this question is important in studies where models are applied for analysis of changes associated with the cardiovascular control system, where the model input is changed as downstream properties are controlled.

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

Organizer: Mansoor A. Haider  
North Carolina State University, USA

#### 4:30-4:55 A Coupled Model of the Left Ventricle and the Systemic Arteries

Nicholas A. Hill, University of Glasgow, Scotland, UK; Weiwei Chen and Hao Gao, University of Glasgow, Scotland, United Kingdom; Boyce Griffith, New York University, USA; Xiaoyu Luo, University of Glasgow, Scotland, United Kingdom

#### 5:00-5:25 Comparison of Inflow Boundary Conditions for Ventriculo-Arterial Coupling in 3D and 1D Fluid-Structure Interaction Models

Kevin D. Lau, Jordi Alastruey, and C. Alberto Figueroa, King's College London, United Kingdom

#### 5:30-5:55 Pulsatile Flow in the Entire Coronary Arterial Tree

Huo Yunlong, Peking University, China

#### 6:00-6:25 Physiological Modeling in Hypertension and Heart Failure

Karim Azer, Merck & Co., Inc., USA

Tuesday, August 5

## MS44

### Mathematical Modeling of Sleep Patterns in Humans

4:30 PM-6:30 PM

Room: Symphony VII

Sleep is a behavioral state in which we spend nearly one third of our lives. This biological phenomenon clearly serves an important role in the lives of most species. While much effort has been put forth in understanding the nature of sleep, many aspects of sleep are still not well understood. Modeling can help to uncover some of the complex underlying dynamics associated with sleep cycles and their regulation. In this minisymposium, speakers will discuss sleep regulation considered at different spatio-temporal scales using various modeling approaches.

Organizer: Shelby Wilson  
Morehouse College, USA

Organizer: Pamela B. Fuller  
Rensselaer Polytechnic Institute, USA

#### 4:30-4:55 Modeling Interindividual Differences in Spontaneous Internal Desynchrony Patterns

Victoria Booth, University of Michigan, USA; Cecilia Diniz Behn, Gettysburg College, USA

#### 5:00-5:25 A Mathematical Model of the Wake/NonREM/REM States

Selenne Garcia-Torres, University of Southern California, USA; Janet Best, The Ohio State University, USA; Gemma Huguet, Universitat Politècnica de Catalunya, Spain; Alicia Prieto Langarica, Youngstown State University, USA; Shelby Wilson, Morehouse College, USA; Pamela B. Fuller, Rensselaer Polytechnic Institute, USA

#### 5:30-5:55 Modeling the Effects of Temperature on Sleep Patterns

Alicia Prieto Langarica, University of Texas at Arlington, USA; Janet Best, The Ohio State University, USA; Gemma Huguet, Universitat Politècnica de Catalunya, Spain; Selenne Garcia-Torres, University of Southern California, USA; Shelby Wilson, Morehouse College, USA; Pamela B. Fuller, Rensselaer Polytechnic Institute, USA

#### 6:00-6:25 Spiking Neuron Vs. Neural Mass Models in the Context of Sleep-Regulatory Circuits

Andrew Phillips, Brigham and Women's Hospital and Harvard Medical School, USA; Victoria Booth, University of Michigan, USA; Elizabeth B. Klerman, Brigham and Women's Hospital and Harvard Medical School, USA

*continued in next column*

Tuesday, August 5

## MS45

### Change and Robustness in the Evolution of Biological Systems

4:30 PM-6:30 PM

Room: Mecklenburg III

Diversity in biology contributes greatly to the adaptivity of living organisms, both enabling survival in a changing environment and underlying the evolution of new phenotypes. We will discuss the relationship between diversity and evolution at various levels of biology within a cell. How selection works at multiple levels, from the function of proteins through genes to cellular architecture, remains an open question, and approaches in mathematical modeling and optimization will be used to address it. These applications enable us to understand mechanisms contributing to robustness within a biological system, and their role in evolution.

Organizer: Loretta Au

State University of New York, Stony Brook, USA

#### 4:30-4:55 Disentangling Protein Fitness Requirements Using Computational Mutagenesis

Loretta Au, State University of New York, Stony Brook, USA

#### 5:00-5:25 Conserved Enhancer Function When Sequence Is Not Conserved: Adventures with Cis-Regulatory Logic

John Reinitz, University of Chicago, USA

#### 5:30-5:55 Decoding Information in Cell Shape

Padmini Rangamani, University of California, Berkeley, USA

#### 6:00-6:25 A Mechanistic Model of the Bacterial Flagellar Motor

Kranthi Mandadapu, Jasmine Nirody, and George Oster, University of California, Berkeley, USA

Tuesday, August 5

## CP5

### Biophysics

4:30 PM-6:00 PM

Room: Symphony III

Chair: To Be Determined

#### 4:30-4:55 Parameter Inference Using Variance Fitting for Markov Models of Voltage Gated Ion Channels

Philipp Kuegler, University of Hohenheim, Germany

#### 5:00-5:25 A Fractional Order Model of Electroporation

Md Mehedi M. Hasan and Corina Drapaca, Pennsylvania State University, USA

#### 5:30-5:55 Compatibility of Slender Bodies and Surface Traction at Low Reynolds Number

Eva M. Strawbridge, James Madison University, USA; Charles Wolgemuth, University of Arizona, USA

Tuesday, August 5

## CP6

### Immunology and Diseases I

4:30 PM-6:30 PM

Room: Mecklenburg I

Chair: Lydia Bourouiba, Massachusetts Institute of Technology, USA

#### 4:30-4:55 Modeling Effects of Drugs of Abuse on Hiv-1 Dynamics

Naveen K. Vaidya, University of Missouri, Kansas City, USA

#### 5:00-5:25 Sensitivity Analysis and Treatment of Hepatitis C Virus Infection

Ariel Cintron-Arias, East Tennessee State University, USA

#### 5:30-5:55 The Effect of Systemic Estrogen and Cortisol on the Inflammatory Phase of Wound Healing

Angela M. Reynolds, Racheal Cooper, Rebecca Segal, and Robert Diegelmann, Virginia Commonwealth University, USA

#### 6:00-6:25 The Role of Interleukin-2 in Immune Response Regulation

Ryan S. Waters and Tomas Gedeon, Montana State University, USA

Tuesday, August 5

## CP7

### Genetic and Biochemical Networks

4:30 PM-6:30 PM

Room: Mecklenburg II

Chair: Eduardo Sontag, Rutgers University, USA

#### 4:30-4:55 On the Perfect Reconstruction of the Topology of Gene Regulatory Networks

Alan Veliz-Cuba, University of Houston, USA

#### 5:00-5:25 Spatial Uniformity of Solutions of Reaction-Diffusion Pde's

Zahra Aminzare and Eduardo Sontag, Rutgers University, USA

#### 5:30-5:55 Scale-Invariant Sensing of Singularly Perturbed Biomolecular Models

Maja Skataric, Evgeni Nikolaev, and Eduardo Sontag, Rutgers University, USA

#### 6:00-6:25 Simulation-Based Simplification of Non-Linear Feed-Forward Models

Richard Allen and Cynthia Musante, Pfizer Inc., USA

## Dinner Break

6:30 PM-8:00 PM

Attendees on their own

Tuesday, August 5

## PP1

### Poster Session

8:00 PM-10:00 PM

Room: Symphony IV

#### Network Bursting in Inhibitory Neural Circuits

Deniz Alacam and Andrey Shilnikov, Georgia State University, USA

#### Test Criterion for Finding the Global Minimum of a Function Using Exclusion Algorithm

Ibraheem Alolyan, King Saud University, Saudia Arabia

#### Staying in Shape: Patterns in Radial Symmetry Provide Protein Structural Stability and Functionality

Loretta Au, State University of New York, Stony Brook, USA

#### Modeling the Deformation of Proteins: from Coarse-Grained to Continuum

George Borleske, Colorado State University, USA

#### Demographics and Modeling of Multisite HPV Infection and Transmission

Andrew Brouwer, Rafael Meza, and Marisa Eisenberg, University of Michigan, USA

#### Binocular Rivalry Waves in Directionally Selective Neural Fields

Sam R. Carroll, University of Utah, USA; Paul C. Bressloff, University of Utah, USA and University of Oxford, United Kingdom

#### Modeling Interactions Between Two Major Southeastern U.S. Sea Turtle Nest Predators and Their Effects on Nest Depredation Rates

Joshua Castro, John Weishampel, Andrew Nevai, and Pedro Quintana-Ascencio, University of Central Florida, USA

#### Intrinsic Mechanisms for Pattern Generation in Three-Node Networks

Jarod Collens, Aaron Kelley, Deniz Alacam, Tingli Xing, Justus T. Schwabedal, and Andrey Shilnikov, Georgia State University, USA

#### Modeling the Dynamics of Opioid Abuse

William Consagra, Rochester Institute of Technology, USA

#### A Computational Model for a Porous Viscoelastic Cytoskeleton with Applications to Cell Mechanics

Calina A. Copos and Robert D. Guy, University of California, Davis, USA

#### Predicting Severity and Periodicity of Mountain Pine Beetle Outbreaks

Jacob P. Duncan, James Powell, and Luis Gordillo, Utah State University, USA; Joe Eason, University of Utah, USA

#### Temperature Effects on REM/Non-REM Sleep Dynamics

Pamela B. Fuller, Rensselaer Polytechnic Institute, USA; Janet Best, The Ohio State University, USA; Gemma Huguet, Universitat Politècnica de Catalunya, Spain; Shelby Wilson, Morehouse College, USA; Alicia Prieto Langarica, Youngstown State University, USA; Selenne Garcia-Torres, University of Southern California, USA

#### How Robust Is the Zero-Lag Synchrony When Two Neurons Interact Via a Third Relay Neuron

Zahra Ghasemi Esfahani and Alireza Valizadeh, Institute of Advanced Studies in Basic Science, Iran

#### Investigating the Effect of Atropine on Baroreceptor Heart Rate Regulation

Christian H. Haargaard Olsen and Mette S. Olufsen, North Carolina State University, USA; Johnny T. Ottesen, Roskilde University, Denmark; Jesper Mehlsen, Frederiksberg Hospital, Denmark; Hien T. Tran, North Carolina State University, USA

#### Accelerated Uzawa Iteration for the Stokes Equations

Nguyenho Ho, Sarah D. Olson, and Homer F. Walker, Worcester Polytechnic Institute, USA

#### Determining An Optimal Mathematical Model for Tumor Growth

Hana Jaafari, Michael Ellis, and Hana Dobrovolny, Texas Christian University, USA

continued in next column

continued on next page

### **Synchrony in Metapopulations with on-off Stochastic Dispersal**

*Russell Jeter* and *Igor Belykh*, Georgia State University, USA

### **Two-Theta Neuron: Phase Models for Bursting Networks**

*Aaron Kelley*, Georgia State University, USA

### **A Linear Analysis of a Straight Rod under Tension Both With and Without Drag**

*Victoria Kelley*, James Madison University, USA

### **Conserved NPZ Models with Time Delay**

*Matt Kloosterman*, Sue Ann Campbell, and Francis Poulin, University of Waterloo, Canada

### **Prediction of Biphasic Mitogenic Activity by Hgf, a Cancer-Associated Stroma-Derived Growth Factor, Using a Multi-Species Continuum Model**

*Anna Konstorum*, University of California, Irvine, USA

### **The Role of CD200-CD200R in Cancer Suppression and Promotion**

*Kang-Ling Liao*, Xue-Feng Bai, and Avner Friedman, The Ohio State University, USA

### **Patient-Specific Modeling of Average Cerebral Blood Flow During Orthostatic Stress**

*Gregory C. Mader*, Mette S. Olufsen, and Adam Mahdi, North Carolina State University, USA

### **Periodic Accumulation of Genetic Variation in the Genome of the Plant *Sorghum Bicolor***

*Ryan F. McCormick*, Sandra K. Truong, and John Mullet, Texas A&M University, USA

### **Gene Regulatory Network Based on a Novel Evolvable Partially Connected Artificial Neural Network**

*Mina Moradi Kordmahalleh*, Mohammad Gorji Sefidmazgi, and Abdollah Homaifar, North Carolina A&T State University, USA

### **Accumulation Behavior**

*Thomas Morrissey*, Infosys, USA

### **Distribution of Correlated Spiking Events in Integrate-and-Fire Networks**

*Katherine Newhall*, Jiwei Zhang, and Adi Rangan, Courant Institute of Mathematical Sciences, New York University, USA; Douglas Zhou, Shanghai Jiao Tong University, China

### **Modeling Dynamics of Mosquito Populations and Assessing Abatement Strategies for West Nile Virus**

*Kasia A. Pawelek*, *Patrick R. Niehaus*, and Cristian Salmeron, University of South Carolina, Beaufort, USA; Elizabeth J. Hager and Gregg J. Hunt, Beaufort County Mosquito Control, USA

### **Activity Patterns of Neuronal Network with Voltage-Sensitive Piecewise Smooth Coupling**

*Choongseok Park*, North Carolina A&T State University, USA; Jonathan Rubin, University of Pittsburgh, USA

### **Modeling the Effects of Craniosynostosis on Intracranial Pressure**

*Jackson Penning*, Madeline Anderson, Emily Van Heel, and Magda Stolarska, University of St. Thomas, USA

### **Investigation of Dual Virus Infection of Human Respiratory Tract**

*Lubna Pinky* and Hana Dobrovolny, Texas Christian University, USA

### **Synchronization of Bursting Neurons: a Synergetic Effect of Excitation and Inhibition**

*Reimbay Reimbayev* and Igor Belykh, Georgia State University, USA

### **Determining Mechanism of Action and Efficacy of Novel Influenza Antivirals**

*Thalia Rodriguez* and Hana Dobrovolny, Texas Christian University, USA

### **Within-Host Models of Influenza Virus Infection: The Role of Macrophages**

*Cristian Salmeron* and Kasia A. Pawelek, University of South Carolina, Beaufort, USA

### **Bursting in the Pituitary Corticotroph: The Role of Bk Ion Channels**

*Sevgi Sengul* and Joel Tabak, Florida State University, USA; Peter Duncan and Mike Shipston, University of Edinburgh, United Kingdom; Richard Bertram, Florida State University, USA

### **Identifiability of Linear Dynamical Systems from a Single Trajectory**

*Shelby R. Stanhope*, Jonathan Rubin, and David Swigon, University of Pittsburgh, USA

### **From Chaos to Periodicity: Revisiting the Logistic Map with an Ecologically Realistic Spatial Structure and Dispersal Mechanism**

*Laura Storch* and James Pringle, University of New Hampshire, USA

### **Identifying Physiological Origins of Baroreceptor Firing Characteristics Through a Conductance Based Neural Model**

*Jacob Sturdy*, North Carolina State University, USA; Johnny T. Ottesen, Roskilde University, Denmark; Mette S. Olufsen, North Carolina State University, USA

### **Leaf Inclination Angle Regulates the Distribution of Light in the Sorghum Canopy**

*Sandra K. Truong*, Ryan F. McCormick, and John Mullet, Texas A&M University, USA

### **Modeling the Effect of Antiarrhythmic Agents on the Action Potential of Human Ventricular Cells**

*Binaya Tuladhar* and Hana Dobrovolny, Texas Christian University, USA

### **Understanding and Distinguishing Three Time Scale Oscillations**

*Yangyang Wang*, University of Pittsburgh, USA; Pingyu Nan and Vivien Kirk, University of Auckland, New Zealand; Jonathan Rubin, University of Pittsburgh, USA

### **Coupling-Induced Synchronization of Mexican Jumping Beans**

*Andrea J. Welsh*, Flavio Fenton, and Ilija Uzelac, Georgia Institute of Technology, USA

### **Phenotypic Modulation of Virulence Facilitates Pathogen Invasion of the Gut**

*Glenn S. Young*, Bard Ermentrout, and Jonathan Rubin, University of Pittsburgh, USA

*continued in next column*

*continued in next column*

## Wednesday, August 6

### Registration

7:30 AM-5:00 PM

Room: Symphony Preconvene Area

### Remarks

8:10 AM-8:15 AM

Room: Symphony I, II & III

## IP5

### Deterministic and Stochastic Thresholds for Disease Extinction in Infectious Disease Models

8:15 AM-9:00 AM

Room: Symphony I, II & III

Chair: Maia Martcheva, University of Florida, USA

Thresholds for disease extinction provide essential information for control, eradication or management of diseases. Relations between branching process theory and corresponding deterministic models show that deterministic and stochastic thresholds are in agreement for discrete-time and continuous-time infectious disease models with multiple infectious groups. Markovian branching process theory in conjunction with deterministic models provide additional information about the probability of disease extinction. These relations are illustrated in discrete-time and continuous-time models of infectious diseases.

Linda J. Allen  
Texas Tech University, USA

### Coffee Break

9:00 AM-9:30 AM

Room: Symphony Preconvene Area



Wednesday, August 6

## MT2

### Modelling Arterial Wall Mechanics and Adaption using Structurally Based Constitutive Laws

9:30 AM-11:30 AM

Room: Symphony VI

Chair: Xiaoyu Luo, University of Glasgow, Scotland, United Kingdom

This mini-tutorial will introduce the four different aspects of modelling in arterial wall mechanics.

#### Constitutive Laws for Artery Wall with Application to Optimal Fibre Angle in Iliac Artery

Xiaoyu Luo, University of Glasgow, Scotland, United Kingdom

#### Arterial Wall Remodelling in Abdominal Aortic Aneurysm

Nicholas A. Hill, University of Glasgow, Scotland, UK

#### Stability of Arterial Wall with Case Study on Acute Aneurysm Initiation as a Bifurcation Phenomenon

Yibin Fu, Keele University, United Kingdom

#### Assessment of Statistical Variability in Wall Model Material Parameters for 1d Arterial Network Simulations

Leif Hellevik, Norwegian University of Science and Technology, Norway

Wednesday, August 6

## MS46

### Mathematical Models in Biology and Epidemiology - Part II of II

9:30 AM-11:30 AM

Room: Symphony I

#### For Part 1 see MS40

Mathematical modeling and analysis are powerful tools to gain important insights on the complicated biological and epidemiological processes by formulating, analyzing, simulating, and interpreting mathematical models. In the proposed minisymposium, we bring together a group of distinguished researchers who have particular expertise in applying mathematical models and theory to study the challenging problems arising from the field of biology and epidemiology. The invited speakers will present the most cutting-edge studies in the field, which may provide valuable opportunities for future modeling improvement and practical applications. The diversity of our speakers may spur new interests and promote participation among underrepresented groups including women in this exciting field.

Organizer: Yun Kang  
Arizona State University, USA

Organizer: Sophia Jang  
Texas Tech University, USA

#### 9:30-9:55 Modeling Drug Resistance in Metastatic Cancers

Doron Levy, University of Maryland, USA

#### 10:00-10:25 Vector Dynamics and Its Impact on the Vector Borne Disease- Malaria

Miranda I. Teboh-Ewungkem, Lehigh University, USA

continued on next page

**10:30-10:55 From Within-Host to Between-Host Dynamics. Systems Biology of Epidemiology**

*Juan B. Gutierrez*, University of Georgia, USA

**11:00-11:25 The Impact of Decay in BedNet Efficacy over Time on Malaria Transmission**

*Jemal Mohammed-Awel*, Valdosta State University, USA; *Calistus Ngonghalaa*, National Institute for Mathematical and Biological Synthesis, USA; *Sara Del Val*, Los Alamos National Laboratory, USA; *Ruijun Zhao*, Minnesota State University Mankato, USA

Wednesday, August 6

**MS47**

**Modeling and Inverse Problems of Complex Biological Systems**

9:30 AM-11:30 AM

*Room: Symphony II*

The analysis of complex hierarchical biological systems 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 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 applications in life sciences including infectious diseases, cancer biology, and kidney disease.

Organizer: *Phillip J. Aston*  
*University of Surrey, United Kingdom*

Organizer: *Hien T. Tran*  
*North Carolina State University, USA*

**9:30-9:55 A New Mathematical Model for Hepatitis C Infection: Derivation, Analysis and Implications**

*Philip J. Aston*, University of Surrey, United Kingdom

**10:00-10:25 Mathematical Modeling of Malignant Brain Tumor with T11 Target Structure As a Potent Immune Stimulator.**

*Sandip Banerjee*, Indian Institute of Technology Roorkee, India

**10:30-10:55 Parameter Subset Selection and Generalized Sensitivities for a Model of Erythropoiesis**

*Franz Kappel*, University of Graz, Austria

**11:00-11:25 Deconvolution of Isotope Signals Mixed from Sampling Bundles of Multiple Hairs**

*Christopher Remien*, University of Tennessee, USA; *Frederick Adler*, Lesley Chesson, Luciano Valenzuela, James Ehleringer, and *Thure Cerling*, University of Utah, USA

Wednesday, August 6

**MS48**

**Recent Advances of Membrane Modeling and Computation - Part I of II**

9:30 AM-11:30 AM

*Room: Symphony III*

**For Part 2 see MS55**

Dynamics of lipid bilayer in vivo involves multiscale interactions with surrounding fluid and other macromolecular complexes. To date, grand challenges remain in high-fidelity modeling and efficient computation of the composition variations, large deformation and topological changes of membrane induced by multiscale electrostatic, entropic, hydrodynamics, and mechanical interactions. This minisymposium will (1) address some of the most interesting topics in modeling of bilayer membranes, including coupling of asymmetric bilayers, protein insertion and pore formation, pattern formation, multicomponent coupling, fluid-vesicle coupling, fluid-electrostatics-vesicle coupling, and fast algorithms; (2) nurture collaborations among young scholars in applied and computational mathematics, biophysics, and mechanical engineering internationally.

Organizer: *Shuwang Li*  
*Illinois Institute of Technology, USA*

Organizer: *Yongcheng Zhou*  
*Colorado State University, USA*

**9:30-9:55 Continuum Models of Membrane Protein Insertion and Stability**

*Michael Grabe*, University of California, San Francisco, USA

**10:00-10:25 Competitive Geometric Evolution of Lipid Bilayers and Pores**  
*Shibin Dai*, New Mexico State University, USA; *Keith Promislow*, Michigan State University, USA

*continued on next page*

Wednesday, August 6

## MS48

### Recent Advances of Membrane Modeling and Computation - Part I of II

9:30 AM-11:30 AM

continued

#### 10:30-10:55 Periodic Migration in a Physical Model of Cells on Micropatterns

*Yanxiang Zhao*, University of California, San Diego, USA

#### 11:00-11:25 On Minimizers of the Bending Energy of Two-Phase Biomembranes

*Marco Veneroni*, University of Pavia, Italy; *Rustum Choksi*, McGill University, Canada; *Marco Morandotti*, Carnegie Mellon University, USA

Wednesday, August 6

## MS49

### Molecular Biosciences: Topological Modeling of Biomolecules - Part I of II

9:30 AM-11:30 AM

*Room: Symphony V*

#### For Part 2 see MS56

In the past two decades, molecular based mathematical biology has emerged as one of the most promising interdisciplinary research areas in the interface of mathematics and biology. This minisymposium will focus on recent advances on topological modeling of the macromolecular structures and interactions. The topics include topological states of DNA, DNA knots and links, neural data analysis, flexibility and rigidity analysis of biomolecule, elasticity modeling of protein, etc. We will emphasize not only the topological theories, methods and algorithms, but also their application in the real biomolecular systems.

Organizer: *Kelin Xia*  
*Michigan State University, USA*

Organizer: *Yuanan Diao*  
*University of North Carolina, Charlotte, USA*

#### 9:30-9:55 Topological Tools for Detecting Hidden Geometric Structure in Neural Data

*Carina Curto*, University of Nebraska, Lincoln, USA

#### 10:00-10:25 Topological Distances on DNA Knots and Links

*Isabel Darcy* and *Annette Honken*,  
University of Iowa, USA

#### 10:30-10:55 The Topological Structure of the Mitochondrial Dna from Trypanosomes

*Yuanan Diao*, University of North Carolina, Charlotte, USA

#### 11:00-11:25 Modeling Dna Packing with Confined Equilateral Random Polygons

*Claus Ernst*, Western Kentucky University, USA

Wednesday, August 6

## MS50

### Dynamics of Multistable Perception and Decision Making - Part I of II

9:30 AM-11:30 AM

*Room: Symphony VII*

#### For Part 2 see MS58

Multi-stable perception (spontaneous changes in subject's perception when confronted with an ambiguous sensory stimulus) and decision making (selecting a course of action from several available options) are two important cognitive processes that have attracted a lot of attention from both experimentalists and modelers. While several models have been proposed, the exact mechanisms underlying the dynamics of these processes remain unclear. This minisymposium brings together scientists studying different aspects of these cognitive processes and sensory modalities. Through enhanced discussion, the minisymposium aims to gain insight into the mechanisms that operate in the brain, and to inspire collaboration.

Organizer: *Rodica Curtu*  
*University of Iowa, USA*

Organizer: *Gemma Huguet*  
*Universitat Politecnica de Catalunya, Spain*

#### 9:30-9:55 Build-Up and Neural Competition in a Model of Auditory Streaming

*Rodica Curtu*, University of Iowa, USA;  
*John M. Rinzal*, Courant Institute of Mathematical Sciences, New York University, USA

#### 10:00-10:25 Modelling the Emergence and Dynamics of Perceptual Organisation in Auditory Streaming

*Sue Denham*, Plymouth University, United Kingdom

#### 10:30-10:55 Bistable Auditory Perception: Neural Competition with Periodic Input

*James Rankin* and *John Rinzal*, New York University, USA

#### 11:00-11:25 Diagnosing Excitation-inhibition Balance using Psychophysics

*Shashaank Vattikuti* and *Carson C. Chow*,  
National Institutes of Health, USA

Wednesday, August 6

## MS51

### The Mathematics of Sudden Cardiac Death - Part I of II

9:30 AM-11:30 AM

*Room: Mecklenburg I*

#### For Part 2 see MS59

Cardiac arrhythmias, in which propagating electrical waves that trigger cardiac contraction become localized and uncoordinated, affect the lives of millions of people around the world and have serious health and economic costs. The most severe arrhythmias can lead to sudden cardiac death if normal electrical wave patterns are not restored. This two-part minisymposium brings together researchers studying cardiac arrhythmias and sudden death from multiple perspectives. The utility of different modeling techniques, including PDEs, delay differential equations, stochastic processes, and data assimilation, as well as approaches to modeling cardiac structure, will be discussed. Applications to arrhythmia development will be presented.

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

#### 9:30-9:55 Delay-Differential Equations in Cardiac Electrophysiology Models

*Elizabeth M. Cherry and Ryan Thompson, Rochester Institute of Technology, USA*

#### 10:00-10:25 The Role of Feedback and Heart Rate Variability on Cardiac Rhythm Stability

*Elena Tolkacheva, Stephen McIntyre, and Yoichiro Mori, University of Minnesota, USA*

#### 10:30-10:55 Experimentally-based Modified Cable Equation That Reproduces Alternans Measured in Cardiac Tissue

*Flavio Fenton and Yanyan Ji, Georgia Institute of Technology, USA*

#### 11:00-11:25 Effects of Intracellular Sodium Accumulation on Cardiac Reentry Dynamics

*Trine Krogh-Madsen and Margo Smith, Cornell University, USA; David Christini, Weill Cornell Medical College, Cornell University, USA*

Wednesday, August 6

## MS52

### Modeling and Numerical Methods for Complex Systems in Developmental and Cell Biology - Part I of II

9:30 AM-11:30 AM

*Room: Mecklenburg II*

#### For Part 2 see MS60

This minisymposium aims to bring researchers to address recent advances of mathematical modeling and numerical methods for complex biological systems including (but not limited to) morphogenesis and stem cells, cell signaling pathways, cell polarization, cancer stem cells, tumor growth, tissue patterning, etc. Many such systems usually consist of multiple interacting components that exhibit complicated temporal and spatial dynamics with multiple scales and high dimensions, which are extremely difficult to describe, model or predict. In this minisymposium, the challenges of modeling these complex systems will be discussed, and more beyond, the new mathematical and numerical methods to analyze and simulate these models will also be presented.

Organizer: Xinfeng Liu  
*University of South Carolina, USA*

Organizer: Yongtao Zhang  
*University of Notre Dame, USA*

Organizer: Lei Zhang  
*Peking University, China*

#### 9:30-9:55 Stochastic Dynamics in Signal Transduction, Stem Cells, and Development Patterning

*Qing Nie, University of California, Irvine, USA*

#### 10:00-10:25 Mathematical Models for Stem Cell Interactions

*Jianjun Paul Tian, College of William & Mary, USA*

#### 10:30-10:55 Computation of Transition State and Its Applications in System Biology

*Lei Zhang, Peking University, China*

#### 11:00-11:25 Numerical Studies on Cell Lineage Models

*Yongtao Zhang, University of Notre Dame, USA*

Wednesday, August 6

## CP8

### Evolution and Ecology I

9:30 AM-11:30 AM

*Room: Mecklenburg III*

*Chair: Marc Harper, University of California, Los Angeles, USA*

#### 9:30-9:55 Linear Algebra of the Quasispecies Model

*Artem S. Novozhilov, North Dakota State University, USA; Alexander Bratus, Lomonosov Moscow State University, Russia; Yuri Semenov, Moscow State University of Railway Engineering, Russia*

#### 10:00-10:25 Species Coexistence Under Eco-evolutionary Dynamics

*Swati Patel and Sebastian Schreiber, University of California, Davis, USA*

#### 10:30-10:55 Stationary Stability for Evolutionary Dynamics in Finite Populations

*Dashiell Fryer, Pomona College, USA; Marc Harper, University of California, Los Angeles, USA*

#### 11:00-11:25 Mutational History Dominates Clonal Selection Within Evolving Tumors

*Scott T. Bickel, Joseph Juliano, and John D. Nagy, Arizona State University, USA*

## Lunch Break

11:30 AM-1:00 PM

*Attendees on their own*

Wednesday, August 6

## IP6

### Is “Good Cholesterol” Always “Good”? New Insights about HDL from an In-Silico Model of Lipoprotein Metabolism and Kinetics

1:00 PM-1:45 PM

*Room: Symphony I, II & III*

*Chair: Dean Bottino, Takeda Pharmaceuticals North America, USA*

Individuals with higher endogenous plasma levels of high-density lipoprotein-cholesterol (HDL-C), the so called “good cholesterol”, have a lower risk of developing cardiovascular disease (CVD) – an effect that is generally attributed to the role of HDL particles in the reverse cholesterol transport process. Nevertheless recent efforts to increase HDL-C levels pharmacologically have failed to lower CVD risk in patients. To understand this apparent paradox, we developed a novel in-silico model of lipoprotein metabolism and kinetics [1.Lu J, Hübner K, Nanjee MN, Brinton EA, Mazer NA. An in-silico model of lipoprotein metabolism and kinetics for the evaluation of targets and biomarkers in the reverse cholesterol transport pathway.]

Our model highlights the geometrical aspects of HDL structure and dynamics, and suggests why certain HDL-C raising therapies have not been successful to date. 1.Lu J, Hübner K, Nanjee MN, Brinton EA, Mazer NA. An in-silico model of lipoprotein metabolism and kinetics for the evaluation of targets and biomarkers in the reverse cholesterol transport pathway.

Norman Mazer

*F. Hoffmann-La Roche Ltd., Switzerland*

## Intermission

1:45 PM-2:00 PM

Wednesday, August 6

## MS53

### Advances in Mathematical Modeling of Complex Aspects and Control of Some Prevalent Infectious Diseases - Part I of II

2:00 PM-4:00 PM

*Room: Symphony I*

#### For Part 2 see MS61

This minisymposium will present recent efforts in understanding underlying mechanisms that drive patterns of infectious pathogens in the population and in the host. The talks will discuss pressing issues relevant to control of infectious diseases such as influenza, malaria, Hepatitis-C, HIV. Amidst active research in controlling them through optimal public health planning (vaccination) and/or therapeutic strategies, discerning complimentary aspects like immunity, nosocomial input, drug resistance will be indispensable in developing ways to eliminate them for good. The sessions promote several women and minorities, and can be of interest to students and researchers in infectious diseases, applied mathematics including public health.

Organizer: Swati Debroy  
*University of South Carolina, Beaufort, USA*

Organizer: Anuj Mubayi  
*Northeastern Illinois University, USA*

#### 2:00-2:25 Optimizing Vaccine Allocation for Influenza

*Jan Medlock, Oregon State University, USA*

#### 2:30-2:55 Malaria Vaccine Efficacy in a Region with Naturally Acquired Immunity

*Olivia Prosper, Dartmouth College, USA;  
Nick Ruktanonchai and Maia Martcheva,  
University of Florida, USA*

#### 3:00-3:25 A Two-Patch Avian Influenza Model

*Omar Saucedo, University of Florida, USA*

#### 3:30-3:55 Mathematical Model of Community-Acquired and Hospital-Acquired Methicillin-Resistant Staphylococcus Aureus Transmission in Hospital Settings

*Folashade Agusto, Austin Peay State University, USA*

Wednesday, August 6

## MS54

### Optimal Control and Optimization in Biological Models

2:00 PM-4:00 PM

*Room: Symphony II*

This minisymposium features talks by advanced students and recent postdocs on optimal control and optimization techniques and numerical results on biological models. Ecological and epidemiological applications will be presented. The types of models include systems of ODEs, PDEs, agent-based models and difference equations.

Organizer: Suzanne M. Lenhart  
*University of Tennessee, USA*

Organizer: Eric Numfor  
*University of Tennessee, USA*

#### 2:00-2:25 The Impact of Spatial Arrangements on Intervention Strategies in Epidemic Models

*Michael Kelly, University of Tennessee, Knoxville, USA*

#### 2:30-2:55 Optimal Control and Analysis of a Coupled Ode/pde Immuno-Epidemiological Model

*Eric Numfor, University of Tennessee, USA*

#### 3:00-3:25 Optimizing Hiv Treatment In a Resource Limited Settings

*Gordon Akudibillah and Jan Medlock,  
Oregon State University, USA*

#### 3:30-3:55 Inferring Equation Models from Agent-Based Model Data

*Matthew Oremland, Virginia Tech, USA*

Wednesday, August 6

## MS55

### Recent Advances of Membrane Modeling and Computation - Part II of II

2:00 PM-4:00 PM

Room: Symphony III

#### For Part 1 see MS48

Dynamics of lipid bilayer in vivo involves multiscale interactions with surrounding fluid and other macromolecular complexes. To date, grand challenges remain in high-fidelity modeling and efficient computation of the composition variations, large deformation and topological changes of membrane induced by multiscale electrostatic, entropic, hydrodynamics, and mechanical interactions. This minisymposium will (1) address some of the most interesting topics in modeling of bilayer membranes, including coupling of asymmetric bilayers, protein insertion and pore formation, pattern formation, multicomponent coupling, fluid-vesicle coupling, fluid-electrostatics-vesicle coupling, and fast algorithms; (2) nurture collaborations among young scholars in applied and computational mathematics, biophysics, and mechanical engineering internationally.

Organizer: Shuwang Li  
Illinois Institute of Technology, USA

Organizer: Yongcheng Zhou  
Colorado State University, USA

#### 2:00-2:25 Electromechanics of Bilayer Membrane: Forces and Fast Algorithms

Michael Mikucki, Colorado State University, USA

#### 2:30-2:55 Three Dimensional Vesicle Electrohydrodynamics: A Numerical Investigation

David Salac and Ebrahim M. Kolahdouz,  
State University of New York at Buffalo, USA

#### 3:00-3:25 A Continuum Model for Simulating Bilipid Membrane Deformation During Vesicle Drying

Chris Vogl, University of Washington, USA

#### 3:30-3:55 Numerical Simulations of Fluctuating Vesicles in Linear Flow

Shuwang Li and Kai Liu, Illinois Institute of Technology, USA

Wednesday, August 6

## MS56

### Molecular Biosciences: Topological Modeling of Biomolecules - Part II of II

2:00 PM-4:00 PM

Room: Symphony V

#### For Part 1 see MS49

In the past two decades, molecular based mathematical biology has emerged as one of the most promising interdisciplinary research areas in the interface of mathematics and biology. This minisymposium will focus on recent advances on topological modeling of the macromolecular structures and interactions. The topics include topological states of DNA, DNA knots and links, neural data analysis, flexibility and rigidity analysis of biomolecule, elasticity modeling of protein, etc. We will emphasize not only the topological theories, methods and algorithms, but also their application in the real biomolecular systems.

Organizer: Kelin Xia  
Michigan State University, USA

Organizer: Yuanan Diao  
University of North Carolina, Charlotte, USA

#### 2:00-2:25 Flexibility-Rigidity Index for Protein Flexibility Analysis

Kristopher Opron, Michigan State University, USA

#### 2:30-2:55 Knotting in Open Chains, Closed Chains, and Proteins

Eric Rawdon, University of St. Thomas, USA

#### 3:00-3:25 Unlinking of Supercoiled DNA Catenanes by Type IIA Topoisomerases

Alexander Vologodskii, New York University, USA

#### 3:30-3:55 Invariant Manifold and Persistent Homology for Biomolecules.

Guo-Wei Wei and Kelin Xia, Michigan State University, USA

*continued in next column*

Wednesday, August 6

## MS57

### Cellular, Tissue, and Organ Level Biofluid Dynamics - Part I of II

2:00 PM-4:00 PM

Room: Symphony VI

#### For Part 2 see MS64

Fluid flows play an important role in animal and plant physiology, from the level of single cells up to the level of organs and organisms. In the first part of this minisymposium, we begin by highlighting the role of fluids at the tissue and organ level by considering the importance of flow to the development of embryonic lung. We then consider the role of structures such as the pericardium in the transport of fluids within the body. In the next session, we consider the importance of non-Newtonian and multiphase flows in biological processes such as biofilm formation, cellular motility, and the tracks of tears.

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

#### 2:00-2:25 Transport in the Embryonic Lung I

Kishore Krishna Bokka and Sharon Lubkin,  
*North Carolina State University, USA*

#### 2:30-2:55 Transport in the Embryonic Lung II

Uduak Z. George, Kishore Krishna Bokka,  
and Sharon Lubkin, *North Carolina State University, USA*

#### 3:00-3:25 Role of the Pericardium in the Tubular Hearts of Tunicates

Lindsay Waldrop, *University of North Carolina, Chapel Hill, USA*

#### 3:30-3:55 Fluid-Composite Structure Interaction in Hemodynamics

Suncica Canic, *University of Houston, USA*;  
Martina Bukac, *University of Pittsburgh, USA*; Boris Muha, *University of Zagreb, Croatia*

Wednesday, August 6

## MS58

### Dynamics of Multistable Perception and Decision Making - Part II of II

2:00 PM-4:00 PM

Room: Symphony VII

#### For Part 1 see MS50

Multi-stable perception (spontaneous changes in subject's perception when confronted with an ambiguous sensory stimulus) and decision making (selecting a course of action from several available options) are two important cognitive processes that have attracted a lot of attention from both experimentalists and modelers. While several models have been proposed, the exact mechanisms underlying the dynamics of these processes remain unclear. This minisymposium brings together scientists studying different aspects of these cognitive processes and sensory modalities. Through enhanced discussion, the minisymposium aims to gain insight into the mechanisms that operate in the brain, and to inspire collaboration.

Organizer: Rodica Curtu  
*University of Iowa, USA*

Organizer: Gemma Huguet  
*Universitat Politècnica de Catalunya, Spain*

#### 2:00-2:25 Noise and Adaptation in Multistable Perception: A Case Study with Tristable Visual Plaids

Gemma Huguet, *Universitat Politècnica de Catalunya, Spain*; John M. Rinzal, *Courant Institute of Mathematical Sciences, New York University, USA*; Jean-Michel Hupé, *Toulouse University & CNRS, France*

#### 2:30-2:55 Network Symmetry and Binocular Rivalry Experiments

Martin Golubitsky, *The Ohio State University, USA*; Casey Diekmann, *New Jersey Institute of Technology, USA*

#### 3:00-3:25 Networks That Learn the Timing of Event Sequences

Alan Veliz-Cuba, Kresimir Josic, and Zachary Kilpatrick, *University of Houston, USA*

#### 3:30-3:55 Integration of Information over Multiple Timescales in a Large-scale Model of the Cortex

Rishidev Chaudhuri, Jorge F. Mejias, and Xiao-Jing Wang, *New York University, USA*

*continued in next column*

Wednesday, August 6

## MS59

### The Mathematics of Sudden Cardiac Death - Part II of II

2:00 PM-4:00 PM

Room: Mecklenburg I

For Part 1 see MS51

Cardiac arrhythmias, in which propagating electrical waves that trigger cardiac contraction become localized and uncoordinated, affect the lives of millions of people around the world and have serious health and economic costs. The most severe arrhythmias can lead to sudden cardiac death if normal electrical wave patterns are not restored. This two-part minisymposium brings together researchers studying cardiac arrhythmias and sudden death from multiple perspectives. The utility of different modeling techniques, including PDEs, delay differential equations, stochastic processes, and data assimilation, as well as approaches to modeling cardiac structure, will be discussed. Applications to arrhythmia development will be presented.

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

#### 2:00-2:25 Predicting Arrhythmias with a Nonlinear Cardiac Fiber Model

Laura Munoz and Niels Otani, Rochester Institute of Technology, USA; Anna Gelzer, Cornell University, USA; Flavio M. Fenton, Georgia Institute of Technology, USA; Weiye Lin and Min Chul Shin, Cornell University, USA; Robert Gilmour, Jr., University of Prince Edward Island, Canada

#### 2:30-2:55 Compositionality Results for Cardiac Cell Dynamics

Md. Ariful Islam and Abhishek Murthy, Stony Brook University, USA; Antoine Girard, Université Joseph Fourier, France; Scott Smolka, Stony Brook University, USA; Radu Grosu, Vienna University of Technology, Austria

#### 3:00-3:25 Microscale Modeling of Cardiac Tissue

Letitia Hubbard and Craig Henriquez, Duke University, USA

#### 3:30-3:55 Intramural Forecasting of Cardiac Electrical Dynamics Using Data Assimilation

Matthew J. Hoffman, Stephen Scorse, and Elizabeth M. Cherry, Rochester Institute of Technology, USA

Wednesday, August 6

## MS60

### Modeling and Numerical Methods for Complex Systems in Developmental and Cell Biology - Part II of II

2:00 PM-4:00 PM

Room: Mecklenburg II

For Part 1 see MS52

This minisymposium aims to bring researchers to address recent advances of mathematical modeling and numerical methods for complex biological systems including (but not limited to) morphogenesis and stem cells, cell signaling pathways, cell polarization, cancer stem cells, tumor growth, tissue patterning, etc. Many such systems usually consist of multiple interacting components that exhibit complicated temporal and spatial dynamics with multiple scales and high dimensions, which are extremely difficult to describe, model or predict. In this minisymposium, the challenges of modeling these complex systems will be discussed, and more beyond, the new mathematical and numerical methods to analyze and simulate these models will also be presented.

Organizer: Xinfeng Liu  
University of South Carolina, USA

Organizer: Yongtao Zhang  
University of Notre Dame, USA

Organizer: Lei Zhang  
Peking University, China

#### 2:00-2:25 Time to Mutation Acquisition in Stem Cell Driven Cancers

Alexandra Jilkine, University of Notre Dame, USA

#### 2:30-2:55 Analysis and Simulations of a Three Dimensional Model of Cell Signal Transduction

David Iron, Dalhousie University, Canada

#### 3:00-3:25 Spatial-Temporal Regulation of the First Embryonic Development Decision

William Holmes, University of California, Irvine, USA

#### 3:30-3:55 Mathematical Modeling of Proliferation Kinetics of Cancer Stem Cells

Xinfeng Liu, University of South Carolina, USA

Wednesday, August 6

## CP9

### Evolution and Ecology II

2:00 PM-4:00 PM

Room: Mecklenburg III

Chair: Dashiell Fryer, Pomona College, USA

#### 2:00-2:25 The Information Player: a Novel Strategy That Dominates Zero Determinant and Other Known Strategies in Multiplayer Evolutionary Games

Christopher Lee and Marc Harper, University of California, Los Angeles, USA; Dashiell Fryer, Pomona College, USA

#### 2:30-2:55 Quantifying the Relationships among Natural Selection, Mutation, and Stochastic Drift in Multidimensional Finite Populations

Marc Harper, University of California, Los Angeles, USA

#### 3:00-3:25 Pest Persistence and Eradication in a Deterministic Model for Sterile Insect Release

Luis Gordillo, Utah State University, USA

#### 3:30-3:55 Quantifying the Impact of the Recent Invasive Species, *Pomacea insularum*

Lihong Zhao, University of Louisiana, Lafayette, USA

## Coffee Break

4:00 PM-4:30 PM



Room: Symphony Preconvene Area

Wednesday, August 6

## MS61

### Advances in Mathematical Modeling of Complex Aspects and Control of Some Prevalent Infectious Diseases - Part II of II

4:30 PM-6:00 PM

*Room: Symphony I*

#### For Part 1 see MS53

This minisymposium will present recent efforts in understanding underlying mechanisms that drive patterns of infectious pathogens in the population and in the host. The talks will discuss pressing issues relevant to control of infectious diseases such as influenza, malaria, Hepatitis-C, HIV. Amidst active research in controlling them through optimal public health planning (vaccination) and/or therapeutic strategies, discerning complimentary aspects like immunity, nosocomial input, drug resistance will be indispensable in developing ways to eliminate them for good. The sessions promote several women and minorities, and can be of interest to students and researchers in infectious diseases, applied mathematics including public health.

Organizer: Swati Debroy  
*University of South Carolina, Beaufort, USA*

Organizer: Anuj Mubayi  
*Northeastern Illinois University, USA*

#### 4:30-4:55 Detailed Viral Kinetics During Liver Transplantation Indicates that the Liver Plays a Role in HCV Clearance

*Harel Dahari, Loyola University, USA*

#### 5:00-5:25 Silibinin As a Drug for Hepatitis C in Patients with Compromised Liver

*Swati Debroy, University of South Carolina, Beaufort, USA; Harel Dahari, Loyola University, USA; Laetitia Canini, Los Alamos National Laboratory, USA; Zoe Marino, Gonzalo Crespo, and Miquel Navasa, CIBERehd, Spain; Massimo D'Amato, Rottapharm Spa, Italy; Xavier Forns, CIBERehd, Spain; Scott Cotler, Loyola University, USA; Alan S. Perelson, Los Alamos National Laboratory, USA*

#### 5:30-5:55 Role of Methamphetamine in Transmission Dynamics of HIV in MSM Population

*Aprillya Lanz, Norfolk State University, USA*

Wednesday, August 6

## MS62

### Uncertainty, Complexity, and Model Qualification for Life Sciences

4:30 PM-6:30 PM

*Room: Symphony II*

How do modelers in life sciences responsibly support decision-making given the potential impact versus the number and complexity of unknowns? Many life science applications have significant consequences: dosing in clinical drug trials, interpretation of data to inform decisions on new drugs or devices, etc. Speakers will balance complexity, uncertainty, and impact via visualization and intentional communication as well as mathematics, statistics, and computation. Examples will include qualifying physiological models in pharmaceutical applications, leveraging visualization and probability to obtain a critical cancer-drug threshold, statistical perspectives on assessing the impact of knowns and unknowns, and incorporating in physiologically-based pharmacokinetic models variability and changes between species.

Organizer: Jeff Sachs  
*Merck Research Laboratories, USA*

Organizer: Karim Azer  
*Merck & Co., Inc., USA*

#### 4:30-4:55 Developing Fit-for-purpose Physiological Models in Drug Discovery and Development - A Framework for Qualification Best Practices

*Karim Azer, Merck & Co., Inc., USA; Jeff Sachs, Merck Research Laboratories, USA; Stefan Willmann, Bayer Technology Services, Germany; Carolyn Cho, Merck & Co., Inc., USA; Thomas Kerbusch, Antonio Cabal, Christopher Gibson, and Sandra Sandra Allerheiligen, Merck Research Laboratories, USA*

*continued in next column*

*continued on next page*

**5:00-5:25 Leveraging Visualization and Probabilistic Thinking to Get Consensus on an Assay Level Target for a Cancer Drug**

*Jeff Sachs*, Jos Lommerse, Jeroen Elassaiss - Schaap, and Yali Zhu, Merck Research Laboratories, USA

**5:30-5:55 A Sensitivity Based Statistical Approach to Parameter Selection and Uncertainty Quantification**

*H. T. Banks*, North Carolina State University, USA

**6:00-6:25 Application of Modelling and Simulation in Oncology: Physiologically-based Pharmacokinetics and Dynamics Examples**

*Michael Block*, Bayer Technology Services, Germany

Wednesday, August 6

## MS63

### Molecular Biosciences: Geometric Modeling in Biomolecular Systems

4:30 PM-6:30 PM

*Room: Symphony V*

Large biological systems such as molecular motors and viruses are of great importance to the processes of life, and now also to biologically inspired engineering. However, the complex interactions between these systems and their aquatic environment pose enormous challenges for theoretical understanding and design, particularly in offering accurate predictions of experimental data. This minisymposium will address how advances in geometric modeling and computation are advancing our understanding of these interactions. Topics include multiscale continuum models, new bio-medical imaging methods, and the interplay between chemical and mathematical approximations. Speakers will address mathematical theories and methods, as well as simulation and software.

Organizer: Jaydeep P. Bardhan  
*Northeastern University, USA*

Organizer: Zhan Chen  
*University of Minnesota, USA*

**4:30-4:55 Chemical Insights, Matrix Approximations, and Boundary-Integral Equations**

*Jaydeep P. Bardhan*, Northeastern University, USA

**5:00-5:25 Geometry of Surfaces in the Protein Images and the Graph Algorithms**

*Jing He*, New Mexico State University, USA

**5:30-5:55 Accurate Electrostatics in 3D Classical Dft**

*Matthew G. Knepley*, University of Chicago, USA

**6:00-6:25 Protein Modeling from Intermediate-Resolution Density Maps Using Geometric Skeletons**

*Tao Ju*, Washington University, St. Louis, USA

Wednesday, August 6

## MS64

### Cellular, Tissue, and Organ Level Biofluid Dynamics - Part II of II

4:30 PM-6:30 PM

*Room: Symphony VI*

**For Part 1 see MS57**

Fluid flows play an important role in animal and plant physiology, from the level of single cells up to the level of organs and organisms. In the first part of this minisymposium, we begin by highlighting the role of fluids at the tissue and organ level by considering the importance of flow to the development of embryonic lung. We then consider the role of structures such as the pericardium in the transport of fluids within the body. In the next session, we consider the importance of non-Newtonian and multiphase flows in biological processes such as biofilm formation, cellular motility, and the tracks of tears.

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

**4:30-4:55 Plant Leaves Reconfigure into Cone Shapes to Reduce Drag and Flutter**

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

**5:00-5:25 Modeling and Simulation of Biofilm Flows**

*Qi Wang*, University of South Carolina, USA; *Jia Zhao*, University of South Carolina, USA

**5:30-5:55 Surface Tension in Human Lungs: Modeling and Experiments**

*Rachel Levy*, Harvey Mudd College, USA; *Karen Daniels*, North Carolina State University, USA; *Ellen Swanson*, Centre College, USA; *Stephen Strickland*, North Carolina State University, USA; *Peter Megson* and *Shreyas Kumar*, Harvey Mudd College, USA

**6:00-6:25 Biofilm Pattern Formation Within Microfluidic Chambers**

*Mark E. Whidden*, Nick Cogan, and Matt Donahue, Florida State University, USA; *Fernando Navarrete* and *Leonardo de La Fuente*, Auburn University, USA

Wednesday, August 6

## MS65

### Recent Advances in Ecosystems and Disease Models

4:30 PM-6:30 PM

Room: Mecklenburg III

Mathematical models have been playing significant roles in life sciences to capture the complex relationship among humans, animals, microorganisms, and infectious diseases. This minisymposium will focus on recent advances in ecosystems and disease models. The purpose of this minisymposium is to bring together researchers from different backgrounds to work together and contribute to the study of biological processes. It will serve as a platform to report on recent progresses, exchange ideas, propose questions for discussion, extend networks, and seek further collaborations. Topics of talks are carefully selected to make the minisymposium interesting and attractive to a diverse audience.

