**Mathematical Neuroscience 2012-2013**

Mathematics describes key dynamical mechanisms for patterns of neural activity and quantifies levels of information in these patterns. At the same time, new mathematics, that often bridges information theory, dynamical systems, and statistical mechanics, has been inspired by the complexity of the underlying networks and the computations they perform. Over the past decade, mathematics has entered different subfields of neuroscience, and has suggested unexpected parallels among others. The first emphasis year workshop, *Mathematical Challenges in Neural Network Dynamics*, will focus on such parallels, in the form of general challenges posed by dynamics of nonlinear, spiking networks, and will organize a series of workshops to follow that will highlight mathematical impact and possibilities in the most active and exciting areas of neuroscience.

Cognitive Neuroscience will present superb opportunities for mathematical contributions, especially in connecting different theoretical and experimental frameworks. On the experimental side, methods ranging from single-neuron recording to human behavioral tests are flourishing, and mathematical models are beginning to suggest how one leads to the other. Rigorous theoretical treatments from microeconomics are often applied, including Bayesian estimation and optimization, but details of how they might be implemented in stochastic, dynamic neural circuits have only recently been proposed. By bringing together theorists working on different levels, this workshop will move the field closer to a long-held goal of understanding and predicting decision-making and choice behavior.

A workshop on Disease will include recent work that has suggested mechanisms for pathological activity patterns in epilepsy and Parkinsons disease, and dynamical models that have been used to explain the function and possible improvement of stimulation-based therapies. Mathematical analysis is also being pursued for prosthetics used in sensory systems (i.e., cochlear implants for deafness) and motor systems (i.e., neural implants that drive artificial limbs). Many open questions remain for other disease states, including addictions, mental illnesses, and memory dysfunction. In parallel, rich mathematical questions arise in the exploding area of non-invasive imaging. Algorithms are needed for more efficient data analysis and especially for combining datasets gathered on different spatial and temporal scales (e.g., fMRI, EEG,
Rhythms and Oscillations will feature increasing evidence that oscillations and appropriate phase relationships are critical for cognitive states and sensory processing.

In Cellular and Subcellular, moving to the smallest spatial scale, the chemical and molecular mechanisms for the dynamics of brain state regulation, development, repair, and adaptation are being uncovered by modern tools of molecular biology and genetics. These small-scale dynamics affect excitability, and bridging across such multiple scales is a frontier in our understanding of patterns of neuronal activity. There is enormous opportunity for mathematics to contribute by combining models at the levels of systems biology and electrophysiology.

In Sensory Systems and Coding, we will address separate modalities, as well as consider commonalities for the representation and processing of stimuli with naturalistic statistics. Here, the establishment of maps and associations, the dynamics of synaptic plasticity, the adaptation to scene statistics, and the mechanisms for multi-modal interactions are of central importance. Special focus will be given to active sensing and feedback loops (central to periphery) in sensory processing, to coding strategies, and to streaming (source separation) in the auditory system. Attention throughout the workshop will be given to plausible neuronal mechanisms for these aspects of sensory processing.

For more details visit: http://www.mbi.osu.edu/2012/scientific2012.html

Continued from page 1 (Mathematical Neuroscience 2012-2013)

and single-neuron recordings).

MBI Congratulates New SIAM Fellows

On April 1 SIAM announced its 2012 Class of SIAM Fellows. The elected fellows, 35 in all, are leaders in applied mathematics. Among those elected were ten researchers with strong ties to MBI. They are:

- Anthony Bloch (workshop organizer)
- Bard Ermentrout (MBI Scientific Advisory Committee and workshop organizer)
- Lisa Fauci (MBI Scientific Advisory Committee, VLP Lecturer, and workshop organizer)
- Greg Forest (MBI Scientific Advisory Committee and workshop organizer)
- Susan Friedlander (contact person for USC Institute Partner)
- Kirk Jordan (Chair of MBI Board of Trustees, MBI Scientific Advisory Committee, chair of MBI Industrial Advisory Committee, and workshop organizer)

