Message from the Director
New Programs at MBI

During the past year MBI successfully re-competed for funds from NSF. We were awarded a five-year grant to continue our missions of stimulating research on the interface between the mathematical sciences and the biosciences and of training young researchers in math biology. The two-year renewal process led to a variety of new programs, which I would like to discuss here. MBI activities mostly fall under five categories (scientific programs, postdoctoral fellows, national impact, education, and diversity) and MBI is developing new programs in each of these categories:

Workshops

Several national panels have noted that the quantification of biology has the potential for revolutionizing biology, while simultaneously creating new fields of mathematics and providing new directions to some mature fields of mathematics. It has been argued that the payoff in both directions will be great, but that the time scale for the impact of biology on the mathematical sciences is longer than is the time scale for the impact of mathematics on biology. Two primary goals of MBI are to promote the impact of the mathematical sciences on the biological sciences and the impact of the biological sciences on the mathematical sciences. We term these math->bio and bio->math. During the first seven years of its existence MBI had stressed math->bio programs and in our new grant we proposed to continue these programs and in addition to feature bio->math programs. The first of these new programs was the very successful November 2009 workshop on Mathematical Developments Arising from Biology (organized by John Guckenheimer, Reinhard Laubenbacher, and Bernd Sturmfels).

MBI programs can be divided into two groups: emphasis year workshops (last year’s theme was Molecular interactions within the cell: Network, scale and complexity) and current topic workshops (which includes the always successful Workshop for Young Researchers in Mathematical Biology) and this year’s theme is Evolution, Synchronization, and Environmental Interactions: Insights in Plants and Insects. We have proposed to have approxi-

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Workshop 3: Ecology and Control of Invasive Species, Including Insects
(February 21-25, 2011)

Organizers: Mark Lewis, Ottar Bjornstadt, Subhash Lele, and Sergei Petrovskii

The spread of invasive species is a key applied problem in ecology. In North America, invasive exotic species are widespread, ranging from gypsy moth to Asian longhorn beetle to weedy plants. The associated costs are immense, by some estimates exceeding $100 billion US per year. While many invasive species are introduced from Asia or Europe, others, like mountain pine beetle, are simply spreading into new areas of North America, due to processes such as climatic change.

The purpose of the MBI workshop on invasive species is to bring together researchers from different groups: mathematicians, biologists and statisticians to develop the new interdisciplinary approaches to biological invasions.

A full description and list of speakers for this workshop can be found at http://www.mbi.osu.edu/2010/ws3description.html.

Workshop 4: Insect Self-organization and Swarming
(March 14-18, 2011)

Organizers: David Sumpter, Madeleine Beekman, Stephen Pratt, Vijay Kumar, and Chad Topaz

Insect groups generate a wide range of interesting collective patterns and behaviours, for example the formation of ant trails, the building of elaborate nests, collective movement of honey bee swarms and marching locust bands, to name just a few. The complex non-linear nature of the mechanisms underlying such collective behaviour has generated a great deal of theoretical interest from mathematicians and physicists. Collective insect behavior is one area where mathematical modeling and experiment have lived well side by side.

Collective insect behavior is interesting from the point of view of evolution because understanding the non-linear dynamics provides insights into self-organization in natural systems which in turn serves as an inspiration for computer algorithms and robots. Many of the emergent collective phenomena involve synchronization where large numbers of individuals move in the same direction or co-ordinate their activities. Lastly, mass movement of insects such as grasshoppers and crickets involve large-scale interactions with the environment, whereby feedback between individuals within a group and their environment determine collective patterns.

A full description and list of speakers for this workshop can be found at http://www.mbi.osu.edu/2010/ws4description.html.
Workshop 5: Coevolution and the Ecological Structure of Plant-insect Communities (April 4-7, 2011)

Organizers: Scott L. Nuismer and Sharon Y. Strauss

Plant-insect interactions have played a pivotal role in the development of modern coevolutionary theory, beginning with Darwin’s initial insights into reciprocal adaptation between plants and pollinators. When Ehrlich and Raven published their now classic study of coevolution between butterflies and plants in 1964, the link between the development of coevolutionary theory and plant-insect interactions was cemented. Since this time, numerous studies of plant-insect interactions have revealed an important role for coevolution, even as the perceived importance of coevolution for the overall structure of plant-insect communities has waxed and waned. Currently, much of the research on the ecology and evolution of plant-insect interactions, both mutualistic and antagonistic, is expanding from simpler two-species frameworks to consider coevolution in the context of multispecies communities.