Organizer: Guihong Fan  
Columbus State University, USA

Organizer: Xiang-Sheng Wang  
Southeast Missouri State University, USA

#### 4:30-4:55 Basic Reproductive Ratios in Ecosystems and Disease Models

Xiang-Sheng Wang, Southeast Missouri State University, USA

#### 5:00-5:25 Parameter Estimation and Model Discrepancy with Application to the Life Sciences

John A. Burns and Eugene Cliff, Virginia Tech, USA

#### 5:30-5:55 Habitat and Abundance Modeling of West Nile Virus Vector

Heidi Brown, University of Arizona, USA

#### 6:00-6:25 Optimal Control in PDE/DE Model for an Anthrax Epizootic

Buddhi Pantha, University of Tennessee, Knoxville, USA; Suzanne M. Lenhart, University of Tennessee, USA

Wednesday, August 6

## CP10

### Neuroscience II

4:30 PM-6:00 PM

Room: Symphony VII

Chair: Janet Best, The Ohio State University, USA

#### 4:30-4:55 Robust Design of Polyhythmic Neural Circuits

Justus T. Schwabedal, Georgia State University, USA; Alexander Neiman, Ohio University, USA; Andrey Shilnikov, Georgia State University, USA

#### 5:00-5:25 Relating Spiking Neural Network to Partial Differential Equations

Li Yang, Olivier Faugeras, and Pierre Kornprobst, INRIA Sophia Antipolis, France

#### 5:30-5:55 Characterization of Transient and Spatially Distributed High-Frequency Oscillations in the Brain with Quasi-Periodic Time Scales

Catherine Stamoulis, Harvard Medical School, USA; Bernard Chang, Harvard Medical School, Beth Israel Medical Center, USA

Wednesday, August 6

## CP11

### Circadian Rhythms

4:30 PM - 6:30 PM

Room: Mecklenburg I

Chair: To Be Determined

#### 4:30-4:55 Glucose and Temperature Compensation in the Neurospora Circadian Clock: Mathematical Modeling and Experimental Validation

Andrey A. Dovzhenok and Mokryun Baek, University of Cincinnati, USA; Arun Mehra, Jennifer Loros, and Jay Dunlap, Dartmouth College, USA; Sookkyung Lim and Christian Hong, University of Cincinnati, USA

#### 5:00-5:25 Molecular Mechanisms That Regulate the Coupled Period of the Mammalian Circadian Clock

Jae Kyoung Kim, The Ohio State University, USA; Zachary Kilpatrick, University of Houston, USA; Matthew Bennett, Rice University, USA; Krešimir Josic, University of Houston, USA

#### 5:30-5:55 Mathematical Modeling of the Hypothalamic-Pituitary-Adrenal Axis in Relation to Major Depression

Johanne Gudmand-Høyer and Johnny T. Ottesen, Roskilde University, Denmark

Wednesday, August 6

## CP12

### Cell Biology

4:30 PM-6:00 PM

Room: Mecklenburg II

Chair: To Be Determined

#### 4:30-4:55 Modeling the Spatio-Temporal Dynamics of Small GTPase Activity at Dendritic Spines

Samuel A. Ramirez and Sridhar Ragavachari, Duke University, USA

#### 5:00-5:25 In Vitro Assay Geometry Affects Estimates of the Cell Diffusivity and Cell Proliferation Rate

Katrina Treloar, Matthew Simpson, and Sean McElwain, Queensland University of Technology, Australia; Ruth E. Baker, University of Oxford, United Kingdom

#### 5:30-5:55 Unravelling the Impact of Obstacles in Diffusion and Kinetics of An Enzyme Catalysed Reaction

Marcio Duarte Albasini Mourao, The Ohio State University, USA; Doree Kreitmann and Santiago Schnell, University of Michigan, USA

Wednesday, August 6

## CP15

### Systems Physiology

4:30 PM-6:00 PM

Room: Symphony III

Chair: To Be Determined

#### 4:30-4:55 Spatial Modelling of Cytokine Dynamics Within Osteoarthritic Articular Cartilage

Michelle Baker, University of Nottingham, United Kingdom

#### 5:00-5:25 In Vivo Volume and Hemoglobin Dynamics in Red Blood Cells

Roy Malka, Harvard Medical School, USA

#### 5:30-5:55 Fractional Model for Neurovascular Coupling

Zehor Belkhatir, King Abdullah University of Science & Technology (KAUST), Saudi Arabia; Taous-Meriem Laleg, INRIA Rocquencourt, France

### Dinner Break

6:30 PM-8:00 PM

Attendees on their own

### SIAG/LS Business Meeting

8:00 PM-8:45 PM

Room: Symphony II

(Open to all SIAG/LS members.)

Complimentary wine and beer will be served.



Wednesday, August 6

## PD3

### Lee Segel Forum

8:45 PM-9:30 PM

Room: Symphony II

Chair: Robert D. Guy

University of California, Davis, USA

The focus of this year's Lee Segel Forum is on careers in mathematical biology with panelists representing different career types including industry, medicine, research and teaching. The Forum will start with brief presentations by panelists, which will be followed by an open question and answer session. The Forum will provide and integrate recommendations for undergraduate, graduate, and postdoctoral training in mathematical biology. 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.

#### Panelists:

##### Timothy David

University of Canterbury, New Zealand

##### Timothy C. Elston

University of North Carolina at Chapel Hill, USA

##### Oliver E. Jensen

University of Manchester, United Kingdom

##### Suzanne M. Lenhart

University of Tennessee, USA

##### Rachel Levy

Harvey Mudd College, USA

##### Jeff Sachs

Merck Research Laboratories, USA

## Thursday, August 7

### Registration

7:30 AM-3:00 PM

Room:Symphony Preconvene Area

### Closing Remarks

8:10 AM-8:15 AM

Room:Symphony I, II & III

## IP7

### Early Warning Signs and Critical Transitions in Ecology: Corals, Theory, Pitfalls, and Advances

8:15 AM-9:00 AM

Room:Symphony I, II & III

Chair: Robert D. Guy, University of California, Davis, USA

I will start by describing specific ecological systems that have multiple stable states, lakes and coral algal grazer systems giving models of the latter. I will then discuss approaches for predicting sudden shifts in the face of slow parameter change. The approach will depend on developing a simple stochastic model and using this model to describe the data. A key element in describing the results will be the use of receiver-operator curves. This part of the talk will include both possibilities and pitfalls. I will then discuss how the use of data can both help and be misleading in judging the efficacy of warning signals.

Alan M. Hastings  
University of California, Davis, USA

### Coffee Break

9:00 AM-9:30 AM



Room:Symphony Preconvene Area

Thursday, August 7

## MS66

### Mathematical Modeling and Control of Ecological and Epidemiological Problems - Part I of II

9:30 AM-11:30 AM

Room:Symphony I

#### For Part 2 see MS74

The management of ecological and epidemiological systems is of importance to agriculture, public health and biodiversity. The complexity of these systems, however, makes it difficult to develop tractable models that can produce actionable control policies, and model validation remains a fundamental difficulty. This session will bring together a diverse group of researchers to discuss innovative methods of modeling and control. Challenges and open questions will be discussed in the context of both application-specific and theoretical presentations. In the process, we will explore the roles of space, time and stochasticity in the modeling, analysis, and management of ecological and epidemiological systems.

Organizer: Wandí Ding  
Middle Tennessee State University, USA

Organizer: Rachel Leander  
Middle Tennessee State University, USA

#### 9:30-9:55 Probability of Extinction in Stochastic Models of Populations and Infectious Diseases: Importance of Time and Location

Linda J. Allen, Texas Tech University, USA

#### 10:00-10:25 Optimal Control Applied to Hospital-Acquired and Community-Acquired Methicillin-Resistant Staphylococcus Aureus Strains in Hospitals

Wandí Ding, Middle Tennessee State University, USA; Glenn Webb, Vanderbilt University, USA

#### 10:30-10:55 Optimal Control of Continuous Systems with Impulse Controls

Rachel Leander, Middle Tennessee State University, USA; S.M. Lenhart, University of Tennessee, USA; Vladimir A. Protopopescu, Oak Ridge National Laboratory, USA

#### 11:00-11:25 How Fish Ecology Affects the Effectiveness of Marine Protected Areas

Patrick DeLeenheer, Oregon State University, USA

continued in next column

Thursday, August 7

**MS67****Practical Parameter Estimation and Uncertainty Quantification Methods for Physiological Models**

9:30 AM-11:30 AM

*Room:Symphony II*

Numerous physiological models has been developed to gain insight into the system dynamics, though few has been combined with data enabling patient specific analysis. One obstacle is the lack of adequate inverse methods for parameter identification and estimation. Two groups of methods exist: methods that rely on linearization around given parameter values and global methods, frequently based on Monte Carlo simulations, predicting a global sensitivity matrix by sampling. Global methods are computationally intensive and are thus less suitable for practical parameter identifiability and estimation. On the other hand they also provide uncertainty quantification as a part of the method.

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

Organizer: Johnny T. Ottesen  
Roskilde University, Denmark

**9:30-9:55 Patient Specific Modelling of the Endocrine HPA-Axis and Its Relation to Depression: Ultradian and Circadian Oscillations**

Johnny T. Ottesen, Stine Timmerman,  
and Johanne Gudmand-Hoyer, Roskilde  
University, Denmark

**10:00-10:25 Uncertainty Quantification in ODE Modeling of Immune Response**

David Swigon, Ericka Mochan, Jonathan  
Rubin, and Gilles Clermont, University of  
Pittsburgh, USA

**10:30-10:55 Model Calibration in Systems Biology: Making the Most of Limited Data**

Brian P. Ingalls and Rahul Rahul,  
University of Waterloo, Canada

**11:00-11:25 Combined Parameter and State Estimation in Ensemble Kalman Filters**

Daniela Calvetti, Andrea N. Arnold, and  
Erkki Somersalo, Case Western Reserve  
University, USA

Thursday, August 7

**MS68****Modeling and Simulation of Complex Biological Systems - Part I of II**

9:30 AM-11:30 AM

*Room:Symphony III***For Part 2 see MS76**

Mathematical modeling and simulation is a powerful approach for understanding complex biological systems. Development of novel mathematical models and simulation algorithms is critical for studying these systems. Recently, several successful attempts have been made for simulating complex biological processes like metabolic pathways, gene regulatory networks, cell signaling pathways, cell dynamics, tissue engineering and biofabrication, etc. These models have not only generated experimentally verifiable hypothesis but also provided valuable insights into the behavior of the complex biological systems. This minisymposium will showcase some new progresses made in developing mathematical and efficient computational approaches for a set of biological systems.

Organizer: Qi Wang  
University of South Carolina, USA

Organizer: Yi Sun  
University of South Carolina, USA

**9:30-9:55 Diffusion in Soft Matter: Theory, Modeling, and Simulations**

M. Gregory Forest and John Mellnik,  
University of North Carolina at Chapel  
Hill, USA; Paula Vasquez, University of  
South Carolina, USA; Scott McKinley,  
University of Florida, USA; David Hill,  
University of North Carolina at Chapel  
Hill, USA

**10:00-10:25 A Multicell Model to Investigate How Vasculogenesis Is Disrupted in Cerebral Cavernous Malformations**

Timothy Elston, University of North  
Carolina, Chapel Hill, USA

**10:30-10:55 Homeostatic Mechanisms in Biochemical Systems**

Michael C. Reed, Duke University, USA

**11:00-11:25 Mathematical Understanding of Cancer Virotherapy**

Jianjun Paul Tian, College of William &  
Mary, USA

Thursday, August 7

**MS69****Molecular Biosciences: Ion Channels and their Roles in Cell Biology - Part I of II**

9:30 AM-11:30 AM

*Room:Symphony V***For Part 2 see MS77**

Ion channels are special proteins embedded in cell membranes and conduct ionic flux from extracellular to intracellular environment or vice versa. Thus, they are among the most fundamental building blocks to understand behaviors (e.g. action potential) of individual cells or their interactions with microenvironment (e.g. angiogenesis, chemotaxis). However, studies of functions of ion channels require molecular scales. The purpose of the proposed minisymposium is to promote multiscale modeling, analysis, and simulations of ion channels and their roles in cellular or developmental biology. The invited speakers include biophysicists, computational biologists, and mathematicians working in areas of modeling, analysis, and scientific computing.

Organizer: Duan Chen  
University of North Carolina, Charlotte,  
USA

Organizer: Wei Cai  
University of North Carolina, Charlotte,  
USA

**9:30-9:55 Ions in Channels: Natural Nanovalves**

Bob Eisenberg, Rush University Medical  
Center, USA

**10:00-10:25 Title Not Available at Time of Publication**

Tai-Chia Lin, National Taiwan University,  
Taiwan, ROC

**10:30-10:55 A Energy-Preserving Scheme for Pnp Equations**

Xiaofan Li, Illinois Institute of Technology,  
USA

**11:00-11:25 The Way Cells Talk: Modeling and Simulations of Ion Transport**

Duan Chen, University of North Carolina,  
Charlotte, USA

Thursday, August 7

## MS70

### Fluid Dynamics of Propulsion and Transport - Part I of II

9:30 AM-11:30 AM

Room: Symphony VI

#### For Part 2 see MS78

The surrounding fluid environment plays an important role in both propulsion and transport in the biological world. In the first part of this minisymposium, we will begin focus on a hydrodynamic level, by first exploring the role of neuronal control mechanisms in swimming organisms. We will then examine transport mechanisms found on an organismal level and in complex fluid environments. In our second session, we will shift our focus to movement of and through air. We will begin by examining scaling effects in insect flight and respiration, before moving on to mechanisms found for pathogen transmission through air.

Organizer: Alexander Hoover  
*University of North Carolina, Chapel Hill, USA*

Organizer: Laura Miller  
*University of North Carolina at Chapel Hill, USA*

#### 9:30-9:55 Neuromuscular Pumping in Jellyfish Bells

Alexander Hoover and Laura A. Miller,  
*University of North Carolina, Chapel Hill, USA*

#### 10:00-10:25 The Metachronal Limb Stroke Pattern in Crustacean Swimming

Calvin Zhang, Courant Institute of Mathematical Sciences, New York University, USA; Robert D. Guy and Timothy Lewis, University of California, Davis, USA; Boyce Griffith, New York University, USA; Charles S. Peskin, Courant Institute of Mathematical Sciences, New York University, USA

*continued in next column*

#### 10:30-10:55 The Effects of In Phase and Out of Phase Pulsations in Groups of Upside-down Jellyfish, *Cassiopea sp*

Julia E. Samson, University of North Carolina, Chapel Hill, USA; Arvind Santhanakrishnan, Oklahoma State University, USA; Laura A. Miller, University of North Carolina, Chapel Hill, USA

#### 11:00-11:25 Experiments and Modeling Study of Low Reynolds Number Flows Generated by a Processing Nodal Cilia

Longhua Zhao, Case Western Reserve University, USA; Roberto Camassa, James D. Martindale and Richard McLaughlin, University of North Carolina at Chapel Hill, USA; Leandra Vicci, University of North Carolina, USA

Thursday, August 7

## MS71

### Mathematical Questions in Neuronal and Neural Network Dynamics - Part I of II

9:30 AM-11:30 AM

Room: Symphony VII

#### For Part 2 see MS79

Understanding the brain and the physiological control mechanisms of neurons is difficult. It necessarily requires understanding electrophysiology, the biochemistry of neurons, the behavior of large-scale neural networks and how neural control is coordinated with other physiological systems. This is a daunting task because these aspects of neural function are related to behavior, to changing levels of gene regulation, and to the endocrine system. The mathematical techniques used to gain understanding range from dynamical systems and partial differential equations to probability theory and stochastic processes. The talks in this minisymposium will illustrate a diversity of biological systems and mathematical techniques.

Organizer: Janet Best  
*The Ohio State University, USA*

Organizer: Michael C. Reed  
*Duke University, USA*

#### 9:30-9:55 The Influence of Neurochemistry

Janet Best, The Ohio State University, USA; Michael C. Reed and H Frederik Nijhout, Duke University, USA

#### 10:00-10:25 Interaction of Two Distinct Timescales in Computational a Model of in-Vitro Sigh Generation

Natalia Toporikova, Washington and Lee University, USA; Muriel Thoby-Brisson, Universite de Bordeaux I, France

#### 10:30-10:55 How Precise Can We Make a Biophysical Neural Integrator?

Michael Schwemmer, The Ohio State University, USA

#### 11:00-11:25 The Effects of Long-Range Coupling on Neural Activity in the Crayfish Swimmeret System

Lucy Spardy, University of Pittsburgh, USA; Brian Mulloney and Tim Lewis, University of California, Davis, USA

Thursday, August 7

**MS72****Mechanisms for Defibrillation and Control of Cardiac Tissue**

9:30 AM-11:00 AM

*Room: Mecklenburg I*

When spiral waves of electrical activity form in the heart, they drive it to a spatiotemporally complex state that prevents contraction. Currently, the only reliable way to eliminate these “reentrant” waves is to apply a strong electric field that activate the whole heart and reset it. In this minisymposium, different alternative methods for defibrillation or control of waves before they become arrhythmic will be presented. These newer methods aim to use lower energies to reduce the risk of damage and pain.

Organizer: Flavio Fenton  
*Georgia Institute of Technology, USA*

**9:30-9:55 Local Termination of Cardiac Alternans Using Isostable Response Curve Techniques**

*Dan D. Wilson and Jeff Moehlis,*  
University of California, Santa Barbara,  
USA

**10:00-10:25 Large Reduction of Defibrillation Threshold Using a Four-Electrode System**

*Jean Bragard,* Universidad de Navarra,  
Spain; Ana Simic and Jorge Elorza,  
University of Navarra, Spain

**10:30-10:55 Unification of Electrical Restitution Dynamics and Ion Channel Dynamics in the Control of Cardiac Rhythm - An Eigenmode Approach**

*Niels Otani,* Rochester Institute of  
Technology, USA

Thursday, August 7

**MS73****Probabilistic Methods in Cell Biology - Part I of II**

9:30 AM-11:00 AM

*Room: Mecklenburg II***For Part 2 see MS81**

With the increasing availability of single-cell experimental data, increasing attention is being focused on the sources and effects of stochasticity in the dynamics of cells. Although deterministic models provide “on average” information, they cannot explain variability key to understanding properties such as robustness and synchronization. Classical probabilistic approaches ranging from stochastic simulations to Langevin approximations have previously been used to study such variability; some newer approaches have focussed on additional sources such as delay and genetic variation. This minisymposium will bring together theorists and experimentalists to discuss different approaches to study stochasticity in biology.

Organizer: Alan Veliz-Cuba  
*University of Houston, USA*

Organizer: Chinmaya Gupta  
*University of Houston, USA*

**9:30-9:55 Extrinsic Noise and Cell-Cycle Dependence of Genetic Oscillators**

*Alan Veliz-Cuba,* University of Houston,  
USA

**10:00-10:25 An Optimal Control Framework for Stochastic Gene Regulatory Networks**

*David Murrugarra,* Georgia Institute of  
Technology, USA

**10:30-10:55 Exact Protein Distributions for Stochastic Models of Gene Expression**

*Rahul Kulkarni and Niraj Kumar,*  
University of Massachusetts, Boston,  
USA; Hodjat Pendar, Virginia Tech, USA;  
Thierry Platini, Coventry University,  
United Kingdom

Thursday, August 7

**CP13****Evolution and Ecology III**

9:30 AM-11:30 AM

*Room: Mecklenburg III**Chair: To Be Determined***9:30-9:55 The Dynamics of Foraging Activity in Harvester Ants**

*Oyita Udiani,* Arizona State University, USA

**10:00-10:25 A Continuous Model of Ant Foraging with Pheromones and Trail Formation**

*Paulo V. Amorim,* Universidade Federal de  
Rio de Janeiro, Brazil

**10:30-10:55 Using Homogenization to Estimate Random-Walk Motility from Gps Collar Data in Variable Landscapes**

*Martha J. Garlick,* South Dakota School of  
Mines & Technology, USA; James Powell  
and Luis Gordillo, Utah State University,  
USA

**11:00-11:25 Respect Versus Disrespect for Ownership: An Iterated Hawk-Dove Game with Relocation Costs**

*Tugba Karabiyik,* Florida State University,  
USA

**Lunch Break**

11:30 AM-1:00 PM

*Attendees on their own*

Thursday, August 7

## IP8

### Synthetic Biology and Biocomputation: Life Redesigned

1:00 PM-1:45 PM

Room: Symphony I, II & III

Chair: Eduardo Sontag, Rutgers University, USA

Synthetic biology is bringing together engineers, computational scientists and biologists to design and construct biological circuits out of proteins, genes and other bits of DNA, and to use these circuits to rewire and reprogram organisms. These re-engineered organisms are going to change our lives in the coming years, leading to cheaper drugs, “green” means to fuel our car and clean our environment, and targeted therapies to attack “superbugs” and diseases such as cancer. In this talk, we highlight recent efforts to create synthetic gene networks and programmable cells, and discuss a variety of synthetic biology applications in biocomputing, biotechnology and biomedicine.

James J. Collins  
Boston University, USA

## Coffee Break

1:45 PM-2:15 PM

Room: Symphony Preconvene Area



Thursday, August 7

## MS74

### Mathematical Modeling and Control of Ecological and Epidemiological Problems - Part II of II

2:15 PM-4:15 PM

Room: Symphony I

#### For Part 1 see MS66

The management of ecological and epidemiological systems is of importance to agriculture, public health and biodiversity. The complexity of these systems, however, makes it difficult to develop tractable models that can produce actionable control policies, and model validation remains a fundamental difficulty. This session will bring together a diverse group of researchers to discuss innovative methods of modeling and control. Challenges and open questions will be discussed in the context of both application-specific and theoretical presentations. In the process, we will explore the roles of space, time and stochasticity in the modeling, analysis, and management of ecological and epidemiological systems.

Organizer: Wandu Ding  
Middle Tennessee State University, USA

Organizer: Rachel Leander  
Middle Tennessee State University, USA

#### 2:15-2:40 Optimal Control in Models of Management Involving Trees and Forest Resources

Suzanne M. Lenhart, University of Tennessee, USA

#### 2:45-3:10 Modeling of Transgenic Or Sterile Mosquitoes in Fighting Vector-Borne Diseases

Jia Li, University of Alabama, Huntsville, USA

#### 3:15-3:40 An Ecological Model for Producers and Scroungers in a Spatial Habitat

Chris Cosner, University of Miami, USA;  
Andrew Nevai, University of Central Florida, USA

#### 3:45-4:10 The Role of Avian Stage-structure in the Transmission and Control of West Nile Virus

Suzanne Robertson, Virginia Commonwealth University, USA; Kevin Caillouet, St. Tammany Parish Mosquito Abatement District, USA

Thursday, August 7

## MS75

### Identifiability and Parameter Estimation in Mathematical Models of Biological Phenomena

2:15 PM-4:15 PM

Room: Symphony II

Mathematical modeling of biological phenomena is a very fast growing area of research. It is a common situation that some of the model's parameters are unknown and have to be inferred from the available data. An important question is: Can all, or at least some, of the model's parameters be estimated uniquely from system's input and output? This is the problem of structural identifiability. This minisymposium will focus on both the current research areas related to structural and practical identifiability as well as parameter estimation techniques in models arising in biology.

Organizer: Adam Mahdi  
North Carolina State University, USA

Organizer: Nicolette Meshkat  
North Carolina State University, USA

#### 2:15-2:40 Identifiability and Parameter Estimation in Modeling Disease Dynamics

Marisa Eisenberg, University of Michigan, USA

#### 2:45-3:10 Identifiability of High-Dimensional Models

Hongyu Miao, University of Rochester, USA

#### 3:15-3:40 Identifiability and Parameter Estimation in Systems Biology and Drug Development

Andreas Raue, University of Freiburg, Germany

#### 3:45-4:10 Identifiability of Linear State Space Models

Seth Sullivant, North Carolina State University, USA

Thursday, August 7

**MS76****Modeling and Simulation of Complex Biological Systems - Part II of II**

2:15 PM-4:15 PM

*Room:Symphony III***For Part 1 see MS68**

Mathematical modeling and simulation is a powerful approach for understanding complex biological systems. Development of novel mathematical models and simulation algorithms is critical for studying these systems. Recently, several successful attempts have been made for simulating complex biological processes like metabolic pathways, gene regulatory networks, cell signaling pathways, cell dynamics, tissue engineering and biofabrication, etc. These models have not only generated experimentally verifiable hypothesis but also provided valuable insights into the behavior of the complex biological systems. This minisymposium will showcase some new progresses made in developing mathematical and efficient computational approaches for a set of biological systems.

Organizer: Qi Wang  
*University of South Carolina, USA*

Organizer: Yi Sun  
*University of South Carolina, USA*

**2:15-2:40 Modeling Cartilage Tissue Engineering in Cell-Seeded Scaffolds**  
*Mansoor A. Haider, North Carolina State University, USA*

**2:45-3:10 Mathematical Modeling of Renal Hemodynamics**  
*Anita T. Layton, Duke University, USA*

**3:15-3:40 Let There be Force: Modeling Cell-ECM Interactions**  
*Yi Jiang, Georgia State University, USA*

**3:45-4:10 Kinetic Monte Carlo Simulations of Multicellular Aggregate Self-Assembly in Biofabrication**  
*Yi Sun, University of South Carolina, USA*

Thursday, August 7

**MS77****Molecular Biosciences: Ion Channels and their Roles in Cell Biology - Part II of II**

2:15 PM-4:15 PM

*Room:Symphony V***For Part 1 see MS69**

Ion channels are special proteins embedded in cell membranes and conduct ionic flux from extracellular to intracellular environment or vice versa. Thus, they are among the most fundamental building blocks to understand behaviors (e.g. action potential) of individual cells or their interactions with microenvironment (e.g. angiogenesis, chemotaxis). However, studies of functions of ion channels require molecular scales. The purpose of the proposed minisymposium is to promote multiscale modeling, analysis, and simulations of ion channels and their roles in cellular or developmental biology. The invited speakers include biophysicists, computational biologists, and mathematicians working in areas of modeling, analysis, and scientific computing.

Organizer: Duan Chen  
*University of North Carolina, Charlotte, USA*

Organizer: Wei Cai  
*University of North Carolina, Charlotte, USA*

**2:15-2:40 Title Not Available at Time of Publication**  
*Chun Liu, Pennsylvania State University, USA*

**2:45-3:10 A Model of Tissue Electrodifusion and Osmosis and Its Application to Cortical Spreading Depression**  
*Yoichiro Mori, University of Minnesota, USA*

**3:15-3:40 Pnp Equations with Steric Effects: A Model of Ion Flow Through Channels**  
*Tzzy-Leng Horng, Feng Chia University, Taichung, Taiwan*

**3:45-4:10 Computer Simulation of Voltage Sensitive Calcium Ion Channels in a Dendritic Spine**  
*Pilhwa Lee, University of Connecticut Health Center, USA*

Thursday, August 7

**MS78****Fluid Dynamics of Propulsion and Transport - Part II of II**

2:15 PM-4:15 PM

*Room:Symphony VI***For Part 1 see MS70**

The surrounding fluid environment plays an important in both propulsion and transport in the biological world. In the first part of this minisymposium, we will begin focus on a hydrodynamic level, by first exploring the role of neuronal control mechanisms in swimming organisms. We will then examine transport mechanisms found on an organismal level and in complex fluid environments. In our second session, we will shift our focus to movement of and through air. We will begin by examining scaling effects in insect flight and respiration, before moving on to mechanisms found for pathogen transmission through air.

Organizer: Alexander Hoover  
*University of North Carolina, Chapel Hill, USA*

Organizer: Laura Miller  
*University of North Carolina at Chapel Hill, USA*

**2:15-2:40 Clap and Fling Interaction of Bristled Wings in Tiny Insect Flight**  
*Arvind Santhanakrishnan, Oklahoma State University, USA; Alice Robinson, University of California, Davis, USA; Tyson Hedrick and Laura A. Miller, University of North Carolina, Chapel Hill, USA*

**2:45-3:10 Fluid Flow Through Many Bristled Wings**  
*Shannon Jones and Laura Miller, University of North Carolina, Chapel Hill, USA*

**3:15-3:40 Microscale Gas Transport in Insect Respiratory Systems**  
*Anne Staples, Virginia Tech, USA*

**3:45-4:10 Roles of Droplets and Bubbles in Pathogen Transmission Through Air**  
*Lydia Bourouiba, Massachusetts Institute of Technology, USA*

Thursday, August 7

## MS79

### Mathematical Questions in Neuronal and Neural Network Dynamics - Part II of II

2:15 PM-4:15 PM

Room:Symphony VII

#### For Part 1 see MS71

Understanding the brain and the physiological control mechanisms of neurons is difficult. It necessarily requires understanding electrophysiology, the biochemistry of neurons, the behavior of large-scale neural networks and how neural control is coordinated with other physiological systems. This is a daunting task because these aspects of neural function are related to behavior, to changing levels of gene regulation, and to the endocrine system. The mathematical techniques used to gain understanding range from dynamical systems and partial differential equations to probability theory and stochastic processes. The talks in this minisymposium will illustrate a diversity of biological systems and mathematical techniques.

Organizer: Janet Best  
*The Ohio State University, USA*

Organizer: Michael C. Reed  
*Duke University, USA*

**2:15-2:40 Multi-Motor Transport in Neurons: Moving Beyond Tug-of-War**  
*Scott McKinley, University of Florida, USA*

**2:45-3:10 Measuring Edge Importance for Random Processes on Networks**  
*Deena Schmidt, Case Western Reserve University, USA*

**3:15-3:40 Stochastic Switching: Mathematical Surprises and Biological Insight**  
*Sean D. Lawley, Duke University, USA*

**3:45-4:10 Spontaneous Neural Activity Caused by Ion Channel Fluctuations**  
*Jay Newby, The Ohio State University, USA*

Thursday, August 7

## MS80

### Mathematical Modeling and Experiments Toward Mechanisms of Pulmonary Hypertension

2:15 PM-3:45 PM

Room:Mecklenburg I

Pulmonary hypertension is a pathophysiological condition of sustained mean pulmonary arterial pressure greater than 25 mmHg at rest. It is a syndrome in which remodeling of pulmonary vasculature leads to increased pulmonary vasculature resistance leading to right ventricular hypertrophy and heart failure. This minisymposium would highlight the current state of our understanding of the mechanisms underlying pulmonary hypertension such as dysfunction of endothelium and arterial stiffening. The discourse goes together with multiscale modeling of the pulmonary blood flow circulation and prediction of right ventricular heart failure.

Organizer: Pilhwa Lee  
*University of Michigan, Ann Arbor, USA*

#### 2:15-2:40 Individualized Pulmonary Arterial Blood Flow Analysis

*Pilhwa Lee, Shivendra Tewari, and Daniel Beard, University of Michigan, Ann Arbor, USA*

#### 2:45-3:10 A Mathematical and Computational Structured-Tree Model of the Pulmonary Circulation

*Nicholas A. Hill, University of Glasgow, Scotland, UK; M. Umar Qureshi, International Islamic University, Pakistan and University of Glasgow, United Kingdom; Gareth D.A. Vaughan and Christopher Sainsbury, University of Glasgow, Scotland, United Kingdom; Martin Johnson, Western Infirmary, Glasgow, United Kingdom; Charles S. Peskin, Courant Institute of Mathematical Sciences, New York University, USA; Mette S. Olufsen, North Carolina State University, USA*

#### 3:15-3:40 Analysis of Cardiovascular Dynamics in Pulmonary Hypertensive C57BL6/J Mice

*Shivendra Tewari, University of Michigan, Ann Arbor, USA; Naomi Chesler, University of Wisconsin, Madison, USA; Daniel Beard, University of Michigan, Ann Arbor, USA*

Thursday, August 7

## MS81

### Probabilistic Methods in Cell Biology - Part II of II

2:15 PM-4:15 PM

Room:Mecklenburg II

#### For Part 1 see MS73

With the increasing availability of single-cell experimental data, increasing attention is being focused on the sources and effects of stochasticity in the dynamics of cells. Although deterministic models provide “on average” information, they cannot explain variability key to understanding properties such as robustness and synchronization. Classical probabilistic approaches ranging from stochastic simulations to Langevin approximations have previously been used to study such variability; some newer approaches have focussed on additional sources such as delay and genetic variation. This minisymposium will bring together theorists and experimentalists to discuss different approaches to study stochasticity in biology.

Organizer: Chinmaya Gupta  
*University of Houston, USA*

Organizer: Alan Veliz-Cuba  
*University of Houston, USA*

#### 2:15-2:40 Rare Events for Genetic Networks: Studying Interactions Between Meta-Stability and Time-Delays

*Chinmaya Gupta, Manuel Lopez, and Robert Azencott, University of Houston, USA; Matthew Bennett, Rice University, USA; Kresimir Josic and William Ott, University of Houston, USA*

#### 2:45-3:10 Queueing Approaches to Multisite Enzyme Kinetics

*William H. Mather, Virginia Tech, USA*

#### 3:15-3:40 First-Passage Time Calculations for Gene Networks: Implications for Phage Lambda Lysis Time

*Abhyudai Singh, University of Delaware, USA; John Dennehy, City University of New York, USA; Khem Ghusinga, University of Delaware, USA*

#### 3:45-4:10 Impact of Stochastic Transcriptional Delay on Gene Networks

*Manuel Lopez, University of Houston, USA*

Thursday, August 7

## CP14

### Immunology and Diseases II

2:15 PM-3:15 PM

*Room: Mecklenburg III*

*Chair: Martha J. Garlick, South Dakota  
School of Mines & Technology, USA*

**2:15-2:40 The Virus of My Virus Is  
My Friend: Modeling the Ecological  
Effect of Virophages**

*Bradford Taylor, Michael H. Cortez,  
and Joshua Weitz, Georgia Institute of  
Technology, USA*

**2:45-3:10 Analyzing the Effects of a  
Non-Host Worm Population on the  
Spread of Whirling Disease in Trout**

*Tamra Heberling, Lisa G. Davis, Ryan  
Lamb, and Billie Karens, Montana State  
University, USA*

## Notes

## LS14 Abstracts



Art courtesy of Bourouiba, Gourley, Liu and Wu, SIAP 71-2

Abstracts are printed as submitted.

**IP1****Perceptual Dynamics in an Ambiguous World**

When experiencing an ambiguous sensory stimulus (e.g., the vase-faces image), subjects may report haphazard alternations (time scale, seconds) between the possible interpretations. I will describe dynamical models for neuronal populations that compete through mutual inhibition for dominance - showing alternations, behaving as noisy oscillators or as multistable systems subject to noise-driven switching. In highly idealized formulations networks are percept specific without direct representation of stimulus features. Our recent work involves perception of ambiguous auditory stimuli (e.g., <http://auditoryneuroscience.com/topics/streaming-galloping-rhythm-paradigm>); the models incorporate feature specificity, tonotopy, so that perceptual selectivity is emergent rather than built-in.

John Rinzel

New York University  
rinzeljm@gmail.com

**IP2****Invited Plenary Speaker - Title Tbd - Swanson**

TBD

Kristin Rae Swanson

Northwestern University, USA  
kristin.swanson@northwestern.edu

**IP3****Modelling Plant Cell and Tissue Growth**

Plant growth typically occurs through the coordinated anisotropic expansion of plant cells. Growth is regulated by hormones and is driven by high intracellular pressures generated by osmosis. This machinery allows a plant primary root, for example, to penetrate soil in a direction guided by gravity, while seeking out nutrients and avoiding obstacles. I will describe the biomechanical aspects of a multiscale model for root gravitropism recently developed with colleagues at the Centre for Plant Integrative Biology at the University of Nottingham, UK. This incorporates descriptions of cell walls as fibre-reinforced viscoelastic polymer networks and adopts upscaling approaches to efficiently describe the growth of multicellular tissues.

Oliver E. Jensen

University of Manchester, United Kingdom  
Oliver.Jensen@manchester.ac.uk

**IP4****Invited Speaker - Title Tbd - Lander**

TBD

Arthur Lander

University of California, Irvine  
adlander@uci.edu

**IP5****Invited Plenary Speaker - Title Tbd - Galvani**

TBD

Alison Galvani

Department of Epidemiology and Public Health  
Yale University School of Medicine  
alison.galvani@yale.edu

**IP6****Is Good Cholesterol Always Good? New Insights about HDL from an In-Silico Model of Lipoprotein Metabolism and Kinetics**

Individuals with higher endogenous plasma levels of high-density lipoprotein-cholesterol (HDL-C), the so called good cholesterol, have a lower risk of developing cardiovascular disease (CVD) - an effect that is generally attributed to the role of HDL particles in the reverse cholesterol transport process. Nevertheless recent efforts to increase HDL-C levels pharmacologically have failed to lower CVD risk in patients. To understand this apparent paradox, we developed a novel in-silico model of lipoprotein metabolism and kinetics [1]. Our model highlights the geometrical aspects of HDL structure and dynamics, and suggests why certain HDL-C raising therapies have not been successful to date. 1.Lu J, Hbner K, Nanjee MN, Brinton EA, Mazer NA. An in-silico model of lipoprotein metabolism and kinetics for the evaluation of targets and biomarkers in the reverse cholesterol transport pathway. PLoS Comput Biol. 2014 Mar 13;10(3):e1003509. doi: 10.1371/journal.pcbi.1003509. eCollection 2014 Mar.

Norman Mazer

F. Hoffmann-La Roche Ltd, Switzerland  
Norman.Mazer@roche.com

**IP7****Early Warning Signs and Critical Transitions in Ecology: Corals, Theory, Pitfalls, and Advances**

I will start by describing specific ecological systems that have multiple stable states, lakes and coral algal grazer systems giving models of the latter. I will then discuss approaches for predicting sudden shifts in the face of slow parameter change. The approach will depend on developing a simple stochastic model and using this model to describe the data. A key element in describing the results will be the use of receiver-operator curves. This part of the talk will include both possibilities and pitfalls. I will then discuss how the use of data can both help and be misleading in judging the efficacy of warning signals.

Alan M. Hastings

UC Davis  
amhastings@ucdavis.edu

**IP8****Synthetic Biology and Biocomputation: Life Redesigned**

Synthetic biology is bringing together engineers, computational scientists and biologists to design and construct biological circuits out of proteins, genes and other bits of DNA, and to use these circuits to rewire and reprogram organisms. These re-engineered organisms are going to change our lives in the coming years, leading to cheaper drugs, "green" means to fuel our car and clean our environment, and targeted therapies to attack "superbugs" and diseases such as cancer. In this talk, we highlight recent efforts to create synthetic gene networks and programmable cells, and discuss a variety of synthetic biology applications

in biocomputing, biotechnology and biomedicine.

James J. Collins

Boston University  
Department of Biomedical Engineering  
jcollins@bu.edu

## CP1

### **A Mathematical Model of Intermittent Androgen Suppression Therapy for Treatment of Advanced Prostate Cancer**

Advanced prostate cancer is often treated with androgen deprivation therapy (ADT) which facilitates the death of androgen-dependent (AD) cancer cells. Androgen-independent (AI) cancer cells may increase with continuous ADT so that intermittent androgen suppression (IAS) therapy is utilized to delay the onset of AI cells. We model the dynamics of IAS therapy with a system of ordinary differential equations and determine the optimal times to collect data relative to model parameters in order to develop better treatment protocols.

John G. Alford, Edward Swim, Alacia M. Voth  
Sam Houston State University  
jalford@shsu.edu, ews007@shsu.edu, amv007@shsu.edu

## CP1

### **Can Mathematical Models Predict the Outcomes of Prostate Cancer Patients Undergoing Intermittent Androgen Suppression Therapy?**

Prostate cancer is often treated by intermittent androgen deprivation therapy since prostate cells depend on androgens for proliferation and survival. We extend an existing prostate cancer model and test the model's predictive accuracy when only a subset of the data is used to find parameter values. The results are compared with those of an existing linear model. We also develop a second method for testing the accuracy in predicting the duration of off-treatment periods.

Rebecca A. Everett, Aaron Packer  
Arizona State University  
rarodger@asu.edu, aaron.packer@asu.edu

Yang Kuang  
Arizona State University  
School of Mathematical and Statistical Sciences  
kuang@asu.edu

## CP1

### **Variance Reduced Model for Tumor Growth**

One of the major challenges when using individual-based models for tumor growth is to reduce the computational cost. We consider an individual-based model for tumor growth, which is continuous in space and time and coupled with a set of reaction diffusion equations to model the environment. We propose a novel variance reduction scheme to reduce the computational cost, based on a control variate that is obtained from a kinetic description.

Annelies Lejon  
KU Leuven  
Dept. Computer Science  
annelies.lejon@cs.kuleuven.be

Giovanni Samaey  
Department of Computer Science, K. U. Leuven  
giovanni.samaey@cs.kuleuven.be

Dirk Roose  
KU Leuven  
Dept. of Computer Science  
Dirk.Roose@cs.kuleuven.be

## CP1

### **On the Accumulation of Mutations in Cancer**

In this work we consider the problem of modeling the stochastic accumulation of somatic mutations in cancer. The integration of mathematical modeling and statistical analysis with sequencing and clinical data represents a new powerful approach for better understanding the evolutionary dynamics of cancer, and for implementing quantitative approaches to cancer classification and treatment. By considering, for the first time, all relevant phases of a tissues history - the model makes unexpected predictions, validated by the analysis of sequencing data: what is the number of somatic mutations that occur prior to the onset of neoplasia? How many rate-limiting mutations are needed for cancer to occur? The talk is partially based on: Tomasetti C, Vogelstein B, Parmigiani G. Half or more of the somatic mutations in cancers of self-renewing tissues originate prior to tumor initiation. Proc Natl Acad Sci USA 2013, 110(6):1999-2004.

Cristian Tomasetti  
Johns Hopkins University  
ctomase2@jhu.edu

## CP2

### **A Simple Model Incorporating Demographic and Epidemiological Processes in a Spatially Heterogeneous**

In this talk, we explore an epidemic model incorporating demographic processes in a spatially heterogeneous environment in which the individuals are subject to a random movement. Our analytical and numerical results reveal that the persistence of the population and disease outbreak be ignited by both individuals mobility and environmental heterogeneity.

Yongli Cai  
Department of Mathematics  
Sun Yat-Sen University  
caiyongli06@163.com

Shangbin Cui  
Department of Mathematics, Sun Yat-Sen University  
cuishb3@yahoo.com.cn

Weiming Wang  
College of Mathematics and Information Science  
Wenzhou University, Wenzhou, 325035 P.R.China  
weimingwang2003@163.com

## CP2

### **An SIRS Epidemic Model with Non-Exponential Probability for Temporary Immunity**

We consider an SIRS model for disease dynamics that accounts for temporary immunity whereby recovered individuals return to the susceptible class. We allow for a general

probability function of remaining immune such that the model is a system of integro-differential equations (IDE). We show how the IDEs can be approximated by a system of delay-differential equations. We then show that different probabilities, whose parameters have been chosen such that they have equal moments, generate equivalent dynamical output. For the case of a linear function we can derive bifurcation equations that determine how the moments affect the intensity and duration of epidemics.

Thomas W. Carr  
Southern Methodist University  
Department of Mathematics  
tcarr@smu.edu

### CP3

#### Comparison of a Deterministic and Stochastic Model for the Transmission Dynamics of Influenza

We consider an extension of the SEIR model for the transmission dynamics of influenza. We describe two stages of the infection, an early and a late stage, in the later stage the infected may or may not take medicine, in addition a fraction from both these groups may be hospitalized. We perform rigorous analysis of the system. It is shown that for the basic reproductive number  $R_0$  the disease free equilibrium is stable and the system has an endemic equilibrium for  $R_0$ . We next consider an analogous Continuous Time Markov Chain (CTMC) based model. Numerical simulations are used to estimate the mean, variance and probability distributions for the various states and are compared to the steady state solutions of the deterministic model. The expected time to extinction in the CTMC model is also estimated.

Adnan Khan  
Lahore Univeristy of Management Sciences  
Department of Mathematics  
adnan.khan@lums.edu.pk

### CP3

#### A Mixed-Strategy Game Theoretical Approach for Infectious Disease Prevention by Social Distancing

We describe a population game in which individuals are allowed to decide between adopting different social distancing strategies in order to lower infection risk and maximize payoffs. When the reduction in infection risk is a convex function of the cost of social-distancing, there is a unique pure-strategy game equilibrium. When the reduction in infection risk is not convex, the existence of equilibria becomes more complicated. We will discuss three cases vis--vis different costs of infection.

Jing Li, Timothy Reluga  
Pennsylvanian State University  
jing.li@csun.edu, treluga@math.psu.edu

### CP3

#### Abms for Infectious Diseases Spreading and Ill-Posed Problems

Usually rules and behavior of agents in ABMs are not known exactly. In the general case a problem of ABMs parameters evaluation is so called ill-posed one and therefore it can have no unique solution for available data describing emergent patterns under consideration or can have unique but unstable solution with respect to small changes

of these data. In my talk I will illustrate that for a model of influenza epidemic spreading in a city.

Valeriy D. Perminov  
BioTeckFarm Ltd.  
vdperm@yandex.ru

### CP3

#### Analysis of Labour Productivity in the Presence of Substance Abuse

Substance abuse impedes the productivity of employees and reduces economic growth. Efficient management of an organizations workforce must involve eradicating drug use. In this paper, we formulate and analyse a mathematical model for labour productivity in the presence of substance abuse transmission dynamics that includes intervention strategies. We investigate the existence and stability of equilibria and use Pontryagin's Maximum Principle to derive necessary conditions for the optimal control of the disease. Numerical simulations are performed to illustrate the analytical results.

Isaac Takaidza  
Vaal University of Technology  
isaact@vut.ac.za

### CP4

#### Nonlinear Stochastic Dynamics of Sensory Hair Cells

Hair cells are mechano-receptors in vertebrate senses of hearing and balance. In lower vertebrates sensory hair cell exhibits spontaneous oscillations of hair bundle and membrane potential. We use modelling to study how mechanical and electrical oscillations emerge, interact and contribute to the overall sensitivity and selectivity of the hair cell. We show that oscillatory regimes result in enhanced sensitivity to harmonic stimuli. Irregular spontaneous dynamics is best suited for sensing broad-band slowly changing external stimuli.

Rami M. Amro, Alexander Neiman  
Department of Physics and Astronomy  
Ohio University  
ra150909@ohio.edu, neimana@ohio.edu

### CP4

#### Large Deviations of An Ergodic System of Hebbian Neurons

We investigate finite-size effects in a system of neurons interacting ergodically. Our model consists of  $N$  Hodgkin-Huxley neurons, with external noise. The noise is correlated in an ergodic manner, meaning that its probability law is invariant under a uniform translation of the neurons. We asymptote  $N$  to infinity and apply the theory of Large Deviations to determine in which direction the system is most likely to deviate from its limit equation.

James Maclaurin  
INRIA SOPHIA ANTIPOLIS  
james.maclaurin@inria.fr

Olivier Faugeras  
INRIA Sophia-Antipolis

olivier.faugeras@inria.fr

#### CP4

##### Fast-Slow Analysis of Neural Excitability with Synaptic Noise

By considering a stochastic Morris-Lecar model with the inclusion of synaptic noise, we study neural excitability using a systematic perturbation analysis. In this presentation, I will talk about our understanding and findings of synaptic noise on neural excitability.

Xueying Wang  
Washington State University  
xueying@math.tamu.edu

James P. Keener  
University of Utah  
keener@math.utah.edu

#### CP5

##### A Fractional Order Model of Electroporation

Electro-chemotherapy and gene electro-transfer have recently emerged as promising new cancer therapies that use locally applied electric fields to facilitate the transport of either chemotherapeutic drugs or genes into tumor cells using the cell membrane electroporation. The continuous evolving microstructure of tissues and tumors affect the distribution of the applied electric field. To account for such complex and mostly unknown dynamics, we propose a novel fractional order model for the local electric field distribution.

Md Mehedi M. Hasan  
The Pennsylvania State University  
mzh204@psu.edu

Corina Drapaca  
Department of Engineering Science and Mechanics  
Pennsylvania State University  
csd12@psu.edu

#### CP5

##### Parameter Inference Using Variance Fitting for Markov Models of Voltage Gated Ion Channels

Voltage gated ion channels play a central role in neuronal and electric signaling and are experimentally studied by the voltage clamp technique with single channel or whole cell current recordings. In this talk we address the inverse problem of identifying rate parameters in Markov chain models that describe the transition between the conformational states the channel can sojourn in. Assuming that single channel data from repeated observations is available we utilize model predictions of the current variance and directly compare it with the sample variance derived from the data. Cost functions that account for variance fitting may feature landscapes in the parameter space with more pronounced curvatures than mean based approaches such that parameter unidentifiability or model ambiguity may be weakened or even overcome.

Philipp Kuegler  
RICAM, Austrian Academy of Sciences  
Austria

philipp.kuegler@uni-hohenheim.de

#### CP5

##### Compatibility of Slender Bodies and Surface Traction at Low Reynolds Number

The past forty years have witnessed an ever-increasing interest in applications of slender-body dynamics (such as Kirchhoff rod theory), in particular with regard to the shape, movement, or material parameters of biomolecules or materials. In most applications, hydrodynamic interactions (i.e. surface traction often approximated by resistive force theory) have been of utmost importance since the biologically relevant scales usually result in very small Reynolds number. However, the formulation of classical Kirchhoff slender-body assumes no surface traction in the development of the constitutive relation. We will discuss an asymptotic approach to reconciling this apparent inconsistency and provide velocity bounds for which the compatibility of Kirchhoff rod and resistive force theory hold.

Eva M. Strawbridge  
University of Chicago  
Department of Mathematics  
strawbem@jmu.edu

Eva M. Strawbridge  
James Madison University  
Department of Mathematics and Statistics  
strawbem@jmu.edu

Charles Wolgemuth  
University of Arizona  
Department of Physics  
wolg@email.arizona.edu

#### CP6

##### Sensitivity Analysis and Treatment of Hepatitis C Virus Infection

The interplay between two types of immune responses, antibodies and CTL cells, is explored in the context of hepatitis C virus (HCV) infection. The competition for HCV is explored with sensitivity analyses, considered under three main steady states: co-existence, dominant CTL response, and dominant antibody response. Sensitivity functions allow temporal ranking of parameters, in relation to their degree of influence in viral load. Comparisons between steady states with and without treatment are discussed.

Ariel Cintron-Arias  
Department of Mathematics and Statistics  
East Tennessee State University  
cintronaarias@etsu.edu

#### CP6

##### The Effect of Systemic Estrogen and Cortisol on the Inflammatory Phase of Wound Healing

A complex combination of interactions initiates and regulate the inflammatory phase of the wound healing response. Many chronic wounds arise due to an improper transition out of this phase. To understand regulation of this transition, we developed a model for key inflammatory cells during wound healing that accounts for the effects of cortisol and estrogen. Latin Hypercube sampling was performed to determine feasible parameters for the model. Experimental

data was used to validate this model.

Angela M. Reynolds  
Department of Mathematics and Applied Mathematics  
Virginia Commonwealth University (VCU)  
areynolds2@vcu.edu

Racheal Cooper  
Virginia Commonwealth University  
cooperrl2@vcu.edu

Rebecca Segal  
Virginia Commonwealth University  
Department of Mathematics and Applied Mathematics  
rasegal@vcu.edu

Robert Diegelmann  
Virginia Commonwealth University  
rdieglm@vcu.edu

## CP6

### Modeling Effects of Drugs of Abuse on Hiv-1 Dynamics

Complications of HIV-1 infection with simultaneous drugs of abuse are an emergent problem. I will present a within-host viral dynamics model that incorporates effects of drugs of abuse on HIV-1 infection. Our model agrees well with experimental data from Simian Immunodeficiency Virus infections in morphine-addicted macaques (animal model of HIV). I will discuss how our model helps evaluate morphine-induced alterations in viral dynamics, steady state viral load, and basic reproduction number.

Naveen K. Vaidya  
Dept of Applied Maths, University of Western Ontario  
London, Ontario, Canada  
vaidyan@umkc.edu

## CP6

### The Role of Interleukin-2 in Immune Response Regulation

The immune system has many adaptive and dynamic components that are delicately regulated to ensure appropriate, precise, and rapid response to a pathogen. Inadequate immune response can lead to prolonged disease, while an excessive or under-regulated response can lead to autoimmunity. We are interested in the role cytokines play in maintaining this balance. Through the use of mathematical models, we attempt to understand cytokine signaling including problems leading to autoimmunity and MS treatment by Daclizumab.

Ryan S. Waters  
Department of Mathematical Sciences  
Montana State University  
waters@math.montana.edu

Tomas Gedeon  
Montana State University  
Dept of Mathematical Sciences  
gedeon@math.montana.edu

## CP7

### Simulation-Based Simplification of Non-Linear

## Feed-Forward Models

Mechanistic modeling of signaling or metabolic pathways is highly valuable for understanding and predicting basic biology, disease, and therapy. However, due to the complexity of biological systems it is necessary to make simplifying assumptions to reduce the degrees of freedom of any model. Here we demonstrate in a simple, yet biologically relevant, case an approach using simulation and data to simplify non-linear feed-forward models. We apply this to a model of hepatic de novo-lipogenesis.

Richard Allen  
University of North Carolina, Chapel Hill  
richard.allen@pfizer.com

Cynthia Musante  
Pfizer, Inc  
cynthia.j.musante@pfizer.com

## CP7

### Spatial Uniformity of Solutions of Reaction-Diffusion Pde's

Motivated by the question of pattern formation, we study the behavior of the solutions of reaction-diffusion PDE's. Applying some techniques from modern functional analysis, such as logarithmic Lipschitz constants and logarithmic norms, we provide conditions for global convergence to uniform solutions. We then illustrate the result by a simple biomolecular model.

Zahra Aminzare, Eduardo Sontag  
Rutgers University  
aminzare@math.rutgers.edu, sontag@gmail.com

## CP7

### Scale-Invariant Sensing of Singularly Perturbed Biomolecular Models

Feedforward motifs such as a simple incoherent feedforward loop have been the subject of extensive research in systems biology, and they are inherent in cellular systems ranging from bacteria to mammalian cells. Additionally, it was observed that multiple time scales are typically inherent in such motifs. Experimentally, it has been shown that certain incoherent feedforward molecular circuits can (approximately) exhibit a scale invariance property, namely, scale invariance of the complete output trajectory with respect to a rescaling of input magnitudes. Even though they may not exhibit the perfect scale invariance property, such circuits can often possess an approximate scale invariance property, and we study conditions under which systems with different time scales can possess the approximate scale invariance property, estimate the accuracy with which this property can be established, and illustrate our theoretical predictions on three examples.

Maja Skataric  
Graduate Student  
skataric@eden.rutgers.edu

Evgeni Nikolaev, Eduardo Sontag  
Rutgers University  
evgeni@math.rutgers.edu, sontag@math.rutgers.edu

## CP7

### On the Perfect Reconstruction of the Topology of

## Gene Regulatory Networks

The network inference problem consists in reconstructing the topology or wiring diagram of a dynamic network from data. Solving this problem is specially important for gene regulatory networks, because in many cases regulation mechanisms are unknown or cannot be detected directly. Even though this problem has been studied in the past, there is no algorithm that guarantees perfect reconstruction of the topology of a dynamic network. In this talk we will present a framework and algorithm to solve the network inference problem for discrete networks that, given enough data, is guaranteed to reconstruct the topology of a dynamic network perfectly. The framework uses tools from algebraic geometry.

Alan Veliz-Cuba  
University of Houston  
Rice University  
alanavc@math.uh.edu

## CP8

### Mutational History Dominates Clonal Selection Within Evolving Tumors

Natural selection acting on clonal diversity within tumors is thought to drive tumor progression, but details remain obscure. Evolutionary mathematical models of the angiogenic switch predict the emergence of hypovascular necrosis caused by hypertumors—“cheating” clones that free-ride on vasculature organized by cooperative clones. Here we show that hypertumors should rarely evolve because the deterministic evolutionary trajectory is overwhelmed by stochastic mutational history. These results highlight mutation pressure as a significant evolutionary force in cancer.

