



The MBI Newsletter

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Special points of interest:

- 2005-2006 scientific program in Ecology and Evolution
- 2006 Summer Education Program
- Second Young Researchers Workshop in Math Biology
- New MBI postdocs

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Director's Letter

The Mathematical Biosciences Institute at the Ohio State University, funded by the National Science Foundation (NSF), was created in 2002 to provide a national forum for mathematical biosciences that can catalyze such interactions between the biological, medical, and mathematical scientists through vigorous programs of research and education, and to nurture a nationwide community of scholars in this emerging field. The MBI aims to reinforce and build upon existing research efforts in mathematical biosciences, and quicken intellectual growth in this area.

The MBI focuses each year on one broad area in the biosciences. It runs tutorials and workshops in their field, as well as a summer education program.

“The MBI aims to reinforce and build upon existing research efforts in mathematical biosciences, and quicken intellectual growth in this area.”

Despite the clear importance of biology for the future of mathematics, it is still not an easy matter for a mathematician to make the switch to working in this area. Vocabulary is different, the methods may seem strange, and the criteria by which one's work is judged can be radically different. In this regard, workshops held at the MBI play an important role; they are, in essence,

role models for those mathematicians interested in broadening their research interests;



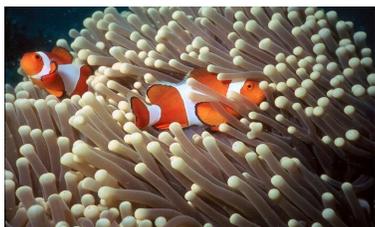
they provide examples of how interdisciplinary work is done, and how to work with experimental colleagues; and, with the provision of extensive tutorials, they provide an introduction to the field of the particular year.

Information on the seminars, workshops, and tutorials held at the MBI is available on the web; we also post streaming videos of all workshop talks. Nevertheless, in this information age, too much information may obscure some particular program or talks, which some individuals would have liked to have. Indeed, we're often told by some individuals that they wished they had known about the MBI talks that they missed. For this reason, we decided to publish and distribute a special newsletter each semester, both in electronic and paper form. The newsletter will provide information on current and near future programs, and, with less detail, on future programs in subsequent years. We reach a broad community of mathematical and biological scientists, and enable more researchers to participate in and benefit from the MBI program.

Avner Friedman

Director





Ecology and Evolution Program

Workshop 1: Phylogeography and Phylogenetics, September 26-30, 2005

Workshop 2: Aspects of Self-Organization in Evolution, November 14-18, 2005

Workshop 3: Spatial Heterogeneity in Biotic and Abiotic Environment: Species Ranges, Co-evolution, & Speciation, February 6-10, 2006

Workshop 4: Spatial Ecology, March 13-17, 2006

Workshop 5: Uncertainty in Ecological Analysis, April 3-7, 2006

Workshop 6: Microbial Ecology, May 15-19, 2006

Workshop 7: Global Ecology, June 26-30, 2006

Further information can be found at: <http://mbi.osu.edu>

Ecology and Evolution 2005-2006

The MBI's 2005-2006 scientific program is on issues related to ecology and evolution. Organizers of the program are: Chris Adami, Sergey Gavrilets, Lou Gross, Craig Moritz, Claudia Neuhauser, John Pastor, Frede Thingstad

Ecology and evolutionary biology have historically been two of the areas of biology that have most benefited from, and made use of, mathematical methods. Many distinguished mathematical biologists have contributed to these areas, and their efforts have illuminated much of ecological and evolutionary theory over the past century. An objective of this special year is to focus on specialized areas that offer particularly challenging mathematical problems, which are relatively unexplored and are of potentially great interest to observational biologists. Thus, an underlying goal of the proposed activities is to maintain direct connections to observable biology.

One thread of connection between the various proposed activities concerns spatial aspects of natural systems. Central questions about the history and structure of biological systems are affected by spatial variation. Additionally, numerous problems, which have great public impact, necessarily involve the spatial heterogeneity of biological systems, both those occurring through natural processes and those deriving from human actions. Conservation biology, biodiversity, harvest planning, invasive species control, and wildlife management are just a few of the applications that utilize mathematical methods to address major public policy issues. These applied areas rely greatly upon general ecological and evolutionary genetics theory. Determining how natural systems are affected by interactions of space and time leads to problems that require mathematical approaches. Although a large body of mathematical literature has developed over the past several decades dealing with spatio-temporal interactions, there are still many biologically important questions that require new mathematical approaches and would benefit from close collaborations between ecologists, evolu-

tionary biologists, and mathematicians.