Goals of the Workshop

1. To discuss metrics (e.g., network structure, local adaptation, community heritability) with robust theoretical/statistical underpinnings that can be used to elucidate the importance of coevolutionary processes in structuring plant-insect communities at local and regional scales.
2. To discuss statistical techniques (e.g., path analysis; selective source analysis, etc.) for evaluating the importance of ongoing coevolutionary selection in multispecies communities of plants and insects.
3. To discuss profitable avenues for the development of a cohesive theoretical framework that incorporates coevolution, multiple interacting species, spatial structure, evolutionary history and variable abiotic environments. This framework will thus formally link several of these different empirical approaches to communities.

A full description and list of speakers for this workshop can be found at http://www.mbi.osu.edu/2010/ws5description.html.
New Developments in Dynamical Systems Arising from the Biosciences (March 22-26, 2011)

Organizers: Tasso Kaper, Bernd Krauskopf, Hinke Osinga, and Martin Wechselberger

The biosciences provide rich grounds for mathematical problems, and many questions require the development of new mathematical theory and algorithms. With this workshop we give particular attention to new ideas and developments in dynamical systems. We have chosen four themes to showcase how the biosciences inspired recent progress: systems with delays, systems with multiple scales, dynamics of networks, and stochastic bifurcation theory. The meeting will highlight and discuss new directions of fundamental research in each of the themes, how they are connected, and how they contribute to the understanding of specific questions in bioscience applications.

A full description and list of speakers for this workshop can be found at http://www.mbi.osu.edu/2010/ddsdescription.html.


Organizer: Guowei Wei, Terrence Conlisk, and Charles Bell

A major feature of biological science in the 21st century will be its transition from phenomenological and descriptive science to quantitative science. Revolutionary opportunities have emerged for mathematically driven advances in biological research. Currently, most experimental research in the life sciences is based on molecular biology or molecular level understanding. However, a much smaller amount of mathematical biology activity is based on molecular level understanding. Therefore, it is imperative to strengthen molecular based mathematical biology, particularly, the modeling and computation of molecular structure and dynamics. It can be envisioned that a dramatic transition in mathematical biology research will occur in the near future. Many of the next generation of leaders in mathematical biology will be working on molecular based research. Multiscale modeling and computation, a subject that has its root in mathematics, will be an important topic in mathematical biology.

This weeklong workshop will cover a wide range of topics in multiscale mathematical modeling of biological/biomolecular systems and their application to specific research problems. Topics include atomistic models; molecular dynamics; Brownian dynamics; continuum-discrete models; micro-macro models; implicit solvation models; electro-elastic models; fluid-electro-elastic models; Poisson-Boltzmann equation; Poisson-Nernst-Planck equations; microfluidics; etc.

A full description and list of speakers for this workshop can be found at http://www.mbi.osu.edu/2010/mltdescription.html.

Current Topic Workshops

MBI is soliciting applications for Current Topic Workshops. These workshops:

1. Focus on emerging areas in the biological sciences that are ripe for association with the mathematical sciences, such as through modeling.
2. Focus on areas in the mathematical sciences that are needed for progress in biology.
3. Focus on emerging areas in the mathematical sciences that are being stimulated by advances in the biosciences.
4. Revisit areas from previous emphasis year programs.

For information on how to submit an application for a CTW or MBI Program, visit: http://www.mbi.osu.edu/suggestions.html

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mately six emphasis year workshops and approximately six current topic workshops each year and we always encourage community members to submit ideas for these workshops. To apply to organize an MBI program, please consult: http://mbi.osu.edu/suggestions.html.