In Sensory Systems and Coding, we will address separate modalities, as well as consider commonalities for the representation and processing of stimuli with naturalistic statistics. Here, the establishment of maps and associations, the dynamics of synaptic plasticity, the adaptation to scene statistics, and the mechanisms for multi-modal interactions are of central importance. Special focus will be given to active sensing and feedback loops (central to periphery) in sensory processing, to coding strategies, and to streaming (source separation) in the auditory system. Attention throughout the workshop will be given to plausible neuronal mechanisms for these aspects of sensory processing.

We congratulate these new SIAM Fellows and take this opportunity to thank them for their service to MBI.

Full list of Events 2012-2013

<table>
<thead>
<tr>
<th>Date</th>
<th>Event</th>
</tr>
</thead>
<tbody>
<tr>
<td>July 16-20, 2012</td>
<td>MBI BioSciences Problem-Solving Workshop (PSW@MBI)</td>
</tr>
<tr>
<td>August 27-30, 2012</td>
<td>Workshop for Young Researchers in Mathematical Biology</td>
</tr>
<tr>
<td>September 19-21, 2012</td>
<td>Math Biology: Looking at the Future</td>
</tr>
<tr>
<td>October 1-5, 2012</td>
<td>Workshop 1: Mathematical Challenges in Neural Network Dynamics</td>
</tr>
<tr>
<td>October 15-18, 2012</td>
<td>Mathematical and Computational Challenges in Cilia- and Flagella-Induced Fluid Dynamics</td>
</tr>
<tr>
<td>November 13-16, 2012</td>
<td>Statistics of Time Warpings and Phase Variations</td>
</tr>
<tr>
<td>December 10-14, 2012</td>
<td>Workshop 2: Cognitive Neuroscience</td>
</tr>
<tr>
<td>February 4-8, 2013</td>
<td>Workshop 3: Disease</td>
</tr>
<tr>
<td>February 18-22, 2013</td>
<td>Mathematical Challenges in Biomolecular/Biomedical Imaging and Visualization</td>
</tr>
<tr>
<td>March 18-22, 2013</td>
<td>Workshop 4: Rhythms and Oscillations</td>
</tr>
<tr>
<td>April 8-12, 2013</td>
<td>Workshop 5: Cellular and Subcellular</td>
</tr>
<tr>
<td>May 6-10, 2013</td>
<td>Workshop 6: Sensory Systems and Coding</td>
</tr>
<tr>
<td>June 24-28, 2013</td>
<td>Keyfitz Symposium on Mathematical Demography</td>
</tr>
</tbody>
</table>
Math Biology: Looking at the Future
MBI’s 10th Anniversary (September 19-21, 2012)

The meeting will feature talks about areas in which exciting progress has been made in recent years and in which future advances can be expected.

Speakers

- Reka Albert (Penn State)
- Bill Bialek (Princeton)
- Emery Brown (MIT, Mass General)
- Jim Collins (HHMI, BU, Harvard)
- Ingrid Daubechies (Duke)
- Nicholas Jewell (Berkeley)
- Nancy Kopell (BU)
- Simon Levin (Princeton)
- Philip Maini (Oxford)
- Martin Nowak (Harvard, Keynote)
- Lior Pachter (Berkeley)

For more details visit: http://www.mbi.osu.edu/2012/10thdescription.html

Workshop for Young Researchers in Mathematical Biology
(August 27-30, 2012)

The workshop is intended to broaden the scientific perspective of young researchers (primarily junior faculty, postdocs, and senior graduate students) in mathematical biology and to encourage interactions with other scientists.

Workshop activities include plenary talks and poster sessions, as well as group discussions on issues relevant to mathematical biologists. Several abstracts will be chosen for short talks as well as to be presented as a poster.

We cordially invite young mathematical biologists to participate. For full consideration, please apply by May 1, 2012.