Beyond emphasizing the spatio-temporal nature of natural systems and the mathematical approaches that are used to address them, the special year is intended to foster interactions between individuals working on problems at different spatial/temporal scales. While the underlying biological questions may operate on quite different scales, the necessary mathematical approaches may be similar. Another theme for the year is linking between scales, for example, how might evolutionary models that account for the dynamics of spatial structure relate to ecological models, which operate on shorter time periods? How might genomic information that is rapidly becoming available assist in developing a theory for whole organism interactions with environment and the functioning of populations, communities, and ecosystems? What new mathematical approaches might contribute to better models for natural system response across the genome/organism/population interfaces? The proposed set of activities will enhance our ability to address these questions and hopefully lead to new collaborations between mathematicians and biologists that are beneficial to both fields.

“Determining how natural systems are affected by interactions of space and time leads to problems that require mathematical approaches.”

Summer Program: Ecology and Evolution

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.

The 2006 Summer Program will concentrate on issues related to ecology and evolution. The dates are July 17 - August 4 and the program leaders are Kate Calder and Yuan Lou.

Specific topics of this year's summer program include:

- Effects of spatial heterogeneity on invasions of rare species
- Patterns of multiallelic polymorphism maintained by migration and selection
- Evolution of ranges of species.

The coherent biological theme behind these three projects is to understand the effect of spatial heterogeneity of environment on the invasion of species when rare, coexistence of multiple competing species, maintenance of multiple alleles, and the range of existing single or multiple species. These problems can be modeled by discrete and continuous systems, and the common tools in analyzing these mathematical models include techniques from differential equations, dynamical system, and numerical computation.



A group works on a project during the 2005 Summer Program.

Second Young Researchers Workshop In Mathematical Biology

To provide a forum for young mathematical biologists to interact with their peers, the MBI will host the Second Young Researchers Workshop in Mathematical Biology on March 27-30, 2006. The workshop will bring together approximately 45 young researchers in mathematical biology, to broaden their scientific perspective and to develop connections that will be important for their future careers.

Postdoctoral researchers and junior faculty are encouraged to apply for participation to this workshop. A limited number of advanced graduate students may also be accepted. Applications can be made on the web page: <http://mbi.odu.edu>.

Each participant will present a poster of current research and give a 5-minute advertisement of the poster. The workshop will also feature working group discussions on broad issues relevant to researchers in mathematical biology.

The MBI will pay for all local expenses. Travel support will also be available on a competitive basis.

The application deadline is December 15, 2005. Applicants will be notified via e-mail regarding acceptance by January 31, 2006. If you have any questions, please contact Rebecca Martin at rebecca@mbi.osu.edu.

Plenary talks given by leading researchers in mathematical biology:

- Catherine Carr, University of Maryland
- Leah Edelstein-Keshet, University of British Columbia
- Bard Ermentrout, University of Pittsburgh
- Hans Othmer, University of Minnesota
- Timothy Secomb, University of Arizona
- Arthur Sherman, National Institutes of Health
- Kristin Swanson, University of Washington
- Raimond Winslow, Johns Hopkins School of Medicine

"The workshop will bring together young researchers in mathematical biology to broaden their scientific perspective and to develop connections that will be important for their future careers."



Poster viewing during the First Young Researchers Workshop.

Future Program: Systems Physiology

The MBI's 2006-2007 scientific program is on issues related to Systems Physiology. Organizers of the program are: Paul Bressloff, Jim Keener, Harold Layton, Ken Lutchten, Andrew McCulloch, Tim Secomb, Artie Sherman, James Sneyd, Rai Winslow

“The goal of systems physiology is to understand how various human organs and tissues are organized and regulated to produce their normal function and pathologies.”

