MBI is a community opportunity, and I have spent my first three months at MBI developing an appreciation for its many possibilities. A decade ago, when Avner Friedman was conceiving the idea of a national institute devoted to math and biology, the quantification of biology was being debated. There were a number of areas where math and biology combined successfully, from Lotka-Volterra (in population dynamics) to Hodgkin-Huxley (in neuroscience) to Turing (in a myriad of biological patterns) to name a few. But, only in relatively few departments did mathematicians embrace biology (at least in the way that mathematicians have long embraced physics and engineering) and only in relatively few areas did bioscientists embrace mathematics. Now, the commingling of math and biology through detailed modeling, based on biological principles and observations, is rampant. Many departments have established math biology programs at either the research level or the curricular level or both, and the case for this effort has been made in a number of academy and professional society publications.

Through this commingling, researchers are finding that old answers are often not quite accurate (for example, the Turing mechanism might not be the right way to describe many biological patterns) and that old tools are often not quite sufficient to describe those areas that are newly quantitative (the buzzwords of multiscale, hybrid systems, complex systems, and stochasticity all have multiple homes in the biosciences). For the optimists among us, this is the opportunity of a lifetime. We can use math skills to solve interesting problems in new application areas and, when we do this, we will ultimately create new mathematics.

So what roles can MBI play? MBI provides a place where mathematical scientists and bioscientists can spend time together and learn from each other, and where a cadre of young mathematical biology post-docs can be trained broadly and deeply. MBI brings the protagonists together by hosting theme years (each with about six theme-related workshops) and by hosting one-off workshops (aimed at specific math topics motivated by biology or specific biology topics whose quantification is near at hand). In another direction, MBI can help the profession by detecting trends in the way math biology is practiced and trends in the way math biologists are trained at all levels.

The post-docs are trained by being exposed to the many topics and tutorials discussed at MBI and by working with mentors who help them hone their research skills on specific problems in math biology. They can also network with the many researchers who visit MBI. This combination of training, networking, and research is possible because of the usual three-year tenure in MBI postdoctoral positions.

So what roles can the community play? After all, MBI is a community opportunity. At the very least, individuals can visit MBI (as workshop participants, as long-term visitors, or as post-docs) and participate in MBI programs. Even more important however, individuals can also suggest ideas for future MBI programs, help lead these programs, mentor MBI post-docs, and find new and better ways to use MBI to stimulate interactions between the mathematical and biological sciences. We are continually exploring ways for individuals to become involved in MBI, and we encourage you to explore ways that you can become involved in MBI.

Marty Golubitsky
Mathematical Challenges in Developmental Biology

The MBI’s 2008-2009 scientific program is on issues related to mathematical challenges in developmental biology. Organizers of the program are: Robert Dillon, Leah Edelstein-Keshet, Philip K. Maini, Hans G. Othmer, Kristin Rae Swanson, Ken Miller, Fred Wolf and Michael Levine.

Growth, movement and differentiation of cells are three key processes involved in pattern formation and morphogenesis in developing systems. Pattern formation involves the expression of genes at the correct point in space at the correct time, and this in turn typically involves spatially- and temporally-varying signals, and mechanisms for signal transduction and activation or repression of gene expression. Gene expression during embryonic development is not a cell-autonomous process, because cell fate in a multicellular embryo usually depends on the cell’s location. This fact led to the theory of positional information, which posits that a cell must ‘know’ its position relative to other cells in order to adopt the correct developmental pathway. Positional information is viewed as a necessary part of pattern formation. Frequently pattern formation results from the response of individual cells to a spatial pattern of chemicals called morphogens: molecules that move through a tissue by diffusion or other means, and regulate gene expression in a concentration-dependent manner. Morphogenesis refers to the processes that shape tissues, organs and organisms and necessarily involves both signaling and force generation for movement and cell rearrangement. While there are many variations on how the different processes are involved in different organisms, it is striking how conserved the basic processes are across the phyla. Also not surprisingly, these same processes are involved in various diseases such as cancer, and this unity and conservation of basic processes provides the rationale for studying various experimental model systems. This same unity and conservation also implies that mathematical models of the fundamental processes can have a wide-ranging impact across the spectrum of normal and pathological development.