Scott T. Bickel  
Arizona State University  
Scottsdale Community College  
bickel777@gmail.com

Joseph Juliano  
Arizona State University  
joejuliano22@gmail.com

John D. Nagy  
Scottsdale Community College  
Arizona State University  
john.nagy@scottsdalecc.edu

## CP8

### Stationary Stability for Evolutionary Dynamics in Finite Populations

We extend the theory of evolutionary stability to multidimensional finite populations with mutation, connecting the theory of the stationary distribution of the Moran process with the Lyapunov theory of evolutionary stability for the replicator dynamic. We show essentially that the local extrema of the stationary distribution minimize the relative entropy of the current population state and the “expected next state” computed by weighting the adjacent states by the appropriate transition probabilities. This holds for a variety of selection processes including the increasingly popular Fermi selection. We present several complete computational examples for illustration and we show that the classical stability theory of the replicator dynamic is recovered in the large population limit. If time allows, we

describe extensions to populations evolving on graphs.

Dashiell Fryer  
Pomona College  
Dashiell.Fryer@Pomona.edu

Marc Harper  
UCLA  
marcharper@ucla.edu

## CP8

### Linear Algebra of the Quasispecies Model

Eigen’s quasispecies model is a famous ‘almost linear’ system of ODEs, for analysis of which intricate methods of classical and quantum mechanics, statistical physics, and elaborate numerical algorithms were applied. In a nutshell, the analysis boils down to studying the leading eigenvalue and the corresponding eigenvector of the matrix describing mutation–selection process. Our approach to this problem is to use the methods of linear algebra. Using the fact that the mutation matrix has a special form, a change of the basis is suggested such that in new coordinates a number of exact results can be obtained.

Artem S. Novozhilov  
North Dakota State University  
artem.novozhilov@ndsu.edu

Alexander Bratus  
Lomonosov Moscow State University  
alexander.bratus@yandex.ru

Yuri Semenov  
Moscow State University of Railway Engineering  
yuri\_semenoff@mail.ru

## CP8

### Species coexistence under eco-evolutionary dynamics

Ecological mechanisms for coexistence of interacting species have been studied extensively. In light of recent evidence that feedbacks between ecological and evolutionary processes are more common and substantial than originally thought, we examine how these feedbacks mediate coexistence in a three-species interaction. We model these processes using a Lotka-Volterra and quantitative genetics framework and use singular perturbation theory to analyze coexistence for this model.

Swati Patel  
Department of Mathematics  
University of California Davis  
swati@math.ucdavis.edu

Sebastian Schreiber  
University of California, Davis  
sschreiber@ucdavis.edu

## CP9

### Pest Persistence and Eradication in a Deterministic Model for Sterile Insect Release

The release of sterile insects is an environment friendly pest control method used in integrated pest management programs. New deterministic population models that include sterile male release are derived and explored numerically.

The differential equations account separately the effects of mating failure due to sterile release and the frequency of mating encounters. When insects spatial spread is incorporated through diffusion terms, computations reveal the possibility of steady pest persistence in finite size patches.

Luis Gordillo  
Utah State University  
luis.gordillo@usu.edu

#### CP9

##### **Quantifying the Relationships among Natural Selection, Mutation, and Stochastic Drift in Multidimensional Finite Populations**

The interrelationships of the fundamental biological processes natural selection, mutation, and stochastic drift are quantified by the entropy rate of Moran processes with mutation, measuring the long-run variation of a Markov process. The entropy rate is shown to behave intuitively with respect to evolutionary parameters such as monotonicity with respect to mutation probability (for the neutral landscape), relative fitness, and strength of selection.

Marc Harper  
UCLA  
marc.harper@gmail.com

#### CP9

##### **The Information Player: a Novel Strategy That Dominates Zero Determinant and Other Known Strategies in Multiplayer Evolutionary Games**

We present a long-history strategy capable of quickly inferring opponent strategies and building coalitions in population games using statistical inference and machine learning techniques. These "information players" very effectively invade existing strategies including tit-for-tat, win-stay-lose-shift, and zero determinant strategies, and conversely block invasion by these strategies, even in the presence of substantial ambient noise (errors in play). Crucially, information players initially seek not to maximize their *score*, but rather their *information* about the opponent's strategy.

Christopher Lee  
Depts. of Chemistry & Biochemistry, and Computer Science  
University of California, Los Angeles  
leec@chem.ucla.edu

Marc Harper  
Institute for Genomics & Proteomics  
UCLA  
marcharper@gmail.com

Dashiell Fryer  
Pomona College  
Dashiell.Fryer@Pomona.edu

#### CP9

##### **Quantifying the Impact of the Recent Invasive Species, *Pomacea insularum***

*Pomacea insularum*, or applesnail, is a relatively new species to the Gulf Coast region and threatens local sugar and rice crops, due to their relatively low predation rates at high sizes and seemingly fast population growth, result-

ing in significant vegetation consumption. In collaboration with the National Wetlands Research Center, we present the estimation of vital rates in a size-structured mathematical model from a population observed in a laboratory setting. We compare these results and estimates of population sizes and growth dynamics with the calibrated model to preliminary field data, highlighting necessary modifications necessary to adapt the model to this natural setting, such as the incorporation of predation. We discuss the possible impact of this species and potential for its control.

Lihong Zhao  
Mathematics Department  
University of Louisiana at Lafayette  
lxz6134@louisiana.edu

#### CP10

##### **Bursting in Networks of Integrate and Fire Neurons**

We use mean field analysis to study bursting in networks of identical, pulse-coupled neurons. The individual neurons are represented using a class of two-dimensional integrate and fire model. The mean field model is a system of switching ordinary differential equations and the transition to bursting involves both standard and nonsmooth bifurcations. The results of the mean field analysis are compared with numerical simulations of large networks.

Sue Ann Campbell  
University of Waterloo  
Dept of Applied Mathematics  
sacampbell@uwaterloo.ca

Wilten Nicola  
University of Waterloo  
wnicola@uwaterloo.ca

#### CP10

##### **Robust Design of Polyrhythmic Neural Circuits**

Neural circuit motifs showing multiple coexistent rhythms are building blocks of neural networks. We study robustness of such circuitry to sustain rhythms by revealing statistics of their switches due to random perturbations. We find a threshold of coupling strength beyond which accidental switching between rhythms occurs frequently. We elucidate mechanisms underlying this stochastic arrhythmia, and show how the type of coupling enhance rhythm robustness. Our findings are applicable to a broad class of oscillator systems.

Justus T. Schwabedal  
Division of Sleep Medicine, Brigham & Women's Hospital  
Harvard Medical School  
jschwabedal@gmail.com

Alexander Neiman  
Department of Physics and Astronomy  
Ohio University  
neimana@ohio.edu

Andrey Shilnikov  
Neuroscience Institute and Department of Mathematics  
Georgia State University

ashilnikov@gsu.edu

## CP10

### Characterization of Transient and Spatially Distributed High-Frequency Oscillations in the Brain with Quasi-Periodic Time Scales

Spatially distributed neural oscillations with characteristic frequencies  $\geq 80$  Hz have recently been identified in non-invasive electroencephalograms. These high-frequency oscillations (HFO) are transient and are thought to be modulated by abnormal and dynamic neurophysiological processes. In continuous multi-day recordings, it is possible to estimate HFO dynamics and their corresponding time scales. In this study we show that transient HFO dynamics have quasi-periodic time scales, with periods of occurrence that are modulated by relatively rare electrophysiological events.

Catherine Stamoulis

Massachusetts Institute of Technology  
Department of Ocean Engineering  
caterina.stamoulis@childrens.harvard.edu

Bernard Chang

Harvard Medical School, Beth Israel Deaconess Medical Center  
Department of Neurology  
bchang@bidmc.harvard.edu

## CP10

### Relating Spiking Neural Network to Partial Differential Equations

In this talk we show that a spiking neural network without the constraint of symmetry can be approximated by the FitzHugh-Nagumo equations. The well-known FitzHugh-Nagumo equations are much easier to analyze than an enormous system of differential equations, describing the activity of each spiking neuron.

Li Yang

Inria at Sophia-Antipolis, France  
li.yang@inria.fr

Olivier Faugeras, Pierre Kornprobst

INRIA Sophia-Antipolis  
olivier.faugeras@inria.fr, pierre.kornprobst@inria.fr

## CP11

### Fractional Model for Neurovascular Coupling

Functional magnetic resonance imaging (fMRI) is an indirect measure of brain activity. To describe the chain from neural activity to the measured fMRI signal namely the Blood Oxygen Level Dependent (BOLD) signal, we propose to use a system of fractional differential equation inspired from the dynamical Balloon Model [K. J. Friston et al, 2000. Nonlinear responses in fMRI: the Balloon model, Volterra kernels, and other hemodynamics. NeuroImage 12, 466-477]. We show that thanks to its non-locality and memory properties, fractional derivatives constitute a powerful tool for the neurovascular coupling.

Zehor Belkhatir

Computer, Electrical and Mathematical Sciences and Engineering, KAUST  
zehor.belkhatir@kaust.edu.sa

Taous-Meriem Laleg

INRIA Rocquencourt  
Taous-Meriem.Laleg@inria.fr

## CP11

### Glucose and Temperature Compensation in the Neurospora Circadian Clock: Mathematical Modeling and Experimental Validation

Circadian rhythms play a vital role in an organisms functions anticipating daily changes in its environment. The period of circadian oscillator is relatively insensitive to changes in physiological temperature and nutrients (e.g. glucose), which are referred to as temperature and glucose compensation, respectively. In this study, we constructed a mathematical model of the Neurospora circadian clock, and investigated molecular mechanisms of glucose and temperature compensation. Our model shows that temperature compensation is achieved by an intricate balance of synthesis and degradation of FRQ and WC-1. We experimentally validated loss of glucose compensation in wc-1 overexpression mutant and maintenance of nuclear abundance of FRQ as predicted in the model.

Andrey A. Dovzhenok

University of Cincinnati  
Department of Mathematical Sciences  
dovzheay@ucmail.uc.edu

Mokryun Baek

University of Cincinnati College of Medicine  
Department of Molecular and Cellular Physiology  
baekmn@ucmail.uc.edu

Arun Mehra

Geisel School of Medicine at Dartmouth  
Department of Genetics  
n/a

Jennifer Loros

Geisel School of Medicine at Dartmouth  
Department of Biochemistry  
jennifer.loros@dartmouth.edu

Jay Dunlap

Geisel School of Medicine at Dartmouth  
Department of Genetics  
jay.c.dunlap@dartmouth.edu

Sookkyung Lim

University of Cincinnati  
Department of Mathematical Sciences  
limsg@ucmail.uc.edu

Christian Hong

University of Cincinnati College of Medicine  
Department of Molecular and Cellular Physiology  
hongca@ucmail.uc.edu

## CP11

### Molecular Mechanisms That Regulate the Coupled Period of the Mammalian Circadian Clock

In the mammalian circadian clock, intercellular coupling synchronizes rhythms with the period close to the population mean of individual periods. With the theory of weekly coupled oscillators, we found that the coupled period stays near the population mean if transcriptional repression oc-

curs with piecewise-linear protein sequestration, but not highly non-linear Hill-type regulation in individual cells. This shows that the behavior of coupled oscillator with the same topology changes depending on the mechanisms underlying individual oscillator.

Jae Kyoung Kim  
Department of Mathematics  
University of Michigan, Ann Arbor, Michigan 48109, USA  
kim.5052@mbi.osu.edu

Zachary Kilpatrick  
University of Houston  
zpkilpat@math.uh.edu

Matthew Bennett  
Department of Biochemistry & Cell Biology, Rice  
University  
matthew.bennett@rice.edu

Kreimir Josic  
Department of Mathematics, University of Houston  
josic@math.uh.edu

## CP11

### In Vivo Volume and Hemoglobin Dynamics in Red Blood Cells

Human red blood cells (RBCs) lose  $\sim 30\%$  of their volume and  $\sim 20\%$  of their protein during their  $\sim 100$ -day lifespan in the bloodstream. We use measurements of RBC size and protein concentration to derive a model for the physical processes controlling RBC volume and hemoglobin. We show that common models of vesicle shedding alone are sufficient to explain surface area lost but insufficient to explain the lost volume and hemoglobin mass. We use single-cell measurements of human RBCs to validate the models and to define requirements for alternative explanations.

Roy Malka  
Systems Biology, Harvard Medical School  
Center for Systems Biology, Massachusetts General  
Hospital  
Roy.Malka@hms.harvard.edu

## CP12

### Unravelling the Impact of Obstacles in Diffusion and Kinetics of An Enzyme Catalysed Reaction

We develop a two-dimensional lattice-based Monte Carlo simulation to model enzyme-catalyzed reactions in diffusion-limited conditions to investigate effects of obstacle density and size on reactant diffusion and rate coefficients. Our results show that these factors affect first- and second-order rates. We also find that particle rotations and weak force interactions affect rate coefficients. Our simulations suggest that the anomalous kinetic observed in cellular crowded environments can appear in less restricted conditions than previously reported.

Marcio Duarte Albasini Mourao  
Mathematical Biosciences Institute  
The Ohio State University  
albasinimourao.1@mbi.osu.edu

Doree Kreitmann, Santiago Schnell  
University of Michigan

doreek@umich.edu, schnells@umich.edu

## CP12

### Mathematical Modeling of the Hypothalamic-Pituitary-Adrenal Axis in Relation to Major Depression

Both circadian and ultradian oscillations are seen in the levels of the hormones of the Hypothalamic-Pituitary-Adrenal axis, including cortisol. With a model consisting of non-linear ordinary differential equations, we investigate enzyme reactions taking place inside the cortisol-producing adrenal cortex cell to see, whether the presence of potential Goldbeter-Koshland switches is instrumental in generating the ultradian oscillations. The performances in model reduction of the standard quasi-steady-state approximation (sQSSA) and the total QSSA are compared.

Johanne Gudmand-Høyer  
Roskilde University  
joguho@ruc.dk

Johnny T. Ottesen  
Roskilde University  
Department of Mathematics  
johnny@ruc.dk

## CP12

### Modeling the Spatio-Temporal Dynamics of Small Gtpase Activity at Dendritic Spines

Signaling through small GTPases at dendritic spines is crucial for synaptic plasticity, a cellular correlate for learning and memory. We implement a computational method in order to model the spatio-temporal dynamics of GTPase activity accounting explicitly for the spine geometry. A question that motivates our research is how does the activity of the GTPase Cdc42 localize persistently to spine membranes despite its rapid lateral diffusion.

Samuel A. Ramirez  
Duke University  
samurami@gmail.com

Sridhar Ragavachari  
Duke University Medical Center  
raghavachari@neuro.duke.edu

## CP12

### In Vitro Assay Geometry Affects Estimates of the Cell Diffusivity and Cell Proliferation Rate

Cells respond to biochemical and physical cues during wound-healing and tumour progression. *In vitro* assays used to study these processes are typically conducted in one geometry. In this work, we investigate the capacity of cell populations to spread in two different *in vitro* assay geometries by comparing estimates of the effective cell diffusivity and effective cell proliferation rate.

Katrina Treloar, Matthew Simpson  
Queensland University of Technology  
k.treloar@qut.edu.au, matthew.simpson@qut.edu.au

Sean McElwain  
School of Mathematical Sciences  
Queensland University of Technology  
s.mcelwain@qut.edu.au

Ruth E. Baker  
Centre for Mathematical Biology  
University of Oxford  
ruth.baker@maths.ox.ac.uk

### CP13

#### A Continuous Model of Ant Foraging with Pheromones and Trail Formation

We propose and numerically analyze a PDE model of ant foraging behavior. Ant foraging is among the most interesting behaviors in the animal kingdom, and a prime example of individuals following simple behavioral rules based on local information producing complex, organized and “intelligent” strategies at the population level. One of its main aspects is the widespread use of pheromones, which are chemical compounds laid by the ants used to attract other ants to a food source. We consider a continuous description of a population of ants and simulate numerically the foraging behavior using a system of PDEs of chemotaxis type. We show that, numerically, this system accurately reproduces observed foraging behavior, such as trail formation, optimization of routes, and efficient removal of food sources. Furthermore, we present a preliminary mathematical analysis of a simplified version of the model.

Paulo V. Amorim  
Instituto de Matemática  
Universidade Federal do Rio de Janeiro  
paulo@im.ufrj.br

### CP13

#### Using Homogenization to Estimate Random-Walk Motility from Gps Collar Data in Variable Landscapes

We compute the probability of an animal passing through various habitat patches between known GPS collar locations using solutions of a homogenized ecological diffusion model. From these probabilities we can obtain the time an animal spends in a particular habitat type to use in estimating motility coefficients. We apply this method to parameterize a model of the spread of chronic wasting disease in mule deer in Utah.

Martha J. Garlick  
Dept. of Mathematics and Statistics  
Utah State University  
martha.garlick@sdsmt.edu

James Powell, Luis Gordillo  
Utah State University  
jim.powell@usu.edu, luis.gordillo@usu.edu

### CP13

#### Respect Versus Disrespect for Ownership: An Iterated Hawk-Dove Game with Relocation Costs

The classic Hawk-Dove game predicts that when “Bourgeois” respect for ownership arises as a pure convention, so does “anti-Bourgeois” disrespect. Why is the former so common in nature, the latter so rare? An iterated model can yield stable strategy mixtures with any degree of partial respect between 0 and 1. This poster describes how their basins of attraction depend on both the relocation costs of “infinite regress” and the probability of further

interaction.

Tugba Karabiyik  
Florida State University  
tugbakarabiyik1@gmail.com

### CP13

#### The Dynamics of Foraging Activity in Harvester Ants

Collective foraging is ubiquitous in social animals. Its utility is largely dependent on the efficient use of social information to communicate changes in environmental profitability and coordinate the actions of individual group members. Here, we develop a simple compartmental model of foraging activity in harvester ant colonies based on non-spatial, interaction-mediated worker recruitment. Our analysis indicate that adaptive changes in worker availability relative to the frequency of contacts with successful foragers can allow colonies to sustain activity when worker activation rates are low. Simulated forager removals exploring the effects of short-term reductions in forager return rates (e.g. due to elevated predation on the trail) show good fits with empirical data. We discuss the biological interpretation of our results and motivate further improvements to the model.

Oyita Udiani  
Applied Mathematics for the Life & Social Sciences  
College of Liberal Arts and Sciences ASU  
oyita.udiani@asu.edu

### CP14

#### Analyzing the Effects of a Non-Host Worm Population on the Spread of Whirling Disease in Trout

We present a mathematical model of the Host/Parasite system describing the *Myxobolus Cerebralis* parasite and the *Tubifex* worms that cause Whirling Disease in trout. A Non-Host worm is incorporated which competes with the Host producing a negative effect but also eliminates the parasite spores causing a positive, indirect effect. System dynamics, parameters and bifurcation analysis will be discussed.

Tamra Heberling, Lisa G. Davis, Ryan Lamb, Billie Karens  
Montana State University  
heberling.t@gmail.com, davis@math.montana.edu,  
ryan.lamb2@gmail.com, bkarens@exchange.montana.edu

### CP14

#### The Virus of My Virus Is My Friend: Modeling the Ecological Effect of Virophages

Virophages are viruses that rely on the replication machinery of other viruses for reproduction. We construct two mean field models of population dynamics between hosts, viruses and virophage to address how different modes of coinfection affect the ecological dynamics. We prove that virophage reduce the viral population and increase the host population at equilibrium. We also identify differences in the frequency and nature of coexistence within the two models.

Bradford Taylor  
Georgia Tech  
btaylor40@gatech.edu

Michael H. Cortez, Joshua Weitz  
Georgia Institute of Technology  
michael.cortez@biology.gatech.edu, jsweitz@gatech.edu

## MS1

### A Structured Model for the Transmission Dynamics of Mycobacterium Marinum Between Aquatic Animals

**Abstract:** Mycobacterium marinum (Mm), a genetically similar bacterium to Mycobacterium tuberculosis, affects a number of fish industries (fisheries, aquaculture, aquariums and research stocks) on a comparable scale to tuberculosis (TB) in humans. Because of this, and the practical advantages of working with animal models as opposed to humans, Mm infections in recently established fish models provide a unique opportunity for the study of mycobacterial infections. We derive a model of transmission dynamics of Mm in fish, which either involves consumption of an infected host or a source of bacteria to ensure activation into a highly infectious state. We derive a model of transmission within a food web, in which infected fish behavior is structured by infection severity. This is a key component as chronic (seemingly asymptomatic) infection is prominent in both fish and human TB. We develop a finite difference method to compute solutions of this model. We illustrate, via this numerical scheme, that this model can be used to reproduce experimental settings.

Azmy S. Ackleh  
Department of Mathematics  
University of Louisiana at Lafayette  
ackleh@louisiana.edu

## MS1

### Mathematics of Anti-Hpv Vaccines

Human papilloma virus (HPV) is a major sexually-transmitted disease that inflicts a significant public health burden globally. HPV causes various cancers and warts in females and males, notably cervical cancer in females (the second highest malignancy in women globally, accounting for over 250,000 deaths annually). The talk is based on the use of mathematical models to gain insight into the population-level impact of the two currently-available anti-HPV vaccines (Cervarix (by GlaxoSmithKline) and Gardasil (by Merck Inc.)).

Abba Gumel  
University of Manitoba  
Department of Mathematics  
gumelab@cc.umanitoba.ca

## MS1

### Transient Periodic Oscillations and the Dynamics of CTL Response to Viral Infections

Abstract not available at time of publication.

Michael Li  
University of Alberta  
mli@math.ualberta.ca

## MS1

### Modeling Avian Influenza and Implications for Control

A mathematical model of avian influenza which involves

human influenza is introduced to better understand the complex epidemiology of avian influenza. The model is used to rank the efficacy of the current control measures used to prevent the emergence of a pandemic strain. We find that culling without re-population and vaccination are the two most efficient control measures. Control measures applied to humans, such as wearing protective gear, are not very efficient. Furthermore, we find that should a pandemic strain emerge, it will invade, possibly displacing the human influenza virus in circulation at that time. Moreover, higher prevalence levels of human influenza will obstruct the invasion capabilities of the pandemic H5N1 strain. This effect is not very pronounced, as 1% increase in human influenza prevalence will decrease the invasion capabilities of the pandemic strain with 0.006%.

Maia Martcheva  
University of Florida  
maia@ufl.edu

## MS2

### Parameter Identifiability in Virus Infection Models

Confidence in the accuracy of estimated parameters is essential for the development of successful treatment protocols. Guidance when designing the experiment is needed for recovery of accurate parameters and identifiability. Noise associated with data collection affects that design. Here, we establish a computational method that investigates the effect of noise on the design of the experiment and the identifiability of parameters. Our method is applied to a model of hepatitis B infection.

Matthias Chung, Stanca Ciupe  
Virginia Tech  
mcchung@vt.edu, stanca@math.vt.edu

## MS2

### Early HIV Infection Predictions: Role of Viral Replication Errors

Less than 0.1% of circulating virus in any HIV+ individual is infectious. Non-infectious virus may arise from errors in viral replication or other processes; the specific mechanism does not affect deterministic modeling predictions. However, during the earliest stages of infection, viral loads are small and more appropriately modeled stochastically. We model viral dynamics using continuous-time branching processes to investigate how viral replication error assumptions change predictions on risk of infection and time to infection clearance/detection.

Jessica M. Conway  
Los Alamos National Laboratory  
conway@lanl.gov

Alan S. Perelson  
Theoretical Biology and Biophysics  
Los Alamos National Lab  
n/a

## MS2

### Coping with Model Uncertainty in the Analysis of Acute Hiv Infection Datasets

HIV datasets are sparse. For example, sampling occurs infrequently relative to the pace of the infection, sampled viral sequences are few in number or lack linkage informa-

tion, and data for the immune response is sparse relative to the complexity of the immune system. I will describe an approach for dealing with this uncertainty in the context of estimating CTL escape rates. CTLs are immune system cells that kill HIV infected cells depending on the viral genotype, thereby mediating selective pressure from which HIV escapes through mutation. Quantifying the rate of this escape is valuable in understanding the role of CTL response in HIV infection.

Sivan Leviyang  
Georgetown University  
sr286@georgetown.edu

## MS2

### Multi-Scale Modeling of Immune Response to Influenza Infection

Many systems in engineering and physics such as a rocket system can be represented by differential equations, which can be derived from well-established physics laws and theories. It is unclear whether the biological systems follow a mathematical representation such as differential equations. Fortunately, recent advances in cutting-edge biomedical technologies allow us to generate intensive high-throughput data to gain insights into biological systems. It is badly needed to develop mathematical models and statistical methods to test whether a biological system follows a mathematical representation based on experimental data. In this talk, I will present our recent work in developing statistical methods to identify high-dimensional ordinary differential equation (HD-ODE) models and solve the associated inverse problems for HD-ODE models in modeling immune responses to influenza infection. The time course high-throughput data from both mice and human experiments will be used to illustrate our methodologies.

Hulin Wu  
University of Rochester  
hulin.wu@urmc.rochester.edu

## MS3

### Mechanical Forces Drive Morphogenesis: How the Embryonic Brain Twists

The embryonic chick brain undergoes progressive, rightward torsion, one of the earliest organ-level symmetry-breaking events. Researchers speculated that heart looping affects the brain torsion direction, but direct evidence rarely exists. Our experiments show that the vitelline membrane exerts loads necessary for torsion and that direction of heart looping determines brain torsion direction. A computational model and a physical model are built to interpret these findings, together classifying mechanical origins of brain torsion.

Zi Chen  
Washington University  
Department of Bimedical Engineering  
chen.z@seas.wustl.edu

Qiaohang Guo  
Fuzhou University  
sheeptj@163.com

Eric Dai, Larry Taber  
Washington University

ericdai93@gmail.com, lat@wustl.edu

## MS3

### Bio-Mechanical Modeling of Tracheal Angioedema by Nonlinear Finite Elasticity

Tracheal angioedema refers to the rapid swelling of tracheal tissue by excess accumulation of fluid from vascular leakage, which can be life threatening if it narrows airway rapidly. We present a bio-mechanical analysis with a swelling dependent natural configuration to reflect the altered tissue volume increment under angioedema. Various localized swelling and far field boundary conditions are studied in order to assess how the interaction between swelling, anisotropy and large deformation affects airway constriction.

Kun Gou  
Texas A&M University  
Department of Mathematics  
kungoukevin@gmail.com

Thomas Pence  
Michigan State University  
Department of Mechanical Engineering  
pence@egr.msu.edu

## MS3

### A Continuum Mechanics Model of Stress Mediated Arterial Growth During Hypertension Using An Eulerian Frame.

In the classical approach to continuum mechanics, one assumes that a material body is deformed from a "stress free" reference configuration into a loaded current configuration. However, a reference configuration is merely a mathematical construct and cannot actually be determined, especially for dynamic physiological processes. We introduce a framework that is formulated entirely in the current configuration and test its effectiveness by showing how well it predicts arterial growth during instantaneous hypertension.

Maya E. Johnson  
Texas A&M University  
Dept. of Mathematics  
mayaj@math.tamu.edu

Jay R. Walton  
Department of Mathematics  
Texas A&M  
jwalton@math.tamu.edu

## MS3

### Estimating Residual Stresses in Soft Tissues by An Inverse Spectral Technique

A mathematical model is studied to estimate residual stresses in the arterial wall using intravascular ultrasound (IVUS) techniques. A BVP is formulated for the nonlinear, slightly compressible elastic wall, the boundary of which is subjected to a quasi-static blood pressure, and then an idealized model for IVUS is constructed by superimposing small amplitude time harmonic vibrations on large deformations. Using the classical theory of inverse Sturm-Liouville problems and optimization techniques, an inverse spectral algorithm is developed to approximate the residual stresses, given the first few eigenfrequencies of several

induced pressures.

Sunnie Joshi  
Temple University  
sjoshi@temple.edu

Jay R. Walton  
Department of Mathematics  
Texas A&M  
jwalton@math.tamu.edu

#### MS4

##### **Modeling the Melanopsin Phototransduction Cascade**

Melanopsin is a recently discovered photopigment found in intrinsically photosensitive retinal ganglion cells (ipRGCs) and is involved in non-image forming vision, such as circadian rhythm entrainment and the pupillary light reflex. We model the activation and inactivation of the melanopsin phototransduction cascade, and compare the model simulations to experimental data. The research was conducted by undergraduates at UMBC and funded by an NSF undergraduate training grant.

Kathleen A. Hoffman  
University of Maryland, Balt. Co.  
Department of Math. and Stat.  
khoffman@umbc.edu

#### MS4

##### **Collective Cell Migration: Modeling from Initiation to Destination**

Collective cell migration is critical in development and pathology. We consider the *Drosophila* ovary as an experimental system for transition to cell. We use a force balance dynamical system approach to capture cell adhesion, repulsion, chemotaxis, and stochastic motion in the migration. We show that basic forces in 3-dimensions can account for observed apparent rotation of the cluster, as well as reduced migration speed in mutants that reduce the number of migrating cells.

David Stonko  
UMBC  
dstonko1@umbc.edu

Bradford E. Percy  
Department of Mathematics and Statistics  
University of Maryland, Baltimore County  
bpercy@umbc.edu

Michelle Starz-Gaiano  
Dept. of Biological Sciences  
UMBC  
starz@umbc.edu

#### MS4

##### **Phototransduction in Melanopsin Expressing Retinal Ganglion Cells**

Intrinsically photosensitive retinal ganglion cells (ipRGCs) in the mammalian retina express the photopigment melanopsin and constitute a third class of photoreceptors. The ipRGCs contribute primarily to non-image forming vision and the melanopsin-based signaling cascade generates a depolarizing light response. Our goal is to characterize

the biochemical pathways that mediate the intrinsic light responses of ipRGCs and mediate its adaptation to light and dopamine.

Phyllis R. Robinson  
Dept. of Biological Sciences  
UMBC  
probinso@umbc.edu

#### MS4

##### **Genetic Regulation of Cell Motility**

Morphogens generate distinct cell fates by differences in concentrations. The release, diffusion, uptake, and decay rates of these molecules impact concentration and thereby cellular responses. We propose that the irregular domains of adjacent tissue also alter the local concentration. To examine this, we utilize the well-studied development of the *Drosophila* ovary. We are characterizing a genetic pathway that promotes cell motility in response to a morphogen and relate pathway activation to tissue architecture.

Michelle Starz-Gaiano  
Dept. of Biological Sciences  
UMBC  
starz@umbc.edu

Lathiena Manning  
UMBC Biological Sciences  
manning1@umbc.edu

#### MS5

##### **Marine Invertebrate Sperm Chemotaxis: Search Trajectories**

In marine invertebrate sperm, chemotaxis guides the sperm towards the egg. The chemoattractant causes changes in intracellular calcium, associated with changes in flagellar waveforms and curvature of path trajectories. We use a fluid-structure interaction model where the calcium concentration is coupled to the forces in the flagellum. Results will be presented to show how trajectories can be modulated by calcium parameters as well as elastic properties of the flagellum.

Sarah D. Olson  
Worcester Polytechnic Institute  
sdolson@wpi.edu

#### MS5

##### **Modeling Tumor and Microenvironment Interactions under Treatment: the Role of the Interstitial Fluid**

The interactions between tumor cells and their microenvironment are complex, and this complexity is leveraged when both tumor and stromal cells are exposed to anti-cancer therapeutic agents. We use fluid-structure interaction methods to systematically explore the role of the interstitial fluid flow and tumor tissue architecture on the extent of drug and biomarker molecule penetration into the tissue.

Katarzyna A. Rejniak  
Moffitt Cancer Research Center  
Integrated Mathematical Oncology

Kasia.Rejniak@moffitt.org

## MS5

### Sperm Altruism and Motility Near Surfaces

As mammalian sperm traverse the oviduct, they undergo significant changes in motility. During this process, sperm are known to bind to the oviductal epithelium and their ability to detach is dependent upon contractions that occur near the time of ovulation. Thus, the impact that surfaces and their motion have upon sperm fertility is significant. Using the method of regularized Stokeslets, we investigate surface interactions and sperm cooperativity to elucidate how epithelial detachment occurs.

Julie Simons, Lisa J. Fauci  
Tulane University  
Department of Mathematics  
jsimons@tulane.edu, fauci@tulane.edu

Ricardo Cortez  
Tulane University  
Mathematics Department  
rcortez@tulane.edu

## MS5

### Swimming Through Highly Heterogeneous, Viscoelastic Media

We present a simple model of a free microswimmer in a highly heterogeneous, viscoelastic medium. An effect of viscoelasticity is modeled by immersing viscoelastic structures into a viscous environment. Varying complexity of those structures allows medium to exhibit different viscoelastic properties. Several tests are performed showing that the model agrees with rheological properties of a medium. Regions of higher structural density can significantly affect a swimming pattern of a microorganism.

Jacek K. Wrobel  
Tulane University  
jwrobel@tulane.edu

Ricardo Cortez  
Tulane University  
Mathematics Department  
rcortez@tulane.edu

Lisa J. Fauci  
Tulane University  
Department of Mathematics  
fauci@tulane.edu

## MS6

### Novel Characterization of Brain Networks Through Low-Rank Network Decomposition

Small-world networks occur naturally throughout the brain on multiple scales. In this work, we develop a new formalism using a low-rank decomposition of network adjacency matrices to classify neuronal networks. This new procedure scales well with network size and connection density, yielding stable results independent of node indexing. We apply our methodology to recent experimental data on cerebral cortex connectivity, proposing such a network may be categorized into a broader class of networks than small-worlds.

Victor Barranca  
Rensselaer Polytechnic Institute  
barranca@nyu.edu

Douglas Zhou  
Shanghai Jiao Tong University  
zdz@sjtu.edu.cn

David Cai  
New York University  
Courant institute  
cai@cims.nyu.edu

## MS6

### Improved Estimation of Neural Correlations Suggests Detailed Interactions in Visual Cortex

How does connectivity impact network dynamics? We address this question by linking network characteristics on two scales. On the global scale we consider the coherence of overall network dynamics. We show that such global coherence in activity can often be predicted from the local structure of the network. To characterize local network structure we use motif cumulants, a measure of the deviation of pathway counts from those expected in a minimal probabilistic network model.

Kresimir Josic  
University of Houston  
Department of Mathematics  
josic@math.uh.edu

Yu Hu  
Department of Applied Mathematics  
University of Washington  
huyupku@gmail.com

James Trousdale  
University of Houston  
Department of Mathematics  
jrtrousd@math.uh.edu

Eric Shea-Brown  
Department of Applied Mathematics  
University of Washington  
etsb@amath.washington.edu

## MS6

### Sparsity and Compressed Coding in Sensory Systems

Considering many natural stimuli are sparse, can a sensory system evolve to take advantage of sparsity? We show significant downstream reductions in the numbers of neurons transmitting stimuli in early sensory pathways might be a consequence of sparsity. Our work points to a potential mechanism for transmitting stimuli related to compressed-sensing (CS) data acquisition. Through simulation, we examine the characteristics of networks that optimally encode sparsity and the role of receptive fields in stimulus sampling.

Gregor Kovacic  
Rensselaer Polytechnic Inst  
Dept of Mathematical Sciences  
kovacg@rpi.edu

Victor Barranca  
Rensselaer Polytechnic Institute  
barranca@nyu.edu

Douglas Zhou  
Shanghai Jiao Tong University  
zdz@sjtu.edu.cn

David Cai  
Courant Institute for Mathematical Sciences, NYU  
Shanghai Jiao-Tong University  
cai@cims.nyu.edu

## MS6

### Spatiotemporal Dynamics of Neuronal Population Response in the Primary Visual Cortex

We use a large-scale computational model of the primary visual cortex (V1) to study the population responses in V1 as observed in experiments in which monkeys performed visual detection tasks. Our model can well capture spatiotemporal activities measured by voltage-sensitive-dye-based optical imaging in V1. Our computational modeling approach allows us to reveal intrinsic cortical dynamics, separating it from those statistical effects arising from averaging procedures in experiment.

Douglas Zhou  
Shanghai Jiao Tong University  
zdz@sjtu.edu.cn

Aaditya Rangan, David McLaughlin  
Courant Institute of Mathematical Sciences  
New York University  
rangan@cims.nyu.edu, david.mclaughlin@nyu.edu

David Cai  
New York University  
Courant institute  
cai@cims.nyu.edu

## MS7

### Bayesian Support Vector Machines and Supervised Factor Modeling for General Omic Data

A new Bayesian formulation is developed for nonlinear support vector machines (SVMs), based on a Gaussian process and with the SVM hinge loss expressed as a scaled mixture of normals. We then integrate the Bayesian SVM into a factor model, in which feature learning and nonlinear classifier design are performed jointly. Inference is performed with expectation conditional maximization (ECM) and Markov Chain Monte Carlo (MCMC). An extensive set of experiments on multiple types of omics data demonstrate the utility of using a nonlinear Bayesian SVM within supervised feature learning and factor modeling, from the standpoints of prediction accuracy and physiological interpretability.

Larry Carin  
Electrical & Computer Engineering  
Duke University  
lcarin@duke.edu

## MS7

### Perfusion Heterogeneity in Tumors As a Challenge for Optimal Nanotherapeutics Delivery

Optimal nanotherapeutics delivery remains elusive because

of heterogeneities in vascular perfusion within solid tumors. Using intravital microscopy data previously obtained, we develop a machine-learning framework to determine which perfusion features most affect nanoparticle transport. Further, nanoparticle surface modifications can provide for increased targeting and uptake within tumor tissue. To guide nanoparticle design, we apply computational modeling to simulate tumor perfusion heterogeneity in order to evaluate uptake and distribution as functions of nanoparticle- and tumor-specific characteristics.

Hermann Frieboes  
University of Louisville  
hbfrie01@louisville.edu

## MS7

### Dynamics of Living Systems: Wave-Based Mechanisms for Contact Guidance and Collective Migration

Guided cell migration is a key aspect of many physiological processes from the immune response to cancer metastasis. I will describe how simple physical measurements of shape dynamics and motion reveal an underlying wave-like process of the cellular scaffolding that drives persistent migration. We find that wave-like dynamics of the scaffolding also contributes to the ability of cells to recognize and follow surface nanotopography, and allows cells to couple to each other during collective motion.

Wolfgang Losert  
Department of Physics  
University of Maryland, College Park  
wlosert@glue.umd.edu

John Fourkas, Meghan Driscoll, Xiaoyu Sun, Can Guven, Chenlu Wang  
University of Maryland  
fourkas@umd.edu, meghan.driscoll@gmail.com,  
xysun1@gmail.com, canguven83@gmail.com,  
clwang@mail.umd.edu

Carole Parent  
National Cancer Institute  
parentc@mail.nih.gov

## MS7

### Random Walks, Markov Chains, and Cancer Progression Models from Longitudinal and Autopsy Data

We will describe our models of metastatic cancer progression using Markov chain modeling on a directed graph of nodes that are the various anatomical sites where metastatic tumors can form for a given type of primary cancer. We use metastatic tumor distributions gathered from historical autopsy data, as well as current longitudinal data sets to estimate the transition probabilities from site to site. This creates a systemic network diagram from which we can calculate reduced two-step diagrams using the fact that the systems converge to their steady-state distribution after roughly two steps. The diagrams are used to categorize metastatic sites as 'sponges' or 'spreaders', as well as to run hypothetical therapeutic scenarios based on Monte Carlo simulations of progression. A useful metric which we describe is the notion of metastatic entropy.

Paul Newton  
Univ Southern California

Dept of Aerospace and Mechanical Engineering  
newton@usc.edu

## MS8

### Modeling and Inverse Problems in Environmental Toxicity

*Daphnia magna* is a vital species in ongoing investigations into the synergistic toxicity of chemicals. *D. magna* is a species with a complex life history; females are parthenogenetic and males are only produced in response to environmental stressors. Males can fertilize the females' eggs, transforming them into diapause eggs which are capable of withstanding extreme conditions and hatch when conditions improve. We model *D. magna* population growth by combining a two-sex age structured partial differential equation model with an ordinary differential equation model to describe their food environment. We then validate this model by performing parameter estimation using structured population data collected from experiments. This work is joint with K. Adoteye (Math), Karissa Cross (Biological Sciences) and a group of toxicologists lead by Gerald LeBlanc.

H. Thomas Banks

North Carolina State Univ  
Dept of Math & Ctr for Rsch in  
htbanks@ncsu.edu

Kevin Flores  
Mathematics  
North Carolina State University  
kbflores@ncsu.edu

## MS8

### Flocculation Dynamics and Cell Sorting

Flocculation is the process whereby particles in suspension aggregate and fragment and size-structured models are the best framework for modeling and simulation. It arises in many natural, environmental, and medical settings such as wastewater treatment and algal dynamics. In this talk, we will present recent results in how size-structured models of cell sorting devices can be used to improve sorting efficiency.

David M. Bortz

University of Colorado  
Department of Applied Mathematics  
dmbortz@colorado.edu

## MS8

### Estimating the Division Rate for a Growth-fragmentation Equation with Self-similar Kernel

Abstract not available at time of publication.

Thibault Bourgeron

UPMC and Inria Paris-Rocquencourt  
Paris, France  
bourgeron@ann.jussieu.fr

## MS8

### Applied Particle Aggregation for Cell Isolation in the Life Sciences

Among the many applications for particle aggregation, controlled assembly of synthetic beads onto the surface of liv-

ing cells is of particular industrial, life science, and therefore commercial interest. By fabricating beads with high affinity for cell surface markers, methods for achieving remarkable levels of enrichment from mixed populations are possible. In this presentation, I'll present current and proposed methods for exploiting aggregative physics towards real world applications, and consider where mathematics will play a large role.

John G. Younger

University of Michigan  
jyounger@med.umich.edu

## MS9

### A Model for the Spatial Transmission of Dengue with Daily Movement between Villages and a City

Dengue is a re-emergent vector-borne disease affecting large portions of the world's population living in the tropics and subtropics. A discrete-time multi-patch model which takes into account the mobility of people as well as processes of infection, recovery, recruitment, and mortality is considered here. One patch (the city) is connected to all other patches (the villages) in a spoke-like network. Vector control, human treatment and vaccination, and different kinds of mobility are studied.

Andrew Nevai

Department of Mathematics  
University of Central Florida  
math.anevai@gmail.com

Edy Soewono

Department of Mathematics, Institut Teknologi Bandung  
Bandung 40132, Indonesia  
esoewono@math.itb.ac.id

## MS9

### Modeling HIV Latency and Viral Blips

HIV cannot be eliminated by combination therapy because of latent infection. The latent reservoir consisting of latently infected CD4<sup>+</sup> T cells is relatively stable. Many patients also experience transient viral load measurements above the detection limit (the so-called "viral blips") even with suppressive treatment for many years. The mechanisms underlying the emergence of intermittent viral blips and stability of the latent reservoir are not fully understood. In this talk, I will introduce a new model based on the establishment of HIV latency to address this issue. Both deterministic and stochastic simulations of the model show that it is able to generate a stable latent reservoir, intermittent viral blips, as well as low-level viremia persistence. The results provide more insights into the latent reservoir replenishment and long-term HIV dynamics in patients on suppressive combination therapy.

Libin Rong

Oakland University  
rong2@oakland.edu

## MS9

### Disease Invasion of Community Networks with Environmental Pathogen Movement

Consider a set of communities (patches), connected to one another by a network. When can disease invade this network? Intuitively, this should depend upon both the prop-

erties of the communities, as well as on the network structure. Here we make this dependence explicit for a broad class of disease models with environmental pathogen movement. In particular, the rooted spanning trees of the network and a generalization of the group inverse of the graph Laplacian play fundamental roles in determining the ability of disease to invade.

Joseph Tien  
Ohio State University  
jtien@math.ohio-state.edu

Zhisheng Shuai  
University of Central Florida  
zhisheng.shuai@ucf.edu

Marisa Eisenberg  
University of Michigan  
marisae@umich.edu

P. van Den Driessche  
U. Victoria  
vandendr@uvic.ca

#### MS9

##### **Dynamics of Low and High Pathogenic Avian Influenza in Wild and Domestic Bird Populations**

An earlier infection with low pathogenic avian influenza (LPAI) provides a partial immunity towards infection with high pathogenic avian influenza (HPAI). We consider a time-since recovery structured model to study the dynamics of LPAI and HPAI in wild and domestic bird populations. The system has a unique disease-free equilibrium which is locally and globally stable when the reproduction number is less than one. There are unique LPAI-only and HPAI-only equilibria, which are locally asymptotically stable as long as the other pathogen can not invade the equilibrium. There exist a coexistence equilibrium when the invasion number of both pathogens are greater than one. We show that both pathogen can coexist in the form of sustained oscillations.

Necibe Tuncer  
University of Tulsa  
necibe-tuncer@utulsa.edu

#### MS10

##### **Within-Host Virus Model with Immune Response and Infected Cell Age Structure**

There is substantial evidence that the CTL (Cytotoxic T Lymphocyte) immune response plays a crucial role in controlling HIV in infected patients. CTLs recognize pathogen-derived proteins (epitopes) presented on the surface of infected cells to mediate their killing. Recent studies have demonstrated the heterogeneity of epitope presentation and recognition with respect to the infected cell lifecycle, which may impact the efficacy of the immune response. This talk concerns modeling the coupled within-host population dynamics of virus and CTL immune response, paying special attention to the cellular infection-age kinetics of recognition and killing of infected cells by CTLs. In particular, we extend a cellular infection-age structured within-host virus model to include immune response and analyze the resulting dynamics.

Cameron Browne  
Vanderbilt University

cameron.j.browne@vanderbilt.edu

#### MS10

##### **Modeling Human Papilloma Virus and the Onset of Cervical Cancer**

High-risk strains of Human Papillomavirus are the dominant cause of cervical cancers. Incorporating the known biology of viral persistence and the generation of cancerous and pre-cancerous cells, we develop and analyze a model the connection between HPV infection and cervical cancer onset. The model provides a framework for understanding the factors relevant to reducing cancer risk and the role of suppressive drug therapies in long-term treatment.

Jonathan Forde  
Hobart and William Smith Colleges  
forde@hws.edu

#### MS10

##### **A Basic Model for In-Host TB Infection**

Tuberculosis (TB) infection can result in clearance, latent infection or active disease. Mathematical models have been used to provide insight into TB infection and progression. The models to date, however, have been very complex or have not been able to produce all disease outcomes. We present a simple 4-dimensional mathematical model of TB infection in-host. The model includes macrophages, T lymphocytes, TB bacteria and their interactions. The model provides a foundation for future studies on the pathogenesis of drug resistant TB and HIV-TB co-infection.

Jane Heffernan, Yimin Du  
York University  
jmheffer@yorku.ca, tigerduhh@yahoo.ca

Jianhong Wu  
York University, Canada  
wujh@yorku.ca

#### MS10

##### **Mechanism Elucidation in Intracellular Signaling Models Via Sensitivity Functions**

Many physiological and cellular processes, from G-protein coupled receptor (GPCR) signaling to circadian rhythms, are regulated by oscillatory signals. Although an actively studied area, even the most well-known and commonly studied pathways can have controversy and lack of clarity on circuit architecture. Time-dependent stimulation, using microfluidics technology, has proven valuable in eliciting previously unseen cellular responses, thereby potentially allowing researchers to glean new insights. We discuss the use of sensitivity functions as tools to decipher the underlying mechanisms driving the responses, and to understand the differences in circuitry under constant and time-dependent stimulation patterns. We further discuss the possible information gained from observing other species in the pathway, and offer suggestions to improve future experimental design.

Karyn L. Sutton  
University of Louisiana  
Lafayette

sutton@louisiana.edu

## MS11

### Quantification of Iliac Artery Tortuosity and Its Implication for Rotation of Fenestrated Aortic Stent Grafts

Tortuosity is a measure of the deviation of an artery from a straight line, and is an indicator of potential problems during deployment of fenestrated aortic stent grafts, which can have unwanted rotation in severely tortuous arteries. We will present mathematical techniques for tortuosity assessment and iliac artery tortuosity values for typical patients and those for which rotation was an issue, with the goal of establishing criteria to predict when tortuosity will cause graft rotation.

Matthew G. Doyle, Cristina Amon  
University of Toronto  
mg.doyle@utoronto.ca, cristina.amon@utoronto.ca

Leonard Tse  
Toronto General Hospital  
leonard.tse@uhn.ca

## MS11

### A Mechanical and Biochemical Model of Intimal Hyperplastic Lesions

We investigate an axisymmetric model of intimal hyperplasia using hyperelasticity theory. Our model incorporates growth of the intima due to cell proliferation which is driven by the release of cytokines. The growth rate is tied to local stresses and concentration of cytokine. We find that rapid intimal thickening coupled to a quiescent media puts the intima in a state of compression. Our results are compared with intima-media thickness measurements of carotid arteries from clinical studies.

Rebecca Vandiver  
St. Olaf College  
Department of Mathematics, Statistics and Computer Science  
vandiver@stolaf.edu

Pak-Wing Fok  
University of Delaware  
pakwing@udel.edu

## MS11

### Understanding the Role of Cell-substrate Interaction in Cell and Focal Adhesion Shapes

Mechanical interaction between a cell and its underlying substrate have important implications in many contexts, and it has been shown experimentally that the material properties of the substrate affect cellular response. We present a two-dimensional mathematical model and finite element simulations of a biological cell interacting with a deformable substrate and use this model to gain a better understanding of how the mechanical interaction between the cell and substrate affects cell shape and focal adhesion (FA) dynamics during cell spreading. The cell is treated as a hypoelastic actively-deforming continuum and the substrate is modeled as a linearly elastic continuum. The active deformation, captured by the addition of an active rate of deformation tensor, models local cytoskeletal reorganization. FAs connecting the cell and the substrate are mod-

eled as a collection of discrete elastic springs, which can be dynamically added and removed. We use this model to investigate how substrate elasticity, cell elasticity, FA strength, and FA spacing affect cell shapes during spreading. We also investigate how cellular active deformation must be coupled to FA forces and intracellular stresses in order to obtain experimentally observed cell spread areas and observed tractions exerted by the cell onto the substrate.

Magdalena Stolarska  
University of St. Thomas  
Department of Mathematics  
mastolarska@stthomas.edu

## MS11

### Modeling the Growth of an Atherosclerotic Lesion

Atherosclerosis is a vascular disease driven by inflammatory processes. Atherogenesis can be viewed as an inflammatory instability of a reaction-diffusion-chemotactic (RDC) system on a fixed domain while modeling atherosclerotic lesion growth requires coupling the RDC system to the momentum balance system for the mechanical response of the affected tissue. This talk presents a model of this process and presents numerical simulations of a free-boundary problem modeling lesion growth.

Jay R. Walton  
Department of Mathematics  
Texas A&M  
jwalton@math.tamu.edu

## MS12

### Collective Effects and Correlations in Semidilute Bacterial Suspensions

To understand the non-trivial correlations emerging from collective swimming, a simple model is introduced where a bacterium is represented as a force dipole subject to two types of interactions: hydrodynamic and excluded volume (collisions). This model allows for efficient direct simulations confirming a striking experimental observation: correlations are independent of concentration and swimming speed, past the concentration threshold for collective motion. The effects of the particle shape, size, and dipole moment will also be presented.

Shawn Ryan  
Department of Mathematics  
Penn State University  
ryan@math.psu.edu

Igor Aranson  
Argonne National Laboratory  
Materials Science Division  
aronson@msd.anl.gov

Leonid Berlyand  
Penn State University  
Department of Mathematics  
berlyand@math.psu.edu

Andrey Sokolov  
Argonne National Laboratory

sokolov@anl.gov

## MS12

### Remarks on Modeling and Identification in Bacterial Chemotaxis

We discuss various topics related to the modeling and identification of bacterial chemotaxis, including the use of advection-diffusion and other PDE's to match microfluidics-generated population behavior, and the inference of signaling dynamics to match single-cell tracking data. Mathematically, the first topic involves the careful modeling of pathways and shallow gradient approximations (following work of Grunbaum, Othmer, and Erban), and the second topic requires the development of tools for the identification of time-varying parameters in nonhomogeneous Poisson processes that model motor events (such as tumbling) as a function of the phosphorylation states of certain enzymes. We present new results on these topics, including a model-based approach to the latter identification problem, and discuss our results in view of new experimental data.

Zahra Aminzare  
Rutgers University  
aminzare@math.rutgers.edu

Maja Skataric  
Graduate Student  
skataric@eden.rutgers.edu

Eduardo Sontag  
Rutgers University  
sontag@math.rutgers.edu

## MS12

### Relating the Chemotactic Sensitivity with Intracellular Signaling and Cell Movement

Chemotaxis of single cells has been extensively studied and a great deal on intracellular signaling and cell movement is known. However, systematic methods to embed such information into continuum PDE models for cell population dynamics are still in their infancy. In this talk, I will present our recent results on relating the chemotaxis sensitivity in the Patlak-Keller-Segel (PKS) model with the detailed biochemistry of intracellular signaling for run-and-tumble bacteria. Our general formulas are useful in explaining relations of single cell behavior and population dynamics. We show that the PKS model is valid when the external signal changes slowly, but inadequate when the signal changes fast. The general theory can also be applied to collective behavior of other individuals that move using a similar strategy.

Chuan Xue  
Ohio State University  
cxue@math.osu.edu

## MS12

### Global Asymptotic Stability of Constant Equilibrium States of a Repulsive Chemotaxis Model with Logarithmic Sensitivity

In contrast to diffusion (random diffusion without orientation), chemotaxis is the biased movement of cells/particles toward the region that contains higher concentration of beneficial or lower concentration of unfavorable chemicals.

The former often refers to the attractive chemotaxis and latter to the repulsive chemotaxis. Chemotaxis has been advocated as a leading mechanism to account for the morphogenesis and self-organization of a variety of biological coherent structures such as aggregates, fruiting bodies, clusters, spirals, spots, rings, labyrinthine patterns and stripes, which have been observed in experiments. In this talk, I will present recent results on the rigorous analysis of a partial differential equation model arising from repulsive chemotaxis, which is a system of hyperbolic balance laws consisting of nonlinear and coupled parabolic and hyperbolic type PDEs. In particular, global wellposedness, large-time asymptotic behavior of classical solutions to such a model are obtained. The long-time behavior result shows that constant equilibrium states are globally stable, which indicates that chemorepulsion problem with non-diffusible chemical signal and logarithmic chemotactic sensitivity exhibits strong tendency against pattern formation. The results are consistent with general results for classical repulsive chemotaxis models.