Accepted Speakers

- Ben Bolker (McMaster)
- Antonio Bru (Complutense de Madrid)
- Thomas Chou (UCLA)
- Lisette de Pillis (Harvey Mudd College)
- Mark Forest (North Carolina at Chapel Hill)
- Kirk Jordan (T.J. Watson Research, IBM)
- Ann Rundell (Purdue)
- Colleen Webb (Colorado State)

For more details and information on how to apply visit: http://www.mbi.osu.edu/wyrmb/wyrmb2012.html
Over the past 40 years, tissue engineering / regenerative medicine (TERM) has grown from concepts to established medical treatments used in over one million patients. As of 2007, there were approximately 50 firms offering TERM products with annual sales in excess of $1.3 billion, which represent more than a ten-fold increase from five years before.

Despite the impressive economic growth of the field and its growing impact on human health, often TERM is understood largely at a phenomenological level. If one considers a historical perspective, developing fields often begin at such a phenomenological stage. For example, chemical engineering initially considered each type of chemical plant as unique. Later in the field’s development, it was recognized that regardless of what chemical is being made, a number of “unit operations” were involved (e.g., distillation, mixing, pumping). A major development in the practice of chemical engineering was made when it was recognized that these different unit operations could be understood in terms of just a few fundamental processes such as transport phenomena (e.g., diffusion, heat transfer, and fluid mechanics), reaction kinetics, and thermodynamics. Importantly these fundamental processes can be rigorously understood with mathematics thereby enabling one to understand and rationally design complex systems from a bottom-up approach. TERM has already advanced from considering each application (e.g., tissue engineering of a skin or blood vessel) as unique to considering the underlying and unifying fundamental processes such as cell proliferation, differentiation, and migration. A critical challenge in the TERM field is to develop a rigorous mathematical understanding of these fundamental processes and to develop appropriate mathematical or computational approaches to enable one to use this rigorous understanding to rationally design complex biological systems relevant to TERM.

This workshop contributed to this critical challenge by bringing together a mix of participants with clinical, biological, engineering, and mathematical backgrounds. To help focus these efforts, cell-matrix interactions in the context of TERM were a central theme of this workshop. Cell-matrix interactions, including cellular responses to biological and mechanical signals from the matrix as well as cell-mediated generation and remodeling of the matrix, had an important role in a wide array of biological systems and TERM applications. Skin/wound healing and cardiovascular tissues were discussed in detail. They were complemented with additional work from an array of other systems/applications.

More details about this event can be found at http://www.mbi.osu.edu/2011/termdescription.html.
Workshop 6: Algebraic Methods in Systems and Evolutionary Biology (May 7-11, 2012)

Organizers: Reinhard Laubenbacher, Ilya Shmulevich, Seth Sullivant, and Ruriko Yoshido

Molecular networks drive many of the cellular and organismal processes that influence the phenotype of an organism, and have become a central focus of systems biology. To understand the complex dynamics underlying these processes, dynamic mathematical and computational models are needed. Several different approaches have been used successfully for this purpose. Beyond differential equations models, a range of discrete models has been used for this purpose, both deterministic and stochastic, for instance Boolean networks and their generalizations, and dynamic Bayesian networks. This workshop focused on modeling of molecular networks, in particular gene regulatory networks, with an emphasis on discrete modeling approaches, including stochastic aspects of networks. In addition to models of specific molecular networks, it explored questions such as the relationship between network structure and their dynamics, design principles of molecular networks, and the evolution of networks. Both mathematical and biological aspects of molecular network modeling were discussed, and the workshop opened with tutorial talks on both. For more details visit http://www.mbi.osu.edu/2011/ws6description.html.