In the last two decades much has been learned about the molecular components involved in signal transduction and gene expression in a number of systems, and the focus is now shifting to understanding how these components are integrated into networks, and how these networks transduce the inputs they receive and produce the desired pattern of gene expression. Several model systems, including Drosophila and limb development, will play a major role during the year. Development is a sequential process in which later stages build on earlier stages, but within stages there are often multiple feedback loops in signaling and gene control networks that may serve to buffer against perturbations caused by fluctuations in morphogen concentration and other components. This suggests two areas in which theoreticians can contribute: (i) the understanding of the relationship between network topology and functionality, and (ii) the development of computational tools for simulating growth, cell movement and differentiation in developing systems. The purpose of the year in Mathematical Challenges in Developmental Biology is to bring together theoreticians who have made significant contributions to various basic processes involved in development with experimentalists working on specific systems for which a quantitative approach has been or may be productive.

Upcoming Workshops

Cancer Development, Angiogenesis, Progression and Invasion: January 26-39, 2009
Organizers: Kristin R. Swanson and Alexander Anderson

Cancer and tumor-induced angiogenesis has a natural place in the Special Year on Developmental Biology as cancer is often thought of as a result of a faulty development process. Experimental and clinical oncology forms a massive literature aimed at understanding and treating cancer. Despite the enormity of the data available, clinical oncologists and tumor biologists proceed without a comprehensive theoretical model to help guide the organization and understanding of such data. To quote a recent Nature article on the topic:

Heeding lessons from the physical sciences, one might expect to find oncology aggressively, almost desperately, pursuing quantitative methods to consolidate its vast body of data and integrate the rapidly accumulating new information. In fact, quite the contrary situation exists. Mathematical models are typically denounced as “too simplistic” for complex tumour-related phenomena (ignoring, of course, the fact that similar simplifying assumptions are required in most experimental designs). Articles in cancer journals rarely feature equation.

Clinical oncologists and those who are interested in the mathematical modelling of cancer seldom share the same conference platforms. -- Nature 421, 321 (2003).

Naturally, successful modeling approaches to cancer requires scientists willing to communicate and interact extensively across disciplinary boundaries. This workshop aims to do exactly this by having truly interdisciplinary scientists as well as giving a shared platform for both experienced modelers and state-of-the-art experimentalists and clinician-scientists discussing their work covering every level of tumor growth.

Each day of the workshop, will consist of 3 primary speakers (one-hour lectures each) that will include an experimentalist laying out the biological problem, a mathematical modeler describing modeling approaches and a imaging specialist describing the type of data (typically imaging) available for model validation and development. Additionally, other attendees will be invited to present posters at the poster session. An expert panel will comprise of leading modelers and experimentalists to discuss current problems in the efficient translation of mathematical modeling techniques to the laboratory and the clinic.
Significant time will be available during the meeting for discussions of current and future problems in the cancer and tumor-induced angiogenesis area.

For more information please visit: http://mbi.osu.edu/2008/ws4description.html

Wound Healing: March 9-13, 2009
Organizers: Philip Maini and Chandan Sen

Abnormal healing of wounds in, for example, diabetics, or aged patients, as well as formation of scar tissue, has resulted in the need to understand the fundamental processes involved in wound healing. This workshop aims to bring together experimentalists, clinicians and theoreticians working at the different scales apparent in this problem and to determine approaches for combining these in a multiscale modeling framework. From a clinical standpoint, we would like to be able to predict from an initial time course what is the longer term prognosis for a wound. At one level, this could be done statistically, as perhaps from data already available trends could be discovered. However, this would not provide a mechanistic understanding which would inform a clinician of what therapeutical intervention to make if the model predicts that a wound would not heal properly.