Much of the biological investigation of the past can be described as a compilation and categorization of the list of parts, whether as the delineation of genomic sequences, genes, proteins, or species. The past decade for example has uncovered the genetic basis for many diseases. A remaining and larger challenge is to provide an understanding of how the interactions of these biological entities across spatial and temporal scales lead to observable behavior and function. This is what systems biology is concerned with. Two important organizing principles need emphasis: (1) An integrated understanding of systems requires mathematics and the development of theory, supplemented by simulations; and (2) Theory cannot be relevant if it is not driven and inspired by experimental data. Thus the development of system biology requires collaborative

work by theoreticians and experimentalists.

The goal of systems physiology is to understand how various human organs and tissues are organized and regulated to produce their normal function and pathologies. This year, the MBI will examine features of several human organ and tissue systems, including the cardiac system, the respiratory system, the microcirculatory system, the renal system, the visual processing system, the endocrine system, and the auditory system. Although these are at first glance quite different, the underlying theme is how cellular level behavior participates in the function of the whole and how feedback from the function of the whole contributes to the regulation of the cellular level behavior. Understanding of these processes may lead to new insights into the causes of diseases and how they can be treated.

MBI Welcomes New Postdocs

The MBI has a very active postdoctoral program. Postdoctoral fellows are immersed in the topics of the MBI's emphasis year programs. The MBI postdoctoral fellow engages 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. Postdoctoral fellows

participate in all aspects of the MBI's scientific programs. Fellows will have two mentors: one in the biological sciences and one in the mathematical sciences. Sponsored Postdoctoral fellows participate in all aspects of the MBI's scientific programs. They are partially supported by a bioscience department or bioscience lab in the public or private sector and spend 50% time on research suggested by the sponsor. Fellows will have two mentors, the sponsor, and a mentor from the mathematical sciences.

This year we are happy to welcome seven new postdoctoral fellows. These are:

Marko Djordjevic: Marko obtained his diploma in Physics at University of Belgrade in Serbia, and PhD in Physics at Columbia University. His research interest is broadly in the area of computational biology and bioinformatics. More specifically, he is interested



Top: Zailong Wang, Diego Pol, Paula Grajdeanu, Richard Schugart, Sookkyung Lim, Janet Best, Jin Zhou/ Bottom: Andrew Nevai, Jianjun (Paul) Tian, German Enciso, Partha Srinivasan, Brandy Stigler, Pranay Goel (Not shown: Marko Djordjevic)

to computationally study regulation of gene expression, by using ideas and methods from statistical physics. In addition to analyzing experimental data, his theoretical research is also aimed at contributing to the experimental design. To accomplish a close interaction of theory with experiment, he is intensively collaborating with experimental biology labs.

German Enciso: While he is currently considering a more applied approach to mathematical biology, German's dissertation research consisted of the study of certain abstract dynamical systems called monotone systems, which are associated with positive feedback and have strong stability properties. Using ideas from control theory, some non-monotone systems were studied using ideas from monotone systems theory. Applications were given to delay and reaction diffusion equations in molecular biology.

Paula B. Grajdeanu: Paula is an applied mathematician specializing in mathematical biology, partial differential equations,

scientific computing, and fluid dynamics. More specifically, she currently works on mathematical modeling for renal physiology projects. The projects model renal function at the level of the nephron: the functional unit of the kidney. She is also part of a research group that implement applications of mathematics to the study of various aspects of cell metabolism, in particular, folate and methionine metabolism.

Andrew Nevai: Andrew received his Ph.D in mathematics from the University of California, Los Angeles in 2005 under the direction of Paul H. Roberts (mathematics) and Richard R. Vance (biology). His dissertation was on mathematical models of plant competition for sunlight. He is interested in many aspects of mathematical ecology including the theory of competition for resources; species persistence and permanence within ecological communities; the dynamics of age, size, and spatially structured populations; behavioral ecology; and formulating ecological models that make use

“MBI facilitated activities for postdoctoral fellows are tailored to the needs of each young scientist.”



Paula Grajdeanu

of mechanistic principles. He also welcomes research opportunities to go out into nature and collect data "in the field".

Richard Schugart: Richard's research interests include mathematical modeling and scientific computing as applied to problems in wound healing and cartilage mechanics. His dissertation work included two problems in cartilage mechanics and is motivated by the need to quantify differences between normal and osteoarthritic mechanical and physico-chemical states in cartilage. The first problem involved the formulation and analysis of mathematical models for osmotically-induced volume change in articular cartilage cells and chondrons, which is the functional cell-matrix unit in cartilage. The second problem was the development of an accelerated numerical method for the continuous spectrum biphasic poroviscoelastic (BPVE) model of articular cartilage deformation. The research was directed under the supervision of his dissertation adviser, Dr. Mansoor Haider, at North Carolina State University and was in collaboration with the Orthopaedic Bioengineering Lab at the Duke University Medical Center.