Kun Zhao  
Department of Mathematics  
Tulane University  
"Zhao, Kun" jkzhao@tulane.edu

## MS13

### Flow Through a Two-Chambered Zebrafish Heart with Trabeculae

Trabeculae form in developing zebrafish hearts for  $Re$  on the order of 0.1; effects of trabeculae in this flow is not well understood. Dynamic processes, such as vortex formation, are important in the generation of shear at the endothelial surface layer and strains at the epithelial layer, which aid in proper morphology and functionality. In this study, CFD is used to quantify the effects of  $Re$  and idealized trabeculae height on the resulting flows.

Nicholas A. Battista  
University of North Carolina at Chapel Hill  
nick.battista@unc.edu

Andrea Lane  
UNC at Chapel Hill  
anlane@live.unc.edu

Laura A. Miller  
University of North Carolina - Chapel Hill  
Department of Mathematics  
lam9@email.unc.edu

## MS13

### The Effects of Perturbations on Lamprey Swimming

The lamprey is a basal vertebrate and a model organism for neurophysiology and locomotion studies. Here a 2D, integrative, multi-scale model of the lamprey's anguilliform (eel-like) swimming is driven by neural activation and muscle kinematics coupled to body interactions with fluid surroundings and implemented using the immersed boundary method. Effects on swimming speed and cost (metabolic work) by nonlinear dependencies associated with muscle force development combined with perturbations to the neural activation are presented.

Christina Hamlet  
Tulane University

New Orleans LA  
chamlet@tulane.edu

Eric Tytell  
Tufts University  
Department of Biology  
eric.tytell@tufts.edu

Lisa J. Fauci  
Tulane University  
Department of Mathematics  
fauci@tulane.edu

### MS13

#### Hydrodynamic Contributions to Amoeboid Cell Motility

In this research, we develop a computational model of crawling *Physarum polycephalum* based on the Immersed Boundary Method. Our model incorporates the effects of cell cytoplasm, the internal cytoskeleton and adhesions to the substrate. Of particular interest are stresses generated by flow and how transmission of stresses to the substrate is coordinated. We attempt to characterize conditions necessary to generate directed motion. Cytoplasmic flows and traction stresses are compared to experimentally measured values in *Physarum*.

Owen Lewis  
University of California, Davis  
ollewis@math.ucdavis.edu

Robert D. Guy  
Mathematics Department  
University of California Davis  
guy@math.ucdavis.edu

Juan Carlos del Alamo, Shun Zhang  
University of California, San Diego  
jalamo@ucsd.edu, shz019@ucsd.edu

### MS13

#### Population Scale Effects of Macrophytes on Plankton Mobility

Small-scale interactions between water and vegetation can have a significant, complex effect on water flow. Using a two-dimensional hydrodynamic model, we represent macrophytes as a simple, flexible and deforming porous layer, varying the bending stiffnesses and porosities of the plants, as well as background flow speeds and type of flow. Studying velocities, shear stress, and mixing, we show that small-scale physical-biological interactions can have major and important implications for plankton patchiness, movement, and ultimate destiny.

Virginia B. Pasour  
U.S. Army Research Office  
pasour@gmail.com

Laura Miller  
UNC-Chapel Hill  
lam9@email.unc.edu

### MS14

#### Path-integrals and large deviations in a stochastic

#### hybrid neural network

We construct a path-integral representation of solutions to a stochastic hybrid system describing the dynamics of synaptically coupled neuronal populations. The state of each local population is described in terms of two stochastic variables, a continuous synaptic variable and a discrete activity variable. The spike-driven dynamical equations for the synaptic currents are only valid between stochastic jumps in spiking activity, which are described by a neural master equation. We use the path-integral representation to derive a large deviation variational principle for a stochastic hybrid neural network. We illustrate the theory by considering the optimal paths of escape from a metastable state in a bistable neural network.

Paul C. Bressloff  
University of Utah and University of Oxford, UK  
Department of Mathematics  
bressloff@math.utah.edu

Jay Newby  
Mathematical Biosciences Institute  
The Ohio State University  
newby.23@mbi.osu.edu

### MS14

#### Vasculature Adaptation and Optimization in Embryonic Zebrafish Brain

During the development of vasculature in the midbrain of embryonic zebrafishes, both angiogenesis and vessel pruning are observed. The vessel pruning occurred preferentially at loop-forming segments, leading to gradual reduction in the vasculature complexity. An shear-stress-driven adaptation model of blood vessels, which naturally optimizes the vessel network, is employed to predict the vessel pruning. The successful prediction suggests that vessel pruning is a consequence of the adaptation process and makes the vasculature more efficient.

Dan Hu  
Shanghai Jiao Tong University  
hudan80@sjtu.edu.cn

### MS14

#### Theoretical Modeling of Nonlinear Dendritic Integration

We address the question of how a neuron integrates excitatory (E) and inhibitory (I) inputs from different dendritic sites. For an idealized neuron with an unbranched dendrite, a conductance-based cable model is derived and its asymptotic solutions are constructed. The solutions reveal the underlying mechanisms of a dendritic integration rule discovered in a recent experiment. We then extend our analysis to the multi-branch case and confirm our analysis through numerical simulation of a realistic neuron.

Songting Li, Douglas Zhou  
Shanghai Jiao Tong University  
songtingli@gmail.com, zdz@sjtu.edu.cn

David Cai  
Courant Institute for Mathematical Sciences, NYU  
Shanghai Jiao-Tong University

cai@cims.nyu.edu

#### MS14

##### **Analytical Evaluation of Targeting Performances at Short and Long Distances in a Stochastic Model for Neural Arborization**

We investigate the behavior of a simplified neural growth model that branches with uniform probability and is subject to a total length constraint. Treating all possible tree instantiations as outcomes drawn from a discrete probability distribution, we compute the expected number of active tree branches as a function of distance. We show analytically that both the rising and decaying part of the resulting curve are respectively described exactly and approximated by geometrical series.

Remus Osan

Georgia State University  
Department of Mathematics and Statistics  
rosan@gsu.edu

Jun Xia

Georgia State University  
jxial@student.gsu.edu

Emily Su

Rutgers University  
mouseai@eden.rutgers.edu

#### MS15

##### **The Dependence of the Existence of Positive Steady States on the Rate Coefficients for Deficiency-One Mass Action Systems**

It is well-known that there exists a unique positive steady state in each of the positive stoichiometric classes for single linkage class weakly reversible (WR) deficiency-one mass action systems. The existence result does not remain valid in general if we omit the weak reversibility assumption. In this talk, we characterise those single linkage class non-WR deficiency-one mass action systems for which the existence of positive steady states does not depend on the rate coefficients.

Balázs Boros

Eötvös Loránd University  
bboros@cs.elte.hu

#### MS15

##### **Degree Two Polynomials for Saddle Node Bifurcations in Mass Action Networks**

Bistability has been recognized an important feature of dynamical systems originating in Biology and it is often established numerically (via a saddle-node bifurcation). However, parameter uncertainty complicates numerical analysis. Hence techniques allowing the analytic computation of parameters where a given system exhibits bistability are desirable. We present a condition involving only polynomials of degree  $\leq 2$  that allows to determine state and parameter vectors where a mass action system generically undergoes a saddle-node bifurcation.

Carsten Conradi

Max-Planck-Institut Dynamik komplexer technischer Systeme

conradi@mpi-magdeburg.mpg.de

#### MS15

##### **Structural Identifiability of Biological Models**

Identifiability concerns finding which unknown parameters of a model can be quantified from given input-output data. Many biological models are unidentifiable, which means that parameters can take on an infinite number of values and yet yield the same input-output data. We study the identifiability properties of several types of models, arising in Systems Biology and Chemical Reaction Networks, and demonstrate how to obtain identifiable reparametrizations of these models when they are unidentifiable.

Nicolette Meshkat, Seth Sullivant

North Carolina State University  
nicolette.meshkat@gmail.com, smsulli2@ncsu.edu

#### MS15

##### **A Global Convergence Result for Processive Multisite Phosphorylation Systems**

Multisite phosphorylation plays an important role in intracellular signaling. There has been much recent work aimed at understanding the dynamics of such systems when the phosphorylation/dephosphorylation mechanism is distributive, that is, when the binding of a substrate and an enzyme molecule results in addition or removal of a single phosphate group and repeated binding therefore is required for multisite phosphorylation. In particular, such systems admit bistability. Here we analyze a different class of multisite systems, in which the binding of a substrate and an enzyme molecule results in addition or removal of phosphate groups at all phosphorylation sites. That is, we consider systems in which the mechanism is processive, rather than distributive. We show that in contrast with distributive systems, processive systems modeled with mass-action kinetics do not admit bistability and, moreover, exhibit rigid dynamics: each invariant set contains a unique equilibrium, which is a global attractor. Additionally, we obtain a monomial parametrization of the steady states. Our proofs rely on a technique of Johnston for using "translated" networks to study systems with "toric steady states", recently given sign conditions for injectivity of polynomial maps, and a result from monotone systems theory due to Angeli and Sontag.

Anne Shiu

University of Chicago  
annejls@math.uchicago.edu

Carsten Conradi

Max-Planck-Institut Dynamik komplexer technischer Systeme  
conradi@mpi-magdeburg.mpg.de

#### MS16

##### **Data Assimilation Methods and Inverse Problem for Protein Polymerization**

Data assimilation methods are particular methods that exploiting some available data give us an estimation of parameters or state variables. In this presentation, we will introduce several data assimilation methods and their application to protein aggregation, a chain reaction which is one of the causes of neurodegenerative diseases called amyloid diseases (among which are Alzheimers, Huntingtons,

Parkinsons etc). Moving from Lifshitz-Slyozov equation, we define a model for protein polymerization. We couple the model and observations to define an inverse problem. The aim is to apply data assimilation methods on this inverse problem to obtain an estimation of kinetic coefficients and/or cluster concentrations, with application on real data.

Aurora Armiento  
Inria, Rocquencourt  
France  
aurora.armiento@inria.fr

Marie Doumic  
INRIA Rocquencourt, France  
marie.doumic-jauffret@inria.fr

## MS16

### Limited Measurement Domains: Robustness of Parameter Estimation in Flocculation Dynamics

While incorporating the Smoluchowski coagulation equation to model aggregation in size structured populations, the actual physical structures we study can exist in clusters smaller than the lower limit and larger than the upper limit of experimental devices. With the motivation of identifying an aggregation kernel under real-world experimental limitations, we aim to rigorously study the impact of the limited measurement domain on the robustness of our parameter estimation inverse problem.

Dustin Keck  
Applied Mathematics  
University of Colorado, Boulder  
dustin.keck@colorado.edu

## MS16

### Impact of Ellipsoid Geometry and Deformation on Flocculation Dynamics

Fragmentation is an important yet poorly understood aspect of flocculation dynamics. Simulations of fragmentation events can be simplified by approximating the floc as a solid ellipsoid. The force on the surface of such an ellipsoid can have a strong dependence on its geometry, further compounded by deformation due to the flow. We present results on the deformation of ellipsoidal flocs in laminar flow.

Eric Kightley  
Interdisciplinary Quantitative Biology  
University of Colorado  
Eric.Kightley@colorado.edu

## MS16

### A General Structured Population Model with the Application to Amphibians Infected with Chytridiomycosis

The disease Chytridiomycosis occurs when the skin of an amphibian is infected by the chytrid fungus *Batrachochytrium dendrobatidis* (Bd). The rapid and widespread growth of Chytridiomycosis has been associated with major population declines and extinctions in many frog species. Studies show that the inoculation of anti-Bd bacterial species *Janthinobacterium lividum* (Jl) could reduce Bd infection on amphibians. We first develop a new and general class of structured metapopulation models with wide

range of application including amphibian dynamics and associated diseases. This modeling approach is then extended to investigate amphibians to understand the effect of the disease Bd and the symbiont Jl on their population dynamics and provide useful insights to biologists in the control of Chytridiomycosis under various scenarios.

Baoling Ma  
University of Louisiana - Lafayette  
bxm4254@louisiana.edu

Azmy S. Ackleh  
Department of Mathematics  
University of Louisiana at Lafayette  
ackleh@louisiana.edu

Jacoby Carter  
USGS National Wetlands Research Center  
carterj@usgs.gov

Vinodh Challamuthu  
University of Louisiana at Lafayette  
vxc1794@louisiana.edu

## MS17

### Merging Population Genetics, Mosquito Behaviour and Epidemiology to Predicting the Success of the Use of GM Mosquitoes for Malaria Control

Transgenic mosquitoes are a potential tool for the control or eradication of insect-vectored diseases. For malaria, one possible strategy relies on the introduction of malaria-refractory transgenes into wild *Anopheles* mosquito populations that would limit their capacity to transmit the disease. This could be done with or without a gene-drive that could facilitate the spread of the allele of interest. By merging population genetics, epidemiology and mosquito life-history traits, it is possible to explore the importance of the gene-drive, the eventual role of mosquito mating preferences as well as the impact of the cost and efficacy of refractoriness on its spread in the mosquito population. As the aim of such approach is not only a modification of the mosquito population but a significant decrease of malaria prevalence in the human population, it is essential to determine how such releases could affect the long-term prevalence of malaria in humans. Those different aspects are going to be discussed in the current context of the fight against malaria.

Christophe Boëte  
Aix Marseille Université, IRD (Institut de Recherche pour le  
EHESP (Ecole des Hautes Etudes en Santé Publique)  
choete@gmail.com

## MS17

### The Effect of IPT on the Spread of Drug Resistant Malaria Parasite When Regions are Connected

The use of IPT is an increasingly popular preventive strategy aimed at reducing malaria incidence in vulnerable individuals. We seek to understand how IPT can affect the spread of antimalarial drug resistance when there is movement between neighboring low and high transmission areas. We expanded a previously published model to include movement between neighboring high and low transmission areas. Our results suggest that population movement results in resistance spreading fastest in high transmission

areas. The more complete the antimalarial resistance, the faster the resistance spread through a population.

Scott Duke-Sylvester  
Department of Biology  
University of Louisiana at Lafayette  
smd3729@louisiana.edu

Jemal Mohammed-Awel  
Valdosta State University  
jmohammedawel@valdosta.edu

Frederick Baliraine  
Department of Biology,  
LeTourneau University, Longview, TX  
FredBaliraine@letu.edu

Miranda Teboh-Ewungkem  
Lehigh University  
Bethlehem, PA, 18020  
mit703@lehigh.edu

## MS17

### Ipt and the Spread of Drug Resistant Malaria

Intermittent Preventive Treatment (IPT) is a malaria control strategy in which vulnerable asymptomatic individuals are given a full curative dose of an antimalarial medication at specified intervals, regardless of whether they are infected with malaria or not. A mathematical model is developed to explore the effect of IPT use on the malaria prevalence and control under different scenarios. The model includes both drug-sensitive and drug-resistant strains of the parasite as well as interactions between human hosts and mosquitoes. The basic reproduction numbers for both strains as well as the invasion reproduction number by the resistant strain are computed and used to examine the role of IPT in the development of resistant infections. Sensitivity and uncertainty analysis is carried out to examine the influence of model parameters in the model outcomes.

Zhilan Feng  
Department of Mathematics  
Purdue University  
zfeng@math.purdue.edu

Miranda Teboh-Ewungkem  
Lehigh University  
Bethlehem, PA, 18020  
mit703@lehigh.edu

Katharine Gurski  
Howard University  
kfgurski@gmail.com

Carrie A. Manore  
Tulane University  
cmanore@tulane.edu

Angela Peace  
Arizona State University  
angela.peace@asu.edu

Olivia Prosper  
Dartmouth University

olivia.f.prosper@dartmouth.edu

## MS17

### Application of *P. falciparum* Gametocyte Sex Ratios Via Competitive and Non-Competitive Strategies: The Evolutionary Implications

A mathematical model that simulates the within-mosquito dynamics of *Plasmodium falciparum* in an Anopheles mosquito is used to investigate optimal gametocyte sex ratios under varying fecundity. Gametocytes are the sexual forms of the *Plasmodium* malaria parasite and understanding mechanisms that determine the ratio of male gametocytes to female gametocytes has engendered considerable interest among researchers. Under unbiased random mating and incomplete fertilization the model illustrate that optimal gametocyte sex ratios vary from a highly female-biased to a slight male-biased sex ratio under a non-competitive strategy. When two distinct fitness optimization strategies for *P. falciparum* with varying fecundity was analyzed, initial results indicate that the non-competitive strategy is the winning strategy.

Miranda I. Teboh-Ewungkem  
Lafayette College  
mit703@lehigh.edu

Thomas Yuster  
Lafayette College  
Easton, PA, 18042  
yustert@lafayette.edu

## MS18

### An Application of Mathematics to Osteoarthritis Related Inflammation

The degenerative joint disease osteoarthritis (OA) has traditionally been viewed as a consequence of aging and “wear and tear.” However, the most recent research indicates that inflammation, as related to the innate immune response, is fundamental in the development and progression of OA. The goal of this talk is to describe mathematical approaches to developing a theoretical foundation for recent discoveries in this area of biological research, and for understanding the connections between OA and inflammation.

Jason Graham  
Department of Mathematics  
University of Scranton  
jason.graham@scranton.edu

## MS18

### Success, Failure, and Spreading Speeds for Invasions on Spatial Gradients

We present a model that describes the spatial spread of a species along a habitat gradient. We demonstrate that the species may succeed or fail in local invasion depending on the species’ growth function and dispersal kernel. We show how a species can escape a region of poor quality habitat by climbing a resource gradient to good quality habitat where it spreads at a constant spreading speed. Joint work with William Fagan and Kimberly Meyer.

Bingtuan Li  
Department of Mathematics  
University of Louisville

bing.li@louisville.edu

## MS18

### Modeling and Analysis of Glioma Tumor Growth

Glioblastoma multiforme is the most common and most deadly primary brain tumor in adults. Gliomas are characterized by highly diffusive growth patterns, thus reaction-diffusion equations are often used in modeling. To give insight on the mechanisms most responsible for tumor growth and the difficult task of forecasting future tumor behavior, numerical and analytical results from various models, including ones with density-dependent diffusion, are compared to experimental data.

Tracy L. Stepien, Erica Rutter  
School of Mathematical and Statistical Sciences  
Arizona State University  
tstepien@asu.edu, erutter1@asu.edu

Yang Kuang  
Arizona State University  
School of Mathematical and Statistical Sciences  
kuang@asu.edu

## MS18

### The Effects of Cross-diffusion on an SIR Model

During the outbreak of infectious diseases, susceptible individuals naturally tend to avoid infective individuals. We use a two-dimensional reaction-diffusion model, adapted from the Shigesada-Kawasaki-Teramoto (1979) model, to describe the effects of cross-diffusion on an SIR model.

Kamuela E. Yong  
Arizona State University  
kamuela.yong@asu.edu

## MS19

### Actin-myosin Spatial Patterns from a Simplified Isotropic Viscoelastic Model

F-actin networks are involved in cell mechanical processes ranging from motility to endocytosis. The mesoscale architecture of assemblies of individual F-actin polymers that gives rise to micrometer-scale rheological properties is poorly understood, despite numerous in vivo and vitro studies. In vitro networks have been shown to organize into spatial patterns when spatially confined, including dense spherical shells inside spherical emulsion droplets. Here we develop a simplified model of an isotropic, compressible, viscoelastic material continually assembling and disassembling. We demonstrate that spherical shells emerge naturally when the strain relaxation rate (corresponding to internal network reorganization) is slower than the disassembly rate (corresponding to F-actin depolymerization). These patterns are consistent with recent experiments, including a collapse of shells to a central high-density focus of F-actin when either assembly or disassembly is reduced with drugs. Our results demonstrate how complex spatio-temporal patterns can emerge without spatially-distributed force generation, polar alignment of F-actin polymers, or spatially non-uniform regulation of F-actin by upstream biochemical networks.

Jun Allard, Owen Lewis  
University of California, Davis  
jun@math.ucdavis.edu, ollewis@math.ucdavis.edu

Robert D. Guy  
Mathematics Department  
University of California Davis  
guy@math.ucdavis.edu

## MS19

### Exploring Motility of Breast Cancer Cells Using a 3D Individual Cell Based Model

Experiments have demonstrated that white blood cells are directly involved in the invasion of breast tumor cells into surrounding tissues and blood vessels. The white blood cells interact with tumor cells via a short-ranged chemical signaling loop involving two signalling molecules. We developed a 3D individual cell based computational model to study these interactions and to understand the observed streaming motility pattern. The cells are simulated as freely moving deformable ellipsoids and the signalling molecule concentrations are estimated using reaction-diffusion equations. The movement and deformation of cells are calculated from equations of motion accounting for all forces acting on each cell. This simplified model is able to reproduce results from both in vitro and in vivo experiments. The model suggests that the removal of the signalling molecules is essential to produce the observed ratio of 3 invasive tumor cells per 1 invasive white blood cell. A preliminary exploration of the parameter space indicates that the ratio between tumor cells and white blood cells is robust to changes in most model parameters, supporting the experimental results. An exception to this robustness is that changes in the decay and secretion rates of the signalling molecules can alter and even eliminate the invasion of tumor cells.

Hildur Knutsdottir  
Department of Mathematics  
The University of British Columbia  
hildurknuts@gmail.com

## MS19

### Insights into Cytoplasmic Rheology Gained from Modeling Cellular Blebbing

Blebbing occurs when the cytoskeleton detaches from the cell membrane, resulting in the pressure-driven flow of cytosol towards the area of detachment and local expansion of the cell membrane. Recent experiments involving blebbing cells have led to conflicting hypotheses regarding the timescale of intracellular pressure propagation. The interpretation of one set of experiments supports a poroelastic cytoplasmic model which leads to slow pressure equilibration when compared to the timescale of bleb expansion. A different study concludes that pressure equilibrates faster than the timescale of bleb expansion. To address this, a dynamic computational model of the cell was developed that includes mechanics of and the interactions between the intracellular fluid, the actin cortex, the cell membrane, and the cytoskeleton. The model results quantify the relative importance of cytoskeletal elasticity and drag in bleb expansion dynamics. This study also shows that recent multi-bleb experimental results can be explained by the combination of cytoskeletal poroelasticity with either dynamic membrane-cortex adhesion or cortical reformation.

Wanda Strychalski  
Department of Mathematics  
University of California, Davis

wis6@case.edu

## MS19

### The Physics of Collective Cell Migration in Wound Healing and Cancer Metastasis

Multicellular organisms require groups of cells to function together as a unit. A common scenario involves the collective movement of cells. For example, when your skin gets cut, one of the first processes is re-epithelialization where epidermal cells crawl over the wounded region. And, in cancer, tumor cells will often move as a group to detach from the primary tumor and invade distal regions of the body. In this presentation, I will describe the work that we have been doing to develop a multiscale model for collective cell migration. This model is based in the fundamental biophysics of a single cell. We show that a combination of directed cell motility, dipole-distributed forces, and adhesion to neighboring cells and the environment is sufficient to explain in vitro wound healing dynamics and gives insight into the biophysical changes that occur when cancer cells become metastatic. This model provides testable predictions that we are now testing with experiments.

Charles Wolgemuth  
University of Arizona  
Department of Physics  
wolg@email.arizona.edu

## MS20

### Impact of Single-Neuron Dynamics on Transfer of Correlations from Common Input

One source of spike train correlations in the nervous system is common input, an inevitable consequence of the ubiquity of coding by populations. The details of how input correlations map onto output spike correlations is surprisingly complex, depending on single-neuron dynamics in subtle ways. Much progress has been made in untangling this relationship in Type I and Type II excitable neurons, in both simplified phase oscillator and conductance-based models. In this talk, we apply these techniques to novel patterns of excitability that arise in the presence of calcium currents.

Andrea K. Barreiro  
Department of Mathematics  
Southern Methodist University  
abarreiro@smu.edu

## MS20

### Integrate-and-Fire Model of Insect Olfaction

When a locust detects an odor, the stimulus triggers a series of synchronous oscillations of the neurons in the antenna lobe. These oscillations are followed by slow dynamical modulation of the firing rates which continue after the stimulus has been turned off. I model this behavior by using an Integrate-and-Fire neuronal network with excitatory and inhibitory neurons. The inhibitory response of both types of neurons contains a fast and slow component. The fast component, together with the excitation, creates the initial oscillations while the slow component suppresses them and aids in the creation of the slow patterns that follow. During the initial oscillations the stimulus can be identified by determining which excitatory neurons participate consistently in every cycle of the oscillations.

Pamela B. Fuller  
Rensselaer Polytechnic Institute

Fullep@rpi.edu

## MS20

### Reduction Methods for Spiking Networks

We consider a simple spiking LIF neuron model driven by excitatory conductance input, and highlight a dimension reduction method to capture the firing rate dynamics. We further consider a QIF population with adaptation and recurrent (all-to-all) excitatory coupling, where an analogous reduction method can be applied with augmentation. Based on the reduction, a linear stability analysis method is applied to capture some of the features of the simulations.

Cheng Ly  
University of Pittsburgh  
Department of Mathematics  
cly@vcu.edu

Wilten Nicola  
University of Waterloo  
wnicola@uwaterloo.ca

Sue Ann Campbell  
University of Waterloo  
Dept of Applied Mathematics  
sacampbell@uwaterloo.ca

## MS20

### The Essential Role of Phase Delayed Inhibition in Decoding Synchronized Oscillations within the Brain

The widespread presence of synchronized neuronal oscillations within the brain suggests that a mechanism must exist that is capable of decoding such activity. Two realistic designs for such a decoder include: 1) a read-out neuron with a high spike threshold, or 2) a phase-delayed inhibition network motif. Despite requiring a more elaborate network architecture, phase-delayed inhibition has been observed in multiple systems, suggesting that it may provide inherent advantages over simply imposing a high spike threshold. We use a computational and mathematical approach to investigate the efficacy of the phase-delayed inhibition motif in detecting synchronized oscillations, showing that phase-delayed inhibition is capable of detecting synchrony far more robustly than a high spike threshold detector. Furthermore, we show that in a system with noisy encoders where stimuli are encoded through synchrony, phase-delayed inhibition enables the creation of a decoder that can respond both reliably and specifically to a stimulus, while a high spike threshold does not.

Mainak Patel  
Duke University  
Department of Mathematics  
mainak@math.duke.edu

Badal Joshi  
California State University, San Marcos  
bjoshi@csusm.edu

## MS21

### The Use of Physiological Model of Menstrual Cycle Regulation in Women's Health: Fertility and

## Contraception

The biology of female menstrual cycle hormonal regulation is complex and not completely understood. The system makes an excellent case study for mathematical modeling due to intrinsic nonlinearities, feedback mechanisms and delays. Several dynamical models with varying complexity and biological plausibility have been proposed. We provide an industrial perspective for how these models can and should be used to inform clinical decisions for therapies targeting contraception, fertility, and endometriosis.

Anna Kondic, Craig Fancourt  
Merck & Co., Inc.  
anna.kondic@merck.com, craig\_fancourt@merck.com

## MS21

### The Role of Insulin and Androgen Dynamics in Female Hormone Dysregulation

Although the physiological role of insulin and androgens in follicle development remains unclear, excess concentrations are commonly associated with ovulatory defects. We incorporate insulin and androgen dynamics into a mathematical model of folliculogenesis, which describes hormone production and pituitary-ovarian feedback through successive growth stages. Changes in model periodicity and gonadotropin/hormone profiles under various biological circumstances are used to characterize the physiological versus pathological influences of insulin and androgens on ovulation.

Erica J. Graham  
North Carolina State University  
Department of Mathematics  
ejgraha2@ncsu.edu

James Selgrade  
North Carolina State University  
selgrade@ncsu.edu

## MS21

### Multiple Cycles and Bifurcation in Models of Hormonal Control of the Menstrual Cycle

Two models for hormonal control of the menstrual cycle are presented using the same system of differential equations but based on different data sets. For the best-fit parameter sets, simulations for the two models agree well with the data but one model also has a stable periodic solution representing an abnormal, nonovulatory menstrual cycle. Differences in model behavior are explained by studying hysteresis curves in bifurcation diagrams with respect to sensitive model parameters.

James F. Selgrade  
Department of Mathematics and Biomathematics  
Program  
selgrade@math.ncsu.edu

## MS21

### A Differential Equation Model for the Bovine Estrous Cycle

Based on the models for the human menstrual cycle by Selgrade and coworkers, a fully coupled feedback model for the bovine estrous cycle has been developed. It has been used for an analysis of follicular wave patterns and for the simulation of synchronization studies. In this talk,

we will present the model and its dynamical properties. Open questions such as the administration of GnRH and an improved modeling of follicular development will be discussed.

Claudia Stoetzel, Julia Ploentzke, Susanna Roeblitz  
Zuse Institute Berlin  
stoetzel@zib.de, ploentzke@zib.de, susanna.roeblitz@zib.de

## MS22

### An Algebraic Framework for Describing and Studying Binary Enzymatic Networks

We present a framework to describe and reason about enzymatic networks. The initial motivation for this construct was to extend examples from the literature into the following theorem: a binary enzymatic network that is futile and cascaded is persistent, i.e. molecular species do not tend to extinction. The framework provides mathematically sound and biochemically applicable definitions for the notions of futile enzymatic cycles and enzymatic cascades, and several prerequisite concepts. The framework could be used to prove more results, or even to help assess the plausibility of models of enzymatic networks during their design.

Gilles Gnacadja  
Amgen  
gilles.gnacadja@gmail.com

## MS22

### Correspondence of Regular and Generalized Mass Action Systems

In this talk, we investigate systems where graph-based correspondence of dynamics for mass action systems may not be made directly, but for which correspondence may be made to a "generalized" mass action system. The constructed generalized mass action system contains different monomials than implied by the chemistry of the system, but has a "well-structured" reaction graph. We will discuss some of the newest results regarding the algorithmic construction of such generalized mass action systems.

Matthew Johnston  
University of Wisconsin Madison  
mjohnston3@wisc.edu

## MS22

### Atoms of Multistationarity in Chemical Reaction Networks

Multistationarity is a prerequisite for a reaction network to act as a biochemical switch. Theoretical tools that help rule out multistationarity include the Jacobian criterion of Craciun and Feinberg. We provide results that are helpful in establishing multistationarity of certain networks. The key result is that if a multistationary network  $N$  is "embedded" in a larger network  $G$  then  $G$  is also multistationary. The partial ordering resulting from the embedding property yields minimal (with respect to number of chemical species and reactions) multistationary networks. We also provide results which identify the smallest such minimal networks.

Badal Joshi  
California State University, San Marcos  
bjoshi@csusm.edu

Anne Shiu  
University of Chicago  
annejls@math.uchicago.edu

## MS22

### Exploiting Reaction Network Structure for Parameter Identification of Biochemical Switches

One key challenge in Systems Biology is the identification of kinetic models from limited quantitative data. In this work we illustrate the potential of Chemical Reaction Network Theory (CRNT) for the parameter identification of kinetic models. We introduce a method for inverse bifurcation of bistable biochemical reaction networks, that exploits inherent structural properties of bistable switches to infer the kinetic parameters from dose response curves. Uniqueness and identifiability properties of the associated inverse problem are analyzed.

Irene Otero-Muras  
CSIC  
ireneotero@iim.csic.es

Pencho Yordanov  
ETH Zurich  
pencho.yordanov@bsse.ethz.ch

Attila Gabor  
CSIC  
attila.gabor@iim.csic.es

Julio R. Banga  
IIM-CSIC  
Vigo, Spain  
julio@iim.csic.es

## MS23

### Real-Time Model Calibration and Prediction Testing with the GPU and Dynamic Clamp

Electrical activity of anterior pituitary cells is heterogeneous, motivating model fitting to individual cells. We use the parallel computational power of the GPU to find parameters of a biophysical model with similar bifurcation structure to live individual cells. The optimization is iteratively improved by making model predictions that induce a qualitative changes in electrical activity, testing the predictions with dynamic clamp on the same cell, then adding the results to the set of optimization constraints.

Patrick A. Fletcher  
Department of Mathematics  
Florida State University  
pfletche@math.fsu.edu

Joël Tabak  
Department of Biological Science  
Florida State University  
joel@neuro.fsu.edu

Richard Bertram  
Department of Mathematics  
Florida State University  
bertram@math.fsu.edu

## MS23

### Hypothalamic Vasopressin Neurons: Signal Pro-

### cessing in An Asynchronous Bursting Population

Vasopressin acts as an antidiuretic hormone, as part of the homeostatic system that maintains osmotic pressure. Experiments show a robust linear relationship between osmotic pressure and vasopressin secretion despite very non-linear properties of spike generation and secretion in the neurons, and highly heterogeneous spiking activity. Here we develop a previous model of the spiking and secretion mechanisms to examine how the heterogeneous population might coordinate a robust signal response using local inter-neuronal (dendritic) communication.

Duncan J. MacGregor, Gareth Leng  
Centre for Integrative Physiology  
University of Edinburgh  
duncan.macgregor@ed.ac.uk, gareth.leng@ed.ac.uk

## MS23

### Leveraging Mathematical Models to Understand Population Variability in Response to Cardiac Drugs

Mathematical models of heart cells and tissues are sufficiently advanced that the models can predict mechanisms underlying pro-arrhythmic or anti-arrhythmic effects of drugs. However, these models are not presently adequate for understanding variability across a population, i.e. why a drug may be effective in one patient but ineffective in another patient. I will discuss novel computational approaches my laboratory has developed that can quantify and predict differences between individuals in the response to cardiac drugs

Eric Sobie  
Mount Sinai Hospital  
eric.sobie@mssm.edu

## MS23

### Paracrine Regulation of Glucagon and Somatostatin Secretion

Pancreatic islets are composed of  $\alpha$ -,  $\beta$ -, and  $\delta$ -cells. These cells secrete the hormones glucagon, insulin, and somatostatin, respectively. Together, these hormones regulate glucose homeostasis in the body. While  $\beta$ -cells are coupled through gap junctions, individual  $\alpha$ - and  $\delta$ -cells are heterogeneous. We investigate the paracrine interactions between these cells, which gives synchronous oscillations of insulin and somatostatin, and anti-synchronous oscillations of insulin and glucagon at high glucose levels.

Margaret A. Watts  
Laboratory of Biological Modeling  
National Institutes of Health  
margaret.watts@nih.gov

Ofer Kimchi  
Princeton University  
okimchi@princeton.edu

Arthur Sherman  
Laboratory of Biological Modeling  
National Institutes of Health  
sherman@helix.nih.gov

## MS24

### Epidemiological and Economic Benefits of Targeted

### **Tuberculosis Screening in a Correctional Facility of New River Health District**

**Objective:** The objective of this study is to conduct cost-effectiveness analysis of pre-screening inmates for tuberculosis compared to no pre-screening in a correctional facility in Southwest Virginia. **Background:** Correctional facilities represent a relatively higher risk for tuberculosis transmission in the United States because they have close living quarters, overcrowding, and poor ventilation, thereby enhancing the risk of tuberculosis acquisition and transmission. **Methods:** We conducted cost effectiveness analysis to evaluate pre-screening measures for tuberculosis compared to the baseline scenario of no pre-screening. We developed a dynamic model to understand and analyze the transmission dynamics of tuberculosis in a correctional facility and its associated costs over a time horizon of 5 years, from the perspective of the correctional facility and the local health department. Data from a tuberculosis outbreak in 2011 at a correctional facility located in Southwest Virginia is incorporated to calibrate the dynamic model. **Results:** We used the ratio of 68 to 200 out of 100,000 inmates will develop active tuberculosis while incarcerated when conducting analysis for the baseline of no pre-screening. Based on preliminary results, the incremental cost-effectiveness ratio of tuberculosis pre-screening is estimated at \$-15,461 per disability adjusted life year averted (cost saving) from the perspective of the correctional facility and the local health department. **Conclusion:** Our findings indicate that tuberculosis pre-screening is a cost-saving intervention; thereby, we recommend adoption of tuberculosis pre-screening programs in correctional facilities.

Kaja Abbas  
Virginia Polytechnic Institute and State University  
kabbas@vt.edu

### **MS24**

#### **A Simple Epidemic Model with Nosocomial Transmission**

The SARS epidemic of 2002-3 drew attention to nosocomial disease transmission, as many of the disease cases were transmitted through hospital staff and visitors. Various types of models have been proposed to describe this, including metapopulation models. We formulate and analyze a simple compartmental model with heterogeneous mixing to describe nosocomial transmission and determine its reproduction number and the final size relations.

Fred Brauer  
University of British Columbia  
Department of Mathematics  
brauer@math.ubc.ca

### **MS24**

#### **Demographic Transition and the Dynamics of Measles in China**

Industrialization and demographic transition generate non-stationary dynamics in human populations that can impact the transmission and persistence of infectious disease. By catalytic transmission model, we show that demographic transition and reduced prevalence has driven a shift in the age distribution of susceptibility to measles in China. The force of infection of measles has declined dramatically in the industrialized eastern provinces in the last decade; while central and western provinces exhibit dynamics con-

sistent with endemic persistence.

Sheng Li  
Pennsylvania State University  
sxl64@psu.edu

### **MS24**

#### **Modeling SIS Disease Dynamics on Random Contact Networks**

Contact networks represent persons by nodes and contacts by edges. It is a more realistic model of disease related human contacts than the random mixing model, which assumes that every pair of individuals have identical contact rate. An effective degree SIS epidemic model was developed before, and was shown to have different disease thresholds than an SIR model. This contradicts with the prediction of classic disease models that SIR and SIS models should have the same disease threshold. But this effective degree model is too complex to derive a closed formula for the disease threshold. In this talk, I will introduce a simplified SIS model on random contact networks, which agrees with stochastic simulations and is mathematically tractable. The model yields a disease threshold formula that bears a clear biological meaning: for the disease to spread, the average number of transmissible neighbours times the average number of times a neighbour can be infected must be greater than unity. The threshold converges to that of the SIR model under the homogeneous mixing limit.

Junling Ma  
University of Victoria, Canada  
junlingm@uvic.ca

### **MS25**

#### **Models of Neurovascular Coupling and Cerebral Autoregulation**

Our research group has developed a parallel numerical model describing neurovascular coupling. NVUs are coupled through a space filling H-tree simulating a vascular tree and spatially embedded in cerebral tissue. The model regulates bloodflow in response to neuronal activity in a 2-dimensional tissue slice of width and depth of the order of millimetres culminating in the dynamic simulation of several million cells. The model thus allows us to study a number of important pathological scenarios.

Tim David  
Centre for Bioengineering  
University of Canterbury, New Zealand  
tim.david@canterbury.ac.nz

### **MS25**

#### **Assessing the Impact of Structural Organization of the Renal Medulla on Oxygen Distribution Using a Mathematical Model**

A theoretical model is presented to analyze the impact on oxygen distribution of the heterogeneous organization of the rat medulla revealed in anatomical studies. Model equations are based on transmural transport and conservation of water and solutes (NaCl, urea, O<sub>2</sub>, HbO<sub>2</sub>, Hb), and are solved to steady state. Results suggest that the structural organization of the renal medulla produces significant axial and radial PO<sub>2</sub> gradients, and impacts the effectiveness of the medullary urine concentrating mecha-

nism.

Brendan C. Fry  
Duke University  
Department of Mathematics  
bfry@math.duke.edu

## MS25

### Can Pre-Glomerular Oxygen Transport Be Used to Investigate Renal Anatomy?

There is a close spatial association of arteries and veins in the pre-glomerular vasculature, which facilitates oxygen shunting and protects the kidney from hyperoxia. However this anatomical structure may lead to hypoxia. We have developed a mathematical model of oxygen transport in the paired pre-glomerular branched vasculature. Here we demonstrate how differences in transit times and shapes of pulses of oxygen and labelled haemoglobin, due to shunting, could be used to explore this pre-glomerular anatomy.

Bruce S. Gardiner  
University of Western Australia  
bruce.gardiner@uwa.edu.au

Saptarshi Kar, David Smith  
The University of Western Australia  
saptarshi.kar@uwa.edu.au, david.smith@uwa.edu.au

Roger Evans  
Monash University  
roger.evans@monash.edu

## MS25

### Development of Hypoxia in a Model of Renal Blood Flow Control and Oxygen Consumption

Hypoxia is an important pathway in the development of acute kidney injury during cardiopulmonary bypass surgery. Using a model of renal hemodynamics we assess the degree to which hypoxia develops under reduced hematocrit, temperature, and systemic pressure that are commonly induced in such surgery. Oxygenation is determined by renal blood flow and the metabolic work of sodium reabsorption. Results suggest that although oxygen supply and consumption both decrease below physiologic levels, fractional extraction increases significantly.

Ioannis Sgouralis  
Duke University  
io-sgou@math.duke.edu

## MS26

### Computational Design of Megadalton-Scale Nucleic Acid Nanoassemblies

Programmed self-assembly of nucleic acids offers the unique opportunity to engineer complex megadalton-scale macromolecular architectures with atomic-level accuracy. The sequence specificity of DNA additionally renders these nanoassemblies spatially addressable structural scaffolds to host secondary molecules such as light-harvesting dyes and chemically active compounds. These properties may be exploited to rationally design, for example, biomimetic light-harvesting constructs to replicate aspects of bacterial photosynthesis. Here, I present our computational design tool CanDo (<http://cando-dna-origami.org>) that quantita-

tively predicts the 3D solution structure of megadalton-scale DNA-based assemblies based on underlying DNA sequence, as well as their emergent light-harvesting properties when decorated with dyes and porphyrins.

Mark Bathe  
MIT  
mark.bathe@mit.edu

## MS26

### The Structural Glycobiology of HIV: Insights from Molecular Simulations and Implications for the Design of Virucidal Lectins

The HIV envelope-glycoproteins are heavily glycosylated to avoid immune recognition, creating both challenges to the effective inhibition of viral-cell recognition and unique opportunities; for example, carbohydrate-binding proteins have been shown to have the potential to act as potent virucides. The development of detailed computational models that explain the relative affinities of distinct oligosaccharides, provide insight into mechanisms of multi-valent binding, and provide a foundation for the rational design of improved inhibitors will be presented.

David F. Green  
Department of Applied Mathematics and Statistics  
Stony Brook University  
dfgreen@stonybrook.edu

## MS26

### 3D Continuum Modeling of Ion Permeation in Ion Channel Systems

As it is hard to apply all-atomic model to simulate the whole process of ion permeation in ion channel, we use continuum electrodiffusion description for ion flow in the channel system. Electrodiffusion process exists in many apparently different physical objects such as electrolyte cell, nanofluidic device, charged porous media, and ion channel in biology. Real 3D ion channel is particularly difficult to simulate due to the multiscale nature of the transport process and the complex geometry/boundary of the channel protein system. For this reason, there are so far only a few software publicly available in this important area of biology. We will present a software platform for ion channel simulations. The platform includes three parts: (1) finite element solver for the Poisson-Nernst-Planck equations and their improved forms, (2) molecular meshing that is required for finite element method. We recently developed a novel and robust molecular surface mesh generation tool TMSmesh that can handle complex and arbitrarily large biomolecular system. (3) a visual system, VCMM, for molecule, mesh and simulation data visualization and analysis. The platform is applied to compute properties such as current-voltage characteristics (curves) and conductance of a few channel systems, and the calculations are compared with Brownian Dynamics simulation and experimental results.

Benzhuo Lu, Bin Tu, Yan Xie  
Institute of Computational Mathematics, China  
bzlu@lsec.cc.ac.cn, tubin@lsec.cc.ac.cn, xieyan@lsec.cc.ac.cn

Linbo Zhang  
LSEC, Chinese Academy of Sciences

zlb@lsec.cc.ac.cn

## MS26

### Monte Carlo Solution of Biochemical Electrostatics Problems

Electrostatic forces and the electrostatic properties of molecules in solution are among the most important issues in understanding the structure and function of large biomolecules. The use of implicit-solvent models, such as the Poisson-Boltzmann equation (PBE), have been used with great success as a way of computationally deriving electrostatics properties such molecules. We discuss how to solve an elliptic system of partial differential equations (PDEs) involving the Poisson and the PBEs using path-integral based probabilistic, Feynman-Kac, representations. This leads to a Monte Carlo method for the solution of this system which is specified with a stochastic process, and a score function. We use several techniques to simplify the Monte Carlo method and the stochastic process used in the simulation, such as the walk-on-spheres (WOS) algorithm, and an auxiliary sphere technique to handle internal boundary conditions. We then specify some optimizations using the error (bias) and variance to balance the CPU time. We show that our approach is as accurate as widely used deterministic codes, but has many desirable properties that these methods do not. In addition, the currently optimized codes consume comparable CPU times to the widely used deterministic codes. Thus, we have an very clear example where a Monte Carlo calculation of a low-dimensional PDE is as fast or faster than deterministic techniques at similar accuracy levels.

Michael Mascagni

Computer Science/Computational Science  
Florida State University, Tallahassee  
mascagni@fsu.edu

## MS27

### Near Wall Motion of a Model Swimmer in a Viscoelastic Fluid

Microorganisms interacting in viscoelastic fluids are ubiquitous in nature; this includes bacteria colonizing in viscoelastic mucus in human and animal bodies, bacteria in biofilms grown on natural and manmade surfaces. Here is this work, we perform a three-dimensional direct numerical simulation of an archetypal low-Reynolds-number swimmer, squirmer, near a surface and investigate the role of viscoelasticity of the background fluid on the swimming speed and trajectory of the swimmer near the surface.

Gaojin Li, Alireza Karimi  
University of Notre Dame  
gli5@nd.edu, akarimi@nd.edu

Arezoo Ardekani

Notre Dame University  
Department of Aerospace and Mechanical Engineering  
arezoo.ardekani.1@nd.edu

## MS27

### Flagellar Kinematics in Complex Fluids: Viscous and Elastic Effects

The motility behavior of microorganisms can be significantly affected by the rheology of their fluidic environment. Here, we experimentally investigate the effects of fluid elas-

ticity on the swimming behavior of the microscopic alga *Chlamydomonas reinhardtii* and on the kinematics of its flagella. We find that the flagellar beating frequency and wave speed are both enhanced by fluid elasticity. Interestingly, the swimming speeds during the alga power and recovery strokes are enhanced by fluid elasticity for Deborah numbers larger than unity,  $De > 1$ . Despite such enhancements, however, the alga net forward speed is hindered by fluid elasticity by as much as 30% compared to Newtonian fluids of similar shear viscosities. We use slender body theory and Principal Component Analysis (PCA) to analyse ciliary waveforms and elucidate the role of fluid elasticity and viscous dissipation in regulating the kinematics of the swimming process.

Arvind Gopinath

MIT  
Mechanical Engineering  
arvind.gopinath@gmail.com

Boyang Qin

Mechanica Engineering and Applied Mechanics  
University of Pennsylvania, Philadelphia.  
qinb@seas.upenn.edu

Jing Yang

Department of Physics and Astronomy  
Haverford College, Haverford, PA 19041  
yangjing.uchc@gmail.com

Jerry P. Gollub

Haverford College  
Department of Physics  
jgollub@haverford.edu

Paulo E. Arratia

Mechanical Engineering and Applied Mechanics  
University of Pennsylvania, Philadelphia.  
parratia@seas.upenn.edu

## MS27

### Finite Length Undulatory Swimmers: Whether to Kick or to Burrow in a Viscoelastic Fluid

We explore finite length undulatory swimmers in viscoelastic fluids. The worm is modeled as an inextensible infinitely thin sheet in 2 dimensions and the swimming is driven using a prescribed target curvature. We look at front-back asymmetries in the prescribed stroke pattern and consider the effect on swimming speed and efficiency. The importance of passive dynamics, where swimmers are given prescribed torques rather than prescribed shapes, is explored. We show that kickers can get a larger boost from viscoelasticity than burrowers.

Becca Thomases

University of California at Davis  
thomases@math.ucdavis.edu

Robert D. Guy

Mathematics Department  
University of California Davis  
guy@math.ucdavis.edu

## MS27

### Lyme Disease and Microorganism Swimming in

## Complex Fluids

Lyme disease is caused by infection of the mammalian host by the highly invasive spirochete, *Borrelia burgdorferi*. These bacteria easily invade and colonize the dermis, joints, connective tissue, heart, and central nervous system. The motility of this organism is, therefore, crucial to the pathogenesis of the disease. I will describe experiments that we have been doing to measure the biophysical parameters of motility of these bacteria in realistic environments, such as matrices that mimic the ECM. These experiments show a number of interesting behaviors that are not predicted by recent theories of swimming in non-Newtonian environments. I will then describe the models and simulations that we have been using to describe the motility of this fascinating organism in complex environments. Using our data, we have also developed a mathematical model to elucidate pathogen-host interactions during early Lyme disease, which explains the spatiotemporal dynamics of the characteristic first sign of the disease, a large (5 cm diameter) rash, known as an erythema migrans (or EM). The model predicts that the bacterial replication and dissemination rates are the primary factors controlling the speed that the rash spreads, whereas the rate that active macrophages are cleared from the dermis is the principle determinant of rash morphology. In addition, the model supports the clinical observations that antibiotic treatment quickly clears spirochetes from the dermis and that the rash appearance is not indicative of the efficacy of the treatment. The quantitative agreement between our results and clinical data suggest that this model could be used to develop more efficient drug treatments and may form a basis for modelling pathogen-host interactions in other emerging infectious diseases.

Charles Wolgemuth  
University of Arizona  
Department of Physics  
wolg@email.arizona.edu

## MS28

### Shilnikov Cornerstone Bifurcation Generates a Family of Mechanisms Governing Dynamics of Central Pattern Generators

The cornerstone Shilnikov bifurcation generates a family of mechanisms that determines temporal characteristics of endogenously bursting, spiking, and silent neurons. We described a model of insect locomotion. The model gait is controlled by the burst duration and interburst interval of protractor and retractor interneurons. The transition from tetrapod to tripod gait is governed by the duty cycle of endogenously silent retractor interneurons, which fire in response to endogenously bursting protractor interneurons.

William H. Barnett  
Neuroscience Institute  
Georgia State University  
wbarnett2@student.gsu.edu

## MS28

### Using Experimental Phase Response Curves to Characterize Inter-Leg Coupling

Walking movements result from a complex interplay of central pattern generating networks (CPGs), local sensory feedback about movements and forces generated in the legs and coordinating signals from neighboring limbs. Cur-

rently, we use a combined experimental and computational approach to investigate the effect of specific front leg sensors onto the middle leg CPGs to gain a deeper insight into the inter-connection of the CPGs of all legs and into the processing of inter-leg sensory signals.

Silvia Daun-Gruhn  
Emmy-Noether Research Group, Department of Animal Physiology  
Zoological Institute, University of Cologne  
sgruhn@uni-koeln.de

Nils Rosjat, Tibor I. Toth  
Emmy-Noether Research Group  
University of Cologne  
nrosjat@uni-koeln.de, ttoth0@uni-koeln.de

## MS28

### Multiple Rhythms from One Network: Phase Plane and Stochastic Analyses of Rhythmic Activity in Turtle Motor Circuits

We analyze a central pattern generators ability to produce differing motor patterns from a single pool of neurons under different tonic drives, focusing on a particular motoneurons response to different phasic synaptic inputs. We study the impact of these phasic inputs on motoneuron phase space, associated trajectories and show how these yield sufficient conditions for reproduction of observed rhythms. We also present preliminary results from stochastic analysis to examine the role of strong synaptic conductances.

Abigail Snyder  
University of Pittsburgh  
acs73@pitt.edu

Jon Rubin  
University of Pittsburgh  
Department of Mathematics  
rubin@math.pitt.edu

## MS28

### Dynamical Architectures for Control of Rhythmic Behavior

How do rhythmic motor systems achieve both robustness to perturbations and sensitivity to variable operating conditions? Do limit cycle (LC) oscillators and chain reflexes (CR) capture two extremes along a continuum of central pattern generation models? We investigate the consequences of different dynamical architectures for incorporating sensory input in motor control, and quantitatively evaluate the advantages of intermediate architectures, such as stable heteroclinic channels, which combine features of both LC and CR dynamics.

Peter J. Thomas, Hillel Chiel, Jeffrey Gill  
Case Western Reserve University  
pjthomas@case.edu, hjc@case.edu, jpg18@case.edu

David Lyttle  
University of Arizona  
Program in Applied Mathematics  
dlyttle@math.arizona.edu

Kendrick Shaw  
Case Western Reserve University  
Department of Biology

kms15@case.edu

**MS29****Therapeutic Implications from a Multiscale Model of Blood Clot Degradation**

We develop a multiscale model of blood clot degradation to study safer, more effective treatments for stroke patients. With a microscale model of a single fibrin fiber, we study how individual activator and inhibitor molecules affect the degradation of the fiber. Data from this microscale model are used in a macroscale model of a full blood clot, where we study the effect of different treatment strategies on clot degradation.

Brittany Bannish  
Department of Mathematics  
University of Central Oklahoma  
bbannish@uco.edu

Aaron L. Fogelson, James P. Keener  
University of Utah  
fogelson@math.utah.edu, keener@math.utah.edu

**MS29****A Model-Based Comparison of Clinical and Biological Determinants for Anticoagulation Therapy**

We combine temporal models of coagulation and fibrinolytic pathways with warfarin pharmacokinetics and pharmacodynamics to study anticoagulation therapy. We compare two modeling frameworks to determine treatment efficacy: a traditional clinical assessment based on a simulated prothrombin time test and a biological assessment influenced by platelet activation and simplified chemical/cellular transport dynamics. We then discuss the roles of these assessment methods in the development and success of individualized treatment strategies.