The first three days will focus on particular spatial scales. Day 1 will begin with an overview talk that will introduce participants to the stages involved in wound healing, together with imaging of actual wound healing processes to illustrate the state of the art in experimental measurement and visualization techniques. It will then investigate aspects of signaling networks within cells which determine cell responses to wounding. Day 2 will focus on angiogenesis, the process by which new vasculature evolves. A specific aim here is to understand the origin of the biphasic response of healing to oxygen tension and its implications, for example, in wound infections where oxygen is used up thus impairing the healing process. Day 3 will address problems arising at the level of cell movement and laying down of matrix with important implications for scar tissue formation.

To arrive at a comprehensive model (or suite of models) one needs to integrate processes occurring on many different time and length scales. It is clearly impossible to simply include everything, so a major challenge for modelers is to extract from detailed models the essence of the processes occurring at each scale and interface them appropriately in a multiscale framework. Day 4 will consist of talks on this subject.

Day 5 will present a number of clinical case studies which will lay down future challenges in developing the generic modeling frameworks presented in the first four days to specific problems. Examples here will include healing in diabetic patients, elderly patients.

For more information please visit: http://mbi.osu.edu/2008/ws5description.html

Systems Biology of Biological Processes and Disease: Biological Problems and Statistical Solutions: April 16-17, 2009
Organizers: Hongzhe Li, Shili Lin, and Tim Huang

The purpose of this two-day workshop is to bring biologists and statisticians/mathematicians together on various aspects of systems biology studies of biological processes and diseases, including both novel biological experiments for systems biology studies of diseases and novel mathematical and statistical methods for integrative analysis of new generation of sequence data, SNP data, gene expression, proteomic, metabolomic and phenotypic data. We propose to have 12 invited talks, about six are on new experimental approaches and new data generation methods for systems biology (mainly given by biologists) and another six talks are on new statistical/computational methods for integrative analysis of these data (mainly given by statisticians or mathematicians). Potential topics to be covered include integrative analysis of sequences and gene expression data for studying complex diseases, methods for analysis of genetic networks and pathways, data generation and analysis methods for epigenetics, methods for analysis of new generations of sequence data and their applications in studying diseases and biological processes.

For more information please visit: http://mbi.osu.edu/2008/ctwdescription.html

Neuroscience Issues in Early Development: April 27-May 1, 2009
Organizers: Ken Miller and Fred Wolf

In the mammalian nervous system, a classic example of pattern formation is the formation of “maps.” These include the continuous mapping of the sensory periphery (e.g. the retina, or a fingertip) onto a central structure, preserving topographic relationships, and the continuous mapping of derived stimulus features such as the dominant eye or the preferred stimulus orientation for driving a central visual neuron. Theories of map formation generally involve an interplay between a number of elements: topographic matching of molecular gradients across axons and across the target structure; activity-dependent rules for synaptic growth or stabilization that typically lead to the outcome “neurons that fire together, wire together”; the patterns of activation of the input axons, in some cases driven by the patterns of sensory stimulation; and the interplay of input drive and intrinsic circuitry, both of which are simultaneously developing, in determining patterns of activation in the target structure.

In recent years, there has been great progress in elucidating the molecules involved in topographic map formation and the often non-intuitive effects on the maps of perturbing them, and models are playing a key role in making sense of these observations. There has also been great progress in understanding the dynami-
cal mechanisms underlying feature map formation, and this theoretical work is leading to a new class of experiments involving perturbation of feature maps even in adulthood. Some aspects of feature map formation show “critical periods” — specific developmental time windows during which abnormal sensory experience greatly alters feature maps, and outside of which the maps are relatively impervious to alterations of sensory experience. Recent years have seen enormous progress in understanding the mechanisms underlying critical periods, in particular with the demonstration that maturation of inhibition in the target structure can be necessary and sufficient to initiate the critical period. This presents enormous challenges for theorists to understand how these changes in target circuitry can radically alter the sensitivity of the development process to changes in input statistics. The workshop will articulate these challenges.