Partha Srinivasan: Membrane proteins are proteins that reside in the membranes of cells. They form an important class of proteins because they are central to a variety of cellular processes. As the functionality of proteins is closely related to its 3-dimensional structure, there is a huge amount of interest in obtaining structures of membrane proteins. Due to the gel-like nature of the membrane environment, it is hard to crystallize membrane proteins in their native environment in order to perform x-ray crystallography on them. Nuclear magnetic resonance (NMR) is becoming an increasingly popular tool to obtain high-resolution structures of membrane proteins by providing distance and orientation information among the various spins (atoms) residing in the backbone of a protein. Due to the variety of spin interactions present in a molecule, it is important to suppress undesired interactions, while keeping the ones of interest. In NMR, this is achieved through a technique called pulse sequences. Partha has previously



German Enciso

worked in the quantum mechanical analysis of pulse sequences. He is interested in designing new pulse sequences and/or modifying existing ones that improve the resolution and sensitivity in NMR experiments of biological samples.

Brandy Stigler: Brandy's research involves the development of a mathematical framework for reverse-engineering biochemical networks using polynomial dynamical systems over finite fields. We have developed a novel algebraic approach to build models from experimental time series data. The approach uses computational algebra to construct the set of all polynomial dynamical systems that fit the given data and to select minimal models from this set. This work is currently being applied to an oxidative stress response network in yeast.

Our other postdocs include:

Janet Best: Janet's principal interests involve understanding essential biological processes at the level of cells and organisms, in terms of mechanisms that operate at the level of ions, proteins, and genes. Much of her work is concerned with establishing how the complex structure of firing patterns observed in neuronal networks arises from intrinsic and synaptic properties of the cells together with the connective architecture of the network. Her work emphasizes a close integration of mathematical modeling with the experimental studies of her collaborators. She uses a variety of dynamical systems methods in analyzing these biophysical models, including geometric singular perturbation theory and iterated maps; the development of mathematical techniques is also an important aspect of her work. Current systems of study include hypothalamic neurons essential to reproduction, pacemaker cells that generate the inspiratory phase of the respiratory rhythm, Parkinson's disease, the human sleep/wake cycle, and plant circadian rhythms.

Pranay Goel: Pranay is interested in how neuronal networks perform computations relevant to behavior. In particular, he studies the properties of spatiotemporal

patterns in coupled oscillator systems. He is also interested in the role of electrophysiology in model development. With Alan Gelperin, he explores neuronal networks to explain the learning logic of associative conditioning in the *Limax*. With Jack Enyeart, he builds accurate models for ion channel dynamics in the bovine AZF cells. With control theorists, Klaus Robenack, and Andrea Serrani, he is involved in developing algorithms designed to take advantage of modern instrumentation (such as the dynamic clamp) for improved parameter estimation in models, and for reverse-engineering neuronal circuitry.

With James Sneyd and Sandor Gyorke (at the Davis Heart and Lung Institute, OSU), he is involved in modeling calcium transients in the cardiac myocyte to better understand the dynamics of intracellular calcium signaling, and its role in excitation-contraction coupling.

Sookkyung Lim: Sookkyung's main research interests are mathematical modeling, scientific computing, and numerical analysis for biological and medical problems. For example, blood circulation in the human embryo before the development of the heart valves, thoracic pump mechanism during cardiopulmonary resuscitation (CPR), swimming motion of bacteria, simulations of aortic aneurysms, and geometry of DNA associated with twist and bent that is important in many biological processes.

Diego Pol: Diego's current research interests are focused on computational methods for understanding the phylogenetic relationships of biological species. The focus of his phylogenetic research is on properties of various models for phylogenetic reconstruction from DNA sequences and on efficient algorithm development for analyzing large datasets of DNA sequences (in the order of thousands of organisms). These datasets present considerable computational challenges requiring synergistic application of parallel computing and simulated annealing and genetic algorithms.