CTW: Statistics, Geometry, and Combinatorics on Stratified Spaces Arising from Biological Problems (May 21-25, 2012)

Organizers: Stephan Huckemann, Huiling Le, Ezra Miller, Megan Owen, and Victor Patrangenaru

Modern statistics problems, from areas such as evolutionary biology, medical imaging, and shape analysis, increasingly deal with data sampled from spaces that are singular but naturally stratified; that is, the spaces behave nicely at most points, but at certain points the smooth structure becomes degenerate, such as when the space is composed of two or more intersecting smooth pieces. Key examples of stratified spaces are shape spaces (representing equivalence classes of point configurations under operations such as rotation, translation, scaling, projective transformations, or other non-linear transformations) and tree spaces (representing metric phylogenetic trees on fixed sets of taxa). Generalizing these two examples leads to algebraic varieties and polyhedral complexes, respectively. Applications require knowledge of the asymptotics of distributions on such spaces.

Developments in this “stratified statistics” take their cue from more classical geometric statistics, where data points are sampled from smooth manifolds, or from neighborhoods of embedded manifolds. Now, however, interesting algebraic geometry and combinatorics join the mix as methods for controlling behavior near strata of lower dimension, where the sample space can be singular nearby. Asymptotics on such spaces are governed not only by their local structure, but also by global topology (of the space and the data).

First results from the systematic study of nonparametric statistics on data sampled from stratified spaces include central limit theorems (CLTs) that illustrate nonclassical behavior, particularly when the mean lies on a lower stratum. The related asymptotics in this surprisingly common circumstance can depend in a crucial way on global geometry. Other first results include concrete combinatorial constructions of sample spaces.

This workshop aims to stimulate progress and cross-fertilization in the rapidly moving areas of theoretical and applied stratified statistics by gathering a mix of researchers with interests in biology, geometry, combinatorics, topology, probability, and statistics. For more details visit: http://www.mbi.osu.edu/2011/pgcdescription.html
Workshop 1: Mathematical Challenges in Neural Network Dynamics (October 1-5, 2012)

Organizers: Nicolas Brunel, Eric Shea-Brown, John Rinzel, and Sara Solla

This workshop will focus on dynamics and information processing in large, nonlinear networks. The aim is to highlight a set of mathematical questions that recur across neuroscience, and to discuss both recent progress and outstanding problems. The final day will feature a series of retrospective talks on the interplay of mathematics and neuroscience, leading into moderated discussions of future prospects. These sessions will align with the major themes of the workshop, which are proposed to be as follows:

1. Linking large-scale network structure and dynamics
2. Bridging scales – mean field models
3. Information and coding in large spiking networks
4. Plasticity and learning in network connections

For more details visit http://www.mbi.osu.edu/2012/ws1description.html

CTW: Mathematical and Computational Challenges in Cilia- and Flagella-Induced Fluid Dynamics (October 15-18, 2012)

Organizers: Kenny Breuer, Greg Forest, Anita Layton, Matthias Salathe, and Peter Satir

Cilia and flagella are ubiquitous in cell biology, acting either in a coordinated fashion to move surrounding fluid such as in lung airways, or as a propeller for cell locomotion such as on sperm or eukaryotic microorganisms, or as a sensory immotile but flexible antenna such as the primary cilia in essentially every cell in vertebrates and many vertebrate and invertebrate sense organs. The fluid dynamics induced by cilia and flagella, the mechanisms of coordination of motile cilia and flagella, and the fluid dynamic feedback to intra-ciliary and intra-flagellar transport and signaling, are essential to biology. The purpose of this workshop is to convene experts in biology, physics, mathematical modeling, and scientific computation to collectively assess progress and identify challenges to be undertaken in cilia- and flagella-induced fluid dynamics.