All workshop talks at MBI are now live video streamed. Instructions for viewing may be found at http://mbi.osu.edu/streaming.html. In addition, MBI archives all talks (in which speakers give permission) on the MBI website. To find this material go to the workshop website and click on the lecture materials link.

Institute Partners and Mentoring

During the past year the number of MBI Institute Partners doubled from 19 to 39 (two of which are industrial IPs). This change was the result of a concerted effort by MBI to involve IP researchers in Institute programs. Perhaps the most dramatic of these has been the effort to promote the offsite mentoring of MBI postdoctoral fellows. Indeed, this year seven of the MBI post-docs have had at least one IP mentor, and their experience has been very positive. We very much encourage Institute Partner researchers to sign up to be a possible MBI post-doc mentor. See http://mbi.osu.edu/about/partners.html.

Education Programs

Each quarter MBI now sponsors a course in mathematical biology broadly construed. This fall we had a team taught course on Topics in Mathematical Ecology. Chiu-Yen Kao and Ching-Shan Chou will teach the winter course on Numerical Methods for PDEs and Their Applications in Biology. In the spring, Dong Li (Univ. of Iowa) will give a course on Stochastic Differential Equations. We are working to have these courses available by live video streaming for all those who would like to attend.

Diversity and Outreach

During the past year MBI established a Diversity Committee co-chaired by Carlos Castillo-Chavez and Trachette Jackson. This committee has made a number of suggestions the most visible of which is the MBI Visiting Lecturer Program (VLP). This program will support visits by a number of mathematical biologists to campuses with large minority enrollments. In addition, this year MBI restarted its successful public lecture series, but with some new twists: the lectures are held at COSI (the Columbus Science Museum) and have been organized with the cooperation of Metro High, a local STEM high school.

All-in-all 2009-10 has been an active and exciting year for MBI, its staff, and its directors. The driving principle behind most of the changes at MBI has been the desire to find ways to further encourage interaction between MBI and its constituent communities. So I end this message with the open invitation to those who work on the interface between the mathematical and biosciences to participate in, to propose, and to lead MBI programs.

Marty Golubitsky
Mathematical Biology
University of Utah

Mathematical Biology at the University of Utah was born in 1970’s under the leadership of Frank Hoppensteadt, and has flourished continuously ever since. The Mathematics Department currently has five faculty, six post-docs and over 20 graduates students in this area, with tentacles of collaboration infiltrating departments across the campus. The group has long emphasized the commonalities among the diverse areas of research of the faculty, and attempted to convey this unified approach to graduate students.

Our four major groups can be broadly classified as Ecology and Evolutionary Biology, Neuroscience, Biofluids, and Cell Physiology. In spite of the biological diversity of these topics, boundaries between these groups are fluid (and often biofluid), as there is significant overlap, interplay and crosstalk between and among them. Indeed, we see the different areas of mathematical biology much like the different organ systems that control the body, which can be studied separately only by destroying the whole.

Research in Ecology and Evolutionary Biology, led by Fred Adler and Biology Department faculty member Jon Seger, has recently focused on the dynamics of host-pathogen and host-symbiont interactions, linking scales ranging from population dynamics of hosts, immunology, competition between pathogens, and genetic evolution. Work on viruses includes a concerted effort to understand the rhinoviruses, the most common cause of the common cold, and deemed by one disinterested party to be “one of the two best adapted viruses infecting humans.” This group is studying the factors maintaining their remarkable biodiversity, mildness and peculiar population dynamics. Not to be thought narrow, students and post-docs address questions as diverse as the interaction between influenza and secondary bacterial infections, the maintenance of Epstein-Barr virus (“the other best adapted human virus”), the spread and maintenance of hantavirus in deer mice, the potential deadly spread of an agent like SARS, and the dynamics that maintain the latent phase of HIV.

Led by Mathematics faculty Alla Borisyuk and Paul Bresslo in close collaboration with Bioengineering professor John White, research in neuroscience spans from cellular to systems neurophysiology. Investigations address such broad questions as how neurons respond to complex, temporally modulated stimuli like those seen in the living animal. Pleasingly, neuronal responses to complex stimuli can be mimicked by rather simple computational models. Neuroscience involves modeling how processes at the single cell level scale up, through network architecture and plasticity of connections, to allow the brain to achieve such advanced tasks as recognizing pattern and reading newsletters.