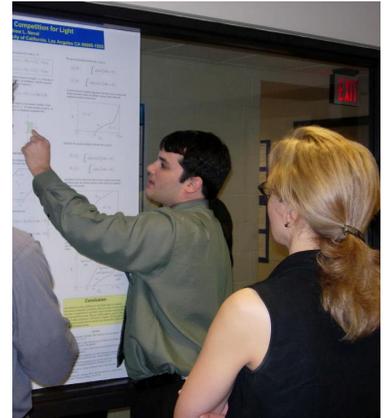
Some of the empirical problems he is currently analyzing consist of comprehensive

microbial datasets important for the diagnosis and study of emerging infectious diseases. He is also developing tree-based methods to correlate the mutational history of single nucleotide polymorphisms and disease phenotypes. This approach is useful for identification of candidate genes related to complex diseases.

Jianjun (Paul) Tian: Paul is trying to use all available mathematical methods to study biological phenomena and also looking for new mathematical objects in biology. He has established a model for virotherapy of brain tumors by using system of PDEs, which fits experimental data and more the prediction also fits new experimental data. He has discovered new algebraic structures from genetics, which are coalgebraic structures and evolution algebras. He has also made a new mathematical coalescent theory, which is colored coalescent theory. He has to model development of tissues (normal and anormal) and organisms, particularly by using stem cells as growth factors.

Zailong Wang: Dr. Wang's research interests include: biostatistics, bioinformatics, data mining, and machine learning. Currently, he focused on applying the Bayesian approach and Markov Chain Monte Carlo (MCMC) methodology to gene expression data analysis such as microarray data, ChIP-on-chip data, and SAGE (Serial Analysis of Gene Expression) library data. The Bayesian Hierarchical models and reversible jump MCMC proposals have been developed for gene expression analysis.

Jin Zhou: MicroRNAs(miRs) are small RNA molecules encoded in the genomes of plants and animals. Each miR is a sequence of about 21 nucleotides, which is highly conserved over species. These miRs regulate the expression of genes by binding to the 3' untranslated regions of specific messenger RNAs. It has been estimated that about 1/3 of all genes are subject to miR regulation. I have developed an algorithm for matching miRs with targets and assessing statistical properties of the miR-targets matching.



Andrew Nevai and Janet Best



Diego Pol

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***The mission of
the MBI is:***

- *to develop mathematical theories, statistical methods, and computational algorithms for the solution of fundamental problems in the biosciences;*
- *to involve mathematical scientists and bioscientists in the solutions of these problems;*
- *to nurture a community of scholars through education and support of students and researchers in mathematical biosciences.*

We're on the web!

<http://mbi.osu.edu>

Apply for a Visit!

Long term visit application: <http://mbi.osu.edu/forms/visitorapplication.html>

Workshop/Tutorial application: <http://mbi.osu.edu/applyworkshop.html>

Postdoctoral application: <http://mbi.osu.edu/forms/postdocapplication.html>

Upcoming Events

2006 Annual Meeting of the Society of Mathematical Biology Joint SMB-SIAM Conference on the Life Sciences

July 31-August 4, 2006

North Carolina State University, Raleigh, NC, USA

<http://www.siam.org/meetings/lso6/>

If you would like us to include information on the following, please contact David Terman at terman@mbi.osu.edu:

- Upcoming meeting/programs
- Employment opportunities

Become an Institute Partner

The MBI welcomes the participation of other academic institutions and invites those interested to join the MBI Institute Partner Program. The program subsidizes the travel and local expenses of IP member faculty, postdoctoral fellows, and students, to allow their participation in research and education programs at the MBI.

Each IP institution commits annual funds to the MBI. These funds are credited to the IP member account and may roll over from one year to the next. Following authorization by the IP member's chair, travel and local expenses of up to twice the balance in the IP member account will be paid in full with 50 percent debited from the IP account and 50 percent debited from the MBI's account.

In addition, IP chairs or representatives are invited to annual meetings to explore educational and research opportunities and provide input for future institute programs. IP members also receive MBI newsletters, proceedings, and annual reports.

If you would like to be an Institute Partner, please contact Avner Friedman at afriedman@mbi.osu.edu.

Current Institute Partners:

- Arizona State University
- Case Western Reserve University
- Drexel University
- Indiana University-Purdue University Indianapolis
- Iowa State University
- Michigan State University
- New Jersey Institute of Technology
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