In addition, theory also addresses how particular neuronal response features are learned, a separate question from the organization of preferred features into continuous maps. Recent years have seen progress in understanding mechanisms for development of spatiotemporal, rather than merely spatial, response features such as selectivity for the direction of motion of a stimulus, and in understanding how certain nonlinear response features (“complex cells”) can arise. Many open questions exist, including the computational function of observed learning rules, and how different nearby neurons can learn to detect quite diverse features from the same overall set of inputs; these questions too will be discussed in the workshop.

For more information please visit: http://mbi.osu.edu/2008/ws6description.html

**Drosophila Development: June 8-12, 2009**

Organizers: Michael Levine and Hans Othmer

The workshop will cover four broad topics that are particularly well-suited for quantitative analysis: genome analysis, pattern formation of the early embryo and wing imaginal disk, computational modeling of signal transduction pathways, and the elucidation and analysis of gene regulation networks.

As of this writing, the genomes of 12 different Drosophilids have been completely sequenced and assembled. These assemblies provide a rich foundation for the identification of conserved noncoding sequences including microRNA genes and regulatory DNAs.

Whole-genome methods provide the comprehensive identification of just about every gene and associated regulatory DNA responsible for complex developmental processes, including segmentation, gastrulation, neurogenesis, and wing morphogenesis. Current progress in each of these areas of research will be discussed with an eye towards future modeling efforts. Several critical processes such as EGF and TGFβ signaling have already been successfully modeled, and the insights gleaned from these efforts will be discussed.

The last sessions will be devoted to gene regulatory networks. A combination of gene disruption assays, DNA binding assays, and cis-regulatory analysis permits the construction of networks, or circuit diagrams, that display the functional inter-connections among all of the regulatory genes and cell signaling components responsible for complex developmental processes. These networks can be used to create predictive changes in patterning processes, and to determine the mechanistic basis for the genesis of embryonic diversity and novelty during insect evolution. We will discuss the logic and topology of these networks, and also consider future goals such as the development of better visualization methods.

For more information please visit: http://mbi.osu.edu/2008/ws7description.html

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**Summer Education Programs and Opportunities**

**2009 Summer Graduate Program**

Each summer the MBI hosts a 3-week education program. The first week is spent in a tutorial, which combines morning lectures with active learning laboratories in the afternoon. The following 2 weeks are spent working on guided team projects and participating in a miniconference to share project results. The program is meant primarily for graduate students; college instructors and qualified undergraduates will also be considered.

**2009 Summer Undergraduate Program**

This program consists of two parts: (a) two weeks of introductory lectures plus short projects and a computer lab, and (b) a summer long research experience (6 weeks to be followed immediately after the 2 weeks) devoted to projects in the interface of mathematics, statistics, and biological sciences. Topics include Mathematical Neuroscience, Statistical Phylogenetics, Chemogenomics, Climate Change and Bioinformatics.

The 2009 Summer Program dates are June 22-July 2, 2009.

To apply: http://mbi.osu.edu/forms/applyundergrad.html
Postdoctoral Fellowships

The Mathematical Biosciences Institute (MBI) at The Ohio State University is accepting applications for Postdoctorate positions to start September, 2009.

Postdoctoral fellows are immersed in the topics of the MBI’s emphasis year programs. The MBI postdoctoral fellow will engage in an integrated program of tutorials, working seminars or journal clubs, participation in workshops, and interactions with local and visiting mentors. These activities are geared toward providing the tools to pursue an independent research program with an emphasis on collaborative research in the mathematical biosciences. MBI facilitated activities for postdoctoral fellows are tailored to the needs of each young scientist. The program provides training in bioscience fundamentals to the mathematically oriented fellow as well as mathematical fundamentals to the bioscience oriented fellow.

The postdoctoral program includes both regular postdoctoral fellows and sponsored postdoctoral fellows. The deadline for applications is January 18, 2009. For more information and to apply please visit the MBI website: http://mbi.osu.edu or call (614) 292-3648.