Lisette G. dePillis  
Harvey Mudd College  
depillis@hmc.edu

Erica J. Graham  
North Carolina State University  
Department of Mathematics  
ejgraha2@ncsu.edu

Yanping Ma  
Loyola Marymount University  
yanping.ma@lmu.edu

Ami Radunskaya  
Pomona College  
Mathematics Department  
aer04747@pomona.edu

Julie Simons  
Tulane University  
Department of Mathematics  
jsimons@tulane.edu

**MS29****Structural Hierarchy Governs Nonlinear Mechanics of Fibrin Networks and Transport of Blood****Clotting Factors**

When a blood vessel ruptures, a hemostatic clot, consisting mainly of platelets and fibrin, is formed to restrict the loss of blood. Salutary blood clotting is highly regulated, but a pathological clot (thrombus) may form within a vessel and restrict blood flow to organs or clot pieces (emboli) can detach and be carried to the lungs, causing a life-threatening complication called pulmonary embolism. Fibrin network plays an important role in determining thrombus mechanical properties. It is responsible for thrombus integrity and redistribution of various mechanical loads acting on the thrombus due to blood flow and vessel deformations. Additionally, the structure of the network affects movement of blood clotting factors through the clot. This study demonstrates that structural changes in fibrin networks exposed to external load strongly correlate with networks mechanics. It is also shown that permeability of the fibrin network and protein diffusivity are important factors determining the transport of blood proteins inside the thrombus. The obtained results combining microfluidic experiments and thrombus hemodynamics model suggests that a fibrin network formed at early stages of thrombus initiation can prevent normally asymptomatic thrombi from developing into pathological clots.

Oleg Kim  
University of Notre Dame  
Dept of Applied and Computational Mathematics and Statistics  
oleg.v.kim.114@nd.edu

**MS29****Fibrin Polymerization in Flow: Gelation and Post Gelation Dynamics**

Blood clots are composed of platelets and a gel of fibrin fibers. The amount and structure of the fibrin fibers depend on conditions during their formation. In this presentation, I will discuss a 2-D advection-diffusion model for fibrin polymerization in flow that includes gelation and post gelation dynamics. Hindered diffusion and a Brinkman resistance term dependent on fiber properties, including branch point density and volume fraction, supply feedback in the system.

Cheryl Zapata-Allegro  
North Carolina State University  
zapata@math.utah.edu

**MS30****Recent Developments, Connections and Open Problems in Chemical Reaction Network Theory**

I'll give a brief overview of some recent developments in chemical reaction network theory, namely the study of the structure-dynamics relationship for chemical reaction networks (CRNs). The talk will outline the nature of conclusions which may be drawn about a CRN based primarily on network structure, and some of the challenges remaining: these include theoretical challenges, but also questions regarding the implementation of theory as algorithms. I will also discuss some connections between claims for mass action kinetics and for more general kinetics.

Murad Banaji  
University of Portsmouth

murad.banaji@port.ac.uk

### MS30

#### Persistence and the Global Attractor Conjecture

A positive trajectory of a dynamical system is called persistent if, in the long run, it does not approach the boundary of the positive orthant. In biological applications, the persistence property is critical in deciding if a species in an ecosystem will become extinct, an infection will die off, or a chemical species will be completely consumed by a reaction network. We describe some classes of dynamical systems for which all positive trajectories are persistent. We also describe connections to the global attractor conjecture, which says that a large class of mass-action systems (called complex balanced or toric dynamical systems) have a global attractor within any invariant subspace.

Gheorghe Craciun

Department of Mathematics, University of  
Wisconsin-Madison  
craciun@math.wisc.edu

### MS30

#### Monotonicity of Chemical Reaction Networks with Respect to Non-Simplicial Cones

The theory of monotone flows has been applied to numerous chemical reaction networks in recent years. A dynamical system is said to be monotone if states preserve a partial ordering as they evolve with time. Monotonicity restricts the possible asymptotics of dynamical systems: stable periodic orbits cannot exist in a monotone dynamical system, and it is frequently possible to draw stronger conclusions, such as generic convergence to equilibria. To date, most applications of the theory of monotone flows to chemical reaction networks focus on networks that are either cooperative, or can be made cooperative by applying a similarity transform to the state space. This talk will explore networks that cannot be made cooperative, yet are still monotone with respect to an ordering defined by a non-simplicial cone. The problem of identifying a suitable cone for a given network will be discussed, along with the consequences for the dynamics.

Pete Donnell, Murad Banaji

University of Portsmouth  
pete.donnell@port.ac.uk, murad.banaji@port.ac.uk

### MS30

#### Sign Vectors in Chemical Reaction Network Theory

Abstract not available at time of publication.

Stefan Mueller

RICAM, Austrian Academy of Sciences  
stefan.mueller@oeaw.ac.at

### MS31

#### Estimating the Functional Connectivity in Networks of Neurons

We will discuss the role of chaotic interplay among voltage gated neural dynamics and intracellular Calcium dynamics. In particular we have analyzed the issues that arise in determining unknown parameters in the dynamical equations of such models when presented with observed data.

Neither voltage data nor Calcium concentration data alone suffices to estimate properties of the model; two measurements are required. We show that both voltage and Ca measurements suffice or measurements based on the waveform of the time course of voltage will suffice. This has strong implications for experiment on neurons where both types of dynamics are present.

Henry D. Abarbanel

Physics Department  
Univ of California, San Diego  
habarbanel@ucsd.edu

### MS31

#### Using Mathematical Models to Determine the Source of Heterogeneity in Cellular Calcium Dynamics

Cell responses to stimuli are commonly heterogeneous. We describe a model-based technique for determining the source of the heterogeneity in the calcium response of pituitary lactotrophs to a calcium-mobilizing agonist. This method samples specific parameters to produce various responses, and then compares scatter plots of features of the response to features from experimental traces to determine the likely sources of response variability. This technique is applicable to any situation in which the heterogeneous biological response is described by a mathematical model.

Richard Bertram

Department of Mathematics  
Florida State University  
bertram@math.fsu.edu

Maurizio Tomaiuolo

University of Pennsylvania  
mtomai@mail.med.upenn.edu

Arturo Gonzalez-Iglesias

Department of Biological Science  
Florida State University  
iglesiasa@neuro.fsu.edu

Joël Tabak

Florida State University  
joel@neuro.fsu.edu

Henry D. Abarbanel

Physics Department  
Univ of California, San Diego  
habarbanel@ucsd.edu

### MS31

#### Heterogeneity As a Consequence of Homeostasis

A fundamental question in neuroscience is how neurons develop, control, and maintain their electrical signaling properties in spite of ongoing protein turnover and activity perturbations. I will introduce some recent modelling work that has tied together experimental data with long-standing questions about the inherent variability of neuronal properties. Interestingly, the model predicts pathological behavior that can arise as a consequence of homeostasis rather than a failure of it.

Timothy O'Leary

Brandeis University

toleary@brandeis.edu

### MS31

#### Inference of Network Structure from Spikes and Time Series

We discuss recent usage of data assimilation techniques to track and infer structure from networks of excitable cells. We emphasize methods that are statistical in nature in the sense of avoiding arbitrary thresholds, and that can be applied in real time to deal with nonstationary systems.

Timothy Sauer  
Department of Mathematical Sciences  
George Mason University  
tsauer@gmu.edu

### MS32

#### Contact and Transmission in Epidemiological Models

The mechanisms of contact leading to the transmission of pathogens from one host to another in a population shape the dynamics of an epidemic. Despite major modeling efforts at the population level in epidemiology; the mechanisms of contact and transmission remain poorly understood and their modeling remain typically rooted in models describing mixing of particles in homogeneous baths. Here, we discuss how a combination of theoretical and experimental approaches can be used to start reformulating the fundamental definitions and formulations of contact and transmission between hosts in a population.

Lydia Bourouiba  
Massachusetts Institute of Technology  
lbouro@MIT.EDU

### MS32

#### Economic Evaluation of the Fungal Meningitis Outbreak Response in New River Valley: Local Health Department and Clinical Perspectives

The objective of this study is to conduct an economic evaluation of the fungal meningitis outbreak response in New River Valley of Virginia from the local public health department and clinical perspectives. The multi-state fungal meningitis outbreak started during September 2012 in Tennessee. The immediate cause of the outbreak was injection of contaminated lots of methylprednisolone acetate used in epidural steroid injections. Roanoke and New River Valley were the epicenter of this outbreak in Virginia, with two clinical centers having administered the contaminated injections to their patients. New River Health District and local hospitals deployed their resources to control the regional impact of the outbreak, starting in October 2012. Public health personnel, in collaboration with clinicians in local hospitals, followed up the exposed patients for 6 months, and provided treatment including lab tests and hospitalizations. The health department continued the outbreak investigation until March 2013 to ascertain that all possible cases were identified and treated. None of the followed-up patients met the case definition, as defined by CDC. Based on preliminary analysis, the local health department expenditure is estimated to be \$30,493 and 73.5 years of disability adjusted life years are averted among the patients, for an incremental cost-effectiveness ratio of \$415 per disability adjusted life year averted. The estimated incremental cost effectiveness ratio assists the local

health department to prioritize and allocate limited public health resources. We are currently extending the analysis to include the clinical perspective.

Nargesalsadat Dorratoltaj  
Virginia Tech  
nargesd@vt.edu

Kaja Abbas  
Virginia Tech  
Department of Population Health Sciences  
kaja.abbas@vt.edu

### MS32

#### Mathematical Modeling of Cholera

Cholera was one of the most feared diseases in the 19th century, and remains a serious public health concern today. It can be transmitted to humans directly by person-to-person contact or indirectly through ingestion of contaminated water. Basic cholera models that include both direct and indirect transmission and assume homogeneous mixing in the host population will be reviewed. Detailed models that incorporate spatial heterogeneity will be applied to understand cholera transmission and to evaluate disease control strategies.

Zhisheng Shuai  
University of Central Florida  
shuai@ucf.edu

### MS32

#### Modeling Cholera in Heterogeneous Environments

We present some recent work in mathematical modeling of cholera, a severe water-borne infectious disease. Particularly, we discuss the impacts of spatial heterogeneity and seasonal variation on the transmission dynamics of cholera, using both mathematical analysis and numerical simulation. Based on a deterministic modeling framework that involves systems of ODEs and PDEs, we establish results of disease extinction and persistence for each model, and compare the threshold dynamics in homogeneous and heterogeneous settings.

Jin Wang  
Old Dominion University  
J3Wang@odu.edu

### MS33

#### Convergence Properties of Gauss-Newton Methods, Well-Posedness of Parameter Estimation Problems and the Reliability of Parameter Estimates

Parameter estimation from measurement data is crucial for model validation. After computing of the estimates the question arises about their reliability. It appears that reliability of the estimates is connected to a convergence rate of Gauss-Newton methods which present good local convergence in so-called small residual problems. We show that bad performance of Gauss-Newton in large residual problems is an advantage rather than a disadvantage of the method, since it indicates ill-posedness of problems.

Ekaterina Kostina  
Fachbereich Mathematik und Informatik  
Philipps-Universität Marburg

kostina@mathematik.uni-marburg.de

### MS33

#### Parameter Estimation for Large-Scale Biological Systems

As scientists continue to make discoveries in the biological sciences, the dynamical systems they are studying continue to grow in size and complexity. These increases make model fitting and parameter estimation more difficult. Hence, the effectiveness and efficiency of such techniques are crucial. This presentation shares a new parameter estimation technique designed to address some of the issues presented by large-scale biological systems by taking advantage of the sparsity often present in such systems.

Justin Krueger  
Department of Mathematics  
Virginia Tech  
kruege2@vt.edu

### MS33

#### Removing Irrelevant Parameters from Complex Biological Models

Parameter inference in biological systems often results in estimates with huge uncertainties. I discuss how these irrelevant parameter combinations can be systematically removed to reveal relevant combinations that govern the collective system behavior and can be accurately inferred from data. Using an information geometric approach, I recast the model reduction problem as a manifold approximation problem. The coarse-grained models vividly illustrate the emergent control mechanisms (e.g. feedback loops) that govern the system's behavior.

Mark K. Transtrum  
Department of Physics and Astronomy  
Brigham Young University  
mktranstrum@byu.edu

### MS33

#### Beyond Acceptable Parameter Fits

Biological time series contain enormous, but hidden information that needs to be extracted with computational means. This extraction is difficult, due to noise, large numbers of parameters, and computational issues. Furthermore, the typical criterion of squared residual errors is often insufficient, especially if the best-suited functional forms for describing the biological system are not known. The structural uncertainty complicates any estimation, but can be ameliorated if the right types of time series data are available.

Eberhard O. Voit  
Georgia Institute of Technology  
eberhard.voit@bme.gatech.edu

### MS34

#### Effect of Intraocular Pressure and Arterial Blood Pressure on Oxygen Saturation Levels in the Retina: a Theoretical Model

Impaired oxygen delivery to the retina has been shown to contribute to the retinal cell death characteristic of glaucoma. A mathematical model is used to predict retinal oxygen saturation as intraocular pressure (IOP) and mean

arterial pressure (MAP) are varied. Model predictions suggest that oximetry data from patients are not sufficient for distinguishing between the factors that alter saturation levels, since nearly identical venous saturation levels are predicted for various combinations of MAP and IOP.

Julia Arciero  
Department of Mathematical Sciences  
Indiana University-Purdue University Indianapolis  
jarciero@math.iupui.edu

Giovanna Guidoboni  
Indiana University-Purdue University at Indianapolis  
Department of Mathematical Sciences  
gguidobo@math.iupui.edu

Brent Siesky, Alon Harris  
Indiana University School of Medicine  
brentsiesky@gmail.com, alharris@indiana.edu

### MS34

#### Computational Modeling of Oxygen and ATP Transport in Skeletal Muscle Capillary Networks of Normal and Pre-Diabetic Rats

In skeletal muscle, capillaries are responsible for delivering oxygen and are involved in regulating the oxygen supply to meet tissue needs. A key mechanism in this regulation is oxygen-dependent release by red blood cells of the signaling molecule ATP, leading to changes in upstream arteriolar resistance and hence blood flow. We present an experiment-based model of oxygen and ATP transport in 3D capillary networks showing how oxygen delivery and RBC ATP-based regulation are disturbed in pre-diabetes.

Daniel Goldman  
University of Western Ontario  
Department of Medical Biophysics  
dgoldma2@uwo.ca

### MS34

#### Green's Function Methods for Simulating Solute Transport in the Microcirculation

Delivery of oxygen and other solutes to tissue is an essential function of the microcirculation, and is critically dependent on the spatial arrangement of microvessels. For numerical simulations involving realistic three-dimensional vascular network geometries, Greens function methods are more computationally efficient than finite-difference or finite-element methods, and are also advantageous with regard to the imposition of appropriate boundary conditions. Steady-state and time-dependent formulations will be presented and applications to several tissue types will be discussed.

Timothy W. Secomb  
University of Arizona  
secomb@u.arizona.edu

### MS35

#### Nonlinear Poisson-Nernst-Planck Equations for Ion Flux Through Confined Geometries

The mathematical modelling and simulation of ion transport through biological and synthetic channels is a challenging problem since at least two major effects have to be taken into account: the electrostatic interaction of ions and

the effects due to size exclusion in narrow regions. We investigate an important modification of the Poisson-Nernst-Planck (PNP) equations due to size exclusion, which is derived from a self-consistent random walk. Next we discuss the stationary solutions as well as the computation of conductance. The need of incorporating nonlinear mobilities in high density situations is demonstrated in an investigation of conductance as a function of bath concentrations, which does not lead to obvious saturation effects in the case of linear mobility.

Marie-Therese Wolfram

Department of Mathematics, University of Vienna  
mt.wolfram@ricam.oeaw.ac.at

### MS35

#### **New Effective Finite Element Algorithms for Solving Local and Nonlocal Poisson-Boltzmann Equations for Biomolecules in Ionic Solvent**

Calculation of electrostatic potential energy for biomolecule (such as protein and DNA) in ionic solvent is a fundamental task in computational biology. To reflect the polarization correlations among water molecules, nonlocal dielectric models were studied in the last thirty years, but only limited to the case of pure water solvent due to modeling and algorithmic difficulties. We recently overcome such difficulties and proposed a new nonlocal dielectric model for protein in ionic solvent, together with a fast finite element solver and an effective program package. In this talk, I will give these new progresses a short review. Specifically, a new nonlocal and nonlinear Poisson-Boltzmann Equation (PBE) model will be discussed in details. Since our nonlocal PBE model includes the classic local PBE model as a special case, our new finite element program package works efficiently and effectively not only for our nonlocal PBE model but also for the local PBE model. This project is a joined work with Prof. L. Ridgway Scott at the University of Chicago under the support by NSF grants (DMS-0921004, DMS-1226259, and DMS-1226019) and the UWM Research Growth Initiative.

Dexuan Xie

Department of Mathematical Sciences  
University of Wisconsin-Milwaukee  
dxie@uwm.edu

### MS35

#### **Fluctuation and Fidelity Control of Single Transcriptional Machine**

Polymerases catalyze gene replication and transcription. We investigated how polymerases achieve high fidelity efficiently by stepwise nucleotide selection. We noticed that early selections outperform the late ones in error reduction, while initial screening seems indispensable for maintaining speed. We studied T7 RNA polymerase in atomistic simulations, and found that substantial nucleotide selection happens prior to full insertion of the nucleotide for Watson-Crick base pairing. Our studies provide a kinetic framework along with molecular mechanisms.

Jin Yu

Beijing Computational Science Research Center,  
China

jinyu@csrc.ac.cn

### MS35

#### **Fast Pseudo-Time Simulations of the Nonlinear Poisson-Boltzmann (NPB) Equation**

Recently, we have developed a pseudo-time approach for solving the NPB equation. In the operator splitting framework, an analytical integration is conducted to suppress the nonlinear instability, and central differences are designed for both sharp and diffused molecular surfaces. Various time splitting schemes that reduce 3D linear systems into 1D ones, such as ADI, LOD, and AOS, have been examined for unconditional stability, accuracy, and efficiency so that a fast NPB solver can be built for biomolecular simulations of large proteins.

Shan Zhao

Department of Mathematics  
University of Alabama  
szhao@ua.edu

### MS36

#### **Swimming Through Heterogeneous Networks**

I will present results for swimmers moving near similar-size microstructural heterogeneities. First, spherical obstructions are used to deduce physical principles linking the swimmer flow field, forces on obstructions, and changes in swimming velocities. Then single rod-like obstructions are studied which are similar to the filaments of networks. Using these results, we deduce the effect of a network of filaments. Notably, swimming properties such as the variance of the swimming speed reflect the density and orientation correlations of the microstructure, and hence swimming properties can be used as probes of microstructure.

Henry Fu

University of Nevada, Reno  
Dept. Mechanical Engineering  
hfu@unr.edu

### MS36

#### **An Active Polar Nematic Model of Microtubule/motor-Protein Assemblies**

We develop a multiscale theory for a class of “bioactive” materials consisting of microtubules and motor-proteins. Brownian dynamics simulations are used to study microscopic organization and identifies two sources of active destabilizing stress: polarity-sorting and crosslink relaxation. A Doi-Onsager theory captures polarity sorting, and the hydrodynamic flows generated by active stresses. In simulating experiments of active flows on immersed surfaces, the model exhibits turbulent-like flows and generation and annihilation of disclination defects.

Tony Gao

Courant Institute of Mathematical Sciences  
New York University  
tgao@cims.nyu.edu

Michael J. Shelley  
New York University  
Courant Inst of Math Sciences  
shelley@cims.nyu.edu

Robert Blackwell, Matthew Glaser, Meredith Betterton

University of Colorado  
 robert.blackwell@colorado.edu,  
 matthew.glaser@colorado.edu,  
 ith.betterton@colorado.edu

mered-

will provide biological examples of oscillations generated by such linear inward currents. The stabilizing role that hyperpolarization-activated inward currents may play will also be discussed.

Jorge Golowasch

Dept of math sciences at NJIT and

Dept of biological sciences at Rutgers-Newark  
 golowasch@njit.edu

### MS36

#### **An Immersed Boundary Method for Two-fluid Mixtures**

We present an Immersed Boundary method for interactions between elastic boundaries and mixtures of two fluids. A penalty method is used to enforce the condition that both fluids' velocities agree with that of the elastic boundaries. The method is applied to several problems: Taylor's swimming sheet problem for a mixture of two viscous fluids, peristaltic pumping of a mixture of two viscous fluids, with and without immersed particles, and peristaltic pumping of a mixture of a viscous fluid and a viscoelastic fluid. Numerical results demonstrate that the method converges and show its capability to handle a number of flow problems of substantial current interest.

Robert D. Guy

Mathematics Department  
 University of California Davis  
 guy@math.ucdavis.edu

Jian Du

Department of Mathematics  
 Florida Institute of Technology  
 jdu@fit.edu

Aaron L. Fogelson

University of Utah  
 fogelson@math.utah.edu

### MS36

#### **Computational Models of Cilia and Flagella in a Brinkman Fluid**

The interaction between dynamic elastic structures and their surrounding fluid is important for sperm navigation and cilia beating within airways. We study a generalized Euler elastica immersed in a Brinkman fluid, a viscous fluid filled with a network of proteins. Regularized Greens functions for Brinkman flow are used to investigate emergent dynamics with preferred kinematics. Results are presented for swimming speeds, synchronization, and efficiency of flagella with planar waveforms in a Brinkman fluid.

Karin Leiderman

Applied Mathematics  
 UC Merced  
 kleiderman@ucmerced.edu

Sarah D. Olson

Worcester Polytechnic Institute  
 sdolson@wpi.edu

### MS37

#### **Linear Currents Can Be Pacemaker Currents**

Regenerative currents necessary for production of oscillatory activity are inward voltage-gated currents. I will show that voltage-dependence is not required. A linear current with negative conductance plus a voltage-gated recovery current are sufficient. We will discuss conditions that these currents need to satisfy for oscillations to be produced, and

### MS37

#### **Robustness and Multifunctionality of Reduced CPG Models**

CPGs stably produce bursting patterns underlying vital rhythmic behaviors. We developed analytical and computational tools reducing the problem of robustness and existence of rhythmic patterns to analysis of attractors in return maps for phase lags between bursters. We identify organizing centers determining CPG outputs and analyze their bifurcations as network circuitry varies. We study sustainability of networks by revealing statistics of rhythms switching due to random perturbations. Our findings are applicable for most oscillatory networks.

Aaron Kelley

GSU  
 aarnkelley@gmail.com

Justus T. Schwabedal

Division of Sleep Medicine, Brigham & Women's Hospital  
 Harvard Medical School  
 jschwabedal@gmail.com

Andrey Shilnikov

Neuroscience Institute and Department of Mathematics  
 Georgia State University  
 ashilnikov@gsu.edu

### MS37

#### **Differential Effects of Conductances on Pyloric CPG Output**

Central pattern generators are neuronal circuits that control rhythmic activities such as breathing and chewing. The output of such circuits can be characterized with relative ease, making them good candidates for studying regulation of neuronal activity at the network and single-cell levels. Our recent work characterizes the effect of specific conductances on the activity of the pacemaker kernel in the pyloric circuit of the crustacean stomatogastric ganglion through a series of computational and electrophysiological studies.

Wafa Soofi

Georgia Institute of Technology and Emory University  
 wsoofi@gmail.com

### MS37

#### **Identifying and Explaining Three Time Scale Oscillations**

CPGs may exhibit behavior, including bursting, involving multiple distinct time scales. Our goal is to understand bursting dynamics in three-time-scale systems, motivated by a model from respiratory CPG neuron. Using geometric singular perturbation theory, we explain the mechanisms underlying some forms of bursting dynamics in a three-

time-scale model. To elucidate which characteristics truly represent three-time-scale features, we investigate certain reductions to two time scales and the parameter dependence of solution features in the three-time-scale framework.

Yangyang Wang  
University of Pittsburgh  
yaw23@pitt.edu

Jon Rubin  
University of Pittsburgh  
Department of Mathematics  
rubin@math.pitt.edu

Vivien Kirk, Pingyu Nan  
University of Auckland  
v.kirk@auckland.ac.nz, pnan011@aucklanduni.ac.nz

### MS38

#### Translational Modeling and Optimal Concurrent Treatment in Oncology

Neutropenia caused by the indiscriminate nature of anti-cancer drugs is a dose-limiting consequence of chemotherapy which necessitates treatment adaptation. To avoid therapy interruption, granulocyte colony-stimulating factor (G-CSF) is administered during chemotherapy. This talk will outline the development of physiologically-based mathematical models of myelopoiesis in conjunction with pharmacokinetic and pharmacodynamic models of zalcypsis and filgrastim, and address their use in the optimisation of chemotherapeutic regimens with G-CSF.

Morgan Craig  
Faculté de Pharmacie  
Université de Montréal  
morgan.craig@umontreal.ca

Anthony Humphries  
McGill University  
humphries@math.mcgill.ca

Jacques Bélair  
Université de Montréal  
Département de Mathématiques  
belair@crm.umontreal.ca

Jun Li  
Université de Montréal  
li@crm.umontreal.ca

Michael Mackey  
McGill University, Canada  
michael.mackey@mcgill.ca

Fahima Nekka  
Université de Montréal, Faculté de Pharmacie  
Centre de Recherches Mathématiques  
fahima.nekka@umontreal.ca

### MS38

#### Systems Pharmacology: Revolutionizing Health Care One Equation at a Time

Similar challenges and questions arise in both the mathematical and pharmaceutical sciences. Unfortunately, differences in culture and approach sometime blur our com-

mon goal: Improving the health and well being of patients. This talk will discuss opportunities within the developmental pipeline where significant contributions can be made by classically trained mathematicians. We will address the unique challenges that pharmaceutical companies face within a highly regulated world and specific areas of greatest need. Novel and symbiotic research opportunities await those with the tools and vision for exploration in this interface where a systems approach to pharmacology is increasingly necessary.

Angelean O. Hendrix  
North Carolina State University  
angelean.o.hendrix@gsk.com

### MS39

#### Elimination of Intermediate Species in the Stochastic Reaction Networks

Biochemical reactions often proceed through the formation of intermediate species. These species are transient species, such as the substrate-enzyme complex appearing in Michaelis-Menten kinetics. For the sake of simplicity the intermediates are often ignored in the description of a reaction network, especially when they happen to be more unstable than the other species and they are degraded at a fast rate. It is not clear, however, whether this simplification can have consequences on the reliability of the model. We focus on stochastically modeled reaction networks and provide a rigorous asymptotic result for the elimination of the eventual intermediate species from the model. In our settings the intermediate species can only appear alone and with unitary stoichiometric coefficient in any reaction involving them. We define a suitable reduced system and we prove that the complete system tends to the reduced one in finite dimensional distribution when the rates of consumption of the intermediate species tend to zero. Further we show that our reduced system coincide with one obtained before in the deterministic settings, where the the number of equilibrium points were studied. Moreover, we extend our results to the situation when the non-intermediate species are described by a single scaled system. We only add the assumption that the rates of the intermediate consumption tend to infinity fast enough compared to the rates of their production.

Daniele Cappelletti, Carsten Wiuf  
University of Copenhagen  
d.cappelletti@math.ku.dk, wiuf@math.ku.dk

### MS39

#### Perturbations of the Lotka-Volterra System

We explore certain large perturbations of the Lotka-Volterra system, and show that they retain persistence, and even periodicity. This is an exploration of how persistence is affected by a reaction network not being endotactic.

Manoj Gopalkrishnan  
Tata Institute of Fundamental Research  
Mumbai, India  
manoj@tcs.tifr.res.in

Gheorghe Craciun  
Department of Mathematics, University of Wisconsin-Madison

craciun@math.wisc.edu

### MS39

#### Bistability in the Dual Futile Cyle

The idea has been around for some years that the system consisting of two successive phosphorylation/dephosphorylation loops exhibits bistability and on the level of heuristic and numerical investigations this can be seen as well-established. After surveying the existing results I will present a purely analytical proof (obtained together with Juliette Hell) that there exist parameter values for which this system has two stable stationary solutions. The methods used are bifurcation theory and geometric singular perturbation theory. I will then go on to discuss possible generalizations to a larger number of loops and to more complicated systems such as those modelling the MAP kinase cascade.

Alan Rendall

Johannes Gutenberg-Universität Mainz  
rendall@aei.mpg.de

### MS39

#### Reaction-Diffusion Equations With Periodic Behavior

We consider the Lotka-Volterra model and the Ivanova reaction. The ODE equations have explicit periodic solutions and equilibrium points. With equal diffusion rates, we give conditions for a solution to converge to a spatially homogeneous periodic solution.

David Siegel

University of Waterloo  
Department of Applied Math  
dsiegel@math.uwaterloo.ca

Blair Davey

University of Minnesota  
edavey@math.umn.edu

### MS40

#### On a Diffusive Predator-prey Model with Nonlinear Harvesting

In this talk, we study the dynamics of a diffusive Leslie-Gower model with a nonlinear harvesting term on the prey. We analyze the existence of positive equilibria and their dynamical behaviors. In particular, we consider the model with a weak harvesting term and find the conditions for the local and global asymptotic stability of the interior equilibrium. The global stability is established by considering a proper Lyapunov function. In contrast, the model with strong harvesting term has two interior equilibria and bistability may occur for this system. We also give the conditions of Turing instability and perform a series of numerical simulations and find that the model exhibits complex patterns.

Peng Feng

Florida Gulf Coast University  
pfeng@fgcu.edu

### MS40

#### Evolutionary Dynamics of a Population Model with

#### Component Allee Effects

We investigate the evolutionary outcomes of a single species prey population subject to component Allee effects within the framework of a continuous strategy evolutionary game theory (EGT) model. Our model assumes a single trait creates a phenotypic trade-off between carrying capacity and predator evasion ability following a Gaussian distribution. This assumption contributes to one of our interesting findings that evolution prevents extinction even when the population is subject to strong Allee effects. However, the extinction equilibrium can be an ESS under some special distributions of anti-predation phenotypes. The ratio of variation in competition and anti-predation phenotypes play an important role in determining the global dynamics of our EGT model: (a) evolution may suppress strong Allee effects for large values of this ratio; (b) evolution may preserve strong Allee effects for small values of this ratio; and (c) intermediate values of this ratio can result in multiple ESSs.

Yun Kang

Applied Sciences and Mathematics, Arizona State  
yun.kang@asu.edu

### MS40

#### An Application of Optimal Control Theory to a Simple Age-of-Infection Sir Model

Abstract not available at time of publication.

Sunmi Lee

Department of Applied Mathematics  
Yongin, Kyung Hee University, South Korea.  
sunmilee@khu.ac.kr

### MS41

#### Form-Function Relationship in *E. coli* Chemotaxis

Cell-to-cell variations in protein abundance in clonal cell populations are ubiquitous in living systems. Because protein composition determines responses in individual cells, it stands to reason that the variations themselves are subject to selective pressures. However, the functional role of these cell-to-cell differences is not well understood. One way to tackle questions regarding relationships between form and function is to perturb the form (e.g., change the protein abundances) and observe the resulting changes in some function. We take on the form-function relationship from the inverse perspective, asking instead what specific constraints on cell-to-cell variations in protein abundance are imposed by a given functional phenotype [1]. We develop a maximum entropy based approach to posing questions of this type and illustrate the method by application to the well-characterized chemotactic response in *Escherichia coli*. We find that full determination of observed cell-to-cell variations in protein abundances is not inherent in chemotaxis itself but, in fact, appears to be jointly imposed by the chemotaxis program in conjunction with other factors (e.g., the protein synthesis machinery and/or additional non-chemotactic cell functions, such as cell metabolism). These results illustrate the power of maximum entropy as a tool for the investigation of relationships between biological form and function. [1] Sayak Mukherjee, Sang-Cheol Seok, Veronica J. Vieland, and Jayajit Das, Proceedings of National Academy of Sciences **110** 18531 (2013).

Jayajit Das

Ohio State University

das.70@osu.edu

## MS41

### From Single Molecule Experiments to Coupled Molecules

Molecular motors convert chemical energy, often stored in the form of ATP, into mechanical energy, a vital activity for living cells. In particular, kinesin and dynein are two molecular motors that convey cargo, such as vesicles and organelles, along microtubules to where they are needed in the cell. This is especially important in neurons which can be up to a meter in length and where a breakdown in motor function has been implicated as a factor in neurodegenerative diseases. Since the early 1990's, experimentalists have been manipulating single motor molecules in vitro using laser traps. This has allowed detailed mechanical information to be gathered from isolated motors, at least in these non-physiological experimental conditions. In living cells, however, a single motor does not move a single cargo. Multiple motors, possibly both kinesin and dynein each biased towards opposite directions, are attached to a single cargo transporting it along the microtubule. A number of questions arise. How do different motors with opposing biases transport the cargo? How are cargos transported to the appropriate locations within the cells? Are there important regulatory proteins which affect this transport process? In this talk, we will discuss data emerging from these multi-motor/single cargo experiments and how information from single molecule experiments can be incorporated into the multi-motor analysis. In addition, we will discuss how these experiments can inform us about the underlying mechanisms which drive this multi-motor transport phenomena using a combination of stochastic models and statistical inference.

John Fricks

Dept of Statistics

Pennsylvania State University

fricks@stat.psu.edu

## MS41

### Estimating Velocity for Processive Motor Proteins with Random Detachment

Processive motor proteins are ATP-powered biological nanomachines that drive many forms of movement in living organisms. For example, kinesin and cytoplasmic dynein motors transport payloads, such as organelles or vesicles, through the cytoplasm of eukaryotic cells. The existence of eukaryotic organisms depends on these tiny motors because the passive process of diffusion is not sufficient to transport large and/or massive payloads through the crowded cytoplasm in a timely fashion. A motor protein overcomes these difficulties by hydrolyzing ATP in order to tow a cargo rapidly and in a directed path along a suitable substrate. An understanding of these motors could lead to important biomedical applications, e.g., anti-tumor technologies; treatments for neurodegenerative diseases; devices for blood testing and genetic screening; and treatments for diseases caused by motor protein defects. We show that, for a wide range of models, the empirical velocity of processive motor proteins has a limiting Pearson type VII distribution with finite mean but infinite variance. We develop maximum likelihood inference for this Pearson type VII distribution. In two simulation studies, we compare the performance of our MLE with the performance of standard Student's t-based inference. The studies show that incorrectly assuming normality (1) can lead to imprecise

inference regarding motor velocity in the one-sample case, and (2) can significantly reduce power in the two-sample case. These results should be of interest to experimentalists who wish to engineer motors possessing specific functional characteristics.

John Hughes

University of Minnesota

hughesj@umn.edu

## MS41

### Superresolution Microscopy As a Quantitative Tool

Protein-protein interaction is the basis for all of communication and information transfer in biology. Nonetheless, protein complexes –the basic interaction subunit– are difficult to image in living cells because of their size (tens of nm). Superresolution imaging methods are now commonly used to generate high resolution images of biological features about 10-100nm in size. We describe a strategy for turning superresolution imaging data into a quantitative tool to enumerate proteins in a complex.

Steve Presse

Indiana University Purdue University Indianapolis

spresse@iupui.edu

## MS42

### A Computational Method for Nearly Singular Integrals

We will describe a relatively simple method for computing singular or nearly singular integrals on a closed curve in 2D or a closed surface in 3D. This method can be used for Stokes flow, e.g., if values of velocity and pressure are needed at regular grid points. In work with Anita Layton, we have used this approach for a moving elastic interface in 2D Stokes flow. We have also devised a second-order accurate method for Navier-Stokes flow coupled with an interface, in which the velocity is decomposed into a Stokes velocity and a more regular part. The advantage is that the interaction of the interface with Stokes flow is much simpler to deal with than the full Navier-Stokes equations. Partially implicit motion of the interface can be used in either case to improve the time step.

J. Thomas Beale

Duke University

beale@math.duke.edu

## MS42

### A Treecode-Accelerated Boundary Integral Poisson-Boltzmann Solver for Electrostatics of Solvated Biomolecules

We present a treecode-accelerated boundary integral (TABI) solver for electrostatics of solvated biomolecules described by the linear Poisson-Boltzmann equation. The method employs a well-conditioned boundary integral formulation for the electrostatic potential and its normal derivative on the molecular surface. The surface is triangulated and the integral equations are discretized by centroid collocation. The linear system is solved by GMRES iteration and the matrix-vector product is carried out by a Cartesian treecode which reduces the cost from  $O(N^2)$  to  $O(N \log N)$ , where  $N$  is the number of faces in the triangulation. We find that the TABI solver exhibits good serial and parallel performance combined with relatively

simple implementation, efficient memory usage, and geometric adaptability.

Weihua Geng  
Southern Methodist University  
wgeng@mail.smu.edu

Robert Krasny  
University of Michigan  
Department of Mathematics  
krasny@umich.edu

## MS42

### On a Parallel Adaptive Fast Multipole Poisson-Boltzmann Solver

In this talk, I will present the mathematical analysis, numerical algorithms, and parallel implementation details of the Adaptive Fast Multipole Poisson-Boltzmann (AFMPB) solver. The package is available under open source license agreement.

Bo Zhang  
Duke University  
zhangb@cs.duke.edu

Xiaolin Cheng  
Oak Ridge National Laboratory  
chengx@ornl.gov

Jingfang Huang  
Department of Mathematics  
University of North Carolina, Chapel Hill  
huang@amath.unc.edu

Benzhuo Lu  
Institute of Computational Mathematics, China  
bzlu@lsec.cc.ac.cn

J Andrew McCammon  
University of California in San Diego  
Department of Chemistry and Biochemistry  
jmccammon@ucsd.edu

Nikos Pitsianis  
Department of Electrical & Computer Engineering  
Aristotle University  
nikos.pitsianis@eng.auth.gr

Xiaobai Sun  
Department of Computer Science  
Duke University  
xiaobai@cs.duke.edu

## MS42

### Surface-Tension Molecular Surfaces for Deployment in Boundary Element Electrostatic Calculations

Molecular surface generators that define the surface by a rolling probe inevitably produce regions with cusps and points, and are not suitable for BEM applications. The SMART algorithm was developed in our laboratory to avoid these issues with a guaranteed continuous surface normal. As an alternative to the rolling-probe approach, we have begun to explore physics-based surfaces whose results will be discussed, along with a new BEM implemen-

tation developed to handle large macromolecules.

Randy Zauhar  
Department of Chemistry & Bioc  
University of the Sciences in Philadelphia  
r.zauhar@usip.edu

## MS43

### Physiological Modeling in Hypertension and Heart Failure

In this talk, we present the application of a fluid mechanics model in drug development. The model is a cardiovascular circulation model which has enabled decisions on compounds in development. The circulation model integrates systemic, pulmonary and cardiac function, and is fit for the purpose of assessing questions arising in heart failure and hypertension drug development. In this presentation, we provide a description of the circulation model, and demonstrate its utility through some examples.

Karim Azer  
Applied Computer Science and Mathematics Dept.  
Merck & Co., Inc.  
Karim\_Azer@Merck.com

## MS43

### A Coupled Model of the Left Ventricle and the Systemic Arteries

A three-dimensional finite-strain model of a human left ventricle is coupled with a one-dimensional physiologically-based structured-tree model of the systemic arteries by matching the pressure and flow rate at the aortic root. The governing equations, which also incorporate fluid-structure interaction and active contraction of the myocardium, are solved using a combined immersed-boundary finite-element method, and a Lax-Wendroff scheme. The effects of changes in vascular compliance and rarefaction on blood pressure and flow are studied.

Nicholas A. Hill  
Department of Mathematics  
University of Glasgow, UK  
Nicholas.Hill@glasgow.ac.uk

Weiwei Chen, Hao Gao  
School of Mathematics and Statistics  
University of Glasgow  
w.chen.3@research.gla.ac.uk, hao.gao@glasgow.ac.uk

Boyce Griffith  
Leon H. Charney Division of Cardiology  
NYU Medical School  
boyceg@gmail.com

Xiaoyu Luo  
School of Mathematics and Statistics  
University of Glasgow  
xiaoyu.luo@glasgow.ac.uk

## MS43

### Comparison of Inflow Boundary Conditions for Ventriculo-Arterial Coupling in 3D and 1D Fluid-Structure Interaction Models

Each cardiac cycle the heart contracts and ejects blood into the systemic circulation. Coupled via the aortic

root, cardiac output into the systemic circulation is governed by both ventricular contractility and haemodynamic impedance of the systemic vasculature. Following a reduced-order coupling approach, a 0D model of cardiac contraction was implemented in 3D and 1D fluid-structure interaction frameworks. Using such models permits the examination of pressure wave propagation under altered physiological states of the heart.

Kevin D. Lau, Jordi Alastruey, C. Alberto Figueroa  
Department of Biomedical Engineering  
Kings College London  
kevin.lau@kcl.ac.uk, jordi.alastruey-arimon@kcl.ac.uk, alberto.figueroa@kcl.ac.uk

#### MS43

##### **Pulsatile Flow in the Entire Coronary Arterial Tree**

The hemodynamic analysis, based on the experimental measurements, plays an important role in the study of coronary circulation given millions of blood vessels in the vasculature. Here, I will show a mathematical model of pulsatile blood flow in the entire coronary arterial tree that is reconstructed from the measured morphometric data. The pathological states (i.e., left ventricular hypertrophy and congestive heart failure) are studied in relation to changes in model parameters and tree structures.

Huo Yunlong  
Department of Mechanics and Engineering Science  
Peking University, China  
yhuo@pku.edu.cn

#### MS44

##### **Modeling Interindividual Differences in Spontaneous Internal Desynchrony Patterns**

Using a physiological model of a sleep-wake regulatory network, we investigated the transition from typical human sleep patterns to spontaneous internal desynchrony. The model describes the neurotransmitter-mediated interactions among neuronal populations that promote wake, REM sleep and non-REM sleep, and the circadian pacemaker in the SCN. Model analysis suggests that similar mechanisms underlie different desynchronized behaviors, and that synchronization of sleep and circadian rhythms may depend on SCN modulation of REM sleep-promoting centers.

Victoria Booth  
University of Michigan  
Depts of Mathematics and Anesthesiology  
vbooth@umich.edu

Cecilia Diniz Behn  
Gettysburg College  
Dept of Mathematics  
cdinizbe@gettysburg.edu

#### MS44

##### **A Mathematical Model of the Wake/NonREM/REM States**

We propose a mathematical model for REM/NonREM dynamics with sleep/wake cycling that illustrates several features observed in humans during sleep. These include first falling into the NonREM stage, oscillating between it and the REM stage during the sleep period, and having four or

five REM bouts which become longer as the night progresses. This model is motivated by one presented by previous authors and is constructed using known neuronal groups involved with sleep and wake.

Selenne Garcia-Torres  
University of Southern California  
Department of Mathematics  
garciato@usc.edu

Janet Best  
The Ohio State University  
Department of Mathematics  
jbest@math.ohio-state.edu

Gemma Huguet  
Centre de Recerca Matemàtica  
Gemma.huguet@upc.edu

Alicia Prieto Langarica  
Youngstown State University  
aprietolangarica@ysu.edu

Shelby Wilson  
Morehouse College  
shelby.wilson@morehouse.edu

Pamela B. Fuller  
Rensselaer Polytechnic Institute  
Fullep@rpi.edu

#### MS44

##### **Spiking Neuron Vs. Neural Mass Models in the Context of Sleep-Regulatory Circuits**

Neural populations can be abstracted in different ways. Neural mass models assign macroscopic state variables to each neural population, whereas spiking neuron models simulate the dynamics of individual neurons. Both types of models are widely used, but it is not always clear under what conditions the two agree when it comes to predicting dynamics of real physiological systems. Here, we consider this problem in the context of sleep-regulatory circuits.

Andrew Phillips  
Brigham & Womens Hospital, Harvard Medical School  
ajphillips@partners.org

Victoria Booth  
University of Michigan  
Depts of Mathematics and Anesthesiology  
vbooth@umich.edu

Elizabeth B. Klerman  
Brigham and Women's Hospital & Harvard Medical School  
ebklerman@hms.harvard.edu

#### MS44

##### **Modeling the Effects of Temperature on Sleep Patterns**

Several studies have been done on human patients that suggest that different temperatures, such as room temperature, core body temperature, and distal skin temperature, have an important effect on sleep patterns, such as length and frequency of REM cycles. A mathematical model is created to investigate the effects of temperature on the

REM/NonREM dynamics. Our model was based on previous well established and accepted models of sleep dynamics and thermoregulation models.

Alicia Prieto Langerica  
The University of Texas at Arlington  
alicia.prietolangarica@mavs.uta.edu

Janet Best  
The Ohio State University  
Department of Mathematics  
jbest@math.ohio-state.edu

Gemma Huguet  
Centre de Recerca Matemàtica  
Gemma.huguet@upc.edu

Sellenne Garcia-Torres  
University of Southern California  
Department of Mathematics  
garciato@usc.edu

Shelby Wilson  
Morehouse College  
shelby.wilson@morehouse.edu

Pamela B. Fuller  
Rensselaer Polytechnic Institute  
Fullep@rpi.edu

#### MS45

##### **Disentangling Protein Fitness Requirements Using Computational Mutagenesis**

Although methods in comparative sequence analysis can measure conservation within a protein family, purely sequence-based methods cannot elucidate the reasons underlying conservation. To deconvolve the multiple roles of amino acids in protein fitness, we have adapted computational protein design algorithms for efficient large-scale mutagenesis, and compare this to alternative in silico modeling approaches. Our method is applied to a G-protein heterotrimer, and provides insight on amino-acid involvement in structural stability, and ligand- or protein-binding interactions.

Loretta Au  
Department of Applied Mathematics & Statistics  
Stony Brook University  
lau@ams.sunysb.edu

#### MS45

##### **A Mechanistic Model of the Bacterial Flagellar Motor**

The bacterial flagellar motor (BFM) drives swimming in many bacterial species. Using structural information from recent experiments, we propose a mechanism for the BFMs conversion of transmembrane ion potential into torque. We also address how the motor reverses the torque direction, allowing bacteria to reorient during chemotaxis. Additionally, we suggest a "mechanical homology" between the BFM and the only other known protein motor driven by a transmembrane ion potential: the Fo motor of ATP synthase.

Kranthi Mandadapu  
University of California, Berkeley

naani.m@gmail.com

Jasmine Nirody  
New York Medical College, NY  
jnirody@gmail.com

George Oster  
Molecular and Cellular Biology  
University of California, Berkeley  
goster@nature.berkeley.edu

#### MS45

##### **Decoding Information in Cell Shape**

Shape is an indicator of cell health. But how is the information in shape decoded? We hypothesize that decoding occurs by modulation of signaling through changes in plasma membrane curvature. Using analytical approaches and numerical simulations, we studied how elongation of cell shape affects plasma membrane signaling. Mathematical analyses reveal transient accumulation of activated receptors at regions of higher curvature with increasing cell eccentricity. In this talk, I will discuss the applicability of reaction-diffusion formulations in understanding the role of cell shape.

Padmini Rangamani  
University of California, Berkeley  
Department of Molecular and Cell Biology  
padmini.rangamani@berkeley.edu

#### MS45

##### **Conserved Enhancer Function When Sequence Is Not Conserved: Adventures with Cis-Regulatory Logic**

The blastoderm stage of *Drosophila* development affords unique advantages for the study of transcriptional control. The embryo can be used as a microarray in which the response of reporters to transcription factors can be quantitatively monitored at cellular resolution. With this data, we have constructed quantitative and predictive models of transcriptional control that shed light on the apparent paradox that conserved gene expression can be driven by highly diverged regulatory sequence.

John Reinitz  
Statistics Dept, Dept. of Ecology & Evolution  
The University of Chicago  
reinitz@galton.uchicago.edu

#### MS46

##### **From Within-Host to Between-Host Dynamics. Systems Biology of Epidemiology**

This talk explores an alternate mechanistic formulation of epidemiological dynamics based upon studying the influence of within-host dynamics in environmental transmission. A basic propagation number is calculated from the host-pathogen interaction; such quantification takes into account antigenic diversity and antigenic variation, and could guide public health policy.

Juan B. Gutierrez  
University of Georgia  
Department of Mathematics

juan@math.uga.edu

#### MS46

##### Modeling Drug Resistance in Metastatic Cancers

The development of drug resistance is a major challenge in the treatment of cancer. In this talk we will overview our recent results on studying the role of cell density and mutations on the dynamics of drug resistance in metastatic cancers. This is a joint work with Jim Greene, Orit Lavi, and Michael Gottesman.

Doron Levy

University of Maryland  
dlevy@math.umd.edu

#### MS46

##### The Impact of Decay in BedNet Efficacy over Time on Malaria Transmission

Insecticide-treated nets (ITNs) are at the forefront of malaria control programs. The potential impact of ITNs on reducing malaria transmission is limited due to inconsistent or improper use, as well as decay in effectiveness. We develop a mathematical model for malaria spread that captures the decrease in ITN effectiveness. We perform uncertainty and sensitivity analyses to identify and rank parameters that play a critical role in malaria transmission. These analyses show that the basic reproduction number  $R_0$ , and the infectious human population are most sensitive to bed-net coverage and the biting rate of mosquitoes. We consider the case in which ITN efficacy is constant over time as well as the case in which ITN efficacy decays over time.

Jemal Mohammed-Awel

Valdosta State University  
jmohammedawel@valdosta.edu

Calistus Ngonghala

National Institute for Mathematical and Biological  
Synthesis  
ngonghala@yahoo.com

Sara Del Val

Energy and Infrastructure Analysis, Los Alamos National  
Lab  
sdelvall@gmail.com

Ruijun Zhao

Minnesota State University, Mankato  
ruijun.zhao@mnsu.edu

#### MS46

##### Vector Dynamics and Its Impact on the Vector Borne Disease-Malaria

Mathematical models have extended our understanding of the biology and transmission dynamics of the vector borne disease malaria, dating back to the models of Sir Ronald Ross and George Macdonald. However, most models either treat the mosquito population density as a constant or do not model the reproductive gains that accrue to the mosquito's population as a result of its lifestyle, feeding and reproductive habits, as well as its interaction with the human population. The interaction between mosquitoes and humans introduce high variability in the mosquito population density and this variability affects both the mosquito

population and the disease dynamics. Using a mathematical model, I will highlight how the lifestyle of the *Anopheles* mosquito and the interaction between the mosquito and humans affect malaria transmission dynamics and introduce complexities not previously observed in unforced continuous time models. Implications for disease control will also be discussed.

Miranda I. Teboh-Ewungkem

Lafayette College  
mit703@lehigh.edu

#### MS47

##### A New Mathematical Model for Hepatitis C Infection: Derivation, Analysis and Implications

The hepatitis C virus was first identified in 1989 and mathematical models for HCV infection followed within a decade. Since then, many models have been proposed. Biological knowledge regarding HCV has also progressed recently and we use this to derive a new model of HCV infection. We analyse the steady states and bifurcations in this model and show how the solutions differ from those of other models. We then consider the implications for HCV treatment.

Philip J. Aston

University of Surrey  
Department of Mathematics  
P.Aston@surrey.ac.uk

#### MS47

##### Mathematical Modeling of Malignant Brain Tumor with T11 Target Structure As a Potent Immune Stimulator.

T11 Target structure, a membrane glycoprotein isolated from sheep erythrocytes, reverses the immune suppressed state of brain tumor induced animals by boosting the functional status of the immune cells. This study aims at aiding in the design of more efficacious brain tumor therapies with T11 target structure as a potent immune stimulator. We propose a mathematical model for brain tumor (glioma) and the immune system (microglial cells, cytotoxic T lymphocytes,  $TGF-\beta$ ,  $IFN-\gamma$ ) interactions, which aims in designing efficacious brain tumor therapy. The system undergoes sensitivity analysis, that determines which state variables are sensitive to the given parameters and the parameters are estimated from the published data. Computer simulations were used for model verification, which highlight the importance of T11 target structure in brain tumor therapy.

Sandip Banerjee

Indian Institute of Technology Roorkee (IITR)  
sandipbanerjee@gmail.com

#### MS47

##### Parameter Subset Selection and Generalized Sensitivities for a Model of Erythropoiesis

We present a model for erythropoiesis involving structured population models for the various cell stages involved. Since the model involves around 30 parameters and only limited data are available, it is necessary to investigate which parameters can be estimated with reasonable accuracy and how the collection of data can be improved within the given limitations. We show how recently devel-

oped methods for parameter subset selection and generalized sensitivity analysis can be applied.

Franz Kappel

Department of Mathematics and Scientific Computing  
University of Graz  
franz.kappel@uni-graz.at

#### MS47

##### **Deconvolution of Isotope Signals Mixed from Sampling Bundles of Multiple Hairs**

Hair records temporal information of body chemical signals, including stable isotopes. Multiple hairs are typically combined into a bundle to obtain enough material for analysis by segmentation. We developed a mathematical model to describe signal averaging from combining multiple hairs for analysis and an inverse method to estimate the original signal from measurements. The inverse method provides a refined interpretation of an oxygen stable isotope chronology from hair of an unidentified murder victim.

Christopher Remien

National Institute for Mathematical and Biological Synthesis  
University of Tennessee  
cremien@nimbios.org

Frederick Adler

University of Utah  
Mathematics Department & Biology Department  
adler@math.utah.edu

Lesley Chesson, Luciano Valenzuela, James Ehleringer, Thure Cerling

Department of Biology  
University of Utah  
chesson@biology.utah.edu, valenzuela@biology.utah.edu, jim.ehleringer@utah.edu, thure.cerling@utah.edu

#### MS48

##### **Competitive Geometric Evolution of Lipid Bilayers and Pores**

We discuss the competitive geometric evolution of co-existing complex structures in amphiphilic mixtures, modeled by the functionalized Cahn-Hilliard (FCH) equation. The system supports lipid bilayers, filamentous pores, micelles, and complex network structures. We analyze the geometric evolution laws of bilayers and pores, respectively, the mechanism under which they compete, and the possibility of co-existence.

Shibin Dai

New Mexico State University  
sdai@math.nmsu.edu

Keith Promislow

Michigan State University  
kpromisl@math.msu.edu

#### MS48

##### **Continuum Models of Membrane Protein Insertion and Stability**

Experimental and computational studies have shown that cellular membranes deform to stabilize the inclusion of transmembrane (TM) proteins harboring charge. Recent

analysis suggests that membrane bending helps to expose charged and polar residues to the aqueous environment and polar head groups. We previously used elasticity theory to identify membrane distortions that minimize the insertion of charged TM peptides into the membrane. Here, we extend our work to consider the energetics of ion and small peptide penetration into the membrane as well as large protein complexes. First, we show that our continuum method accurately reproduces energy profiles and membrane shapes generated from molecular simulations of bare ion permeation at a fraction of the computational cost. Importantly, we find that the energetics of membrane deformation strongly depend on membrane patch size both for ions and peptides. Finally, we present experimental and theoretical analysis that suggests that the antibacterial protein RegIIIa, a C-type lectin, forms channel like complexes that disrupt cellular homeostasis by inserting into membranes containing anionic lipids. We believe that our work presents a novel, computationally efficient method to simulate the effects of small molecules, peptides and large complexes with the membrane.