The biofluids and physiological gels group, led by Aaron Fogelson and Jim Keener, in close collaboration with Mike Kirby from the Department of Computer Science, focuses on two overlapping physiological areas: exploring the processes that lead blood to clot inside blood vessels, and investigating the formation and dynamic behavior of physiological gels. These challenging problems involve multifaceted, dynamic, and spatially-distributed interactions that occur on multiple spatial and temporal scales, with modeling relying heavily on partial differential equations to describe the motion of the fluid and gel and the transport and reaction of chemicals. To demonstrate their mathematical chops, the group uses stochastic Markov models to describe the receptor-ligand binding that mediates adhesion between cells and sur-

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Institute Partner

Focus on MBI Institute Partner

Mathematical Biology
University of Utah

Institute Partner
faces during clot development, and develops novel and sophisticated numerical methods to make cool movies. Some of the rest of these show simulated blood flow at the cellular level and may have potential as the basis for the next Pixar release “A Clot’s Life.”

The physiology group research, under the leadership of Jim Keener, studies the dynamics of physiological processes, both at the cellular and systems level, to understand emergent properties of reaction and transport in both normal and pathological contexts. Three sub-areas of cell and systems physiology are of particular interest: 1) the dynamics of cardiac cells and the relationship to cardiac arrythmias; 2) the size regulation of organelles; and 3) the dynamics of biochemical networks involved in cellular decision making processes. In addition to unleashing the full range of sophisticated methods to study these problems, some of the work resolves back to a more elementary question, “how do cells count?” Bacteria, for example, regulate the lengths of flagellar hooks and laments without counting molecular units, but instead with analogue computations driven by diffusion.

Modern biology is undergoing an unprecedented explosion of knowledge. Together with the fundamental principles of genetics and evolution, mathematical models play a central role in unifying this eld and making sense of this burgeoning complexity. Inspired by this pivotal moment, our group has founded a new Center for Quantitative Biology, dedicated to the proposition that all biological systems are endowed with the inalienable right to be studied mathematically. Our goal is to find new collaborations drawn from the diverse research done on the University of Utah campus and beyond, ranging from medicine and engineering to environmental science and anthropology.
Harsh Vardhan Jain joined the MBI in November 2009 after completing a postdoctoral fellowship at the Frankfurt Institute for Advanced Studies (FIAS), in Germany. Harsh’s interest in the field of mathematical biology came about quite by chance, while he was a graduate student at the University of Michigan, looking to make his mark in commutative algebra. In order to fulfill a cognate requirement, Harsh took a course with Prof. Trachette Jackson on mathematical methods in biology. He found the idea of applying math to better understand biological problems so novel and interesting that he decided to switch his major, and asked Prof. Jackson to be his thesis advisor. Fortuitously at this time, a senior researcher in the University of Michigan’s Cancer Center approached Prof. Jackson with an exciting problem. Prof. Jacques Nor had been working with the tumor secreted pro-angiogenic factor VEGF. In his lab, experiments with head and neck cancer implants in mice indicated a vital signaling pathway that VEGF initiated in co-implanted human endothelial cells, that appeared to make tumor progression much worse. The question Prof Nor wanted answered was ‘What is the therapeutic potential of targeting the various proteins involved in this pathway, and what parameters are key to drug development in the indicated case?’ This became the focus of Harsh’s thesis, and he graduated in the Fall of 2008.