Early Career Visitors

The MBI is accepting applications for Early Career Visitors during the 2009-2010 year on Molecular Interactions Within the Cell: Network, Scale, and Complexity.

Early Career Visitors are hired for up to a one-year term. They are engaged in the integrated program of tutorials, working seminars, and workshops tied to the scientific them of the year, and are expected to interact with local and visiting researchers. Early career visiting positions are aimed at nontenured scientists who currently have continuing employment.

The deadline for applications is January 18, 2009. To access the application form or for more information, visit the MBI website at http://mbi.osu.edu or call (614)292-3648.

Suggest a Focus Group Meeting

The MBI is calling for proposals for Focused-Discovery Groups (FDG). The FDG idea is for a group of researchers from different institutions to get together at the MBI for a period of (typically) one week in order to discuss, intensively investigate, and aim to resolve a significant problem in the biosciences. The MBI will pay the local expenses of the participants, and will provide facilities (office space, computer support).

Proposals should be sent to the Director or one of the Associate Directors. A proposal should describe the problem to be addressed (one or two pages) and list the people who have agreed to participate.

The proposed dates of MBI residence for the FDG should be between six months and one year from the time of submission.

If you are interested in participating in these meetings please send your CV and an explanation of your interests to rebecca@mbi.osu.edu.

Suggest New Ideas and Programs

The MBI programs are aimed at bringing mathematical scientists and bioscientists together to interact on significant problems from the biosciences. It is expected that such activities will also open new research areas for mathematicians and statisticians. The MBI wishes to encourage the mathematical sciences community and the biosciences community to solicit program ideas.

Your suggestions may be submitted in the form of a preproposal for:

- a workshop that falls within a thematic year;
- a stand-alone workshop;
- an extended program, several months to a year; and
- a summer education program.

We welcome ideas from the broad spectrum of mathematical biosciences: you may focus more on the mathematics/statistics motivated by biology, or on biological problems which will require the development of new mathematical/statistical methods.

Please submit your ideas in the form of a few pages describing the background and motivation, and what the program is going to accomplish.

If you want to suggest a specific workshop, we would like to have a list of organizers, a description of the workshop, and a tentative list of speakers and participants.

Please contact the Director or one of the Associate Directors as you develop your ideas for preproposal:

Marty Golubitsky, Director: mg@mbi.osu.edu
David Terman, Senior Associate Director: terman@mbi.osu.edu
Libby Marschall, Associate Director: marschall.2@osu.edu
Dennis Pearl, Associate Director: dpearl@mbi.osu.edu
Andrej Rotter, Associate Director: arotter@mbi.osu.edu
Ever heard of a Division of Biological Sciences being housed within a Mathematics Department? Strange as it may seem, until recently, this was the status quo at the New Jersey Institute of Technology (NJIT), an Institute Partner of the MBI. Surprisingly, it turned out to be a great arrangement that allowed mathematics and biology at NJIT to grow in an interdisciplinary manner, and it created a truly unique Mathematical Biology group. Visit NJIT today and you will find an active community of mathematicians and biologists who work collaboratively on research problems, who provide research training opportunities at the undergraduate, graduate and post-doctoral levels and who have developed undergraduate and graduate curricula to train scientists for the 21st century.

Over the past ten years, the Department of Mathematical Sciences (DMS) at NJIT has developed a strong faculty in the area of Mathematical Biology. This group consists of faculty members trained as applied mathematicians as well as other faculty with primary training in quantitative biology. One of the main streams of research within the group is in mathematical and computational neuroscience, with seven faculty members currently working in this area. Of these faculty, three run wet labs where experiments are performed on central pattern generating networks such as those found in the crustacean stomatogastric ganglion. Current research problems focus on identifying the effect of neuromodulation on rhythmic activity, elucidating the mechanisms and effects of short-term synaptic plasticity; deriving minimal models for mixed mode oscillations, and more generally, developing new mathematical methods to study problems within neuroscience. A second area of concentration is in computational and mathematical ecology with a focus on community and ecosystem ecology. Ongoing research includes: development of automated species identification systems, focusing on coral reef fish and spiders; development of bioinformatic methods to curate and integrate disparate ecological datasets; use of computational geometric methods to quantify biodiversity; and quantifying extinction threat with metapopulation models. In the past five years, the research and training programs of the Mathematical Biology faculty have been supported by over $3 million from external agencies such as the National Science Foundation (NSF), the National Institutes of Health and the Howard Hughes Medical Institute (HHMI).