Michael Grabe

Department of Pharmaceutical Chemistry  
University of California, San Francisco  
michael.grabe@ucsf.edu

#### MS48

##### **On Minimizers of the Bending Energy of Two-Phase Biomembranes**

We consider the problem to find the shape of multiphase biomembranes, modeled as closed surfaces enclosing a fixed volume and having fixed surface area. The surface energy is assumed to be the sum of two terms: the Canham-Helfrich energy, in which the bending rigidities and spontaneous curvatures depend on the phase, and a line tension penalization for the phases interface. By restricting attention to axisymmetric surfaces and phase distributions, we prove existence of a global minimizer. This is a joint work with Rustum Choksi (McGill University, Montreal) and Marco Morandotti (Istituto Superior Tecnico, Lisbona).

Marco Veneroni

Department of Mathematics  
University of Pavia  
marco.veneroni@unipv.it

Rustum Choksi

Department of Mathematics  
McGill University  
rchoksi@math.mcgill.ca

Marco Morandotti

Carnegie Mellon University  
marcomor@andrew.cmu.edu

#### MS48

##### **Periodic Migration in a Physical Model of Cells on Micropatterns**

We extend a model for the morphology and dynamics of a crawling eukaryotic cell to describe cells on micropatterned substrates. This model couples cell morphology, adhesion, and cytoskeletal flow in response to active stresses induced by actin and myosin. We propose that protrusive stresses are only generated where the cell adheres, leading to the cell's effective confinement to the pattern. Consistent with experimental results, simulated cells exhibit a

broad range of behaviors, including steady motion, turning, bipedal motion, and periodic migration, in which the cell crawls persistently in one direction before reversing periodically. We show that periodic motion emerges naturally from the coupling of cell polarization to cell shape by reducing the model to a simplified one-dimensional form that can be understood analytically. Additionally, we will discuss a turning instability arising from our model applying onto a free moving cell without interaction with the micropatterned substrates. Some attempts have made to test how the instability depends on the parameters in the model numerically. For a much simplified model, we do find that surface tension is a key factor to stabilize the cell turning.

Yanxiang Zhao  
Department of Mathematics  
University of California, San Diego  
y1zhao@ucsd.edu

#### MS49

##### **Topological Tools for Detecting Hidden Geometric Structure in Neural Data**

Experimental neuroscience is undergoing a period of rapid progress in the collection of neural activity and connectivity data. This promises to allow more direct testing of a variety of theoretical ideas, and thus advance our understanding of "how the brain works." Detecting meaningful structure in neural data, however, remains a significant challenge. A major obstacle is that these data often measure quantities that are related to more "fundamental" variables by an unknown nonlinear transformation. This transformation obscures the underlying structure, diminishing the power of traditional linear algebra-flavored tools. Methods from computational topology, however, are often capable of detecting the hidden structure. We adapt these methods for the analysis of correlation matrices, and illustrate their use for testing the "coding space" hypothesis on neural data.

Carina Curto  
Department of Mathematics  
University of Nebraska-Lincoln  
ccurto2@math.unl.edu

#### MS49

##### **Topological Distances on DNA Knots and Links**

Topoisomerases and recombinases are two classes of proteins which can knot circular DNA. Type II topoisomerases are proteins which cut one double-stranded DNA segment, allowing a second DNA segment to pass through before resealing the break. This is mathematically modeled by changing a crossing. Recombinases break two segments of DNA, exchanging the DNA ends before resealing the breaks. This action can be mathematically modeled by smoothing a crossing. Distances between knots have been defined based upon the minimum number of times these proteins must act to convert one knot into another knot. Methods for calculating these distances will be discussed. Applications and ways to visualize and analyze these distances via graphs and KnotPlot will be discussed.

Isabel Darcy, Annette Honken  
Department of Mathematics  
University of Iowa

idarcymath@gmail.com, annette-honken@uiowa.edu

#### MS49

##### **The Topological Structure of the Mitochondrial Dna from Trypanosomes**

Trypanosomatid parasites are the cause of disease and death in many third world countries. One of the most unusual features of these organisms is the 3 dimensional organization of their mitochondrial DNA into maxi and minicircles. Here we investigate the effects of the confinement on the topology of the network using a simplified model where randomly oriented minicircles are placed on the plane with their centers on the vertices of the simple square lattice.

Yuanan Diao  
Department of Mathematics and Statistics  
University of North Carolina at Charlotte  
ydiao@uncc.edu

#### MS49

##### **Modeling Dna Packing with Confined Equilateral Random Polygons**

We introduce and study a model of equilateral random polygons confined in a sphere. DNA packed in a virus head motivates this model. The difference between the biologically observed topological characteristics and benchmark data created by our model reveals the bias of DNA packed in the viral capsids and possibly lead to a better understanding of the DNA packing mechanism.

Claus Ernst  
Department of Mathematics  
Western Kentucky University  
claus.ernst@wku.edu

#### MS50

##### **Build-Up and Neural Competition in a Model of Auditory Streaming**

A two-population rate model is built to study the perceptual organization of tones in the auditory cortex. When repetitive sequences of tones alternating between two frequencies are presented, the system's dynamics switches between two distinct states: (1) a coherent, galloping-like single stream ("integration"), and (2) two separate streams of constant pitch tones ("segregation"). The model accounts for the dynamics observed for such stimuli, in single unit recordings in monkey primary auditory cortex. The underlying mechanism for the build-up of the stream segregation is also investigated.

Rodica Curtu  
University of Iowa  
Department of Mathematics  
rodica-curtu@uiowa.edu

John M. Rinzl  
Courant Institute and Center for Neural Science  
New York University  
rinzeljm@gmail.com

#### MS50

##### **Modelling the Emergence and Dynamics of Percep-**

## tual Organisation in Auditory Streaming

Auditory perception solves the problem of associating causes with sound events by switching between alternative solutions. I present a model of auditory scene analysis at the core of which is a process that seeks to discover predictable patterns in the ongoing sound sequence. Representations are created on the fly, and maintained, strengthened or weakened depending on predictive success and conflict with other representations. Auditory perceptual organisation emerges spontaneously through the competition between these representations.

Sue Denham

Plymouth University, UK  
s.denham@plymouth.ac.uk

## MS50

### Bistable Auditory Perception: Neural Competition with Periodic Input

Spontaneous switches in perception occur for auditory stimuli where high A and low B tones are repeated in ABA-sequences [van Noorden 1975, Pressnitzer and Hupé 2006]. We extend a classical neural competition model to include periodic onset-like inputs and capture the parametric organisation of percepts reported in the psychoacoustics literature. We use the model to carry out a comparison study between bistability in auditory perception and other sensory modalities.

James Rankin, John Rinzel

New York University  
james.rankin@nyu.edu, rinzeljm@gmail.com

## MS50

### Diagnosing Excitation-inhibition Balance using Psychophysics

Excitation-inhibition imbalance is a potential cause of mental illness such as Autism. It is useful to understand how such a perturbation may be manifested in psychophysical tests, such as perceptual rivalry. Here, I will discuss recent experimental and theoretical work that makes this connection explicit.

Shashaank Vattikuti

National Institutes of Health, NIDDK  
vattikutis@niddk.nih.gov

Carson C. Chow

Laboratory of Biological Modeling  
NIDDK, NIH  
carsonc@niddk.nih.gov

## MS51

### Delay-Differential Equations in Cardiac Electrophysiology Models

In the heart, period-2 behavior of electrical responses, referred to as alternans, often gives rise to more complicated arrhythmias. To date, alternans has been generated mathematically from coupled nonlinear ODE/PDE systems. We use the fact that delays arise naturally in non-instantaneous cellular processes to suggest an alternative approach using delay-differential equations (DDEs), which are known to promote complex dynamics. We analyze the dynamical behaviors of our DDE system and discuss the

implications of our findings.

Elizabeth M. Cherry, Ryan Thompson

Rochester Institute of Technology  
School of Mathematical Sciences  
excsma@rit.edu, rpt1914@rit.edu

## MS51

### Experimentally-based Modified Cable Equation That Reproduces Alternans Measured in Cardiac Tissue

We incorporate a data-based model to regulate gap junction conductance by transjunction potentials into the cable equation. This modification results in a dynamic decrease of gap-junction conductance during the action potential (AP) plateau, which lowers coupling at high membrane potentials without altering AP restitution dynamics and conduction velocities. Inclusion of a voltage-dependent gap-junction conductance in the cable equation allows spatial alternans to develop in realistic tissue sizes without altering other predictions from the cable equation.

Flavio Fenton, Yanyan Ji

Georgia Institute of Technology  
flavio.fenton@physics.gatech.edu, yji47@gatech.edu

## MS51

### Effects of Intracellular Sodium Accumulation on Cardiac Reentry Dynamics

The morphology and duration of cardiac action potentials is controlled partly by ionic currents that depend on intracellular sodium concentration. We demonstrate how the dynamics of cardiac reentry vary with intracellular sodium accumulation and how this plays a special role in simulated chronic atrial fibrillation.

Trine Krogh-Madsen

Cornell University - Weill Medical College  
trk2002@med.cornell.edu

Margo Smith

Cornell University - Weill Medical College Division of Cardiology  
margo.lee.smith@gmail.com

David Christini

Cornell University - Weill Medical College  
Division of Cardiology  
dchristi@med.cornell.edu

## MS51

### The Role of Feedback and Heart Rate Variability on Cardiac Rhythm Stability

Cardiac dynamics is usually analyzed under the assumption of periodic stimulation, i.e. in the presence of feedback. However, under physiological conditions, the heart rate exhibits substantial variations in time, known as heart rate variability (HRV), which introduces deviations from periodic stimulation. We incorporated HRV into pacing protocols, both with and without feedback, and investigated the role of HRV and feedback on rhythm stability using numerical simulations of an ionic model of the cardiac action potential.

Elena Tolkacheva

Department of Biomedical Engineering  
University of Minnesota  
talkacal@umn.edu

Stephen McIntyre  
University of Minnesota  
mcint144@umn.edu

Yoichiro Mori  
School of Mathematics  
University of Minnesota  
ymori@umn.edu

## MS52

### Stochastic Dynamics in Signal Transduction, Stem Cells, and Development Patterning

Abstract not available at time of publication.

Qing Nie  
University of California at Irvine  
qnie@math.uci.edu

## MS52

### Mathematical Models for Stem Cell Interactions

Abstract not available at time of publication.

Jianjun Paul Tian  
Mathematics Department  
College of William and Mary  
jptian@math.wm.edu

## MS52

### Computation of Transition State and Its Applications in System Biology

Abstract not available at time of publication.

Lei Zhang  
Department of Math  
University of California, Irvine,  
zhangl@math.pku.edu.cn

## MS52

### Numerical Studies on Cell Lineage Models

Multistage cell lineages, typically comprising of a stem cell stage and several subsequent progenitor cell stages (also referred to as transit-amplifying or TA cells), underlie the production of different terminally differentiated (TD) cell types within a tissue. Genetic studies and tissue culture experiments have shown that control of stem and progenitor cell proliferation and differentiation, which ultimately control the TD cell number, is mediated by secreted morphogens through feedback regulation. In this talk, I shall present our recent work on using numerical simulations of advection-reaction-diffusion model to study the formation and regeneration of intestinal crypts, which is based on our early model on tissue stratification patterning of the olfactory epithelium of the mouse. This is a joint work with Tian Jiang (University of Notre Dame), Lei Zhang (Peking University), and Qing Nie (University of California, Irvine).

Yongtao Zhang  
University of Notre Dame

yzhang10@nd.edu

## MS53

### Mathematical Model of Community-Acquired and Hospital-Acquired Methicillin-Resistant Staphylococcus Aureus Transmission in Hospital Settings

In this paper a deterministic model to quantifying the interactions of community-acquired and hospital-acquired methicillin-resistant staphylococcus aureus transmission in a hospital settings is developed. The model include environmental contaminants and isolation of colonized and infected patients. The reproduction number is determined and sensitivity analysis is carried out to determine the impact of model parameters to various outputs. The results of the stochastic version of the deterministic model is discussed.

Folashade Augusto  
Austin Peay State University  
fbagusto@gmail.com

## MS53

### Optimizing Vaccine Allocation for Influenza

The emergence of the 2009 H1N1 influenza A strain and delays in production of vaccine against it illustrate the importance of optimizing vaccine allocation. We have developed computational optimization models to determine optimal vaccination strategies with regard to multiple objective functions: e.g. deaths, years of life lost, economic costs. Looking at single objectives, we have found that vaccinating children, who transmit most, is robustly selected as the optimal allocation. I will discuss ongoing extensions to this work to incorporate multiple objectives and uncertainty.

Jan Medlock  
Oregon State University  
jan.medlock@oregonstate.edu

## MS53

### Malaria Vaccine Efficacy in a Region with Naturally Acquired Immunity

The advent of malaria vaccines raises the question of how effective vaccination will be in regions with naturally acquired immunity (NAI). Our malaria model incorporating vaccination and NAI suggests that disproportionately treating non-immune individuals increases the likelihood of subthreshold endemic equilibria, a dangerous scenario that increases the risk for malaria epidemics and renders vaccination ineffective. Additionally, optimal control theory suggests that efforts to vaccinate should increase as the level of NAI in a population decreases.

Olivia Prosper  
Dartmouth College  
prosper.olivia@gmail.com

Nick Ruktanonchai  
University of Florida  
Department of Biology  
nrukt00@gmail.com

Maia Martcheva  
University of Florida

maia@ufl.edu

## MS53

### A Two-Patch Avian Influenza Model

Abstract not available at time of publication.

Omar Saucedo

University of Florida  
Department of Mathematics  
osaucedo1987@ufl.edu

## MS54

### Optimizing Hiv Treatment In a Resource Limited Settings

Antiretroviral drugs have a clinical benefit of substantially reducing infectiousness thus making them potentially an important strategy in the fight against AIDS. Recent advances in drug therapy have seen the use of antiretroviral medications as a prophylaxis. In this study, we constructed a compartmental heterosexual transmission model based on the dynamics of HIV in heterosexual population in Sub-Saharan. The model classifies the male and female populations by risk (low, medium and high) according to their sexual preferences. Data from South Africa was used to parameterize the model. For a finite amount of drugs we implemented a numerical optimization algorithm to find optimal allocation of the drugs that minimizes objective functions such as Total Number of Deaths and Total Number of Infections. Preliminary results suggest that, the priority should be given to the high-risk females during drug allocations to minimize the number of deaths or infection per year

Gordon Akudibillah, Jan Medlock

Oregon State University  
akudibig@onid.oregonstate.edu,  
jan.medlock@oregonstate.edu

## MS54

### The Impact of Spatial Arrangements on Intervention Strategies in Epidemic Models

The role of spatial arrangements in a metapopulation on the spread and optimal intervention strategies of a cholera epidemic is investigated. We consider how human and pathogen movement affects the optimal vaccination strategy. For each patch, the model has an SIR system of differential equations coupled with an equation modeling the concentration of *Vibrio cholerae* in an aquatic reservoir. The model will be used to compare two basic spatial arrangements of populations along a water source. The work is motivated by the recent cholera outbreak in Haiti. Optimal control results are found numerically.

Michael Kelly

University of Tennessee - Knoxville  
Mkelly14@utk.edu

## MS54

### Optimal Control and Analysis of a Coupled Ode/pde Immuno-Epidemiological Model

Optimal control can be used to design intervention strategies for the management of infectious diseases, and has been applied in immunological and epidemiological models separately. We formulate an immuno-epidemiological

model of coupled within-host model of ODEs and between-host model of ODE and PDE. Existence and uniqueness of solution to the between-host model is established, and an explicit expression for the basic reproduction number of the between-host model is derived. Stability of disease-free and endemic equilibria of the between-host model is investigated. An optimal control problem with drug-treatment control on the within-host system is formulated and analyzed. Numerical simulations based on the forward-backward sweep method are obtained.

Eric Numfor

University of Tennessee  
numfor@math.utk.edu

## MS54

### Inferring Equation Models from Agent-Based Model Data

Abstract not available at time of publication.

Matthew Oremland

Virginia Tech University  
moremlan@vt.edu

## MS55

### Numerical Simulations of Fluctuating Vesicles in Linear Flow

In this talk, we present the fluctuation dynamics of a 2D vesicle in extensional flow. In the quasi-circular limit, we derive a Langevin type SDEs. We then simulate a vesicle dynamics using an immersed boundary method, and achieve good agreement with the theoretical predictions for the equilibrium deformation correlations. Preliminary results show that thermal noise can change the characteristic wavelength of the wrinkles, and prevent the rotation of a tilted vesicle in extensional flow.

Shuwang Li, Kai Liu

Department of Applied Mathematics  
Illinois Institute of Technology  
sli@math.iit.edu, kliu11@iit.edu

## MS55

### Electromechanics of Bilayer Membrane: Forces and Fast Algorithms

Lipid bilayers appear ubiquitously in living systems. Defining and computing the forces on lipid membranes is critical to understanding how these systems operate. In this talk, the electrostatic potential energy for membrane-protein interactions is defined and used to compute the dielectric boundary force via the shape derivative. We then describe a fast algorithm for minimizing the electromechanical energy of vesicles using a spherical harmonic parameterization of the membrane surface. We conclude with examples and numerical results.

Michael Mikucki

Department of Mathematics  
Colorado State University  
mikuckimonster@comcast.net

## MS55

### Three Dimensional Vesicle Electrohydrodynamics:

## A Numerical Investigation

The dynamics of three-dimensional vesicles when exposed to electric fields is complex. There is a nonlinear relationship between the material parameters and the shape of the vesicle. This talk will present a numerical method developed to investigate the electrohydrodynamics of three-dimensional vesicles is presented. This represents a first step towards modeling the electroporation of vesicles in a general, fully three-dimensional framework. Here, the numerical method will be outlined and an investigation of vesicle dynamics will be shown.

David Salac

University at Buffalo - SUNY  
davidsal@buffalo.edu

Ebrahim M. Kolahdouz  
SUNY Buffalo  
mkolahdo@buffalo.edu

## MS55

### A Continuum Model for Simulating Bilipid Membrane Deformation During Vesicle Drying

Bilipid membranes are of interest due to their similar dynamics to certain cells under flow and the ability to manufacture them in a lab. Modeled as a homogeneous, continuum material, the deformation of a vesicle undergoing drying is studied. The level set method is modified to explicitly capture the curvature in order to avoid stability issues when calculating curvature derivatives. The results will guide lyopreservation approaches, where cell drying is used as a storage technique.

Chris Vogl

Department of Applied Mathematics, University of Washington  
chris.j.vogl@gmail.com

## MS56

### Flexibility-Rigidity Index for Protein Flexibility Analysis

We introduce a simple method, flexibility-rigidity index (FRI), to analyze macromolecular flexibility and rigidity in atomic detail. The FRI measures the topological connectivity of protein atoms or residues and characterizes the geometric compactness of the protein structure. The FRI bypasses matrix diagonalization, which underpins most other flexibility analysis methods and FRI's computational complexity is of  $O(N^2)$  at most, where  $N$  is the number of atoms, in contrast to  $O(N^3)$  for Hamiltonian based methods.

Kristopher Opron

Department of Biochemistry and Molecular Biology  
Michigan State University  
kopron@gmail.com

## MS56

### Knotting in Open Chains, Closed Chains, and Proteins

Some proteins are now classified as being knotted. However, proteins have free ends and knotting, mathematically, is only defined for closed curves. Defining knotting in open chains (like proteins) is tricky and ambiguous. We show one definition of open knotting and search for knotted arcs

within knotted open chains, closed chains, and proteins. This is joint work with Ken Millett, Andrzej Stasiak, and Joanna Sulkowska.

Eric Rawdon

Department of Mathematics  
University of St. Thomas  
ejrawdon@stthomas.edu

## MS56

### Unlinking of Supercoiled DNA Catenanes by Type IIA Topoisomerases

It was found recently that DNA catenanes, formed during replication of circular plasmids, become positively (+) supercoiled, and the unlinking of such catenanes by type IIA topoisomerases proceeds much more efficiently than the unlinking of negatively (-) supercoiled catenanes. In an attempt to explain this striking finding we studied, by computer simulation, conformational properties of supercoiled DNA catenanes. Although the simulation showed that conformational properties of (+) and (-) supercoiled replication catenanes are very different, these properties per se do not give any advantage to (+) supercoiled over (-) supercoiled DNA catenanes for unlinking. An advantage became evident, however, when we took into account the established features of the enzymatic reaction catalyzed by the topoisomerases. The enzymes create a sharp DNA bend in the first bound DNA segment and allow for the transport of the second segment only from inside the bend to its outside. We showed that in (-) supercoiled DNA catenanes this protein-bound bent segment becomes nearly inaccessible for segments of the other linked DNA molecule, inhibiting the unlinking.

Alexander Vologodskii

Department of Chemistry  
alex.vologodskii@nyu.edu

## MS56

### Invariant Manifold and Persistent Homology for Biomolecules.

We introduce molecular nonlinear dynamics (MND) as a theoretical framework for describing protein folding. We unveil the existence of intrinsically low dimensional manifolds (ILDMS) in the chaotic dynamics of folded proteins. We reveal that the transition from disordered to ordered conformations in protein folding increases the transverse stability of the ILDM, which yields some the best quantification of protein uncertainty or protein thermal factors. Persistent homology is employed to characterize protein folding pathways and protein flexibility. The predicted cut-off distance is highly consistent with the numerical results from our ILDM model and other state-of-art methods.

Guo-Wei Wei

Department of Mathematics  
Michigan State University  
wei@math.msu.edu

Kelin Xia

Department of Mathematics Michigan State University  
xiakelin2010@gmail.com

## MS57

### Fluid-Composite Structure Interaction in Hemody-

**namics**

The speaker will talk about modeling and simulation of FSI between an incompressible, viscous fluid and a composite structure. Examples include FSI between blood flow and arterial walls, which are composed of several layers, each with different mechanical characteristics, and FSI between blood flow, arterial walls, and vascular devices called stents. A stable loosely coupled scheme will be introduced, and numerical results, showing novel features of this class of FSI problem, will be discussed.

Suncica Canic

Department of Mathematics  
University of Houston  
canic@math.uh.edu

Martina Bukac  
University of Pittsburgh  
Department of Mathematics  
martinab@pitt.edu

Boris Muha  
Department of Mathematics, Faculty of Science  
University of Zagreb  
borism@math.hr

**MS57****Transport in the Embryonic Lung II**

Numerous studies have led to the identification of genes and morphogens that play important roles in lung branching morphogenesis. However the mechanism by which these signaling molecules regulate lung branching is not fully understood. It is also known that physical processes such as transport of morphogens could drive biological responses during development. Thus, in this study, we utilize a computational model to investigate the role of solute transport in lung morphogenesis.

Uduak Z. George  
University of Wisconsin  
uzgeorge@ncsu.edu

Kishore Krishna Bokka, Sharon Lubkin  
North Carolina State University  
kbokkas@ncsu.edu, lubkin@ncsu.edu

**MS57****Transport in the Embryonic Lung I**

Airway peristalsis (AP) begins as soon as the smooth muscle forms, and persists until birth. We analyze a model of the fluid-structure interactions between embryonic tissues and lumen fluid resulting from peristaltic waves that partially occlude the airway. We conclude that AP has a strong effect on flow sensing away from the tip and on transport of morphogens. These effects may be the intermediate mechanisms for the enhancement of branching seen in occluded embryonic lungs.

Kishore Krishna Bokka, Sharon Lubkin  
North Carolina State University  
kbokkas@ncsu.edu, lubkin@ncsu.edu

**MS57****Role of the Pericardium in the Tubular Hearts of****Tunicates**

Tubular hearts of tunicates have a stiff, outer pericardium that encloses a layer of myocardium which contracts to drive fluid flow through the tube. Most models of heart function have not included the pericardium or its possible contributions to the fluid flow produced by myocardial contractions. Here I present both experimental and model evidence that the pericardium fulfills an important mechanical role in the tunicate hearts ability to produce fluid flow through the circulatory system.

Lindsay Waldrop

University of North Carolina at Chapel Hill  
lwaldrop@email.unc.edu

**MS58****Integration of Information over Multiple Timescales in a Large-scale Model of the Cortex**

Models of the neural mechanisms of decision-making typically focus on local circuits operating within a single functionally-defined cortical area. To move beyond this, we study the dynamics of distributed decision-making in an anatomically-constrained model of multiple interacting areas in the macaque cortex. The anatomical constraints produce a hierarchical architecture where cortical areas are optimized to integrate information over different timescales. We investigate how such dynamical heterogeneity can be combined to allow flexible decision-making.

Rishidev Chaudhuri, Jorge F. Mejias, Xiao-Jing Wang  
New York University  
rishidev.chaudhuri@gmail.com, jorge.f.mejias@gmail.com, xjwang@nyu.edu

**MS58****Network Symmetry and Binocular Rivalry Experiments**

This talk discusses a generalized network model for rivalry proposed by Hugh Wilson. The application shows how symmetry-breaking Hopf bifurcation can lead to rigid phase-shift synchrony in periodic solutions of coupled systems of differential equations that in turn can predict percepts in a variety of binocular rivalry experiments.

Martin Golubitsky

Ohio State University  
Mathematical Biosciences Institute  
mg@mbi.osu.edu

Casey Diekman  
Department of Mathematical Sciences  
New Jersey Institute of Technology  
casey.o.diekman@njit.edu

**MS58****Noise and Adaptation in Multistable Perception: A Case Study with Tristable Visual Plaids**

We study the dynamics of perceptual switching in ambiguous visual scenes that admit more than two interpretations to gain insight into the dynamics of perceptual multistability and their underlying neural mechanisms. We focus on a classical paradigmatic stimulus, the visual plaids, consisting of two superimposed drifting gratings with transparent intersections. For visual plaids, tristable perception is

experienced: one coherent percept (the gratings move together as a single pattern) and two transparent percepts (the gratings slide across one another) with alternating depth order. In order to decipher the complex mechanisms of tristable perception, we gathered a large amount of psychophysical data on tristable plaids and developed a firing-rate model based on mutual inhibition and adaptation that involves stochastic dynamics of multiple-attractor systems. The model can account for the dynamical properties (transition probabilities, distributions of percept durations, etc) observed in the experiments. Noise and adaptation have been shown to both play a role in the dynamics of bistable perception. Here, tristable perception allows us to specify the role of noise and adaptation in our model. Noise is critical when considering the time of a switch. However, adaptation mechanisms are critical when considering perceptual choice (in tristable perception, each time a percept ends, there is a possible choice between two new percepts).

Gemma Huguet  
Centre de Recerca Matemàtica  
Gemma.huguet@upc.edu

John M. Rinzel  
Courant Institute and Center for Neural Science  
New York University  
rinzeljm@gmail.com

Jean-Michel Hupé  
Toulouse University & CNRS  
jean-michel.hupe@cerco.ups-tlse.fr

## MS58

### Networks That Learn the Timing of Event Sequences

We discuss a neuronal network model capable of learning the timing of a sequence of events, each of which lasts milliseconds to seconds. Short term facilitation is a second-timescale accumulation process that controls switching between events. Long term plasticity allows the network to learn event timings quickly and accurately. Time scale separations, between the plasticity processes and neuronal activity dynamics, allow us to describe how long term plasticity parameters should depend upon short term facilitation parameters for the network to be able to learn **any** sequence of timings.

Alan Veliz-Cuba  
University of Houston  
Rice University  
alanavc@math.uh.edu

Kresimir Josic  
University of Houston  
Department of Mathematics  
josic@math.uh.edu

Zachary Kilpatrick  
University of Houston  
zpkilpat@math.uh.edu

## MS59

### Intramural Forecasting of Cardiac Electrical Dynamics Using Data Assimilation

As a first step in reconstructing the three-dimensional

propagation and breakup of electrical waves, a data-assimilation system is coupled to a simple model of cardiac electrical dynamics. Data assimilation is a technique—common in numerical weather prediction—for combining observations with a numerical model to derive an improved estimate of the state of a dynamical system. Here an ensemble Kalman filter is used on synthetic data for both 1D and 3D models.

Matthew J. Hoffman, Stephen Scorse  
Rochester Institute of Technology  
mjhsma@rit.edu, sts2766@rit.edu

Elizabeth M. Cherry  
Rochester Institute of Technology  
School of Mathematical Sciences  
excsma@rit.edu

## MS59

### Microscale Modeling of Cardiac Tissue

Focal activity in localized regions of cardiac tissue with poor, heterogeneous gap junction coupling can lead to long conduction delays, isolated wavefront breakthrough sites, and reentry as the wavefront propagates into healthy surrounding tissue. In this study we use two-dimensional, microstructural computer models of ventricular monolayers (1 cm x 1 cm) to investigate the effect of modulating sodium and calcium currents on the formation of breakthrough sites and the development of sustained reentry.

Letitia Hubbard  
Duke University  
mlh23@duke.edu

Craig Henriquez  
Dept of Biomedical Engineering  
Duke University  
ch@duke.edu

## MS59

### Predicting Arrhythmias with a Nonlinear Cardiac Fiber Model

A dynamical model of a cardiac fiber was developed to help investigate the relationship between premature beats and ventricular fibrillation (VF), a lethal cardiac arrhythmia. When tested with canine ventricular data, the model was shown to predict which patterns of premature beats were more likely to produce VF *in vitro*. In addition, model-predicted spatial changes in action potential duration were positively correlated with the observed values.

Laura Munoz  
Rochester Institute of Technology  
School of Mathematical Sciences  
lmmsma@rit.edu

Niels Otani  
Rochester Institute of Technology  
nfosma@rit.edu

Anna Gelzer  
Department of Biomedical Sciences  
Cornell University  
arg9@cornell.edu

Flavio M. Fenton

Georgia Institute of Technology  
flavio.fenton@physics.gatech.edu

Weiye Lin, Min Chul Shin  
Department of Biomedical Sciences  
Cornell University  
wyl7@cornell.edu, ms929@cornell.edu

Robert Gilmour, Jr.  
University of Prince Edward Island  
rgilmour@upei.ca

#### MS59

##### **Compositionality Results for Cardiac Cell Dynamics**

We show that the 13-variable Markovian sodium-channel component of the 67-variable Iyer Mazhari Winslow cardiac cell model can be replaced by an approximately equivalent 2-variable Hodgkin-Huxley-type abstraction. This substitution of (approximately) equals for equals is safe in the sense that the approximation error between the sodium channel models does not get amplified by the feedback-loop context in which the components are placed. The proof entails automatic computation of Lyapunov-like functions that characterize input-to-output stability of dynamical systems.

Md. Ariful Islam, Abhishek Murthy  
Computer Science  
Stony Brook University  
mdaislam@cs.stonybrook.edu,  
amurthy@cs.stonybrook.edu

Antoine Girard  
Université Joseph Fourier  
antoine.girard@imag.fr

Scott Smolka  
Computer Science  
Stony Brook University  
sas@cs.stonybrook.edu

Radu Grosu  
Vienna University of Technology  
radu.grosu@tuwien.ac.at

#### MS60

##### **Spatial-Temporal Regulation of the First Embryonic Development Decision**

Abstract not available at time of publication.

William Holmes  
Department of Mathematics  
University of California, Irvine  
wrholmes@uci.edu

#### MS60

##### **Analysis and Simulations of a Three Dimensional Model of Cell Signal Transduction**

We consider a model of cell signal transduction in a spherical cell. Signal molecule production is restricted to specific areas of the cell. We use asymptotic analysis to construct an system of ordinary differential equations which approximate the full partial differential equation. We then con-

sider the effect of adding in a delay to the production of signal molecules and analyze the resulting Hopf bifurcation.

David Iron  
Dalhousie University, Canada  
iron@mathstat.dal.ca

#### MS60

##### **Time to Mutation Acquisition in Stem Cell Driven Cancers**

Abstract not available at time of publication.

Alexandra Jilkine  
University of Notre Dame  
ajilkine@nd.edu

#### MS60

##### **Mathematical Modeling of Proliferation Kinetics of Cancer Stem Cells**

Abstract not available at time of publication.

Xinfeng Liu  
University of South Carolina  
xliu@math.sc.edu

#### MS61

##### **Detailed Viral Kinetics During Liver Transplantation Indicates that the Liver Plays a Role in HCV Clearance**

While the liver is widely accepted as the main site for hepatitis C virus (HCV) production, its role in the clearance of circulating HCV remains unknown. By analyzing and modeling HCV kinetics during liver transplantation we were able to shed light on the function of the liver in clearing free virus from the circulation. In vitro experiments in HCV-infected hepatocytes support in part our findings.

Harel Dahari  
Loyola University Medical College  
Chicago  
harel.dahari@gmail.com

#### MS61

##### **Silibinin As a Drug for Hepatitis C in Patients with Compromised Liver**

Hepatitis C patients with compromised liver and those awaiting liver transplant rarely respond to standard therapy. Silibinin lowered viral load in such patients in two pilot clinical trials. We use treatment data from these studies to understand the mode of action, efficacy and compare these between the two cohorts. We also aim at describing Hepatitis C viral kinetics in patients treated with Silibinin, according to severity of liver disease, from the two clinical trials.

Swati Debroy  
University of Missouri -Kansas City  
debroy.swati@gmail.com

Harel Dahari  
Loyola University Medical College  
Chicago  
harel.dahari@gmail.com

Laetitia Canini  
5Theoretical Biology and Biophysics, Los Alamos  
National Lab  
Los Alamos, NM 87545  
laetitia.canini@gmail.com

Zoe Marino  
3Liver Unit, CIBERehd, IDIBAPS. Barcelona, Spain  
zmarino@clinic.ub.es

Gonzalo Crespo, Miquel Navasa  
Liver Unit, CIBERehd, IDIBAPS. Barcelona, Spain  
gcrespo@clinic.ub.es, mnavaa@clinic.ub.es

Massimo D'Amato  
Rottapharm SpA, Monza  
Italy  
massimo.damato@rottapharm.com

xavier Forns  
Liver Unit, CIBERehd, IDIBAPS. Barcelona, Spain  
xforns@clinic.ub.es

Scott Cotler  
Loyola University Medical College  
scotler@lumc.edu

Alan S. Perelson  
Los Alamos National Laboratory  
asp@lanl.gov

## MS61

### Role of Methamphetamine in Transmission Dynamics of HIV in MSM Population

Methamphetamine is an addictive stimulant that releases high levels of neurotransmitter dopamine. The use of methamphetamine have shown to increase libido and reduces inhibition. As a result, methamphetamine is commonly used among men who have sex with men to initiate, enhance, and prolong sexual encounters. This, in turns, promotes high risk sexual behavior in this community of methamphetamine users which increases the risk of acquiring an STD. Furthermore, studies have shown that the use of methamphetamine is associated with more frequent risky sexual behaviors among HIV positive men when compared with HIV negative men. This study seeks

to evaluate the dynamics of the methamphetamine abuse and HIV incidence through the stability analysis. The reproduction number of the system is identified. All parameters are approximated and the system is explored by simulations. The implications of preventative measures will be discussed.

Aprillya Lanz  
Norfolk State University  
700 Park Avenue Norfolk, VA 23504  
alanz@nsu.edu

## MS62

### Developing Fit-for-purpose Physiological Models in Drug Discovery and Development - A Framework for Qualification Best Practices

Physiological models are used in drug discovery and development programs to enable decisions such as dose selection, risk assessment, or competitive strategy. We have

developed a framework for the qualification of physiological models, which employ statistical or other techniques to explain variability from various sources. The adoption and application of this framework will support the goals of effective physiological model development, communication, and increased acceptance of physiological models for enabling critical decisions.

Karim Azer  
Applied Computer Science and Mathematics Dept.  
Merck & Co., Inc.  
Karim\_Azer@Merck.com

Jeff Sachs  
Merck Research Laboratories  
Quantitative Pharmacology and Pharmacometrics  
jeff\_sachs@merck.com

Stefan Willmann  
Bayer Technology Services  
stefan.willmann@bayer.com

Carolyn Cho  
Merck & Co., New Jersey  
carolyn.cho@merck.com

Thomas Kerbusch, Antonio Cabal  
Merck Research Laboratories  
Quantitative Pharmacology and Pharmacometrics  
thomas.kerbusch@merck.com, antonio.cabal@merck.com

Christopher Gibson  
Merck Research Laboratories  
PPDM  
christopher.gibson@merck.com

Sandra Sandra Allerheiligen  
Merck Research Laboratories  
Quantitative Pharmacology and Pharmacometrics  
sandra.allerheiligen@merck.com

## MS62

### A Sensitivity Based Statistical Approach to Parameter Selection and Uncertainty Quantification

We discuss both global and local sensitivity analysis in the context of statistical approaches (requiring a good statistical model as well an adequate mathematical model) to assessing and quantifying the effect of known and unknown parameters in complex systems. We use recently developed parameter subset techniques to investigate the impact of estimated parameters on the corresponding selection scores and uncertainty. These ideas are presented in the context of an in-host model for HIV-1 infection dynamics developed and validated with patient data.

H. T. Banks  
CRSC, NC State University  
htbanks@ncsu.edu

## MS62

### Application of Modelling and Simulation in Oncology: Physiologically-based Pharmacokinetics and Dynamics Examples

A physiologically-based model applicable for oncological questions in drug development was developed by use of the systems biology platform including PK-Sim and MoBi.

It includes representation of all relevant processes and its typical variability for small molecules and biologics at a physiological level.

By means of different examples it will be demonstrated that such models are able to represent the pharmacokinetics and related tumor growth dynamics in preclinical species and to provide useful insight into scenarios relevant for the clinic including exploration and separation of variability and uncertainty by the model process.

Michael Block

Bayer Technology Services GmbH  
Technology Dev., Enabling Tech., Comp. Sys. Bio.  
michael.block@bayer.com

**MS62**

**Leveraging Visualization and Probabilistic Thinking to Get Consensus on an Assay Level Target for a Cancer Drug**

Quantitative thresholds can support effective clinical oncology program decisions. Such thresholds are often derived from preclinical and (sparse) clinical data. Here, nonlinear mixed-effect modeling allowed integration of variability and uncertainty in data, and enabled simulations identifying an biochemical assay level (threshold) predictive of clinical efficacy. A kernel-based probabilistic model integrating these simulations captured the necessary phenomena. The model allowed non-mathematical visualization enabling effective collaboration with the development team on the complex, multi-dimensional, probabilistic data.

Jeff Sachs, Jos Lommerse, Jeroen Elassaiss - Schaap  
Merck Research Laboratories  
Quantitative Pharmacology and Pharmacometrics  
jeff\_sachs@merck.com, jos.lommerse@merck.com,  
jeroen.elassaiss-schaap@merck.com

Yali Zhu  
Merck Research Laboratories  
Quantitative Pharm & PMx (current: Hurley Consulting)  
yzhu@hurleyconsulting.com

**MS63**

**Chemical Insights, Matrix Approximations, and Boundary-Integral Equations**

Abstract not available at time of publication.

Jaydeep P. Bardhan  
Department of Electrical and Computer Engineering  
Northeastern University  
jbardhan@ece.neu.edu

**MS63**

**Geometry of Surfaces in the Protein Images and the Graph Algorithms**

Abstract not available at time of publication.

Jing He  
Computer Science Dept.  
NMSU, Las Cruces, NM

jinghe@cs.nmsu.edu

**MS63**

**Protein Modeling from Intermediate-Resolution Density Maps Using Geometric Skeletons**

This talk will present our continuing work on protein modeling from density maps that are captured at intermediate resolutions (6-10Å), which have become increasingly available for imaging macromolecular complexes. Our work computes and makes use of the geometric skeleton of the density map to automate several model-building tasks, including detecting secondary structure elements, identifying their topology on the backbone, and flexibly fitting probe structures into the map. The algorithms are distributed in our open-source tool, Gorgon.

Tao Ju

Washington University in Saint Louis  
Department of Computer Science & Engineering  
taoju@cse.wustl.edu

**MS63**

**Accurate Electrostatics in 3D Classical Dft**

Abstract not available at time of publication.

Matthew G. Knepley  
University of Chicago  
knepley@ci.uchicago.edu

**MS64**

**Surface Tension in Human Lungs: Modeling and Experiments**

Naturally produced surfactant, which lowers surface tension is required for normal human lung function. Premature babies born before surfactant production begins, are at risk for respiratory distress, and often require surfactant replacement therapy. For 20 years mathematicians and scientists have sought to model the complicated flow of fluid lining the passageways and alveoli of the lungs. New experiments allow us to visualize a simplified system that includes a thin film of glycerol and a surface layer of surfactant. This talk will describe what we can learn from such experiments, how the results compare to a commonly accepted model, and how we might modify the experiments to better capture dynamics in the lungs.

Rachel Levy  
Harvey Mudd College  
levy@hmc.edu

Karen Daniels  
North Carolina State University  
kdaniel@ncsu.edu

Ellen Swanson  
Centre College  
ellen.swanson@centre.edu

Stephen Strickland  
North Carolina State University  
slstric2@ncsu.edu

Peter Megson, Shreyas Kumar  
Harvey Mudd College

peter.megson@gmail.com, shreyas.kumar@gmail.com

Auburn University  
lzd0005@auburn.edu

## MS64

### Fluid Dynamics of the Tracks of Tears

In humans, tears are used to wash away irritants, lubricate the eye, and express emotion. The chemical makeup of tears, as well as their mechanical properties, also varies. In addition to changes in chemical properties, the path that the tear exists the eye can change from the corner of the eye to directly over the lid and eyelashes. In this presentation, we use high-speed video to construct simple models of the dynamics of different tears.

Laura A. Miller

University of North Carolina - Chapel Hill  
Department of Mathematics  
lam9@email.unc.edu

## MS64

### Modeling and Simulation of Biofilm Flows

Biofilms are ubiquitous in nature. It consists of bacteria, polysaccharides, water and nutrient. Bacteria are live organisms while polysaccharides, also known as EPS, are biopolymers that cross-link into a resilient network encasing the bacteria. In this talk, we will report our efforts in developing a hydrodynamic theory to study the viscoelasticity of the EPS and how they interact with the live bacteria and the host solvent matrix. Different bacterial phenotypes and quorum sensing effect will be considered in the model. 3-D numerical simulation will be carried to benchmark the model with some available experiments.

Qi Wang, Jia Zhao

University of South Carolina  
qwang@math.sc.edu, zhao62@mailbox.sc.edu

## MS64

### Biofilm Pattern Formation Within Microfluidic Chambers

Recently, many biological phenomena involving complex mechanical and biochemical interactions of multiple components have been successfully modeled using a multiphase framework, including tumorigenesis, cell motility, and developmental processes. In this talk, I will present a two-dimensional multiphase model of the biofilm formation by *Xylella fastidiosa*, the causative agent of Pierce's Disease. Numerical simulations of this model demonstrate the regular spatial patterning observed in microfluidic experiments representing an artificial plant xylem.

Mark E. Whidden

Florida State University  
mwhidden@math.fsu.edu

Nick Cogan, Matt Donahue  
Department of Mathematics  
Florida State University  
cogan@math.fsu.edu, mdonahue@math.fsu.edu

Fernando Navarrete  
Auburn University  
fzn0001@auburn.edu

Leonardo de La Fuente  
Department of Entomology and Plant Pathology

## MS65

### Optimal Control in PDE/DE Model for an Anthrax Epizootic

Anthrax is a fatal, infectious disease which occurs in many animal species, particularly land mammals. It is a cause of population decline in several national parks worldwide such as in bison at northern Canada in 1993. Due to the ability for anthrax spores to survive in soil for a long time even under harsh conditions, clearing anthrax spores from the environment is practically impossible. As infected animals die, their carcasses contribute bacteria in the surrounding environment. Proper disposal of the carcasses and effectively controlling new infections are feasible ways to help control the disease. In this talk, I will present some preliminary results of these measures of controlling the spread of the disease.

Buddhi Pantha

University of Tennessee, Knoxville  
pantha@math.utk.edu

Suzanne M. Lenhart  
University of Tennessee  
Department of Mathematics  
lenhart@math.utk.edu

## MS65

### Habitat and Abundance Modeling of West Nile Virus Vector

Mosquito-borne disease incidence is particularly influenced by climate through two main pathways. First, climate dictates the habitat available for breeding, immature development, and adult resting. Second, fluctuations in temperature and precipitation drive pathogen and mosquito development as well as changes in availability of breeding habitat. As a result of these associations researchers can predict where mosquitoes and mosquitoes-borne diseases are likely to occur and, using dynamic simulation models, researchers can estimate mosquito abundance for specified locations (i.e., climates). Such estimations facilitate our understanding of disease dynamics and spread. Using the mosquito-borne West Nile Virus disease as a case study, I will discuss how spatial and temporal models can be used to understand emerging diseases and where they fall short in our ability to predict new invasions.

Heidi Brown

University of Arizona  
heidibrown@email.arizona.edu

## MS65

### Parameter Estimation and Model Discrepancy with Application to the Life Sciences

In this presentation we consider the problem of parameter estimation for systems governed by ordinary and delay differential equations and discuss the impact of modeling errors which are an important source of model discrepancy. We present an approach based on assuming the model is defined as a dynamical system with uncertain disturbances. This approach can be used to develop prior knowledge about model discrepancy in order to improve

the models predictive usefulness.

John A. Burns, Eugene Cliff  
Virginia Tech  
Interdisciplinary Center for Applied Mathematics  
jaburns@vt.edu, ecliff@vt.edu

## MS65

### Basic Reproductive Ratios in Ecosystems and Disease Models

In this talk, we will discuss the basic reproductive ratios in ecosystems and disease models. In general, for a periodic differential system with time delay, it is difficult to obtain explicit formula for the basic reproductive ratio in terms of model parameters. We will provide a novel technique in finding approximate formulas for basic reproductive ratios in various ecosystems and disease models.

Xiang-Sheng Wang  
Southeast Missouri State University  
Cape Girardeau, MO 63701, USA  
xswang@semo.edu

## MS66

### Probability of Extinction in Stochastic Models of Populations and Infectious Diseases: Importance of Time and Location

Multitype branching process theory is used to estimate the probability of population or disease extinction in multi-patch, multi-group, and multi-stage models. The success of a species invasion or of a disease outbreak often depends on the conditions of the environment at a specific time and location. Applications of the theory are discussed in terms of several zoonotic diseases.

Linda J. Allen  
Dept. of Mathematics and Statistics  
Texas Tech University  
linda.j.allen@ttu.edu

## MS66

### How Fish Ecology Affects the Effectiveness of Marine Protected Areas

MPAs (Marine Protected Areas) are regions where fishing is restricted or prohibited. As a fisheries management tool, their purpose is to protect overharvested species and their habitats. Assume that the fish population consists of a predator and a prey. One system of nonlinear ODEs describes the predator-prey interaction in the MPA where fishing is prohibited. A similar but different system describes the interaction of predator and prey in the Fishing Grounds where fishing is allowed. Now assume that both predator and prey can move between MPA and Fishing Ground, in a way that mimics Fick's albeit in an ODE context. How does the resulting coupled model, consisting of 4 nonlinear ODEs behave? I will show that the coupling tends to stabilize the system. In the special case that the prey is immobilized, but the predator can move, I will outline a proof showing global stability based on the construction of a Lyapunov function, in conjunction with Lasalle's invariance principle. I will also discuss when diffusion is equalizing.

Patrick DeLeenheer  
Oregon State University

deleenhp@science.oregonstate.edu

## MS66

### Optimal Control Applied to Hospital-Acquired and Community-Acquired Methicillin-Resistant Staphylococcus Aureus Strains in Hospitals

Optimal control are applied to a deterministic mathematical model to characterize the factors contributing to the replacement of hospital-acquired Methicillin-resistant Staphylococcus aureus (MRSA) with community-acquired MRSA, and quantify the effectiveness of three interventions aimed at limiting the spread of CA-MRSA in health care settings. Adjoint equations and the characterization of the optimal control strategies are established, and various numerical simulations are provided to illustrate the results.

Wandi Ding  
Department of Mathematical Sciences  
Middle Tennessee State University  
wandi.ding@mtsu.edu

Glenn Webb  
Department of Mathematics  
Vanderbilt University  
gglen.f.webb@vanderbilt.edu

## MS66

### Optimal Control of Continuous Systems with Impulse Controls

Impulse control problems, in which a continuously evolving state is modified by discrete control actions, have applications in epidemiology, medicine, and ecology. In this paper we present a simple method for solving impulse control problems for systems of differential equations. In particular, we show how impulse control problems can be reformulated and solved as discrete optimal control problems. The method is illustrated with two examples.

Rachel Leander  
Middle TN State University  
rachel.leander@mtsu.edu

S.M. Lenhart  
University of Tennessee, Knoxville  
lenhart@math.utk.edu

Vladimir A. Protopopescu  
Oak Ridge National Laboratory  
vvp@ornl.gov

## MS67

### Combined Parameter and State Estimation in Ensemble Kalman Filters

Ensemble Kalman filtering techniques have traditionally been developed to perform state estimation for nonlinear dynamical systems with fixed parameters. However, in many biological applications, there is often uncertainty in the model parameter values. We propose a method for estimating the system parameters along with the states in an ensemble Kalman filter framework. The effectiveness of the resulting algorithm is demonstrated in estimating the maximum reaction rates and affinity constants of Michaelis-Menten flux expressions in a model for skeletal

muscle metabolism.

Daniela Calvetti  
Case Western Reserve Univ  
Department of Mathematics  
dxc57@case.edu

Andrea N. Arnold  
Case Western Reserve University  
Dept. of Mathematics, Applied Mathematics and  
Statistics  
ana33@case.edu

Erkki Somersalo  
Case Western Reserve University  
ejs49@case.edu

### MS67

#### **Model Calibration in Systems Biology: Making the Most of Limited Data**

The field of Systems Biology was developed in response to experimental advances that allow system-level observations of intracellular networks. While such high-throughput assays provide valuable insight into cellular processes, they typically fall short of providing sufficient data to calibrate mechanistic models of intracellular dynamics. This talk will relate our experience with modelling in metabolism and signal transduction, highlighting the tools we used to gain insight from models that were calibrated against limited data.

Brian P. Ingalls  
Department of Applied Mathematics  
University of Waterloo  
bingalls@math.uwaterloo.ca

Rahul Rahul  
Department of Applied Mathematics, University of  
Waterloo  
Waterloo, Canada  
r2rahul@math.uwaterloo.ca

### MS67

#### **Patient Specific Modelling of the Endocrine HPA-Axis and Its Relation to Depression: Ultradian and Circadian Oscillations**

Correlation between depression and a recently defined index characterizing the hypothalamus-pituitary-adrenal (HPA) axis is established. A novel capturing circadian as well as ultradian oscillations of hormone concentrations related to the HPA-axis is suggested. Three parameters related to depression are identified and estimated based on data from 29 subjects using non-linear mixed effects modelling and statistical hypothesis testing. These parameters represent underlying physiological mechanisms of the HPA-axis and may be used for diagnosing and understanding depression.

Johnny T. Ottesen  
Roskilde University  
Department of Mathematics  
johnny@ruc.dk

Stine Timmerman  
Lundbeck  
stot@lundbeck.com

johanne Gudmand-Hoyer  
Roskilde University  
joguho@ruc.dk

### MS67

#### **Uncertainty Quantification in ODE Modeling of Immune Response**

Our team has utilized Bayesian inference for quantifying the uncertainty in parameter estimation for several models of host immune response to bacterial and viral infection. Due to the scarcity of data we have supplemented the likelihood function with heuristic criteria designed to impose restrictions on the qualitative behavior of modeled systems. I will discuss our experience with the feasibility and utility of ensemble modeling, including the use of parallel tempering for speeding up convergence.

David Swigon  
Department of Mathematics  
University of Pittsburgh  
swigon@pitt.edu

Ericka Mochan  
University of Pittsburgh  
erickamochan@gmail.com

Jonathan Rubin  
University of Pittsburgh  
Pittsburgh, PA  
jonrubin@pitt.edu

Gilles Clermont  
University of Pittsburgh  
Critical Care Medicine  
clermontg@upmc.edu

### MS68

#### **A Multicell Model to Investigate How Vasculogenesis Is Disrupted in Cerebral Cavernous Malformations**

Abstract not available at time of publication.

Timothy Elston  
University of North Carolina, Chapel Hill  
telston@med.unc.edu

### MS68

#### **Diffusion in Soft Matter: Theory, Modeling, and Simulations**

This lecture highlights anomalous diffusion of particles in soft matter in general, and in lung airway fluids in particular. We present particle path data from experiments, discuss models that are consistent with the data, and predictive simulations of models that have been fitted to the data. Relevance to pulmonary medicine will be presented.

M. Gregory Forest  
University of North Carolina at Chapel Hill  
Dept of Math & Biomedical Engr.  
forest@unc.edu

John Mellnik  
UNC Chapel Hill

Bioinformatics and Computational Biology Graduate Program  
jmellnik@gmail.com

Paula Vasquez  
University of South Carolina  
pvasquez@math.sc.edu

Scott McKinley  
University of Florida  
scott.a.mckinley@gmail.com

David Hill  
University of North Carolina at Chapel Hill  
Cystic Fibrosis Center  
dbhill@med.unc.edu

## MS68

### Homeostatic Mechanisms in Biochemical Systems

We will discuss the structure of homeostatic mechanisms in a variety of metabolic systems including folate metabolism, methylation reactions, and detoxification by glutathione in the liver. These mechanisms are designed to allow cells to regulate crucial functions in the face of large fluctuations in inputs due to meals. From a mathematical point of view, the question is how these mechanisms dampen stochastic fluctuations as they propagate through the biochemical network.

Michael C. Reed  
Duke University  
reed@math.duke.edu

## MS68

### Mathematical Understanding of Cancer Virotherapy

Abstract not available at time of publication.