Following his time at Michigan, Harsh decided to take up a post-doctoral fellowship offer in Dr. Michael Meyer-Hermann’s Systems Immunology group at FIAS. Here, they started work on developing a model to evaluate the potential of an emerging therapy for the treatment of ovarian carcinomas. The new therapy acted by targeting

Harsh Jain (MBI) and Helen Byrne (University of Nottingham).
the pro-survival protein Bcl-2 in cancer cells, and showed some degree of synergism when co-administered with carboplatin, a DNA-damage inducing agent. Using a biochemical framework, coupled with an age-structured approach to simulating the action of carboplatin, Harsh’s model was able to propose a possible molecular basis for the observed synergism. After rigorously validating the model against experimental data, it was used to predict optimal drug doses, and scheduling protocols. The model has since been submitted to Cancer Research, where it has been conditionally accepted pending minor revisions, and has led to a collaboration involving researchers in the UK and Germany.

“By conducting a postscriptive analysis on a large data set of patient case histories, Harsh hopes to develop a truly prescriptive tool to aid physicians in treatment choices for prostate cancer patients.”

In 2009, an unexpectedly welcome opportunity came Harsh’s way; the Obama administration made available stimulus funds in the sciences, creating new postdoctoral opportunities at the NSF institutes, including at the MBI. He was encouraged to apply by his thesis advisor, and was offered a position starting in Fall, 2009. At this time he started talking with Prof. Helen Byrne, at the University of Nottingham, with a view to starting collaboration, and she agreed to be his math mentor at the MBI. The institute facilitated this by making it possible for Harsh to visit her frequently during his tenure. They are currently working on a project in conjunction with researchers at the Davis Heart and Lung Institute, on modeling the foreign body reaction that occurs in response to the implantation of biomedical devices, and the effect stem cell therapy can have in alleviating this. Realizing the importance of such collaborative efforts, Harsh has also started a joint project involving researchers from the Universities of Nottingham, Oxford, Michigan, and Stuttgart, which will entail developing a hybrid model of tumor angiogenesis, with detailed intracellular signaling pathways determining the behavior of each individual tumor, endothelial and host tissue cell. This will be used to test a number of cancer therapies currently in various stages of clinical trial, primarily aimed at targeting cell apoptosis, or angiogenic signaling. Harsh is also a part of an R01 grant proposal submitted to the NIH by his thesis advisors at Michigan, aimed at elucidating the nature of the cross-talk between tumor and microvascular cells, in the case of head and neck cancers. This will be a natural extension of his graduate thesis and, in a departure form the norm in the cancer-modeling field, will involve model-driven experimentation.

Soon after arriving at the MBI, Harsh met with Prof. Avner Friedman to explore the possibility of joint work with researchers at the Cancer Center in OSU. They eventually started collaborating with Prof. Steven Clinton, director of the Prostate and Genitourinary Oncology Clinic, on a comprehensive model of the progression and evolution of prostatic cancer. The focus of this work is to gain a quantitative understanding of the emergence of castrate-resistance observed in patients who are put on androgen ablation therapy, and which ultimately leads to treatment failure. By conducting a postscriptive analysis on a large data set of patient case histories, Harsh hopes to develop a truly prescriptive tool to aid physicians in treatment choices for prostate cancer patients. Given its potential for impact in the field of prostate cancer treatment, coupled with its translational significance, he plans on submitting a K-series grant to the NIH next year as PI, under the mentorship of Prof. Clinton in order to make rapid progress on this project.

Most of Harsh’s work at the MBI, and leading up to his appointment here, has been in the field of cancer therapeutics. The models he is working with involve large systems of delayed or partial differential equations, and are as such intractable analytically. He recognizes the need for honing his theoretical skills in the highly competitive job market for applied mathematicians. To this end, he has started work on the analysis of delay differential equations arising from his model of ovarian cancer therapy, under the guidance of Profs. Byrne and Meyer-Hermann.
Kesh Govinder (Long-Term Visitor, University of KwaZulu-Natal)
Kesh’s research is on finding solutions to differential equations (ordinary and partial). A variety of techniques are used including group analysis (symmetry methods), singularity analysis and dynamical systems analysis. Part of his research focuses on research into these techniques themselves, while other aspects deal with applications of the techniques. Most of the applications thus far have been in Cosmology and Relativistic Astrophysics. However, at MBI he intends bringing these techniques to bear on the many differential equations that proliferate Mathematical Biology. There are two projects that he is working on. The first deals with Allometric Scaling Theory. Many physiological processes vary with body mass and do so in a power–law manner. His group intends using group theory to underpin the observation that these scaling relationships are power–law relationships and hope to use this to further pinpoint the actual value of the power–law exponent. The other project is that of synchronisation. They hope to supplement existing epidemiological models with a modification of the Kuramoto equation to investigate the phenomenon of synchronisation with regards to human behavior. It is envisaged that this approach will shed insight into appropriate intervention strategies in epidemiology. They intend applying this idea to a simple model of cholera transmission.