The interactions between mathematicians and biologists within DMS facilitated the growth of educational and training programs that lie at the interface of the two disciplines. An undergraduate degree option in Mathematical Biology and a double major between mathematics and biology were created. A quantitative B.S. in Biology was developed that requires 20 credits of mathematics. These degree programs mesh very nicely with the NSF funded Undergraduate Biology and Mathematics (UBM) program that has existed at NJIT since 2004. The program has trained about 25 students with participants engaged in year-long experimental and modeling research projects. All UBM trainees, who have graduated, have moved on to graduate or medical programs. At the graduate level, HHMI recently funded NJIT, in cooperation with Rutgers-Newark and the University of Medicine and Dentistry of New Jersey, to create a Quantitative Neuroscience Ph.D. program. This program complements the Mathematical Sciences Ph.D. program in DMS that has graduated eight students in Mathematical Biology since 2002 and the recently developed Computational Biology M.S. program. DMS hosts the annual conference on Frontiers in Applied and Computational Mathematics. FACM 09 will focus on Mathematical Biology and will be held on June 1-2, 2009. Those interested in participating can get more details at http://www.math.njit.edu.

As evidenced by the rapid growth of Mathematical Biology at NJIT, having a Division of Biological Sciences within Mathematical Sciences can ease the development of interdisciplinary programs. At NJIT, we have, however, become the victim of our own success. Biology has thrived in DMS, resulting in the creation in 2007 of an independent Department of Biological Sciences. The good news is that because this department grew out of DMS, it is stocked with faculty who are quantitative and modeling oriented, thereby promising many more years of fruitful collaboration between biologists and mathematicians. In closing, the way in which mathematical biology grew at NJIT can serve as a model for ways to build sustainable and stable programs. It was initiated through the hiring of a group of faculty who shared common research interests and who were given the freedom to create a surrounding educational infrastructure. There are many reasons to believe that this basic idea can be duplicated at campuses across the country.

New Postdocs and Long Term Visitors

Paula Federico
Postdoctoral Fellow
Paula’s research interests are in the area of mathematical and computational ecology with applications to population dynamics, management and conservation of natural resources, and epidemic/epizootic dynamics. At the MBI she’ll be working on modeling fish movement behavior as a response to seasonal hypoxia in the Gulf of Mexico using different modeling approaches. This zone of low oxygen or “dead zone” is of particular concern because it threatens valuable commercial and recreational Gulf fisheries. She’ll be collaborating in this project with Dr. Yuan Lou from the Department of Mathematics and with Dr. Elizabeth Marschall and Dr. Stuart Ludsin from the Evolution, Ecology, and Organismal Biology Department.
Dan Siegel Gaskins  
Postdoctoral Fellow  
Dan’s research focus lies in the general area of Systems Biology. In particular, he’s interested in how genetic regulatory network architecture can support novel properties such as cellular memory and multistability.

Dan is currently collaborating with Dr. Erich Grotewold and Dr. Greg Smith on these questions using the Arabidopsis thaliana epidermal cell as a model system.

In addition, he’s interested in how single cell-level properties are manifested at the level of populations. He’s currently working on using inverse methods to extract average single-cell information from population microarray expression data.

Tong Li  
Long Term Visitor  
Tong is a Professor of Mathematics at the University of Iowa. Dr. Li’s research area involves nonlinear partial differential equations and their applications. Her research results span the areas of shock wave theory, combustion theory, mathematical modeling and theory of traffic flow, computational fluid dynamics, and mathematical biology.