A list of outstanding challenges and computational strategies will be highlighted through lectures and subsequent discussions and open forums. Find the detailed strategies at http://www.mbi.osu.edu/2012/mccdescription.html

CTW: Statistics of Time Warpings and Phase Variations  
(November 13-16, 2012)

Organizers: J. S. Marron, J. O. Ramsay, L. Sangalli, and A. Srivastava

**Background:** A common feature of functional measurements of data over time, space and other continua, is that salient features in the resulting curves and surfaces vary in position from one recording to the next. For example, the growth patterns of children vary in the timing of puberty, human movements in activities like handwriting and golf swings speed up and slow down from one instance to another, seasonal events like hurricanes arrive early some years and late in others, and traffic jams vary in location over city streets from one day to another. At the same time, each of the events can also vary in intensity. We refer to positional variation as phase variation, and intensity variation as amplitude variation. It is now evident that many processes unfold over a system time that not only does not unroll at the same rate as physical clock time, but also tends to vary in a significant way from one realization of a functional event to another.

The registration or alignment of features in curves and images by smooth, one-to-one transformations of time or space, respectively, is an emerging hot topic that presents many challenges. From its beginnings with dynamic time warping in the late 50’s, followed by the landmark registration methods of Fred Bookstein, the registration of brain images to a fixed atlas, and its widespread application in functional data analysis, statisticians have realized that nonlinear phase variation is pervasive in data distributed over continua. Happily, a considerable variety of methods for separating amplitude from phase variation now exist, and connections with shape analysis methods have been made. It seems time to do some comparative tests, review progress to date, and consider new research opportunities.

**Workshop Ideas:** Instead of the usual passive speaker-audience format, workshop activities will be centered around applying a wide variety of statistical methods to a common collection of data sets. The focus will be on various analytic approaches of several different Analysis Groups, to some common data sets, featuring careful discussion of the strengths and weaknesses of the various analyses.

More details can be found at:  
http://www.mbi.osu.edu/2012/stwdescription.html

---

**Slipped strand mispairing**

Translational

Start: AATGCTTTGTC

-35: ACGAGACCTTCTGA

-10: 

Promoter

OFF:

Start: AATGCTTTGTC

-35: TGG

-10: TGA

Preliminary stop codon

Transcriptional

ON:

Start: AATGCTTTGTC

-35: ACCGAGACCTTCTGA

-10: 

OFF:

Start: AATGCTTTGTC

-35: 

-10: TGA

Phase Variation Slipped Strand Mispairing - Purple oval can either be a transcription factor (TF) or RNA polymerase (RNAP). Black boxes are short sequence repeats, Start (ATG) is the start codon in which the ribosome initiates translation of nucleotide sequence into amino acids and -10:-35 is the promoter which is the binding site for the RNAP to initiate transcription of DNA into RNA.
Spotlight on Casey Diekman

Casey Diekman arrived at MBI in Fall 2010 after completing his PhD at the University of Michigan in Bioinformatics and Industrial & Operations Engineering. His dissertation dealt with two different aspects in modeling and analysis of electrical activity in neuronal systems. It developed: (1) a statistical method for inferring the functional connectivity of neuronal networks from spike train data, and (2) a coupled nonlinear ordinary differential equations model of the electrophysiology of the suprachiasmatic nucleus (SCN), the specific neuronal network responsible for the generation of circadian (~24-hour) rhythms in mammals. The SCN model made a prediction that was verified by an experimental collaborator; namely that during the afternoon, some SCN neurons enter an extremely depolarized state and do not fire action potentials. This result was surprising, as the traditional view is that SCN neurons fire more during the day than at night, and has important consequences for phase shifting of the circadian clock.

Since joining MBI, Casey has continued to focus his research in the areas of mathematical neuroscience and biological rhythms and has established collaborations both within and outside of OSU. Casey is currently investigating neural control of the mammalian breathing rhythm (with Peter Thomas and Christopher Wilson, Case Western Reserve University), the dynamics of binocular rivalry and other oscillations in perception (with Marty Golubitsky, OSU), and the role of mitochondrial excitability in stroke (with David Terman, OSU).