Carl Toews (Early Career Visitor, Duquesne University)
Carl’s primary research interests are in applied computational mathematics, with an emphasis on inverse problems and parameter estimation. His current work is focused on several projects arising from biomedical imaging and ecology. With collaborators at St. Jude Medical he is working on a prototype scheme for real-time intra-coronary position registration, with applications to atrial fibrillation surgery. A second project, undertaken in collaboration with colleagues at NIMBioS, involves applications of robust control to a variety of problems in ecosystem service management, specifically in the setting of marine fisheries. Together with several biologists at OSU, he has recently launched an effort to construct robust statistical classifiers capable of leveraging categorically disparate data types to source individuals from mixed populations.

Casey Diekman (Postdoctoral Fellow)
Casey’s research interests are in mathematical neuroscience and biological rhythms. His dissertation was on modeling the electrophysiology of the mammalian circadian clock and statistical analysis of multi-neuronal spike trains. While at MBI, Casey plans to use simulation and dynamical systems analysis tools to study the neuronal bursting underlying breathing, the role of mitochondrial excitability in stroke, and the circadian clock in the retina.
Annie Lindgren (Postdoctoral Fellow)

Annie's research focuses on understanding evolutionary relationships of cephalopods. Cephalopods are a unique class of mollusc whose members exhibit a great deal of morphological, behavioral, and ecological variability. For example, the cornea, an eye component, has evolved at least twice in cephalopods, once in squids and once in octopods. To determine how the cornea evolved multiple times in cephalopods, she used a phylogenetic approach to resolve relationships among cephalopod species, to test for ecological correlates and to address issues of homology. She also implements next-generation sequencing techniques to identify the underlying genes involved in corneal morphology, with the end goal of improving our knowledge of cephalopod evolution. While at MBI, she is working with researchers to develop novel computer programs that better process and integrate gene expression data that can then be used to increase our understanding of the molecular mechanisms that lead to convergent evolution.

Richard Gejji (Postdoctoral Fellow)

Richard’s research interests are on using stochastic computational simulations and mathematics to model the aggregation and swarming of bacteria and amoebas under volume exclusion conditions. By using computer simulations and continuous limit partial differential equations with nonlinear diffusion, he hopes to predict the macroscopic behavior of the microbes. These predictions will provide new insights into how they can aggregate together and form structures capable of defending against traditional anti-biotic treatments. He is also studying problems in ecology concerning when speciation events may occur and when new species can coexist as the result of different movement strategies.

Juan Gutierrez (Postdoctoral Fellow)

Juan is interested in PDEs, ODEs, differential geometry, and pattern classification applied to the following problems: (i) Dynamical Systems in Ecology & Epidemiology: spread and contention of biological agents (from micro-organisms to invasive species) released intentionally (bioterrorism, naïve release, etc.) or accidentally, (ii) Bioinformatics: geometric and statistical features for pattern classification of biological entities of different scales (from biomolecules to populations). He is currently developing collaborations and research projects, among which there is the problem of moving-boundary PDEs (Stefan-type) as a paradigm to model spread of invasive species in dendrite domains.

Rachel Leander (Postdoctoral Fellow)

Rachel’s research is in optimal control theory and its application. Currently she uses control theory to investigate the relation between a network’s structure and its dynamics. Specifically, she uses optimal control theory to identify structures that promote synchrony in networks of nonlinear oscillators. She is also interested in the structural controllability of networks and impulse control.
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.

If you would like us to include information on upcoming meetings/programs, employment opportunities, or long term visitors, please contact Yuan Lou at lou@math.ohio-state.edu