Jianjun Paul Tian  
Mathematics Department  
College of William and Mary  
jptian@math.wm.edu

## MS69

### The Way Cells Talk: Modeling and Simulations of Ion Transport

Ion channels are fundamental components that conduct ionic exchanges through cellular membranes, thus they are critical in many biological process such as change of action potentials, signaling and interactions with extracellular microenvironment. In this talk I will first briefly overview the methodologies and models of ion channels, then focus a specific ionic transport, the proton transport through cellular membranes. A multi scale and multi physic model is proposed based on a total energy functional, from which the governing equations of proton dynamics and electrostatics are derived. A set of highly accurate and efficient numerical algorithms are developed to perform the simulations. A specific application of proton transport could be a better understanding of abnormal acidity in tumor microenvironment.

Duan Chen, Duan Chen  
Department of Mathematics and Statistics  
University of North Carolina at Charlotte

dchen10@uncc.edu, dchen10@uncc.edu

## MS69

### Ions in Channels: Natural Nanovalves

Ions in channel proteins are the ultimate multiscale device. They are natural nanovalves in which a handful of atoms control many processes crucial to life by controlling macroscopic flows of ions. Statistical mechanics was not designed with interacting systems in mind, let alone systems in which atoms control macroscopic flows and living machines. Variational mechanics (of dissipative flowing systems like complex fluids) is needed to engineer the nanovalves of life, in my opinion.

Bob Eisenberg  
Department of Molecular Biophysics and Physiology  
Rush University  
beisenbe@rush.edu

## MS69

### A Energy-Preserving Scheme for Pnp Equations

In this talk, we present a finite difference scheme that satisfies the energy dissipation law of the Poisson-Nerst-Planck equation exactly. We formulate the chemical potential differently and show that the energy-preserving scheme comes out of the new formulation. Numerical results comparing the energy-preserving scheme with the standard scheme will be shown.

Xiaofan Li  
Illinois Institute of Technology  
lix@iit.edu

## MS69

### Title Not Available at Time of Publication

Abstract not available at time of publication.

Tai-Chia Lin  
National Taiwan University, Taiwan, ROC  
tclin@math.ntu.edu.tw

## MS70

### Neuromuscular Pumping in Jellyfish Bells

A current question in jellyfish propulsion is how the underlying neuromuscular organization of their bell allows for maneuvering. Using an immersed boundary framework, we will examine the neuromechanics of swimming by incorporating neural and muscles models into a model of the elastic jellyfish bell. We then use this model to understand how variability in the electrophysiology allows for complicated swimming behavior, such as steering. We will compare the results of the simulations with experiment.

Alexander Hoover  
University Of North Carolina at Chapel Hill  
hooverap@email.unc.edu

Laura A. Miller  
University of North Carolina - Chapel Hill  
Department of Mathematics

lam9@email.unc.edu

peskin@cims.nyu.edu

**MS70****The Effects of In Phase and Out of Phase Pulsations in Groups of Upside-down Jellyfish, *Cassiopea* sp**

Upside-down jellyfish of the genus *Cassiopea* use bell contractions to generate feeding currents. These jellyfish typically situate themselves on the bottom of the ocean floor in groups. Little is known about the costs and advantages of the different pulsation modes within a group and how these trade-offs are related to the size of the individual jellyfish. In this study, the effects of synchronous and asynchronous pulsations are investigated using particle image velocimetry.

Julia E. Samson

University of North Carolina at Chapel Hill  
jesamson@live.unc.edu

Arvind Santhanakrishnan  
Oklahoma State University  
askrish@okstate.edu

Laura A. Miller  
University of North Carolina - Chapel Hill  
Department of Mathematics  
lam9@email.unc.edu

**MS70****The Metachronal Limb Stroke Pattern in Crustacean Swimming**

Crayfish and other long-tailed crustaceans swim by rhythmically moving four or five pairs of limbs. Despite variations in limb size and stroke frequency, movements of ipsilateral limbs always maintain a tail-to-head metachronal rhythm with an approximate quarter-period inter-limb phase-difference. Relatively few studies have examined the fluid dynamics of metachronal limb stroke for the range of Reynolds numbers under which crustaceans operate. Here, we use a computational fluid dynamics model to address this issue.

Calvin Zhang

Courant Institute of Mathematical Sciences  
calvinz@cims.nyu.edu

Robert D. Guy  
Mathematics Department  
University of California Davis  
guy@math.ucdavis.edu

Timothy Lewis  
Department of Mathematics  
University of California, Davis  
tjlewis@ucdavis.edu

Boyce Griffith  
New York University School of Medicine  
griffith@cims.nyu.edu

Charles S. Peskin  
Courant Institute of Mathematical Sciences  
New York University

**MS70****Experiments and Modeling Study of Low Reynolds Number Flows Generated by a Processing Nodal Cilia**

Theoretical study and experiments are developed to emulate dynamics biological interest such as primary cilia in developing embryos, where primary cilia are the main agent for the embryonic forms of nutrient circulation. Experiments are performed using high viscosity silicon oil with magnetically actuated precessing rod in a table-top setup. Stereoscopic Lagrangian tracking show quantified long-time agreement with an appropriately imaged slender body theory to enforce the no-slip condition at the floor. In contrast, breaking symmetry by a bent rod creates additional flow components which destroy quantitative short time agreement with the theory while maintaining its qualitative features including the creation of large scale Lagrangian tori.

Longhua Zhao

Case Western Reserve University  
lxz315@case.edu

Roberto Camassa  
University of North Carolina  
camassa@amath.unc.edu

James D. Martindale  
University of North Carolina at Chapel Hill  
jmartind@live.unc.edu

Richard McLaughlin  
UNC Chapel Hill  
rmm@amath.unc.edu

Leandra Vicci  
Department of Computer Science  
University of North Carolina  
vicci@cs.unc.edu

**MS71****The Influence of Neurochemistry**

Mathematical models in neuroscience often treat individual neurons as nodes in networks and biochemistry appears, if at all, as some intermediate variables by which the neurons communicate with each other. In fact, many neurons change brain function not by communicating in one-to-one fashion with other neurons, but instead by projecting changes in biochemistry over long distances. This biochemical network is of crucial importance for brain function and it influences and is influenced by the more traditional electrophysiological networks.

Janet Best

The Ohio State University  
Department of Mathematics  
jbest@math.ohio-state.edu

Michael C. Reed, H Frederik Nijhout  
Duke University

reed@math.duke.edu, hfn@duke.edu

muriel.thoby-brisson@u-bordeaux2.fr

## MS71

### How Precise Can We Make a Biophysical Neural Integrator?

Recently, Boerlin et al 2013 derived a recurrent network of leaky-integrate-and-fire neurons with instantaneous synaptic dynamics that can perform a variety of computations. Although this framework is flexible in that the derived network can perform any linear computation, it is important to ask whether the framework generalizes to more realistic synaptic and spike-generating dynamics. Here, we show that this framework can indeed be extended to include slow, alpha function synaptic dynamics and Hodgkin-Huxley-like spike-generating currents.

Michael Schwemmer

The Ohio State University  
schwemmer.2@mbi.osu.edu

## MS71

### The Effects of Long-Range Coupling on Neural Activity in the Crayfish Swimmeret System

The crayfish swimmeret system exhibits a stable stroke pattern during forward swimming, where the limbs move in a back to front metachronal wave with a delay of approximately 25%. A chain of nearest neighbor coupled oscillators indicates that the network topology of the crayfish neural circuit promotes the robust generation of this pattern (Zhang et al.). We extend this modeling work to consider the influence of the long-range connections that are present in this system.

Lucy Spardy

Mathematical Biosciences Institute  
spardy.1@mbi.osu.edu

Brian Mulloney

University of California Davis  
bcmulloney@ucdavis.edu

Tim Lewis

University of California, Davis  
tjlewis@ucdavis.edu

## MS71

### Interaction of Two Distinct Timescales in Computational a Model of in-Vitro Sigh Generation

Augmented breaths, or sighs, increase air intake and a lack of sighing is associated with sudden infant death syndrome. Since sighs operate on significantly slower time scale than eupnoea, it is still debated if they are produced by the same network of neurons or by distinct sub-networks. We developed a mathematical model that proposes that sighs and eupnoea are generated by the two neural sub-networks. The model accounts for dynamics of sigh and eupnoea and reproduces several in-vitro experiments.

Natalia Toporikova

Washington and Lee University  
toporikovan@wlu.edu

Muriel Thoby-Brisson

thoby-brisson@u-bordeaux2.fr) , collaborator INCIA

## MS72

### Large Reduction of Defibrillation Threshold Using a Four-Electrode System

In this talk we propose a new shock protocol that is based on a four electrode system instead of the of standard procedure based with only two electrodes. The model is tested using one-dimensional ring with bidomain properties and with the Beeler-Reuter model for the active properties of the membrane. Three different shock types are tested: monophasic and two types of biphasic shock. The results are compared with those obtained with standard two electrode protocol. Substantial reduction in defibrillation threshold is achieved with respect to the standard protocol.

Jean Bragard

Depto de Física y Matemática Aplicada  
Universidad de Navarra, Pamplona, Spain  
jbragard@unav.es

Ana Simic

University of Navarra, Spain  
asimic@unav.es

Jorge Elorza

University  
jelorza@unav.es

## MS72

### Unification of Electrical Restitution Dynamics and Ion Channel Dynamics in the Control of Cardiac Rhythm - An Eigenmode Approach

The characterization of action potential dynamics in cardiac tissue has traditionally followed two parallel tracks: use of the dependence of action potential duration and wave propagation speed on the preceding diastolic interval (called electrical restitution theory), and use of intricate ion channel models. In our work, we unify these two approaches by applying eigenmode theory to the mapping of perturbations of both sets of dynamical variables from one action potential to the next. This link between the two approaches provides us with an important foundation on which we can discuss in a rigorous manner how drugs and electrical interventions impact the onset and control of fibrillation in the heart.

Niels Otani

Rochester Institute of Technology  
nfosma@rit.edu

## MS72

### Local Termination of Cardiac Alternans Using Isostable Response Curve Techniques

Phase reduction methods have been tremendously useful for understanding the dynamics of nonlinear oscillators, but have been difficult to extend to excitable systems with stable fixed points, such as those that commonly describe individual cardiac cells. Here, we extend the notion of phase reduction to include excitable media, and use this reduction to formulate an energy-optimal control strategy for terminating cardiac alternans in a high-dimensional model

of cardiac cellular activity.

Dan D. Wilson

Mechanical Engineering  
University of California, Santa Barbara  
dan.d.wilson8@gmail.com

Jeff Moehlis

Dept. of Mechanical Engineering  
University of California – Santa Barbara  
moehlis@engineering.ucsb.edu

### MS73

#### Exact Protein Distributions for Stochastic Models of Gene Expression

In this talk, I will discuss approaches developed by my group for obtaining analytical results for protein distributions in stochastic models of gene expression. We invoke the partitioning property of Poisson processes to develop a mapping that significantly simplifies the analysis of such models. Using this mapping, we derive exact analytical results for steady-state and time-dependent protein distributions for the basic 2-stage model of gene expression. Considering extensions of the basic model, we obtain exact protein steady-state distributions for models that include the effects of post-transcriptional and post-translational regulation. Finally, I will introduce a model which includes the interplay between bursting and feedback regulation and discuss insights gained from analyzing the corresponding steady-state protein distribution.

Rahul Kulkarni, Niraj Kumar

University of Massachusetts Boston  
rahul.kulkarni@umb.edu, niraj.kumar@umb.edu

Hodjat Pendar

Virginia Tech  
hpendar@vt.edu

Thierry Platini

COventry University  
ab3334@coventry.ac.uk

### MS73

#### An Optimal Control Framework for Stochastic Gene Regulatory Networks

Modeling stochasticity in gene regulation is an important and complex problem in molecular systems biology due to probabilistic nature of gene regulation. This talk will introduce a stochastic modeling framework for gene regulatory networks which is an extension of the Boolean modeling approach. This framework incorporates propensity parameters for activation and degradation and is able to capture the cell-to-cell variability. In this setting, optimal control problems can be studied using methods from control theory for Markov decision processes for the purpose of developing optimal intervention strategies. These control methods will then be applied to the p53-mdm2 complex.

David Murrugarra

School of Mathematics, Georgia Tech  
davidmur@math.gatech.edu

### MS73

#### Extrinsic Noise and Cell-Cycle Dependence of Ge-

#### netic Oscillators

Understanding the effect of noise and the cell cycle on gene networks is fundamental in developing accurate models. Typically, comparing experimental data and simulations only takes into account individual trajectories, but not the lineage and the corresponding variability and correlation. Here we show that a model that includes extrinsic noise can capture the variability seen in a synthetic gene oscillator. Furthermore, we show that it is sufficient to model extrinsic noise as cell-to-cell variability at cell division.

Alan Veliz-Cuba

University of Houston  
Rice University  
alanavc@math.uh.edu

### MS74

#### Optimal Control in Models of Management Involving Trees and Forest Resources

Two applications of optimal control are presented in examples of managing populations related trees and forest products. One example is a discrete model of gypsy moth populations affecting tree defoliation. The other example is a system of ordinary differential equations modeling the harvesting (lethal and non-lethal) for forest products.

Suzanne M. Lenhart

University of Tennessee  
Department of Mathematics  
lenhart@math.utk.edu

### MS74

#### Modeling of Transgenic Or Sterile Mosquitoes in Fighting Vector-Borne Diseases

To prevent the transmission of malaria or other mosquito-borne diseases, an effective weapon is to use genetically-altered (transgenic) mosquitoes or mosquitoes carrying genetically-modified bacteria, that are resistant to the infection, to replace the wild mosquitoes, or to release sterile mosquitoes to reduce the wild mosquito population. To study the impact of these mosquitoes mixing with wild mosquitoes on the diseases transmission and different strategies in releasing sterile mosquitoes, we formulate simple continuous- or discrete-time mathematical models of interactive wild and transgenic or sterile mosquitoes. We present fundamental analysis of the model equations, and demonstrate the rich dynamical features of the models by numerical examples.

Jia Li

Department of Mathematical Sciences  
University of Alabama in Huntsville  
li@math.uah.edu

### MS74

#### An Ecological Model for Producers and Scroungers in a Spatial Habitat

We describe the dynamics of a producer-scrounger system in a spatial habitat using a partial differential equation model. Both species are assumed to increase logistically and to move randomly in their environment. Producers can obtain the resource directly from the environment, whereas scroungers must steal it from nearby producers. When possible, parameter combinations which allow producers

and/or scroungers to persist either alone or together are distinguished from those in which they cannot.

Chris Cosner  
University of Miami  
Department of Mathematics  
gcc@math.miami.edu

Andrew Nevai  
Department of Mathematics  
University of Central Florida  
math.anevai@gmail.com

## MS74

### The Role of Avian Stage-structure in the Transmission and Control of West Nile Virus

The seasonal occurrence of West Nile Virus in humans has been associated with the end of the avian nesting season. Newly hatched nestlings are more vulnerable to mosquitoes than older birds. While total avian population size increases throughout the season, nestling abundance declines at the end of the brooding season. This temporal variation in host stage abundance may play an important role in structuring WNV transmission. We develop and analyze a stage-structured differential equation model for WNV and investigate the impact of vector preference for specific host life stages on the timing of WNV activity as well as implications for public health interventions.

Suzanne Robertson  
Virginia Commonwealth University  
srobertson7@vcu.edu

Kevin Caillouet  
St. Tammany Parish Mosquito Abatement District  
caillouet@stpamad.org

## MS75

### Identifiability and Parameter Estimation in Modeling Disease Dynamics

Connecting differential equation models with data to yield predictive results requires a variety of parameter estimation, identifiability, and uncertainty quantification techniques. Identifiability analysis addresses the question of whether it is possible to uniquely recover the model parameters from a given set of data. In this talk, I will discuss some recent work using and developing identifiability methods based on tools from computational differential algebra and systems theory, and present several clinical and public health applications to problems in human disease, including cholera and other infectious disease transmission processes.

Marisa Eisenberg  
University of Michigan  
marisae@umich.edu

## MS75

### Identifiability of High-Dimensional Models

The structure of a complex system ultimately determines whether key unknown parameters can be unambiguously quantified from experimental observations. Although many identifiability techniques have been proposed to examine model structures before parameter estimation, we have never gained the capability to explore the territory

of high-dimensional problems due to various limitations in existing methods. Here we develop the very first graphical approach to analyze the identifiability of high-dimensional systems that are governed by dynamic laws. We apply this method to several real model structures, and show how model topology and experimental inputs and outputs affect the identifiability. The proposed method provides a basis to systematically examine and refine the structures of a wide range of complex dynamic systems.

Hongyu Miao  
University of Rochester  
hongyu\_miao@urmc.rochester.edu

## MS75

### Identifiability and Parameter Estimation in Systems Biology and Drug Development

Due to the high complexity of biological data it is difficult to disentangle cellular processes relying only on intuitive interpretation of measurements. A Systems Biology approach, that combines quantitative experimental data with dynamic mathematical modeling promises to yield deeper insights into these processes and makes a more rational drug design possible. Nevertheless, with growing complexity and increasing amount of quantitative experimental data, building realistic and reliable mathematical models can become a challenging task: unknown model parameters need to be estimated from the experimental data and uncertainties in model predictions has to be considered realistically. I will present a case study (Raue et al., Bioinformatics 2014) using three current approaches for identifiability analysis for an application from cell biology (Raia et al., Cancer Research 2011). The approaches are conceptually different and are developed independently. The results of the three approaches are in agreement but have different strength and weaknesses. For the estimation of unknown model parameters, the performance of different optimization algorithms is compared systematically (Raue et al., PLOS ONE 2013). The results show that deterministic derivative-based optimization employing the sensitivity equations in combination with a multi-start strategy based on Latin hypercube sampling outperforms the other methods by orders of magnitude in accuracy and speed.

Andreas Raue  
Physics Institute, University of Freiburg  
araue@merrimackpharma.com

## MS75

### Identifiability of Linear State Space Models

Dynamical systems models described by linear systems of ordinary differential equations are ubiquitous in applied mathematics and mathematical biology. Such a model is said to be identifiable if the parameters of the model can be uniquely determined from given input and output data. I will discuss recent progress on developing precise combinatorial methods to determine if a system is identifiable. Joint work with Nicolette Meshkat and Adam Mahdi.

Seth Sullivant  
North Carolina State University  
smsulli2@ncsu.edu

## MS76

### Modeling Cartilage Tissue Engineering in Cell-

## Seeded Scaffolds

Chondrocytes or stem cells can be used to regenerate cartilage extracellular matrix via tissue engineering approaches in which cells are seeded into porous scaffold materials. In such systems, cell-mediated biosynthesis results in regeneration and accumulation of extracellular matrix constituents concurrent with scaffold degradation. Continuum models are presented for such systems and quantify the effects of evolving porosity on functional outcomes. Both tissue-scale mixture models and microscopic models with individual cells will be presented.

Mansoor A. Haider

North Carolina State University  
Department of Mathematics  
m\_haider@ncsu.edu

## MS76

### Let There be Force: Modeling Cell-ECM Interactions

Extracellular matrix (ECM), a fibrous material that forms a network in a tissue, significantly affects many aspects of cellular behavior, including cell movement and proliferation. Transgenic mouse tumor studies indicate that excess collagen, a major component of ECM, enhances tumor formation and invasiveness. Moreover, cell interactions with the collagen matrix result in aligned fibers that facilitate cell invasion. However, the underlying mechanisms are unclear since the properties of ECM are complex, with diverse topographies and mechanical properties depending on various biophysical parameters. We have developed a three-dimensional elastic computational fiber network model, and parameterized it with in vitro collagen tensile experiments. Using this model, we simulate mechanical testing of fiber networks and examine the mechanical properties of fiber networks with varying density, alignment, and crosslinking. The computational model and simulation results can fill in the gap between microscopic single collagen fiber studies and macroscopic collagen gel studies. This model is the first step toward a fully biomechanical cell-matrix interaction model for changes in matrix organization during cell migration and tumor invasion.

Yi Jiang

Georgia State University  
yjjiang12@gsu.edu

## MS76

### Mathematical Modeling of Renal Hemodynamics

We have developed a mathematical model of the rat kidney's blood flow control, and used that model to study the individual contributions of two autoregulatory mechanisms. The model represents an afferent arteriole, glomerular filtration, and a segment of a short-loop nephron. The afferent arteriole exhibits the an autoregulatory mechanism called the myogenic response, such that it responds to transmural pressure elevation with constriction, and to pressure reduction with dilation. Another autoregulatory mechanism is the tubuloglomerular feedback (TGF): The tubule model predicts tubular fluid and  $\text{Cl}^-$  transport. Macula densa  $\text{Cl}^-$  concentration is sensed as the signal for TGF, which acts to constrict or dilate the afferent arteriole. In other words, TGF contributes to hemodynamics control by adjusting single nephron glomerular filtration rate according to the chloride concentration sensed downstream. With this configuration, the model afferent arteriole main-

tains stable glomerular filtration rate within a physiologic range of perfusion pressure (80-180 mmHg). The contribution of TGF to overall autoregulation is significant only within a narrow band of perfusion pressure values (80-110 mmHg).

Anita T. Layton

Duke University  
Department of Mathematics  
alayton@math.duke.edu

## MS76

### Kinetic Monte Carlo Simulations of Multicellular Aggregate Self-Assembly in Biofabrication

We present a three-dimensional lattice model to study self-assembly and fusion of multicellular aggregate systems by using kinetic Monte Carlo (KMC) simulations. This model is developed to describe and predict the time evolution of postprinting morphological structure formation during tissue or organ maturation in a novel biofabrication process (or technology) known as bioprinting. In this new technology, live multicellular aggregates as bio-ink are used to make tissue or organ constructs via the layer-by-layer deposition technique in biocompatible hydrogels; the printed bio-constructs embedded in the hydrogels are then placed in bioreactors to undergo the self-assembly process to form the desired functional tissue or organ products. Here we implement our model with an efficient KMC algorithm to simulate the making of a set of tissues/organs in several designer's geometries like a ring, a sheet and a tube, which can involve a large number of cells and various other support materials like agarose constructs etc. We also study the process of cell sorting/migration within the cellular aggregates formed by multiple types of cells with different adhesivities.

Yi Sun

University of South Carolina  
yisun@math.sc.edu

## MS77

### Pnp Equations with Steric Effects: A Model of Ion Flow Through Channels

Abstract not available at time of publication.

Tzyy-Leng Horng

Department of Applied Mathematics  
Feng Chia University  
tlhorng@math.fcu.edu.tw

## MS77

### Computer Simulation of Voltage Sensitive Calcium Ion Channels in a Dendritic Spine

Abstract not available at time of publication.

Pilhwa Lee

Department of Cell Biology  
University of Connecticut Health Center

plee@uchc.edu

## MS77

### Title Not Available at Time of Publication

Abstract not available at time of publication.

Chun Liu

Penn. State University  
liu@math.psu.edu

## MS77

### A Model of Tissue Electrodifffusion and Osmosis and Its Application to Cortical Spreading Depression

We propose a PDE model of tissue-level electrodifffusive and osmotic phenomena. An important feature of this model is that it satisfies an energy inequality. This model will be applied to the study of cortical spreading depression, a pathophysiological phenomenon in the brain that is thought to underlie migraine aura and other pathologies.

Yoichiro Mori

University of Minnesota  
ymori@math.umn.edu

## MS78

### Roles of Droplets and Bubbles in Pathogen Transmission Through Air

Pathogen-bearing droplet creation from contaminated fluids results from the interplay between interfacial flow dynamics and pathogens. Such interplay leads to various modes of formation and ejection of contaminated droplets into the air, thus shaping infectious disease transmission indoors. Particular mechanisms of fluid breakup leading to the creation of pathogen-bearing droplets from bursting bubbles and violent expirations will be discussed.

Lydia Bourouiba

Department of Mathematics/Civil and Environmental  
Eng 48-333  
#48-333, Massachusetts Institute of Technology  
lydia.bourouiba@math.mit.edu

## MS78

### Fluid Flow Through Many Bristled Wings

The smallest flying insects are roughly 1mm in length and at this scale viscous effects are significant. Interestingly, these insects commonly possess wings with long bristles on the fringes, and the physiological importance of the bristles remains a mystery. Depending on the Reynolds number and the local environment, bristled wings could act either as leaky sieves or solid paddles. We used the immersed boundary method to investigate the aerodynamic role of bristles in insect flight.

Shannon Jones

University of North Carolina at Chapel Hill  
skjohnsn@email.unc.edu

Laura Miller  
UNC-Chapel Hill

lam9@email.unc.edu

## MS78

### Clap and Fling Interaction of Bristled Wings in Tiny Insect Flight

The flapping flight of the smallest insects that fly at Reynolds numbers ( $Re$ ) on the order of 10 is often characterized by a ‘clap and fling’ of the wings. The effect of a bristled wing characteristic of these insects is investigated using 2D numerical simulations based on a porous version of the immersed boundary method. A comparison of the aerodynamic forces generated between solid and porous wings undergoing wing-wing interaction will be presented.

Arvind Santhanakrishnan

Oklahoma State University  
askrish@okstate.edu

Alice Robinson

University of California, Irvine  
alicekrobinson37@gmail.com

Tyson Hedrick

University of North Carolina, Chapel Hill  
thedrick@bio.unc.edu

Laura A. Miller

University of North Carolina - Chapel Hill  
Department of Mathematics  
lam9@email.unc.edu

## MS78

### Microscale Gas Transport in Insect Respiratory Systems

Insects and some other terrestrial arthropods breathe using a complex network of tracheal tubes. Air is drawn in through sets of openings called spiracles, and follows a branching path down to the tracheoles, which deliver oxygen directly to the cells for respiration. These tracheal networks have recently been found to consist of essentially inelastic but locally (in time and space) collapsible tubes. Mathematical modeling and meshfree computations are presented to describe this transport paradigm.

Anne Staples

Department of Engineering Science and Mechanics  
Virginia Tech  
staplesa@vt.edu

## MS79

### Stochastic Switching: Mathematical Surprises and Biological Insight

Motivated by several biological questions, we consider ODEs with stochastically switching right-hand sides and PDEs with stochastically switching boundary conditions. In a variety of situations, we prove that the system exhibits surprising behavior. In this talk, we will highlight some of the most interesting results and describe their implications both for the mathematical study of stochastic hybrid systems and for the motivating biological problems.

Sean D. Lawley  
Duke University

lawley@math.duke.edu

dschmidt@case.edu

## MS79

### Multi-Motor Transport in Neurons: Moving Beyond Tug-of-War

Transport in neurons is intrinsically bidirectional, with each movement modality carried out by molecular motors in either the kinesin (anterograde) or the dynein (retrograde) families. Because all motors are present at a given time there must be competition and/or cooperation among motors that simultaneously bind a single vesicle to nearby microtubules. It has been assumed for much of the last decade that the competition must resolve itself through some kind of tug-of-war; but recent evidence shows conclusively that this is not the case in vivo. In this talk, we will see a few biological mechanisms (and associated mathematical models) that may lead to resolving theory with experimental observations. Joint work with Will Hancock (Penn State), John Fricks (Penn State), and Pete Kramer (RPI).

Scott McKinley  
University of Florida  
scott.mckinley@ufl.edu

## MS79

### Spontaneous Neural Activity Caused by Ion Channel Fluctuations

The membrane voltage of a neuron is modeled with a piecewise deterministic stochastic process. The membrane voltage changes deterministically while the population of open ion channels, which allow current to flow across the membrane, is constant. Ion channels open and close randomly, and the transition rates depend on voltage, making the process nonlinear. In the limit of infinite transition rates, the process becomes deterministic. The deterministic process is the well known Morris-Lecar model. Under certain conditions, the deterministic process has one stable fixed point and is excitable. An excitable event, called an action potential, is a single large transient spike in voltage that eventually returns to the stable steady state. I will discuss recent development of large deviation theory to study noise induced action potentials.

Jay Newby  
Mathematical Biosciences Institute  
The Ohio State University  
newby.23@mbi.osu.edu

## MS79

### Measuring Edge Importance for Random Processes on Networks

Many neural systems can be represented as a Markov process on a graph. We derived a new measure of the contribution of individual edges in the graph to the accuracy of an approximate process on the graph. We apply this measure to the Hodgkin-Huxley system and extend it for a broad class of random graph models. These results shed new light on the contributions of different ion channel transitions to the variability of neural systems.

Deena Schmidt  
Case Western Reserve University

## MS80

### A Mathematical and Computational Structured-Tree Model of the Pulmonary Circulation

A multiscale mathematical and computational model of the pulmonary circulation is presented and used to analyse both arterial and venous pressure and flow. This work is a major advance over previous studies using structured trees to model vascular beds, e.g. Olufsen et al. (2012), which only address the arterial circulation. For the first three generations of vessels within the pulmonary circulation, the geometry is specified from patient-specific measurements obtained using magnetic resonance imaging (MRI). Blood flow and pressure in the larger arteries and veins are predicted using a nonlinear, cross-sectional-area-averaged system of equations for a Newtonian fluid in an elastic tube. The inflow to the main pulmonary artery is obtained from MRI measurements, while pressure entering the left atrium from the main pulmonary vein is kept constant at the normal mean value of 2 mmHg. Each terminal vessel in the network of 'large' arteries is connected to its corresponding terminal vein via a network of vessels representing the vascular bed of smaller arteries and veins. We develop and implement an algorithm to calculate the admittance of each vascular bed, using bifurcating structured trees and recursion. The structured-tree models take into account the geometry and material properties of the 'smaller' arteries and veins of radii  $\geq 50$  microns. We study the effects on flow and pressure associated with three classes of pulmonary hypertension expressed via stiffening of larger and smaller vessels, and vascular rarefaction. The results of simulating these pathological conditions are in agreement with clinical observations, showing that the model has potential for assisting with diagnosis and treatment of circulatory diseases within the lung. References: Olufsen, M.S., Hill, N.A., Vaughan, G.D.A., Sainsbury, C. & Johnson, M. (2012) Rarefaction and blood pressure in systemic and pulmonary arteries. *J Fluid Mech* 705:280-305

Nicholas A. Hill  
Department of Mathematics  
University of Glasgow, UK  
Nicholas.Hill@glasgow.ac.uk

M. Umar Qureshi  
International Islamic University, Pakistan  
& University of Glasgow, U.K.  
m.qureshi.2@research.gla.ac.uk

Gareth D.A. Vaughan  
School of Mathematics and Statistics University of Glasgow,  
gdavaughan@gmail.com

Christopher Sainsbury  
School of Medicine, University of Glasgow, U.K.  
Chris.Sainsbury@glasgow.ac.uk  
chris.sainsbury@glasgow.ac.uk

Martin Johnson  
Scottish Pulmonary Vascular Unit  
Western Infirmary, Glasgow, U.K.  
martin.johnson@northglasgow.scot.nhs.uk

Charles S. Peskin  
Courant Institute of Mathematical Sciences  
New York University

peskin@cims.nyu.edu

Mette S. Olufsen  
Department of Mathematics  
North Carolina State University  
msolufse@math.ncsu.edu

## MS80

### Individualized Pulmonary Arterial Blood Flow Analysis

We propose an individualized pulmonary arterial blood flow analysis coupled to the lumped windkessel model of heart circulation and mechanics. The pulmonary arterial vasculature is from image segmentation of a mouse simplified as 1D centerline embedded in 3D with cross-sectional radius. We reveal the changes in blood flow patterns and right ventricular adaptation from vascular remodeling and rarefaction, which are consequences of pulmonary hypertension.

Pilhwa Lee, Shivendra Tewari, Daniel Beard  
University of Michigan, Ann Arbor  
pilee@umich.edu, stewari@umich.edu, beardda@med.umich.edu

## MS80

### Analysis of Cardiovascular Dynamics in Pulmonary Hypertensive C57BL6/J Mice

Data on RV pressure and volume, and systemic arterial pressure obtained before, during, and after inferior vena cava occlusion are analyzed using a mathematical model of realistic ventricular mechanics coupled with a simple model of pulmonary and systemic vascular systems. Model analysis suggests monotonic increase in PVR and PA elastance, consistent with prior experimental measurements. Model findings indicate a compensatory remodeling phase of RV precedes pathological remodeling that concludes with heart failure in pulmonary hypertension.

Shivendra Tewari  
University of Michigan, Ann Arbor  
stewari@umich.edu

Naomi Chesler  
University of Wisconsin, Madison  
chesler@engr.wisc.edu

Daniel Beard  
University of Michigan, Ann Arbor  
beardda@umich.edu

## MS81

### Rare Events for Genetic Networks: Studying Interactions Between Meta-Stability and Time-Delays

The dynamics of gene networks are sometimes non-trivially influenced by events that happen on relatively short time scales. To study the impact of such events on gene networks it is not sufficient to study the steady state behavior. Instead, transient behaviors become very important. However, it is difficult to study relevant transient events numerically because they are rare, and the majority of the simulation time is spent sampling events that are not of interest. Therefore, theoretical methods for reliably sampling relevant transient methods for gene networks are re-

quired. In the absence of time delays, Langevin equations have proved to be a very important theoretical tool for the study of genetic networks. However, in models of gene networks that include transcriptional delay, such theoretical tools do not currently exist. In this talk, we present a proof of the weak convergence of time-delayed birth death processes to a class of functional Langevin equations. We further prove that as the system size approaches infinity, both these descriptions converge to the mean field limit. Finally, we obtain quantitative estimates on the distance between the birth-death process and the approximating Langevin process. This lays a rigorous groundwork for studying the dynamics of time-delayed birth-death processes by using functional stochastic differential equations.

Chinmaya Gupta, Manuel Lopez  
University of Houston  
chinmaya@math.uh.edu, jmlopez@math.uh.edu

Robert Azencott  
Department of Mathematics  
University of Houston  
razencot@math.uh.edu

Matthew Bennett  
Rice University  
matthew.bennett@rice.edu

Kresimir Josic  
University of Houston  
Department of Mathematics  
josic@math.uh.edu

William Ott  
University of Houston  
ott@math.uh.edu

## MS81

### Impact of Stochastic Transcriptional Delay on Gene Networks

Abstract not available at time of publication.

Manuel Lopez  
University of Houston  
jmlopez@math.uh.edu

## MS81

### Queueing Approaches to Multisite Enzyme Kinetics

Queueing theory was developed long ago to understand the stochastic dynamics of discrete elements processed by a finite number of servers. Researchers have been developing a new biological queueing theory to describe how processing bottlenecks can strongly influence the dynamics of cellular systems. We now present a biological queueing theory for enzymes that can bind multiple substrates simultaneously, as with the *E. coli* protease ClpXP.

William H. Mather  
Virginia Tech Physics  
wmather@vt.edu

## MS81

### First-Passage Time Calculations for Gene Net-

**works: Implications for Phage Lambda Lysis Time**

The inherent stochastic nature of biochemical processes can drive differences in gene expression between otherwise identical cells. While cell-to-cell variability in gene expression has received much attention, randomness in timing of events has been less studied. We investigate event timing at the single-cell level in a simple system, the lytic pathway of the bacterial virus phage lambda. In genetically identical single-cells, lysis occurs on average at 65 mins, with a standard deviation of 3.5 mins. Interestingly, mutations in the lysis protein, holin, alters both the lysis time mean and variance. Mathematically, lysis time is formulated as the first-passage time for cellular holin levels to cross a critical threshold. Analytical expressions for the first-passage time moments reveal how different model parameters modulate lysis time moments, and these predictions are verified with experiments. Finally, our analysis reveals regulatory motifs that enhance the robustness of lysis timing to cellular noise.

Abhyudai Singh  
University of Delaware  
absingh@udel.edu

John Dennehy  
CUNY  
john.dennehy@qc.cuny.edu

Khem Ghusinga  
University of Delaware  
khem@udel.edu

**PP1****Network Bursting in Inhibitory Neural Circuits**

We study the rhythmogenesis of oscillatory patterns emerging in network motifs composed of inhibitory-coupled parabolic bursters represented by the Plant model of Aplysia-15 nerve cells. Such motifs are the building blocks of larger neural networks including central pattern generators controlling swim locomotion of sea slug *Melibe leonine*.

Deniz Alacam  
Georgia State University  
Mathematics Department  
dalacam1@student.gsu.edu

Andrey Shilnikov  
Neuroscience Institute and Department of Mathematics  
Georgia State University  
ashilnikov@gsu.edu

**PP1****Test Criterion for Finding the Global Minimum of a Function Using Exclusion Algorithm**

The problem of finding the global minimum of a vector function is very common in science, economics and engineering. One of the most notable approaches to find the global minimum of a function is that based on interval analysis. In this area, the exclusion algorithms (EAs) are a well-known tool for finding the global minimum of a function over a compact domain. There are several choices for the minimization condition. In this paper, we introduce a new exclusion test and analyze the efficiency and computational complexity of exclusion algorithms based on this approach. We consider Lipschitz functions and give a new minimization condition for the exclusion algorithm. Then

we study the convergence and complexity of the method.

Ibraheem Alolyan  
King Saud University  
ialolyan@ksu.edu.sa

**PP1****Staying in Shape: Patterns in Radial Symmetry Provide Protein Structural Stability and Functionality**

Toroidal WD40 repeat proteins, such as the beta subunit of heterotrimeric G-proteins, are important in cell signaling. Each repeating unit has about 40 amino acids, comprised of a trademark tryptophan and aspartate. With conventional comparative sequence analysis techniques, the strong signal from these signature positions can mask the importance of less conserved ones. We discuss how computational mutagenesis can overcome these limitations, explaining both the fundamental features of WD40 stability and the advantages of symmetry.

Loretta Au  
Department of Applied Mathematics & Statistics  
Stony Brook University  
lau@ams.sunysb.edu

**PP1****Modeling the Deformation of Proteins: from Coarse-Grained to Continuum**

There has been much research in the area of mathematically modeling of protein complexes using coarse-grained models or continuum models. We are proposing a new approach that will combine the potential energy found in elastic network model or residual based coarse-grained models, and stress/strain components to produce a stiffness matrix. This matrix will have the proteins anisotropic properties encoded within it. The computed anisotropic elastic moduli will be then used for simulating the deformation of protein-complexes.

George Borleske  
Graduate Student at Colorado State University  
borleske@math.colostate.edu

**PP1****Demographics and Modeling of Multisite HPV Infection and Transmission**

The Human Papillomavirus (HPV) infects the epithelial layer at several anatomical sites in the human body (anogenital and oral/nasopharyngeal), and certain HPV genotypes can lead to the development of cancer. We present a statistical analysis characterizing HPV trends in the National Health and Nutrition Examination Survey (NHANES), with an emphasis on demographic differences in multiple site concurrent and type-concordant infection. Based on this data, we develop an ODE model of multisite HPV infection and transmission.

Andrew Brouwer  
University of Michigan  
brouweaf@umich.edu

Rafael Meza  
University of Michigan  
Department of Epidemiology  
rmeza@umich.edu

Marisa Eisenberg  
University of Michigan  
marisae@umich.edu

## PP1

### **Binocular Rivalry Waves in Directionally Selective Neural Fields**

Binocular rivalry is the phenomenon that occurs when an observer is presented with two different conflicting images in the two eyes and the visual perception switches back and forth between the two images. We have analyzed this by constructing traveling wave solutions to a system of integro-differential equations describing the network activity of a population of directionally selective neurons. We have shown that waves travel faster in the direction of stimulus motion than against it.

Sam R. Carroll  
University of Utah  
carroll@math.utah.edu

Paul C. Bressloff  
University of Utah and University of Oxford, UK  
Department of Mathematics  
bressloff@math.utah.edu

## PP1

### **Modeling Interactions Between Two Major South-eastern U.S. Sea Turtle Nest Predators and Their Effects on Nest Depredation Rates**

This project is investigating intraguild predation between two major sea turtle nest predators, North American raccoons and Atlantic ghost crabs. In addition, ghost crab predation assists raccoons in finding nests, thereby facilitating secondary nest depredation (i.e., facilitative predation). Our objectives are to characterize the dynamic interactions between intraguild predators and their effects on prey through the use of an ODE model and determine the role that facilitative predation has in influencing nest densities.

Joshua Castro  
University of Central Florida  
castroucf@knights.ucf.edu

John Weishampel  
University of Central Florida  
Department of Biology  
john.weishampel@ucf.edu

Andrew Nevai  
Department of Mathematics  
University of Central Florida  
math.anevai@gmail.com

Pedro Quintana-Ascencio  
University of Central Florida  
Department of Biology  
pedro.quintana-ascencio@ucf.edu

## PP1

### **Intrinsic Mechanisms for Pattern Generation in Three-Node Networks**

Bursting patterns can be qualified and modeled using low-dimensional models. We show that, depending on intrinsic

mechanisms of release, escape, and post-inhibitory rebound, reciprocally inhibitory Fitzhugh-Nagumo type networks can produce a range of phase-locked states such as anti-phase bursting, propagating waves, and peristaltic patterns with recurrently phase-varying lags. Phase-lag return maps identify phase states, with rhythm switching and attractor robustness revealed using external inhibition. Our qualification promotes the use of simplified modeling for CPG circuitries.

Jarod Collens  
Georgia State University  
jcollens1@student.gsu.edu

Aaron Kelley  
GSU  
aarnkelley@gmail.com

Deniz Alacam  
Georgia State University  
Mathematics Department  
dalacam1@student.gsu.edu

Tingli Xing  
Georgia State University  
USA  
txing1@student.gsu.edu

Justus T. Schwabedal  
Division of Sleep Medicine, Brigham & Women's Hospital  
Harvard Medical School  
jschwabedal@gmail.com

Andrey Shilnikov  
Neuroscience Institute and Department of Mathematics  
Georgia State University  
ashilnikov@gsu.edu

## PP1

### **Modeling the Dynamics of Opioid Abuse**

We extend previous models of the population-level dynamics of drug abuse to describe opioid abuse. In particular, we derive a compartmental model that accounts for light and heavy prescription opioid users, heroin users, and the treatment-relapse cycle often observed in opioid addiction. We investigate the sensitivity of the models parameters to the heavy-prescription-opioid and heroin-using population. Finally, we derive and analyze the stability of the models fixed points, estimate several model parameters, and make predictions.

William Consagra  
Rochester Institute of Technology  
School of Mathematical Sciences  
wxc5756@rit.edu

## PP1

### **A Computational Model for a Porous Viscoelastic Cytoskeleton with Applications to Cell Mechanics**

Cell movement is crucial to physiological processes such as wound healing, cancer metastasis, and embryonic development. We present a computational framework to investigate cell movement involving either pressure-driven or polymer-rich protrusions. Our framework incorporates a porous viscoelastic cytoskeleton, a model of adhesion to the substrate, and a cell environment with changing material

properties. We quantify how cells mechanically sense their surroundings and react to changing environments by altering their shape and adhesion to the substrate to achieve optimal migration.

Calina A. Copos  
University of California Davis  
ccopos@math.ucdavis.edu

Robert D. Guy  
Mathematics Department  
University of California Davis  
guy@math.ucdavis.edu

## PP1

### Predicting Severity and Periodicity of Mountain Pine Beetle Outbreaks

We develop an age-structured forest demographic model that incorporates temperature dependent bark beetle infestation. The model is parametrized using data from a 1995-2005 outbreak in central Idaho. The stability of fixed points is analyzed as a function of (thermally controlled) growth rates, and indicates the existence of periodic outbreaks which increase with severity as growth rates increase. We devise an analytical method to predict outbreak severity and duration as well as expected time between outbreaks.

Jacob P. Duncan, James Powell, Luis Gordillo  
Utah State University  
jacob.duncan@aggiemail.usu.edu, jim.powell@usu.edu, luis.gordillo@usu.edu

Joe Eason  
University of Utah  
eason@math.utah.edu

## PP1

### Temperature Effects on REM/Non-REM Sleep Dynamics

Experimental work and prior models suggest changes in ambient temperature can affect sleep patterns in humans. We have designed a mathematical model describing numerous features of the human sleep/wake cycle and aspects of REM/non-REM dynamics. The model simulates temperature changes detected by neurons in the POAH that, in turn, affect the REM/non-REM cycles during sleep through a state-dependent homeostatic process. This model will help to better understand temperature and sleep relationships and support experimental findings.

Pamela B. Fuller  
Rensselaer Polytechnic Institute  
Fullep@rpi.edu

Janet Best  
The Ohio State University  
Department of Mathematics  
jbest@math.ohio-state.edu

Gemma Huguet  
Centre de Recerca Matematica  
Gemma.huguet@upc.edu

Shelby Wilson  
Morehouse College

shelby.wilson@morehouse.edu

Alicia Prieto Langarica  
Youngstown State University  
aprietolangarica@ysu.edu

Selenne Garcia-Torres  
University of Southern California  
Department of Mathematics  
garciato@usc.edu

## PP1

### How Robust Is the Zero-Lag Synchrony When Two Neurons Interact Via a Third Relay Neuron

A remarkable zero time lag synchronization of two cerebral cortical areas with long distant, which results significant conduction delays, have revealed experimentally and numerically. It has been proposed that the synchronization of two delay-coupled oscillators can be achieved by relaying the dynamics via a third mediating element. Using phase oscillators, we have analytically investigated the dynamical relay problem for three oscillators. Our results show that the complete zero-lag synchrony can be achieved only in symmetric case, when the outer neurons are identical and the connections are symmetric. We have also shown that how phase lag of the outer neurons in the locked state depends on inhomogeneity in presence of small mismatch in the parameters of the neurons and the synapses. The results show very good agreement with numerical results of the conductance based models.

Zahra Ghasemi Esfahani, Alireza Valizadeh  
Institute of Advanced Studies in Basic Science, Iran  
ghasemi.zahra@gmail.com, valizadeh@iasbs.ac.ir

## PP1

### Investigating the Effect of Atropine on Baroreceptor Heart Rate Regulation

Atropine and metoprolol (betablockers) act as competitive antagonists of the neurotransmitters acetylcholine and noradrenaline within the autonomic nervous system. This study presents a non-linear baroreflex differential equations model, incorporating neurotransmitter concentrations. We investigate the impact of admission of atropine and metoprolol on heart rate dynamics during head-up tilt. Global sensitivity analysis and optimization is used to validate and investigate the model using experimentally measured blood pressure and heart rate data for different doses of medication.

Christian H. Haargaard Olsen  
PhD student Biomathematics Program  
North Carolina State University  
chaarga@ncsu.edu

Mette S. Olufsen  
Department of Mathematics  
North Carolina State University  
msolufse@math.ncsu.edu

Johnny T. Ottesen  
Roskilde University  
Department of Mathematics  
johnny@ruc.dk

Jesper Mehlsen

Frederiksberg Hospital  
Denmark  
jesper.mehlsen@frh.regionh.dk

Hien T. Tran  
Department of Mathematics  
North Carolina State University  
tran@math.ncsu.edu

## PP1

### Accelerated Uzawa Iteration for the Stokes Equations

The finite-element discretization of the Stokes equations leads to a saddle-point problem

$$\begin{bmatrix} A & B^T \\ B & 0 \end{bmatrix} \begin{bmatrix} \mathbf{u} \\ p \end{bmatrix} = \begin{bmatrix} \mathbf{f} \\ 0 \end{bmatrix} \quad (1)$$

where  $A$  is symmetric positive-definite and  $B$  is full-rank. The system (1) is explored using the Uzawa iteration

$$\begin{aligned} A\mathbf{u}_{k+1} &= \mathbf{f} - B^T p_k \\ p_{k+1} &= p_k + \omega B\mathbf{u}_{k+1}. \end{aligned}$$

Regarding this as a fixed-point iteration on  $\mathbf{u}$  and  $p$ , we augment it with Anderson acceleration to improve the convergence. We show the results of a numerical study in which we compare the performance in several test cases of Uzawa iteration with and without acceleration as well as several alternative solution approaches.

Nguyenho Ho  
Mathematical Sciences Department  
Worcester Polytechnic Institute  
nho@wpi.edu

Sarah D. Olson, Homer F. Walker  
Worcester Polytechnic Institute  
sdolson@wpi.edu, walker@wpi.edu

## PP1

### Determining An Optimal Mathematical Model for Tumor Growth

Cancer proves to be a major medical issue that is a leading cause of death and much research is devoted to finding effective treatments. Mathematical models play an important role in this effort by providing a framework to optimize proposed treatments. In order to make accurate predictions, models need to correctly predict tumor growth. We test previously proposed models of tumor growth by fitting them to data to determine an optimal model.

Hana Jaafari, Michael Ellis  
Texas Christian University  
h.k.jaafari@tcu.edu, m.e.ellis@tcu.edu

Hana Dobrovolny  
Department of Physics  
Ryerson University  
h.dobrovolny@tcu.edu

## PP1

### Synchrony in Metapopulations with on-off Stochastic Dispersal

We consider ecological networks in which migration between patches and other intrinsic system parameters are

stochastic in nature. We study the role of this stochasticity and how it relates to synchronization, especially in cases when the time scale of the stochastic process is slow with regard the inherent time scale of the system. We find that such a system can favor synchrony, despite the network being disconnected for large time intervals.

Russell Jeter, Igor Belykh  
Department of Mathematics and Statistics  
Georgia State University  
russell.jeter@outlook.com, ibelykh@gsu.edu

## PP1

### Two-Theta Neuron: Phase Models for Bursting Networks

We propose a reduction approach to study bursting outcomes of central pattern generators using coupled two-theta phase models. We examine several configurations of 3-cell CPGs with inhibitory, excitatory and electrical synapses, and compare our findings with corresponding exemplary networks comprised of plausible Hodgkin-Huxley models. Occurrence, robustness and transformations of CPG outcomes are studied using 2D return maps, whose stable fixed points and invariant circles correspond to bursting patterns with fixed and varying phase lags.

Aaron Kelley  
GSU  
aarnkelley@gmail.com

## PP1

### A Linear Analysis of a Straight Rod under Tension Both With and Without Drag

Starting with a straight rod under tension, we are studying the perturbations in twist and bend using the Kirchhoff Rod Model. Additionally, we can include the effects of drag approximated by resisted force theory. Finally, this model can inform us about the response of internal forces compared to external ones. This work has applications to the study of worm locomotion, bacterial flagella, and DNA.

Victoria Kelley  
James Madison University  
kelleyvm@dukes.jmu.edu

## PP1

### Conserved NPZ Models with Time Delay

Nutrient-Phytoplankton-Zooplankton (NPZ) models are used to describe the bottom two trophic levels of an underwater ecosystem. Time delays arise naturally in these models, such as the time it takes for juvenile plankton to reach maturity. Our focus is on models in which the total biomass in the system is conserved. We then explore how the quantity of biomass and the delay properties have on behaviour such as persistence and stability.

Matt Kloosterman  
University of Waterloo  
mklooste@uwaterloo.ca

Sue Ann Campbell  
University of Waterloo  
Dept of Applied Mathematics  
sacampbell@uwaterloo.ca

Francis Poulin  
Department of Applied Mathematics  
University of Waterloo  
fpoulin@uwaterloo.ca

# PP1

## Prediction of Biphasic Mitogenic Activity by Hgf, a Cancer-Associated Stroma-Derived Growth Factor, Using a Multi-Species Continuum Model.

A large number of growth factors and drugs are known to act in a biphasic manner: at lower concentrations they cause increased division of target cells, whereas at higher concentrations the mitogenic effect is inhibited. Often, the molecular details of the mitogenic effect of the growth factor are known, whereas the inhibitory effect is not. Hepatocyte Growth Factor, HGF, has recently been recognized as a strong mitogen that is present in the microenvironment of solid tumors. Recent evidence suggests that HGF acts in a biphasic manner on tumor growth. We build a multi-species model of HGF action on tumor cells using different hypotheses for high dose-HGF activation of a growth inhibitor and show that the shape of the dose-response curve is directly related to the mechanism of inhibitor activation. We thus hypothesize that the shape of a dose-response curve is informative of the molecular action of the growth factor on the growth inhibitor.

Anna Konstorum

University of California, Irvine  
akonstor@uci.edu

# PP1

## The Role of CD200-CD200R in Cancer Suppression and Promotion

CD200-CD200R is an inhibitive signal that tumor cells use it to silence macrophages in tumor microenvironment. It has been shown that CD200-CD200R has apparently two contradictory experimental results in tumor growth: inhibition and promotion. We develop a mathematical model to qualitative fits with experimental results and explain why these two opposite experimental results can both take place depending on the "affinity" of M1 and M2 macrophages to form the complex CD200-CD200R with tumor.

Kang-Ling Liao, Xue-Feng Bai, Avner Friedman  
Ohio State University  
liao.92@mbi.osu.edu, ., .

# PP1

## Patient-Specific Modeling of Average Cerebral Blood Flow During Orthostatic Stress

Cerebral autoregulation is a combination of local mechanisms responsible for maintaining a stable cerebral blood flow during changes in arterial blood pressure. This talk presents a simple patient-specific autoregulatory model that predicts the average cerebral blood flow velocity amidst dramatic changes in arterial blood pressure during the sit-to-stand procedure. The model will be validated against experimental data and results will be compared to explore physiological differences between healthy young, healthy elderly, and hypertensive elderly individuals.

Gregory C. Mader, Mette S. Olufsen  
Department of Mathematics  
North Carolina State University

gmader16@gmail.com, msolufse@math.ncsu.edu

Adam Mahdi  
North Carolina State University  
adam.mahdi@gmail.com

# PP1

## Periodic Accumulation of Genetic Variation in the Genome of the Plant *Sorghum bicolor*

An organism's genome is a key determinant of its phenotype. Genetic variation produces much of the phenotypic variation on which evolutionary forces act, and we aim to identify signatures of factors influencing the accumulation of genetic variation. We show that periodic accumulation of genetic variation exists in the genome of the plant *Sorghum bicolor* and suggest that this periodicity is the result of biological phenomena, such as chromatin structure and selection.