Casey’s work on breathing addresses a common challenge faced by rhythmic processes as diverse as heartbeat, locomotion, feeding, and cortical activity: adaptive regulation of central pattern generator (CPG) activity in response to fluctuating operational demands. Respiratory control in the mammalian brainstem provides a clinically significant case-in-point. To study adaptive regulation of the breathing rhythm, Casey and his collaborators have developed a closed-loop model of respiratory control incorporating a conductance-based CPG, low-pass filtering of CPG output by the respiratory musculature, gas exchange in the lung, metabolic oxygen demand, and chemosensation. During the summer of 2012, Casey will record from cells in the pre-Bōtzinger complex, the region of the brainstem believed to contain the inspiratory CPG. These experiments, to be performed in C. Wilson’s lab at Case Western, have been designed to test predictions of their closed-loop model.

Binocular rivalry is a visual phenomenon that occurs when different images are presented to each eye. Rather than perceiving a single blend of the two images, one's perception alternates back and forth between each image. Casey's research into rivalry began after Hugh Wilson introduced a neuronal network model for generalized rivalry among learned patterns during his MBI colloquium talk in March 2011. Casey and Golubitsky, along with MBI long-term visitor Tyler McMillen (California State University, Fullerton) and Yunjiao Wang (former MBI postdoc, now at Rice University) became interested in H. Wilson’s model and are analyzing it using the theory of coupled cell systems. Their initial work has focused on the case of networks with two learned patterns, which they have shown can be rigorously reduced to much smaller quotient networks that facilitate insights into the dynamics of the original networks.

Recent experimental data suggests that enhancing calcium-sensitive mitochondrial metabolism in mouse cortical astrocytes after ischemia can have a protective effect and reverse cellular swelling and depolarization. To test this hypothesis, Casey has worked with Terman, Christopher Fall (University of Illinois at Chicago), and James Lechleiter (University of Texas Health Science Center at San Antonio) to construct a mathematical model of an astrocyte that integrates cellular membrane potential and volume with mitochondrial ATP production and calcium handling. An important goal of the project is to analyze this model mathematically, in order to better understand mechanisms underlying the experimental results and model behavior.

Casey has found the environment at MBI to be exceptionally stimulating, and his research interests in dynamical systems continue to grow. He is very much looking forward to the workshops associated with the 2012-2013 Emphasis Year on Mathematical Neuroscience.
Spotlight on Rachel Leander

Rachel Leander graduated from the University of Tennessee with a PhD in mathematics in 2010. Her graduate research was in optimal control theory. In collaboration with her advisor Suzanne Lenhart, she used optimal control theory to promote synchronization in populations of non-identical oscillators and developed a method to perform optimal impulse control of continuous dynamical systems. While completing her PhD she became a mother. Her son Viggo is now two years old.

After joining the MBI in 2010, Rachel began working with Avner Friedman to construct models of intracellular signaling associated with disease pathogenesis. In collaboration with Larry Schlesinger and Shi Pan Dai of the Center for Microbial Interface Biology, they constructed a model of membrane proximal signaling in the context of Francisella tularensis infection. When a bacterium makes contact with an immune cell, intracellular signaling networks are triggered. These networks control diverse tasks including the production of cytokines and the progression of phagocytosis. Although each individual signaling cascade is complex in its own right, crosstalk between pathways makes the outcome of a specific host-pathogen interaction difficult to anticipate. Parameterized by the existing literature, their model showed that phagocytosis associated alterations in the composition of the cell membrane can inhibit cytokine production through Toll-like Receptor 2. In addition, the model predicts that the combined actions of two negative regulators of cytokine signaling, Akt and Ras-GAP, is synergistic. Friedman and Rachel are currently investigating how interactions between diverse G proteins shape cAMP production. This model has the potential to provide general insights into the control and modulation of cAMP signaling in various cell types and disease states.