In a series of papers, Li has studied extensively nonlinear stability of detonation waves through various partial differential equation models including two-step chain-branching reaction models and models which have curvature effects. She has published extensively on innovative approaches to the nonlinear dynamics of traffic jams and obtained the well-posedness and zero relaxation limit for nonequilibrium traffic flow models.

Robert M. Miura  
Long Term Visitor  
Robert is a Distinguished Professor of Mathematical Sciences at the New Jersey Institute of Technology, and his current research interests include the modeling of cortical spreading depression (CSD) in the brain and the stretching of heated threads. Waves of CSD are slowly propagating chemical waves in the cortex of different brain structures in a variety of experimental animals. In humans, it has been associated with migraine with aura where the aura is attributed to waves of CSD in the visual cortex. CSD was discovered over 60 years ago by A.A.P. Leao, but we still do not know which are the most important mechanisms and how they conspire to form CSD waves. At MBI, he is incorporating various mechanisms into a continuum model for CSD. These mechanisms include ion diffusion, effects of neurotransmitters, spatial buffering of potassium, and volume changes of the extracellular and intracellular spaces due to osmotic effects. He is a member of the MBI Board of Trustees.

Deena Schmidt  
Postdoctoral Fellow  
Deena’s research interests are in applying probability to problems in population genetics and molecular biology. Her Ph.D. research focused on stochastic models of DNA regulatory sequence evolution in different organisms. She’s currently working on a gene regulatory network model of an experimental system with Timothy Newman (Arizona State University) and Vincent Noireaux (University of Minnesota). Recently at the MBI, she started working on a model of microRNA regulation involved in cancer development with Baltazar Aguda, Yangjin Kim, and Patrick Nana-Sinkam (OSU Davis Heart and Lung Research Institute).

Chuan Xue  
Postdoctoral Fellow  
Chuan’s research involves multi-scale modeling in bacterial pattern formation and wound healing. She received her Ph.D. in mathematics from the University of Minnesota in Aug. 2008 under the direction of Hans G. Othmer. In her thesis, she focused on unveiling the mechanism of spatial pattern formation in the bacterial colonies found in her collaborator’s lab. She developed a hybrid cell-based model which incorporated intracellular signal transduction, cell movement and extracellular signal dynamics. The model yields biologically-based explanations to radial and spiral stream formation in P. mirabilis colonies. To reduce the computational cost due to large number of cells, she lifted the cell-based model to a continuum model by deriving macroscopic chemotaxis equations of cell density using perturbation techniques and moment closure methods. She is also working on mathematical models for ischemic wound healing. The goal is to understand how the supply of oxygen affects the wound healing process and how hyperbaric treatment helps with chronic wound closure in patients with circulation diseases.

For information on how to apply for a postdoctoral fellowship:

http://www.mbi.osu.edu/postdoctoral/postdoctoral.html
Application: http://www.mbi.osu.edu/forms/papp.html

For information on how to apply for a visit to the MBI:

http://www.mbi.osu.edu/visitors/visit_mbi.html
Application: http://www.mbi.osu.edu/forms/applyvisit.html

For information on how to apply to be an Early Career Visitor:

http://www.mbi.osu.edu/postdoctoral/early_career.html
Application: http://mbi.osu.edu/forms/papp.html
The mission of the MBI is:

- to foster innovation in the development and application of mathematical, statistical, and computational methods for the solution of significant problems in the biosciences;
- to engage mathematical and biological scientists in the solution of these problems; and
- to expand the community of scholars in mathematical biosciences through education, training, and support of students and researchers.

Apply for a visit!

Postdoctoral Fellowship: http://mbi.osu.edu/forms/papp.html
Early Career Visitor: http://mbi.osu.edu/forms/papp.html
Workshop/Tutorial: http://mbi.osu.edu/forms/applyworkshop.html
Long-Term Visit: http://mbi.osu.edu/forms/applyvisit.html

If you would like us to include information on upcoming meetings/programs or employment opportunities, please contact David Terman at terman@mbi.osu.edu.