Ryan F. McCormick, Sandra K. Truong, Sandra K. Truong, John Mullet  
Department of Biochemistry & Biophysics  
Texas A&M University  
ryanabashbash@neo.tamu.edu, thkhavi@neo.tamu.edu, thkhavi@neo.tamu.edu, jmullet@neo.tamu.edu

# PP1

## Gene Regulatory Network Based on a Novel Evolvable Partially Connected Artificial Neural Network

DNA microarray technology provides the expression levels of thousands of genes and make it possible to investigate the complex biological processes. Finding relationships between genes and construct a Gene regulatory Network (GRN) is subject of interest. To this aim, we proposed a novel Partially connected Artificial Neural Network with Evolvable Topology (PANNET) in inferring the GRN from time series gene expression data. This approach can illustrate the underlying biological behaviors without prior knowledge of the system

Mina Moradi Kordmahalleh  
North Carolina A&T State University  
mmoradik@aggies.ncat.edu

Mohammad Gorji Sefidmazgi  
PhD Student  
North Carolina A&T State University  
mgorjise@aggies.ncat.edu

Abdollah Homaifar  
North Carolina A&T State University  
homaifar@ncat.edu

# PP1

## Accumulation Behavior

We introduce a Markov Chain variant to model the accumulation behavior of a population and provide a forecasted confidence set of items to be accumulated in a future period which may differ in length from the derived period. In non-sequential accumulation it will be established that the eigenvalues of this model are always real.

Thomas Morrissey  
Infosys

thomas.j.morrissey@verizon.net

### PP1

#### Distribution of Correlated Spiking Events in Integrate-and-Fire Networks

Randomly connected populations of spiking neurons display a rich variety of dynamics. We address the conceptual issue of how to mathematically characterize the partially synchronous multiple firing events (MFEs) which manifest in between homogeneous and total synchronous dynamics. Using a geometric method for obtaining the distribution of magnitudes of these MFEs, we recast the cascading firing event process as a first-passage time problem, establishing a link between the voltage distribution of excitatory and inhibitory neurons and the number of neurons firing in an MFE.

Katherine Newhall

Courant Institute of Mathematical Science  
New York University  
newhall@cims.nyu.edu

Jiwei Zhang

New York University  
Courant Institute of Mathematical Science  
jzhang@cims.nyu.edu

Adi Rangan

Courant Institute of Mathematical Sciences  
rangan@cims.nyu.edu

Douglas Zhou

Shanghai Jiao Tong University  
zdz@sjtu.edu.cn

### PP1

#### Modeling Dynamics of Mosquito Populations and Assessing Abatement Strategies for West Nile Virus

We designed a mathematical model and compared it with surveillance data for mosquitoes that are primary vectors of West Nile Virus (WNV). Based on the best fit of the model to the data, we estimated key parameters such as the effectiveness of insecticide treatments. We used these estimates for modeling the spread of WNV to obtain more reliable disease outbreak predictions and performed numerical simulations to test various mosquito abatement strategies.

Kasia A. Pawelek, Patrick R. Niehaus, Cristian Salmeron  
University of South Carolina Beaufort  
kpawelek@uscb.edu, niehaupr@email.sc.edu,  
salmeron@email.uscb.edu

Elizabeth J. Hager, Gregg J. Hunt  
Beaufort County Mosquito Control  
lhager@bcgov.net, ghunt@bcgov.net

### PP1

#### Activity Patterns of Neuronal Network with Voltage-Sensitive Piecewise Smooth Coupling

We present an analysis of activity patterns in a neuronal network of three mutually inhibitory cells with voltage-sensitive piecewise smooth coupling. While standard fast-slow analysis fails to describe the dynamics during fast jumps due to the voltage-sensitive nature of coupling,

piecewise smoothness of coupling enables us to consider a sequence of fast subsystems in piecewise way. Our analysis shows that slow dynamics as well as fast dynamics incorporate to determine where fast jumps actually go.

Choongseok Park

Department of Mathematics  
North Carolina A&T State University  
cpark@ncat.edu

Jonathan Rubin

University of Pittsburgh  
Pittsburgh, PA  
jonrubin@pitt.edu

### PP1

#### Modeling the Effects of Craniosynostosis on Intracranial Pressure

Craniosynostosis is a condition where the plates in a newborn's skull fuse prematurely. In some cases cognitive development is impaired. Impairment is caused by increased intracranial pressure that arises in untreated craniosynostosis. Our research attempts to quantify the effect of craniosynostosis by mathematically modeling the growing skull/brain system and investigating how the fusion of various plates affects pressures in this system. We use the finite element method to solve the model equations, and conclude that in certain cases intracranial pressures rise above the critical value of 15 mmHg.

Jackson Penning, Madeline Anderson, Emily Van Heel,  
Magda Stolarska

University of St. Thomas  
penn5708@stthomas.edu, ande2354@stthomas.edu,  
vanh3676@stthomas.edu, mastolarska@stthomas.edu

### PP1

#### Investigation of Dual Virus Infection of Human Respiratory Tract

Recent studies have revealed that about 40 percent of influenza like illness are caused by simultaneous infections by more than one virus. The effect of multiple virus infections on the severity of illness is not clear. We investigate a mathematical model of dual virus infections to determine conditions that make these infections more or less severe than single virus infections.

Lubna Pinky

Graduate student(Ph.D),  
Physics & Astronomy Department,TCU  
lubna.pinky@tcu.edu

Hana Dobrovolny

Assistant Professor  
Physics and Astronomy Department,TCU  
h.dobrovolny@tcu.edu

### PP1

#### Synchronization of Bursting Neurons: a Synergetic Effect of Excitation and Inhibition

We study synchronization of bursting neurons with excitatory and inhibitory connections. Fast inhibition is known to promote pairwise asynchrony in inhibitory bursting networks. We show that the addition of such repulsive inhibition to excitatory networks induces bursting synchrony,

in contrast to one's expectations. Through stability and geometrical analysis, we reveal the mechanism underlying this purely synergetic phenomenon and show that it originates from the transition between bursting of different types caused by excitatory-inhibitory synaptic coupling.

Reimbay Reimbayev, Igor Belykh  
Department of Mathematics and Statistics  
Georgia State University  
reimbayev2@student.gsu.edu, ibelykh@gsu.edu

## PP1

### **Determining Mechanism of Action and Efficacy of Novel Influenza Antivirals**

Influenza is a serious viral infection common in humans that can cause deadly pandemics. Drug treatment is a first line of defense against pandemics and many compounds are tested as influenza antivirals. We use mathematical models to identify experiments that can determine the mechanism of action of an influenza antiviral.

Thalia Rodriguez  
Texas Christian University  
thalia.rodriguez@tcu.edu

Hana Dobrovolny  
Department of Physics  
Ryerson University  
h.dobrovolny@tcu.edu

## PP1

### **Within-Host Models of Influenza Virus Infection: The Role of Macrophages**

Influenza strains can be categorized as either with low (LP) or high pathogenicity (HP). We developed a mathematical model which includes the pathogenic role of the immune system cells to study the within-host dynamics influenza infections caused by the HP viruses. By comparing modeling predictions with both macrophage and viral kinetic data, we examined their contribution to the overall pathogenesis of HP viruses and quantified the difference between seasonal and HP viruses.

Cristian Salmeron, Kasia A. Pawelek  
University of South Carolina Beaufort  
salmeron@email.uscb.edu, kpawelek@uscb.edu

## PP1

### **Bursting in the Pituitary Corticotroph: The Role of Bk Ion Channels**

Pituitary corticotrophs from male rats exhibit a variety of electrical activity patterns, including spiking and several forms of bursting. Stimulation with corticotrophin releasing hormone and arginine vasopressin convert the spiking to bursting. Surprisingly, the bursting occurs even though the SK type of calcium-activated potassium ion channels are not expressed. We use mathematical modeling to understand how calcium- and voltage-dependent BK channels can produce the bursting produced by stimulated corticotrophs.

Sevgi Sengul  
Department of Mathematics  
Florida State University  
ssengul@math.fsu.edu

Joel Tabak  
Dept of Biological Sciences  
Florida State University  
joel@neuro.fsu.edu

Peter Duncan, Mike Shipston  
Centre for Integrative Physiology  
University of Edinburgh  
p.j.duncan@sms.ed.ac.uk, mike.shipston@ed.ac.uk

Richard Bertram  
Department of Mathematics  
Florida State University  
bertram@math.fsu.edu

## PP1

### **Identifiability of Linear Dynamical Systems from a Single Trajectory**

In parameter estimation, before implementing numerical methods, it is important to determine whether the parameter estimation problem will have a unique solution in the presence of unlimited and error free data. This is the question of structural identifiability. For linear systems of ODEs, I will present a straightforward criterion for identifiability from one trajectory, solely based on geometric properties of the trajectory. Several illustrative examples will be discussed.

Shelby R. Stanhope  
University of Pittsburgh  
srs114@pitt.edu

Jonathan Rubin  
University of Pittsburgh  
Pittsburgh, PA  
jonrubin@pitt.edu

David Swigon  
Department of Mathematics  
University of Pittsburgh  
swigon@pitt.edu

## PP1

### **From Chaos to Periodicity: Revisiting the Logistic Map with an Ecologically Realistic Spatial Structure and Dispersal Mechanism**

We improve on traditional applications of the logistic map to spatially extended systems by explicitly introducing spatial length scale, dispersal shape, and absorbing boundary conditions. In this way we greatly improve ability to apply model outputs to real-world ecological systems. For a large range of parameters we find spatiotemporally chaotic population distributions abruptly give way to periodicity. As growth rate and dispersal distance increase, we witness an evolving metapopulation structure with three phases.

Laura Storch, James Pringle  
University of New Hampshire  
lmh66@wildcats.unh.edu, jpringle@unh.edu

## PP1

### **Identifying Physiological Origins of Baroreceptor Firing Characteristics Through a Conductance Based Neural Model**

In this study we investigate aortic baroreceptors, stretch

sensitive neurons with endings embedded in the arterial walls. The firing rate of these neurons is a key physiological signal in cardiovascular regulation. We investigate the physiological basis of key characteristics of this firing pattern through an ion channel based model of the membrane voltage. Comparisons of models with differing ensembles of ion channels provide insight into the origins of certain firing characteristics.

Jacob Sturdy  
North Carolina State University  
jsturdy@ncsu.edu

Johnny T. Ottesen  
Roskilde University  
Department of Mathematics  
johnny@ruc.dk

Mette S. Olufsen  
Department of Mathematics  
North Carolina State University  
msolufse@math.ncsu.edu

## PP1

### Leaf Inclination Angle Regulates the Distribution of Light in the Sorghum Canopy

Light interception is the first step in photosynthesis. Mathematical modeling of the light environment of sorghum, an agriculturally important crop, predicts that changes in the angle that a leaf emerges on a plant will confer changes in its light interception. This led to the identification of loci associated with the genetic regulation of leaf inclination angle and continues to guide field experimentation toward optimizing light interception in sorghum.

Sandra K. Truong, Sandra K. Truong, Ryan F. McCormick, John Mullet  
Department of Biochemistry & Biophysics  
Texas A&M University  
thkhavi@neo.tamu.edu, thkhavi@neo.tamu.edu, ryan-abashbash@neo.tamu.edu, jmmullet@neo.tamu.edu

## PP1

### Modeling the Effect of Antiarrhythmic Agents on the Action Potential of Human Ventricular Cells

Sudden cardiac death from ventricular fibrillation is a major cause of death worldwide. Several different classes of antiarrhythmia drugs are currently available each of which alters a different membrane ion conductance. A human cardiac cell model is used to study the effect of the different antiarrhythmia drugs on the physical characteristics of cardiac action potentials.

Binaya Tuladhar  
Texas Christian University  
Fort Worth, TX  
binaya.tuladhar@tcu.edu

Hana Dobrovolny  
Department of Physics  
Ryerson University  
h.dobrovolny@tcu.edu

## PP1

### Understanding and Distinguishing Three Time

## Scale Oscillations

Our goal is to understand bursting dynamics in three time scale systems. Such systems arise in biological settings such as the interaction of intrinsic calcium oscillations with a calcium-dependent, voltage-gated membrane potential oscillation mechanism. With this motivation, we construct a model having three time scales with two copies of Morris-Lecar equations. Using techniques from geometric singular perturbation theory, we explain the mechanisms underlying the dynamics and elucidate which characteristics truly represent three time scale features.

Yangyang Wang  
University of Pittsburgh  
yaw23@pitt.edu

Pingyu Nan, Vivien Kirk  
University of Auckland  
pnan011@aucklanduni.ac.nz, v.kirk@auckland.ac.nz

Jonathan Rubin  
University of Pittsburgh  
Pittsburgh, PA  
jonrubin@pitt.edu

## PP1

### Coupling-Induced Synchronization of Mexican Jumping Beans

Mexican jumping beans jump to move from higher to lower temperatures for optimal survival. By characterizing their jumping pattern containing two characteristic frequencies of jumping and rest, and by inducing a physical nearest neighbor coupling through the attachment of string, we seek to synchronize their motions experimentally. We compare this to computational results relating the behavior of the beans to an adaptation of Kuramoto model with frequency modulated oscillators accounting for the atypical jumping behavior.

Andrea J. Welsh, Flavio Fenton, Ilija Uzelac  
Georgia Institute of Technology  
awelsh8@gatech.edu, flavio.fenton@physics.gatech.edu, ilija.uzelac@physics.gatech.edu

## PP1

### Phenotypic Modulation of Virulence Facilitates Pathogen Invasion of the Gut

The interior lining of the human intestine is inhabited by populations of commensal microbiota, which provide defense against invasive bacteria. Surprisingly, *Salmonella Typhimurium* gains an environmental advantage over the commensals by provoking the hosts inflammatory defenses. We develop and analyze a model of the competition between the commensals and *Salmonella*, which incorporates a simple model of the inflammatory response, to explore possible mechanisms by which *Salmonella* exploits the immune response to outcompete the commensals.

Glenn S. Young, Bard Ermentrout  
University of Pittsburgh  
Department of Mathematics  
gsy2@pitt.edu, bard@pitt.edu

Jonathan Rubin  
University of Pittsburgh  
Pittsburgh, PA

jonrubin@pitt.edu

## LS14 Speaker and Organizer Index



Art courtesy of Bourouiba, Gourley, Liu and Wu, SIAP 71-2

*Italicized names indicate session organizers.*

**A**

Abarbanel, Henry D., MS31, 9:30 Tue  
 Abbas, Kaja, MS24, 10:00 Tue  
 Ackleh, Azmy S., MS1, 11:00 Mon  
 Agosto, Folashade, MS53, 3:30 Wed  
 Akudibillah, Gordon, MS54, 3:00 Wed  
 Alacam, Deniz, PP1, 8:00 Tue  
 Albasini Mourao, Marcio Duarte, CP12, 5:30 Wed  
 Alford, John G., CP1, 2:00 Mon  
 Allard, Jun, MS19, 6:00 Mon  
 Allen, Linda J., MS66, 9:30 Thu  
 Allen, Richard, CP7, 6:00 Tue  
 Alolyan, Ibraheem, PP1, 8:00 Tue  
 Aminzare, Zahra, CP7, 5:00 Tue  
 Amorim, Paulo V., CP13, 10:00 Thu  
 Amro, Rami M., CP4, 2:30 Tue  
 Arciero, Julia, MS34, 2:00 Mon  
 Ardekani, Arezoo, MS27, 10:30 Tue  
 Armiento, Aurora, MS16, 3:00 Mon  
 Arnold, Andrea N., MS67, 11:00 Thu  
 Aston, Philip J., MS47, 9:30 Wed  
 Aston, Philip J., MS47, 9:30 Wed  
 Au, Loretta, MS45, 4:30 Tue  
 Au, Loretta, MS45, 4:30 Tue  
 Au, Loretta, PP1, 8:00 Tue  
 Azer, Karim, MS43, 6:00 Tue  
 Azer, Karim, MS62, 4:30 Wed  
 Azer, Karim, MS62, 4:30 Wed

**B**

Baker, Michelle, CP15, 4:30 Wed  
 Banaji, Murad, MS30, 9:30 Tue  
 Banerjee, Sandip, MS47, 10:00 Wed  
 Banks, H. T., MS62, 5:30 Wed  
 Banks, H. Thomas, MS8, 10:30 Mon  
 Bannish, Brittany, MS29, 9:30 Tue  
 Bannish, Brittany, MS29, 11:00 Tue  
 Bardhan, Jaydeep P., MS63, 4:30 Wed  
 Bardhan, Jaydeep P., MS63, 4:30 Wed  
 Barnett, William H., MS28, 10:30 Tue  
 Barranca, Victor, MS6, 9:30 Mon

Barranca, Victor, MS6, 11:00 Mon  
*Barranca, Victor, MS14, 2:00 Mon*  
*Barreiro, Andrea K., MS20, 4:30 Mon*  
 Barreiro, Andrea K., MS20, 4:30 Mon  
 Bathe, Mark, MS26, 9:30 Tue  
 Battista, Nicholas A., MS13, 2:30 Mon  
 Beale, J. Thomas, MS42, 4:30 Tue  
*Belair, Jacques, MS38, 2:00 Tue*  
 Belkhatir, Zehor, CP15, 5:30 Wed  
*Bertram, Richard, MS23, 4:30 Mon*  
*Bertram, Richard, MS31, 9:30 Tue*  
 Bertram, Richard, MS31, 10:30 Tue  
*Best, Janet, MS71, 9:30 Thu*  
 Best, Janet, MS71, 9:30 Thu  
*Best, Janet, MS79, 2:15 Thu*  
 Bickel, Scott T., CP8, 11:00 Wed  
 Block, Michael, MS62, 6:00 Wed  
 Boëte, Christophe, MS17, 5:30 Mon  
 Booth, Victoria, MS44, 4:30 Tue  
 Borleske, George, PP1, 8:00 Tue  
 Boros, Balázs, MS15, 3:30 Mon  
*Bortz, David M., MS8, 9:30 Mon*  
 Bortz, David M., MS8, 10:00 Mon  
*Bortz, David M., MS16, 2:00 Mon*  
 Bourgeron, Thibault, MS8, 11:00 Mon  
 Bourouiba, Lydia, MS32, 2:30 Tue  
 Bourouiba, Lydia, MS78, 3:45 Thu  
 Bragard, Jean, MS72, 10:00 Thu  
 Brauer, Fred, MS24, 9:30 Tue  
 Bressloff, Paul C., MS14, 2:00 Mon  
 Brouwer, Andrew, PP1, 8:00 Tue  
 Brown, Heidi, MS65, 5:30 Wed  
 Browne, Cameron, MS10, 2:00 Mon  
 Burns, John A., MS65, 5:00 Wed

**C**

*Cai, Wei, MS69, 9:30 Thu*  
*Cai, Wei, MS77, 2:15 Thu*  
 Cai, Yongli, CP2, 5:00 Mon  
 Canic, Suncica, MS57, 3:30 Wed  
 Cappelletti, Daniele, MS39, 3:00 Tue

Carin, Larry, MS7, 10:00 Mon  
 Carr, Thomas W., CP2, 4:30 Mon  
 Carroll, Sam R., PP1, 8:00 Tue  
 Castro, Joshua, PP1, 8:00 Tue  
 Chaudhuri, Rishidev, MS58, 3:30 Wed  
*Chen, Duan, MS69, 9:30 Thu*  
 Chen, Duan, MS69, 11:00 Thu  
*Chen, Duan, MS77, 2:15 Thu*  
*Chen, Zhan, MS63, 4:30 Wed*  
*Chen, Zi, MS3, 9:30 Mon*  
 Chen, Zi, MS3, 11:00 Mon  
*Cherry, Elizabeth M., MS51, 9:30 Wed*  
 Cherry, Elizabeth M., MS51, 9:30 Wed  
*Cherry, Elizabeth M., MS59, 2:00 Wed*  
 Cho, Carolyn, MS38, 3:30 Tue  
*Chung, Matthias, MS2, 9:30 Mon*  
 Chung, Matthias, MS2, 9:30 Mon  
*Chung, Matthias, MS10, 2:00 Mon*  
*Chung, Matthias, MS33, 2:00 Tue*  
 Cintron-Arias, Ariel, CP6, 5:00 Tue  
*Ciupe, Stanca, MS2, 9:30 Mon*  
*Ciupe, Stanca, MS10, 2:00 Mon*  
 Collens, Jarod, PP1, 8:00 Tue  
 Collins, James J., IP8, 1:00 Thu  
 Conradi, Carsten, MS15, 3:00 Mon  
 Consagra, William, PP1, 8:00 Tue  
 Conway, Jessica M., MS2, 10:30 Mon  
 Copos, Calina A., PP1, 8:00 Tue  
 Craciun, Gheorghe, MS30, 11:00 Tue  
 Craig, Morgan, MS38, 2:30 Tue  
 Curto, Carina, MS49, 9:30 Wed  
 Curtu, Rodica, MS50, 9:30 Tue  
*Curtu, Rodica, MS50, 9:30 Wed*  
*Curtu, Rodica, MS58, 2:00 Wed*

**D**

Dahari, Harel, MS61, 4:30 Wed  
 Dai, Shibin, MS48, 10:00 Wed  
 Darcy, Isabel, MS49, 10:00 Wed  
 Das, Jayajit, MS41, 6:00 Tue  
 Daun-Gruhn, Silvia, MS28, 10:00 Tue  
 David, Tim, MS25, 11:00 Tue

*continued on next page*

David, Timothy, PD3, 8:45 Wed  
 Debroy, Swati, MS53, 2:00 Wed  
*Debroy, Swati, MS61, 4:30 Wed*  
 Debroy, Swati, MS61, 5:00 Wed  
 DeLeenheer, Patrick, MS66, 11:00 Thu  
 Denham, Sue, MS50, 10:00 Tue  
*Diao, Yuanan, MS49, 9:30 Wed*  
 Diao, Yuanan, MS49, 10:30 Wed  
*Diao, Yuanan, MS56, 2:00 Wed*  
*Ding, Wandí, MS66, 9:30 Thu*  
 Ding, Wandí, MS66, 10:00 Thu  
*Ding, Wandí, MS74, 2:15 Thu*  
 Donnell, Pete, MS30, 10:00 Tue  
 Dorratoltaj, Nargesalsadat, MS32, 2:00 Tue  
 Dovzhenok, Andrey A., CP11, 4:30 Wed  
 Doyle, Matthew G., MS11, 3:00 Mon  
 Duke-Sylvester, Scott, MS17, 5:00 Mon  
 Duncan, Jacob P., PP1, 8:00 Tue

## E

Eisenberg, Bob, MS69, 9:30 Thu  
 Eisenberg, Marisa, MS75, 2:15 Thu  
 Elston, Timothy, PD3, 8:45 Wed,  
 Elston, Timothy, MS68, 10:00 Thu  
 Ernst, Claus, MS49, 11:00 Wed  
 Everett, Rebecca A., CP1, 2:30 Mon

## F

*Fan, Guihong, MS65, 4:30 Wed*  
 Fancourt, Craig, MS21, 5:30 Mon  
 Faulwell, Cullen J., PP1, 8:00 Tue  
 Feliu, Elisenda, MT1, 8:00 Tue  
*Feliu, Elisenda, MS15, 2:00 Mon*  
*Feliu, Elisenda, MS22, 4:30 Mon*  
 Feng, Peng, MS40, 4:30 Tue  
*Feng, Zhilan, MS17, 4:30 Mon*  
 Feng, Zhilan, MS17, 4:30 Mon  
 Fenton, Flavio, MS51, 10:30 Wed  
*Fenton, Flavio, MS72, 9:30 Thu*  
 Fletcher, Patrick A., MS23, 5:30 Mon  
*Fok, Pak-Wing, MS11, 2:00 Mon*  
 Fok, Pak-Wing, MS11, 2:00 Mon  
 Forde, Jonathan, MS10, 2:30 Mon

Forest, M. Gregory, MS68, 9:30 Thu  
 Fricks, John, MS41, 5:00 Tue  
 Frieboes, Hermann, MS7, 10:30 Mon  
*Fry, Brendan C., MS25, 9:30 Tue*  
 Fry, Brendan C., MS25, 9:30 Tue  
*Fry, Brendan C., MS34, 2:00 Tue*  
 Fryer, Dashiell, CP8, 10:30 Wed  
 Fu, Henry, MS36, 3:00 Tue  
 Fu, Yibin, MT2, 9:30 Wed  
 Fuller, Pamela B., MS20, 5:30 Mon  
*Fuller, Pamela B., MS44, 4:30 Tue*  
 Fuller, Pamela B., PP1, 8:00 Tue  
*Fung, Isaac Chun-Hai, MS24, 9:30 Tue*  
*Fung, Isaac Chun-Hai, MS32, 2:00 Tue*

## G

Galvani, Alison, IP5, 8:15 Wed  
 Gao, Tony, MS36, 3:30 Tue  
 Garcia-Torres, Selenne, MS44, 5:00 Tue  
 Gardiner, Bruce S., MS25, 10:00 Tue  
 Garlick, Martha J., CP13, 10:30 Thu  
*Geng, Weihua, MS42, 4:30 Tue*  
 Geng, Weihua, MS42, 6:00 Tue  
 George, Uduak Z., MS57, 2:30 Wed  
 Ghasemi Esfahani, Zahra, PP1, 8:00 Tue  
 Gnacadja, Gilles, MS22, 5:00 Mon  
 Goldman, Daniel, MS34, 2:30 Mon  
 Golowasch, Jorge, MS37, 3:30 Tue  
 Golubitsky, Martin, MS58, 2:30 Wed  
 Gopalkrishnan, Manoj, MS39, 2:00 Tue  
 Gopinath, Arvind, MS27, 10:00 Tue  
 Gordillo, Luis, CP9, 3:00 Wed  
*Gou, Kun, MS3, 9:30 Mon*  
 Gou, Kun, MS3, 9:30 Mon  
 Grabe, Michael, MS48, 9:30 Wed  
 Graham, Erica J., MS21, 6:00 Mon  
*Graham, Erica J., MS29, 9:30 Tue*  
 Graham, Erica J., MS29, 9:30 Tue  
 Graham, Jason, MS18, 5:00 Mon  
 Green, David F., MS26, 10:00 Tue  
 Gudmand-Høyer, Johanne, CP11, 5:30 Wed  
 Gumel, Abba, MS1, 10:00 Mon

*Gupta, Chinmaya, MS73, 9:30 Thu*  
*Gupta, Chinmaya, MS81, 2:15 Thu*  
 Gupta, Chinmaya, MS81, 2:15 Thu  
 Gutierrez, Juan B., MS46, 10:30 Wed  
*Guy, Robert D., MS27, 9:30 Tue*  
*Guy, Robert D., MS36, 2:00 Tue*  
 Guy, Robert D., MS36, 2:30 Tue

## H

Haargaard Olsen, Christian H., PP1, 8:00 Tue  
*Haider, Mansoor A., MS43, 4:30 Tue*  
 Haider, Mansoor A., MS76, 2:15 Thu  
*Hamlet, Christina, MS5, 9:30 Mon*  
*Hamlet, Christina, MS13, 2:00 Mon*  
 Hamlet, Christina, MS13, 3:00 Mon  
 Harper, Marc, CP9, 2:30 Wed  
 Hasan, Md Mehedi M., CP5, 5:00 Tue  
 Hastings, Alan M., IP7, 8:15 Thu  
 He, Jing, MS63, 5:00 Wed  
 Heberling, Tamra, CP14, 2:45 Thu  
 Heffernan, Jane, MS10, 3:00 Mon  
 Hellevik, Leif, MT2, 9:30 Wed  
 Hendrix, Angelean O., MS38, 3:00 Tue  
 Hill, Nicholas A., MS43, 4:30 Tue  
 Hill, Nicholas A., MT2, 9:30 Wed  
 Hill, Nicholas A., MS80, 2:45 Thu  
 Ho, Nguyenho, PP1, 8:00 Tue  
 Hoffman, Kathleen A., MS4, 10:00 Mon  
 Hoffman, Matthew J., MS59, 3:30 Wed  
 Holmes, William, MS60, 3:00 Wed  
*Hoover, Alexander, MS70, 9:30 Thu*  
 Hoover, Alexander, MS70, 9:30 Thu  
*Hoover, Alexander, MS78, 2:15 Thu*  
 Horng, Tzyy-Leng, MS77, 3:15 Thu  
 Hu, Dan, MS14, 3:30 Mon  
 Huang, Jingfang, MS42, 5:00 Tue  
 Hubbard, Letitia, MS59, 3:00 Wed  
 Hughes, John, MS41, 4:30 Tue  
*Huguet, Gemma, MS50, 9:30 Wed*  
*Huguet, Gemma, MS58, 2:00 Wed*  
 Huguet, Gemma, MS58, 2:00 Wed

*continued on next page*

**I**  
Ingalls, Brian P., MS67, 10:30 Thu  
Iron, David, MS60, 2:30 Wed

**J**  
Jaafari, Hana, PP1, 8:00 Tue  
*Jang, Sophia, MS40, 4:30 Tue*  
Jang, Sophia, MS40, 5:00 Tue  
*Jang, Sophia, MS46, 9:30 Wed*  
Jensen, Oliver E., IP3, 8:15 Tue  
Jensen, Oliver E., PD3, 8:45 Wed  
Jeter, Russell, PP1, 8:00 Tue  
Jiang, Yi, MS76, 3:15 Thu  
Jilkine, Alexandra, MS60, 2:00 Wed  
Johnson, Maya E., MS3, 10:00 Mon  
Johnston, Matthew, MS22, 6:00 Mon  
Jones, Shannon, MS78, 2:45 Thu  
Joshi, Badal, MS22, 4:30 Mon  
Joshi, Sunnie, MS3, 10:30 Mon  
Josic, Kresimir, MS6, 9:30 Mon  
Josic, Krešimir, CP11, 5:00 Wed  
Ju, Tao, MS63, 6:00 Wed

**K**  
*Kang, Yun, MS40, 4:30 Tue*  
Kang, Yun, MS40, 6:00 Tue  
*Kang, Yun, MS46, 9:30 Wed*  
Kappel, Franz, MS47, 10:30 Wed  
Karabiyik, Tugba, CP13, 11:00 Thu  
Keck, Dustin, MS16, 2:00 Mon  
Kelley, Aaron, PP1, 8:00 Tue  
Kelley, Victoria, PP1, 8:00 Tue  
Kelly, Michael, MS54, 2:00 Wed  
Khan, Adnan, CP3, 9:30 Tue  
Kightley, Eric, MS16, 3:30 Mon  
Kilpatrick, Zachary, MS58, 3:00 Wed  
Kim, Oleg, MS29, 10:00 Tue  
Kloosterman, Matt, PP1, 8:00 Tue  
Knepley, Matthew G., MS63, 5:30 Wed  
Knutsdottir, Hildur, MS19, 5:00 Mon  
Kondic, Anna, MS21, 5:30 Mon  
Konstorum, Anna, PP1, 8:00 Tue  
Kostina, Ekaterina, MS33, 3:30 Tue

Kovacic, Gregor, MS6, 10:00 Mon  
Krogh-Madsen, Trine, MS51, 11:00 Wed  
Krueger, Justin, MS33, 2:00 Tue  
Kuegler, Philipp, CP5, 4:30 Tue  
Kulkarni, Rahul, MS73, 10:30 Thu

**L**  
Lander, Arthur, IP4, 1:00 Tue  
Lanz, Aprillya, MS61, 5:30 Wed  
Lau, Kevin D., MS43, 5:00 Tue  
Lawley, Sean D., MS79, 3:15 Thu  
Layton, Anita T., MS76, 2:45 Thu  
*Leander, Rachel, MS66, 9:30 Thu*  
Leander, Rachel, MS66, 10:30 Thu  
*Leander, Rachel, MS74, 2:15 Thu*  
Lee, Christopher, CP9, 2:00 Wed  
*Lee, Pilhwa, MS80, 2:15 Thu*  
Lee, Pilhwa, MS80, 2:15 Thu  
Lee, Pilhwa, MS77, 3:45 Thu  
Lee, Sunmi, MS40, 5:30 Tue  
Leiderman, Karin, MS36, 2:00 Tue  
Lejon, Annelies, CP1, 3:00 Mon  
*Lenhart, Suzanne M., MS54, 2:00 Wed*  
Lenhart, Suzanne M., PD3, 8:45 Wed  
Lenhart, Suzanne M., MS74, 2:15 Thu  
Leviyang, Sivan, MS2, 10:00 Mon  
Levy, Doron, MS46, 9:30 Wed  
Levy, Rachel, MS64, 5:30 Wed  
Levy, Rachel, PD3, 8:45 Wed  
Lewis, Owen, MS13, 2:00 Mon  
Li, Bingtuan, MS18, 6:00 Mon  
Li, Jia, MS74, 2:45 Thu  
Li, Jing, CP3, 10:30 Tue  
*Li, Jun, MS38, 2:00 Tue*  
Li, Michael, MS1, 10:30 Mon  
Li, Sheng, MS24, 10:30 Tue  
*Li, Shuwang, MS48, 9:30 Wed*  
*Li, Shuwang, MS55, 2:00 Wed*  
Li, Shuwang, MS55, 3:30 Wed  
Li, Songting, MS14, 2:30 Mon  
Li, Xiaofan, MS69, 10:30 Thu  
Liao, Kang-Ling, PP1, 8:00 Tue  
Lin, Tai-Chia, MS69, 10:00 Thu

Liu, Chun, MS77, 2:15 Thu  
*Liu, Xinfeng, MS52, 9:30 Wed*  
*Liu, Xinfeng, MS60, 2:00 Wed*  
Liu, Xinfeng, MS60, 3:30 Wed  
Lopez, Manuel, MS81, 3:45 Thu  
Losert, Wolfgang, MS7, 11:00 Mon  
*Lu, Benzhuo, MS26, 9:30 Tue*  
Lu, Benzhuo, MS26, 10:30 Tue  
*Lu, Benzhuo, MS35, 2:00 Tue*  
Lubkin, Sharon, MS57, 2:00 Wed  
*Luo, Xiaoyu, MT2, 9:30 Wed*  
Luo, Xiaoyu, MT2, 9:30 Wed  
Ly, Cheng, MS20, 5:00 Mon

**M**  
Ma, Baoling, MS16, 2:30 Mon  
Ma, Junling, MS24, 11:00 Tue  
*MacGregor, Duncan J., MS23, 4:30 Mon*  
MacGregor, Duncan J., MS23, 5:00 Mon  
*MacGregor, Duncan J., MS31, 9:30 Tue*  
Maclaurin, James, CP4, 3:00 Tue  
Mader, Gregory C., PP1, 8:00 Tue  
*Mahdi, Adam, MS75, 2:15 Thu*  
Malka, Roy, CP15, 5:00 Wed  
Malutina, Elena, CP4, 3:30 Tue  
*Martcheva, Maia, MS1, 9:30 Mon*  
Martcheva, Maia, MS1, 9:30 Mon  
*Martcheva, Maia, MS9, 2:00 Mon*  
Mascagni, Michael, MS26, 11:00 Tue  
Mather, William H., MS81, 2:45 Thu  
Mazer, Norman, IP6, 1:00 Wed  
McCormick, Ryan F., PP1, 8:00 Tue  
McKinley, Scott, MS79, 2:15 Thu  
Medlock, Jan, MS53, 2:00 Wed  
Meshkat, Nicolette, MT1, 2:00 Wed  
Meshkat, Nicolette, MS15, 2:30 Mon  
*Meshkat, Nicolette, MS75, 2:15 Thu*  
Miao, Hongyu, MS75, 2:45 Thu  
Mikucki, Michael, MS55, 2:00 Wed  
*Miller, Laura A., MS57, 2:00 Wed*  
*Miller, Laura A., MS64, 4:30 Wed*  
Miller, Laura A., MS64, 4:30 Wed  
*Miller, Laura, MS70, 9:30 Thu*

*continued on next page*

Miller, Laura, MS78, 2:15 Thu

Mincheva, Maya, MS30, 9:30 Tue

Mincheva, Maya, MS39, 2:00 Tue

Mohammed-Awel, Jemal, MS46, 11:00 Wed

Moradi Kordmahalleh, Mina, PP1, 8:00 Tue

Mori, Yoichiro, MS77, 2:45 Thu

Morrissey, Thomas, PP1, 8:00 Tue

Mubayi, Anuj, MS53, 2:00 Wed

Mubayi, Anuj, MS61, 4:30 Wed

Mueller, Stefan, MS30, 10:30 Tue

Munoz, Laura, MS59, 2:00 Wed

Murrugarra, David, MS73, 10:00 Thu

Murthy, Abhishek, MS59, 2:30 Wed

## N

Nagahara, Larry, MS7, 9:30 Mon

Nekka, Fahima, MS38, 2:00 Tue

Nekka, Fahima, MS38, 2:00 Tue

Nevai, Andrew, MS9, 3:00 Mon

Nevai, Andrew, MS74, 3:15 Thu

Newby, Jay, MS79, 3:45 Thu

Newhall, Katherine, MS20, 4:30 Mon

Newhall, Katherine, PP1, 8:00 Tue

Newton, Paul, MS7, 9:30 Mon

Nie, Qing, MS52, 9:30 Wed

Niehaus, Patrick R., PP1, 8:00 Tue

Nirody, Jasmine, MS45, 6:00 Tue

Novozhilov, Artem S., CP8, 9:30 Wed

Numfor, Eric, MS54, 2:00 Wed

Numfor, Eric, MS54, 2:30 Wed

## O

O'Leary, Timothy, MS31, 11:00 Tue

Olson, Sarah D., MS5, 11:00 Mon

Olufsen, Mette S., MS43, 4:30 Tue

Olufsen, Mette S., MS67, 9:30 Thu

Opron, Kristopher, MS56, 2:00 Wed

Oremland, Matthew, MS54, 3:30 Wed

Osan, Remus, MS14, 3:00 Mon

Otani, Niels, MS72, 10:30 Thu

Ottesen, Johnny T., MS67, 9:30 Thu

Ottesen, Johnny T., MS67, 9:30 Thu

## P

Pantea, Casian, MS30, 9:30 Tue

Pantea, Casian, MS39, 2:00 Tue

Park, Choongseok, PP1, 8:00 Tue

Pasour, Virginia B., MS13, 3:30 Mon

Patel, Mainak, MS20, 6:00 Mon

Patel, Swati, CP8, 10:00 Wed

Peercy, Bradford E., MS4, 9:30 Mon

Peercy, Bradford E., MS4, 11:00 Mon

Penning, Jackson, PP1, 8:00 Tue

Perminov, Valeriy D., CP3, 11:00 Tue

Phillips, Andrew, MS44, 6:00 Tue

Pinky, Lubna, PP1, 8:00 Tue

Presse, Steve, MS41, 4:30 Tue

Presse, Steve, MS41, 5:30 Tue

Prieto Langerica, Alicia, MS44, 5:30 Tue

Prosper, Olivia, MS53, 2:30 Wed

## R

Ramirez, Samuel A., CP12, 4:30 Wed

Rangamani, Padmini, MS45, 5:30 Tue

Rankin, James, MS50, 10:30 Tue

Raue, Andreas, MS75, 3:15 Thu

Rawdon, Eric, MS56, 2:30 Wed

Reed, Michael C., MS71, 9:30 Thu

Reed, Michael C., MS68, 10:30 Thu

Reed, Michael C., MS79, 2:15 Thu

Reimbayev, Reimbay, PP1, 8:00 Tue

Reinitz, John, MS45, 5:00 Tue

Rejniak, Katarzyna A., MS5, 10:00 Mon

Remien, Christopher, MS47, 11:00 Wed

Rendall, Alan, MS39, 3:30 Tue

Reynolds, Angela M., CP6, 5:30 Tue

Rinzel, John, IP1, 8:15 Mon

Robertson, Suzanne, MS74, 3:45 Thu

Robinson, Phyllis R., MS4, 9:30 Mon

Rodriguez, Thalia, PP1, 8:00 Tue

Rong, Libin, MS9, 2:30 Mon

Rubin, Jonathan E., MS28, 9:30 Tue

Rubin, Jonathan E., MS37, 2:00 Tue

Ryan, Shawn, MS12, 3:00 Mon

## S

Sachs, Jeff, MS62, 4:30 Wed

Sachs, Jeff, MS62, 5:00 Wed

Sachs, Jeff, PD3, 8:45 Wed

Salac, David, MS55, 2:30 Wed

Salmeron, Cristian, PP1, 8:00 Tue

Samson, Julia E., MS70, 10:30 Thu

Santhanakrishnan, Arvind, MS78, 2:15 Thu

Saucedo, Omar, MS53, 3:00 Wed

Sauer, Timothy, MS31, 10:00 Tue

Schmidt, Deena, MS79, 2:45 Thu

Schwabedal, Justus T., CP10, 4:30 Wed

Schwemmer, Michael, MS71, 10:30 Thu

Secomb, Timothy W., MS34, 3:00 Mon

Selgrade, James F., MS21, 4:30 Mon

Selgrade, James F., MS21, 4:30 Mon

Sengul, Sevgi, PP1, 8:00 Tue

Sgouralis, Ioannis, MS25, 10:30 Tue

Shilnikov, Andrey, MS37, 2:30 Tue

Shiu, Anne, MS15, 2:00 Mon

Shuai, Zhisheng, MS24, 9:30 Tue

Shuai, Zhisheng, MS32, 2:00 Tue

Shuai, Zhisheng, MS32, 3:30 Tue

Siegel, David, MS39, 2:30 Tue

Simons, Julie, MS5, 9:30 Mon

Singh, Abhyudai, MS81, 3:15 Thu

Skataric, Maja, CP7, 5:30 Tue

Snyder, Abigail, MS28, 9:30 Tue

Sobie, Eric, MS23, 6:00 Mon

Sontag, Eduardo, MS12, 2:00 Mon

Soofi, Wafa, MS37, 3:00 Tue

Spardy, Lucy, MS28, 9:30 Tue

Spardy, Lucy, MS37, 2:00 Tue

Spardy, Lucy, MS71, 11:00 Thu

Stamoulis, Catherine, CP10, 5:30 Wed

Stanhope, Shelby R., PP1, 8:00 Tue

Staples, Anne, MS78, 3:15 Thu

Starz-Gaiano, Michelle, MS4, 10:30 Mon

Stepien, Tracy L., MS18, 4:30 Mon

Stepien, Tracy L., MS18, 4:30 Mon

*continued on next page*

Stoetzel, Claudia, MS21, 5:00 Mon  
 Stolarska, Magdalena, MS11, 2:30 Mon  
 Storch, Laura, PP1, 8:00 Tue  
 Strawbridge, Eva M., CP5, 5:30 Tue  
*Strychalski, Wanda, MS19, 4:30 Mon*  
 Strychalski, Wanda, MS19, 5:30 Mon  
 Sturdy, Jacob, PP1, 8:00 Tue  
 Sullivant, Seth, MS75, 3:45 Thu  
*Sun, Yi, MS68, 9:30 Thu*  
*Sun, Yi, MS76, 2:15 Thu*  
 Sun, Yi, MS76, 3:45 Thu  
 Sutton, Karyn L., MS10, 3:30 Mon  
 Swanson, Kristin Rae, IP2, 1:00 Mon  
 Swigon, David, MS67, 10:00 Thu

**T**  
 Takaidza, Isaac, CP3, 10:00 Tue  
 Taylor, Bradford, CP14, 2:15 Thu  
*Teboh-Ewungkem, Miranda I., MS17, 4:30 Mon*  
 Teboh-Ewungkem, Miranda I., MS17, 6:00 Mon  
 Teboh-Ewungkem, Miranda I., MS46, 10:00 Wed  
 Tewari, Shivendra, MS80, 3:15 Thu  
 Thomas, Peter J., MS28, 11:00 Tue  
*Thomases, Becca, MS27, 9:30 Tue*  
 Thomases, Becca, MS27, 9:30 Tue  
*Thomases, Becca, MS36, 2:00 Tue*  
 Tian, Jianjun Paul, MS52, 10:00 Wed  
 Tian, Jianjun Paul, MS68, 11:00 Thu  
 Tien, Joseph, MS9, 3:30 Mon  
 Tolkacheva, Elena, MS51, 10:00 Wed  
 Tomasetti, Cristian, CP1, 3:30 Mon  
 Toporikova, Natalia, MS71, 10:00 Thu  
*Tran, Hien T., MS47, 9:30 Wed*  
 Transtrum, Mark K., MS33, 3:00 Tue  
 Treloar, Katrina, CP12, 5:00 Wed  
 Truong, Sandra K., PP1, 8:00 Tue  
 Tuladhar, Binaya, PP1, 8:00 Tue  
*Tuncer, Necibe, MS1, 9:30 Mon*  
*Tuncer, Necibe, MS9, 2:00 Mon*  
 Tuncer, Necibe, MS9, 2:00 Mon

**U**  
 Udiani, Oyita, CP13, 9:30 Thu

**V**  
 Vaidya, Naveen K., CP6, 4:30 Tue  
*Vandiver, Rebecca, MS11, 2:00 Mon*  
 Vattikuti, Shashaank, MS50, 11:00 Tue  
 Veliz-Cuba, Alan, CP7, 4:30 Tue  
*Veliz-Cuba, Alan, MS73, 9:30 Thu*  
 Veliz-Cuba, Alan, MS73, 9:30 Thu  
*Veliz-Cuba, Alan, MS81, 2:15 Thu*  
 Veneroni, Marco, MS48, 11:00 Wed  
 Vogl, Chris, MS55, 3:00 Wed  
 Voit, Eberhard O., MS33, 2:30 Tue  
 Vologodskii, Alexander, MS56, 3:00 Wed

**W**  
 Waldrop, Lindsay, MS57, 3:00 Wed  
 Walton, Jay R., MS11, 3:30 Mon  
 Wang, Jin, MS32, 3:00 Tue  
 Wang, Qi, MS64, 5:00 Wed  
*Wang, Qi, MS68, 9:30 Thu*  
*Wang, Qi, MS76, 2:15 Thu*  
*Wang, Xiang-Sheng, MS65, 4:30 Wed*  
 Wang, Xiang-Sheng, MS65, 4:30 Wed  
 Wang, Xueying, CP4, 2:00 Tue  
 Wang, Yangyang, MS37, 2:00 Tue  
 Wang, Yangyang, PP1, 8:00 Tue  
 Waters, Ryan S., CP6, 6:00 Tue  
 Watts, Margaret A., MS23, 4:30 Mon  
 Wei, Guo-Wei, MS56, 3:30 Wed  
 Welsh, Andrea J., PP1, 8:00 Tue  
 Whidden, Mark E., MS64, 6:00 Wed  
 Wilson, Dan D., MS72, 9:30 Thu  
*Wilson, Shelby, MS44, 4:30 Tue*  
*Wiuf, Carsten, MT1, 9:30 Mon*  
 Wiuf, Carsten, MT1, 9:30 Mon  
*Wiuf, Carsten, MS15, 2:00 Mon*  
*Wiuf, Carsten, MS22, 4:30 Mon*  
 Wolfram, Marie-Therese, MS35, 2:00 Tue  
 Wolgemuth, Charles, MS19, 4:30 Mon

Wolgemuth, Charles, MS27, 11:00 Tue  
*Wrobel, Jacek K., MS5, 9:30 Mon*  
 Wrobel, Jacek K., MS5, 10:30 Mon  
*Wrobel, Jacek K., MS13, 2:00 Mon*  
 Wu, Hulin, MS2, 11:00 Mon

**X**  
*Xia, Kelin, MS49, 9:30 Wed*  
*Xia, Kelin, MS56, 2:00 Wed*  
 Xie, Dexuan, MS35, 2:30 Tue  
*Xue, Chuan, MS12, 2:00 Mon*  
 Xue, Chuan, MS12, 3:30 Mon

**Y**  
 Yang, Li, CP10, 5:00 Wed  
*Yong, Kamuela E., MS18, 4:30 Mon*  
 Yong, Kamuela E., MS18, 5:30 Mon  
 Yordanov, Pencho, MS22, 5:30 Mon  
 Young, Glenn S., PP1, 8:00 Tue  
*Younger, John G., MS8, 9:30 Mon*  
 Younger, John G., MS8, 9:30 Mon  
*Younger, John G., MS16, 2:00 Mon*  
 Yu, Jin, MS35, 3:00 Tue  
 Yunlong, Huo, MS43, 5:30 Tue

**Z**  
 Zapata-Allegro, Cheryl, MS29, 10:30 Tue  
 Zauhar, Randy, MS42, 5:30 Tue  
 Zhang, Calvin, MS70, 10:00 Thu  
*Zhang, Lei, MS52, 9:30 Wed*  
 Zhang, Lei, MS52, 10:30 Wed  
*Zhang, Lei, MS60, 2:00 Wed*  
*Zhang, Yongtao, MS52, 9:30 Wed*  
 Zhang, Yongtao, MS52, 11:00 Wed  
*Zhang, Yongtao, MS60, 2:00 Wed*  
 Zhao, Kun, MS12, 2:30 Mon  
 Zhao, Lihong, CP9, 3:30 Wed  
 Zhao, Longhua, MS70, 11:00 Thu  
*Zhao, Shan, MS26, 9:30 Tue*  
*Zhao, Shan, MS35, 2:00 Tue*  
 Zhao, Shan, MS35, 3:30 Tue  
 Zhao, Yanxiang, MS48, 10:30 Wed  
 Zhou, Douglas, MS6, 9:30 Mon

Zhou, Douglas, MS6, 10:30 Mon

*Zhou, Douglas, MS14, 2:00 Mon*

*Zhou, Yongcheng, MS48, 9:30 Wed*

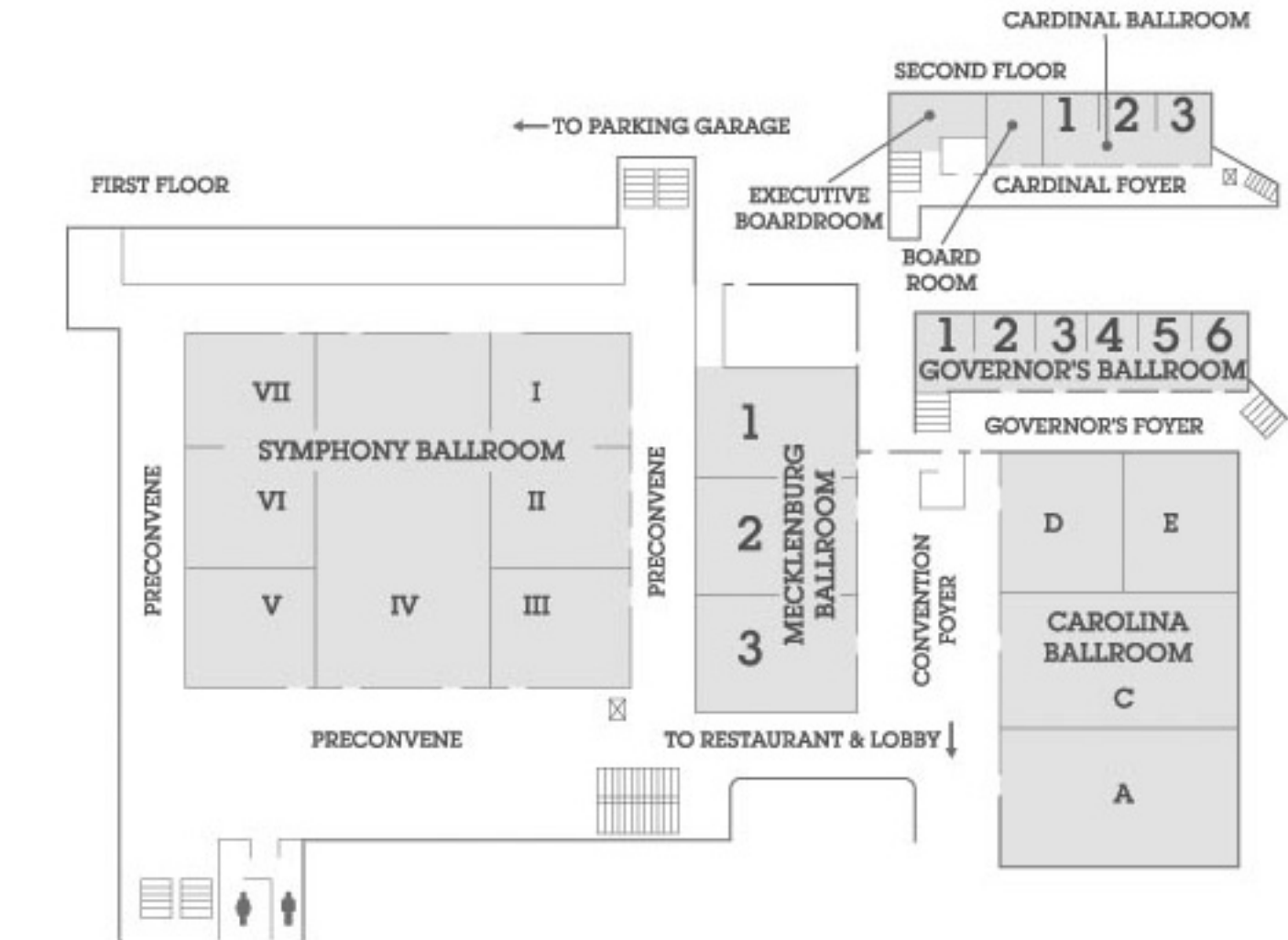
*Zhou, Yongcheng, MS55, 2:00 Wed*

## LS14 Budget

**Conference Budget**  
**SIAM Conference on Life Sciences**  
**August 4-7, 2014**  
**Charlotte, North Carolina**

Expected Paid Attendance	320	
Revenue		
Registration Income		\$103,910
Total		\$103,910
Expenses		
Printing		\$2,800
Organizing Committee		\$3,600
Invited Speakers		\$9,800
Food and Beverage		\$22,000
AV Equipment and Telecommunication		\$15,900
Advertising		\$7,000
Conference Labor (including benefits)		\$34,514
Other (supplies, staff travel, freight, misc.)		\$8,000
Administrative		\$11,287
Accounting/Distribution & Shipping		\$5,542
Information Systems		\$9,910
Customer Service		\$3,670
Marketing		\$5,700
Office Space (Building)		\$3,112
Other SIAM Services		<u>\$3,528</u>
Total		\$146,363
Net Conference Expense		(\$42,453)
Support Provided by SIAM		<u>\$42,453</u>
		\$0
Estimated Support for Travel Awards not included above:		
Early Career and Students	35	\$23,250

## Sheraton Charlotte



FSC logo text box indicating size & layout of logo.  
Conlins to insert logo.