More recently Rachel began working with Ed Allen on the derivation and study of a cell-division probability density. Cancer is a disease in which cells divide uncontrollably. The time between successive divisions is called the intermitotic time. Healthy cells must pass a series of checkpoints before division can occur. Genetic mutations can enable cancer cells to bypass some of these checkpoints so that intermitotic time may be shortened in cancer. Cancer drugs are designed to arrest the cell cycle and induce death. Experimentalists examine the effect that a drug has on the distribution of intermitotic times in order to evaluate the efficacy of the drug and its mode of action. They have designed simple stochastic models of cell cycle progression. In these models the intermitotic time corresponds to a first exit time and, in some simple cases, that distribution of intermitotic times can be calculated explicitly. Data provided by our experimental collaborators; Shawn Garbett, Vito Quaranta, and Darren Tyson of Vanderbilt, enabled them to show their model distributions closely approximate real intermitotic time distributions. By fitting the models to the data we estimated the parameters that determine how the cell progresses toward division after treatment with a specific drug. In comparing the parameters that characterize cell cycle progression for control and drug treated cells they were excited to find that their model yields insights into the ways in which basic cellular processes (i.e. protein synthesis) and specific proteins (i.e. EGFR) control cell cycle progression.

In collaboration with Suzanne Lenhart and Vladimir Popopescu, she also continues to pursue her interest in control, refining and further developing ideas first explored in her thesis. She is particularly interested in identifying feasible control policies that meet specific goals.

Rachel has had a wonderful time working at the MBI. She feels very fortunate to have had the opportunity to collaborate with and learn from the many remarkable people who inhabit this institute.
Ed Allen (Texas Tech University) Professor Allen’s current research interests involve derivation of stochastic differential equation (SDE) models for biological and physical processes. In addition, he is interested in development and analysis of numerical methods for computational solution of SDE models. His current work at MBI involves derivation of stochastic versions of several discrete-delay and continuous-delay differential equation models useful in mathematical biology. In particular, stochastic delay differential equation models are being derived and studied for glucose/insulin levels, bacteriophage/bacteria dynamics, and logistic population growth with delay. Numerical methods for approximating the delay SDE models are simultaneously being developed and tested.

Linda Allen (Texas Tech University) Professor Allen’s research interests include applications of stochastic processes to problems in the spread of zoonotic diseases in wildlife and in virus-cell dynamics. Her current work at the MBI is to better understand and model the virus and immune system dynamics in reservoir versus spillover hosts.

In the reservoir host, the immune response is downregulated which leads to a persistent infection, whereas in the spillover host, the strong immune response leads to clearance of the infection.

Peter Kramer (Rensselaer Polytechnic Institute) Professor Kramer is generally interested in developing statistical or stochastic methods for describing the dynamics of complex systems in terms of physical models for the dynamics of their components and their interactions. He is pursuing three such projects in the context of microscale biology with other long-term visitors, OSU faculty, and MBI postdocs on the following topics: 1) quantitatively connecting network dynamics and structure to the timing of important events, motivated by neuroscience applications, 2) developing physically sound multiscale modeling frameworks for intracellular transport and regulation, and 3) examining the role of hydrodynamic interactions on the efficiency of microscopic swimming organisms in finding nutrients.

Rongsong Liu (University of Wyoming) Professor Liu’s research interests are mathematical biology, differential equations, dynamical systems, and their interface. Her research projects involve formulation, analysis and applications of deterministic mathematical models for infectious diseases and ecological systems. The models are aimed to answer questions and help gain useful insights for the biological systems being investigated. Based on the theoretical analysis and numerical simulations, she describes useful quantitative behaviors of model solutions and tackles which factors are most important in determining these behaviors. Together with collaborating biologists, she provides biological interpretations of the mathematical results, as insights and predictions. From time to time, they need to develop new or improve existing mathematical theories and techniques to provide satisfactory solutions to questions posed by collaborating biologists.

John McSweeney (SAMSI) Many biological systems exhibit bistable behavior — switching back and forth between two distinct states, even if there is theoretically a continuum of possible states for the system. This is seen in sleep-wake cycling dynamics, where the brain alternates between wake and sleep, or in gene expression, where certain genes seem to switch between transcription at full rate or not at all. Moreover, the switching periods for these processes are not uniform, but have a random distribution. Professor McSweeney is working to build simple, first-principles mathematical models that can explain such behavior. Ultimately, it involves making use of the randomness inherent in biological processes such as intracellular biochemical reactions, cell division, or neuron firing, and showing how that can produce bistability in the output.
Brandilyn Stigler (Southern Methodist University) Professor Stigler is continuing her work on the development of mathematical tools for reverse engineering gene regulatory networks. Specifically, she has been working on hybrid methods that incorporate diverse modeling classes, which she has applied to networks in C. elegans and S. cerevisiae. She and colleagues are also looking into questions about data quality and quantity that ensure successful reverse engineering of networks. She has been working with Helen Chamberlin comparing knowledge-driven versus data-driven models of tissue development in C. elegans; a manuscript describing their work has recently been accepted in BMC Systems Biology. She is also initiating a project with Postdoctoral Fellow Franziska Hinkelmann on a web-based modeling tool designed specifically for experimentalists.

Kajetan Sikorski (Rensselaer Polytechnic Institute) Professor Sikorski’s research interests generally lie in exploring the effects of stochasticity in biological systems. During his time at MBI he has been working on developing a mean field theory for suspensions of swimming bacteria. The goal of the work is to treat pair correlations among swimmers in an explicit way, something that has not been done previously. At MBI Kajetan has also interacted with groups exploring molecular motors, beehive dynamics and the structure of neural networks.

Scott McKinley (University of Florida) Professor McKinley is an applied probabilist whose research is focused on diffusion in biological fluids. Unlike the presumed physical environment of classical Brownian motion, biological media can be highly heterogeneous and often exhibit viscoelastic properties. In one line of research he is collaborating with a pharmaceutical engineer and an expert in fluid mechanics to model the movement of foreign particles in human mucus. One current application is the formulation of a model for the interaction of antibodies with various sexually transmitted viruses that invade cervical mucus. In a second line of research, he is collaborating with another MBI Visitor, Peter Kramer, to model molecular motors and other mechanisms of microtubule-based intracellular transport.

MBI Program Applications: Submit your ideas for events

MBI programs are aimed at bringing mathematical scientists and bioscientists together to discuss ways in which the mathematical sciences are being used to solve significant problems in the bio and biomedical sciences or how problems from the biosciences are opening new areas of research for mathematicians, statisticians, and computational scientists.

MBI encourages members from the mathematical sciences and the biosciences community to propose ideas for MBI programs.

MBI Program Options

- Semester or yearlong emphasis programs (consisting of a number of related workshops and supported by MBI long-term visitors)
- Current Topic Workshops or CTWs (typically stand alone meetings of up to one week)
- Education programs

Applications for programs may be submitted via e-mail to the Director (mg@mbi.osu.edu) or in the case of a CTW using the form at http://www.mbi.osu.edu/forms/applyctw.html.

We suggest that applicants not expend too much effort on making the application; MBI will require more details if the basic idea is accepted. The questions that you should address at this stage are: Why is your topic timely, is there a community who is interested in the topic, and is your proposed program relevant to the MBI mission?
**The mission of the MBI is:**

- to foster innovation in the application of mathematical, statistical, and computational methods in the resolution of significant problems in the biosciences;
- to foster the development of new areas in the mathematical sciences motivated by important questions in the biosciences;
- to engage mathematical and biological scientists in these pursuits; and
- to expand the community of scholars in mathematical biosciences through education, training, and support of students and researchers.

**Propose an Idea**

MBI encourages members from the mathematical sciences and the biosciences community to propose ideas for MBI programs. MBI programs fall into three categories:

- Semester or yearlong emphasis programs.
- Current Topic Workshops (typically stand alone meetings of up to one week).
- High level education programs.

Please contact Tony Nance (tony@mbi.osu.edu) to submit your idea.