MBI DIVERSITY COMMITTEE

MBI is enhancing its approach to diversity issues by establishing a Diversity Committee, whose roles will be to advise MBI on effective approaches to diversity and to help MBI assess its progress in this area. Each member of this committee has been involved in successful diversity programs.

The committee members are:

- Carlos Castillo-Chavez (Arizona State, Executive Director of MTBI/SUMS and SUMS-MSHP)
- Joan Herbers (EEOB, OSU and President Elect of AWIS)
- Trachette Jackson (Associate Professor, Department of Mathematics, University of Michigan)
- Maeve Lewis McCarthy (Murray State, Executive Director AWM)
- Yi Li (Iowa, Math Department chair)
- Elizabeth Marschall (Associate Director, MBI and committee liaison)
- Abdul-Aziz Yakubu (Howard University, Math Department chair).

The charge of the Diversity Committee is:

- To suggest individuals from underrepresented groups who can participate in MBI programs.
- To suggest individuals from underrepresented groups and people who are active in diversity efforts for membership on MBI committees.
- To identify individuals from underrepresented groups who can be invited as long-term visitors.
- To suggest programs that can increase participation of underrepresented groups in math biology in general and at MBI in particular.
- To assess the success of MBI diversity building programs.

For more information on the MBI Diversity Committee, please see our web page at:

http://mbi.osu.edu/about/diversity.html

Apply for a visit!

Workshop/Tutorial:
http://mbi.osu.edu/forms/applyworkshop.html

Long-Term Visit:
http://mbi.osu.edu/forms/applyvisit.html

Postdoctoral Fellowship:
http://mbi.osu.edu/forms/papp.html

Early Career Visitor:
http://mbi.osu.edu/forms/papp.html

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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 dynamical 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, see:
http://www.mbi.osu.edu/2008/ws6description.html
WORKSHOP 7: 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 interconnections 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, see: http://www.mbi.osu.edu/2008/ws7description.html

2009 WORKSHOP FOR YOUNG RESEARCHERS IN MATHEMATICAL BIOLOGY (AUGUST 24-26, 2009)

The workshop is intended to broaden the scientific perspective of young researchers in mathematical biology and to encourage interactions with other scientists.

Workshop activities include plenary talks and poster sessions, as well as group discussions on issues relevant to mathematical biologists.

We cordially invite young mathematical biologists to participate.

The deadline for applications is May 1, 2009.

Accepted Speakers:

- Kirk Jordan, Computational Science Center, IBM, T.J. Watson Research
- Yang Kuang, Department of Mathematics and Statistics, Arizona State University
- Suzanne Lenhart, Department of Mathematics, University of Tennessee
- Johan Paulsson, Department of Systems Biology, Harvard Medical School
- Pejman Rohani, School of Ecology, The Center for Tropical and Emerging Global Diseases

For updates and changes please visit: http://www.mbi.osu.edu/wyrmb/wyrmb2009.html
CURRENT TOPICS WORKSHOPS

SYSTEMS BIOLOGY OF BIOLOGICAL PROCESSES AND DISEASES: BIOLOGICAL PROBLEMS AND STATISTICAL SOLUTIONS (APRIL 16-17, 2009)

Organizers: Tim Huang, Hongzhe Li, and Shili Lin

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:
http://www.mbi.osu.edu/2008/ctwdescription.html

COMPUTATIONAL CHALLENGES IN INTEGRATIVE BIOLOGICAL MODELING (OCTOBER 5-9, 2009)

Organizers: Suncica Canic, Lisa Fauci, and Mette Olufsen

Many mathematical models of biological systems have addressed only an isolated aspect of the system -- such as its biochemistry or mechanics -- and these simplified (yet not simple) models have shed much light on fundamental processes. Recently, biological modeling has now advanced to the point where integrative models that couple multiple processes are often developed. Typically, such models involve different spatial and temporal scales. Examples include models of tumor growth that couple solid mechanics with cell signaling and biochemistry and models of blood flow in the heart that couple solid mechanics, fluid mechanics, and bioelectricity. Common to these integrative models is the inclusion of experimental data that has high resolution both in time and space. The effective use of such models calls for new mathematical and numerical techniques; for instance, in the solution of inverse problems, in the derivation of more robust methods for parameter estimation, and in the determination of better numerical methods for the handling of multiscale coupling. This workshop seeks to address some of these challenges through a series of lectures and discussions.

For more information:

MATHEMATICAL DEVELOPMENTS ARISING FROM BIOLOGY (NOVEMBER 8-10, 2009)

Organizers: John Guckenheimer, Reinhard Laubenbacher, and Bernd Sturmfels

This workshop will focus on significant theorems, theories and algorithms in mathematics that have been or are being inspired by problems in biology. Topics will be chosen from dynamical systems, combinatorics, partial differential equations, probability, statistics, topology, algebraic geom-
SUMMER EDUCATION PROGRAMS

2009 SUMMER GRADUATE PROGRAM (JULY 27 - AUGUST 14, 2009)

This year the program will focus on Mathematical Ecology and Evolution. The program leaders are Ian Hamilton (Department of Ecology, Evolution and Organismal Biology, Ohio State University) and Yuan Lou (Department of Mathematics, Ohio State University).

The first week is spent in a tutorial, which combines morning lectures with active learning laboratories in the afternoon. Dr. Hamilton will give five lectures on the evolutionary ecology of interacting phenotypes, including such topics as the use of game theory in evolutionary ecology, levels of selection, the evolution of cooperation, competition and predator-prey games. Dr. Lou will give five lectures on the theory of Adaptive Dynamics with applications to the evolution of dispersal, consumer-resource models and the evolution of virulence.

The following two weeks are spent working on guided team projects and participating in a mini-conference to share project results. The program is meant primarily for graduate students; college instructors and qualified undergraduates will also be considered. Team projects include the following topics:

1. Maintenance of variation in mate choice and mate quality
2. Sanctions and cooperative behavior
3. Evolution of dispersal in heterogeneous landscapes

4. Evolution of virulence

2009 SUMMER PROGRAM IN MATHEMATICAL BIOLOGY FOR UNDERGRADUATES (JUNE 22-JULY 2, 2009)

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, Bioinformatics.

For more information, please visit: http://www.mbi.osu.edu/edupprograms/education.html

For more information: http://www.mbi.osu.edu/2009/mdbdescription.html

To apply for any of the Current Topics Workshops, see: http://www.mbi.osu.edu/forms/applyworkshop.html
Biological processes can be characterized by different degrees of complexity at microscopic (genes, molecules), mesoscopic (protein-DNA complexes) and macroscopic (cells, organisms) levels. Historically, all biological systems have been studied at different levels. However, an increasing amount of experimental results and theoretical studies suggest that a more comprehensive system approach would tackle better biological problems. It would require a collaboration and intensive exchange between experimental and theoretical researchers from physics, chemistry, biology, mathematics, computer science, and engineering.

The proposed activity will answer the following fundamental questions: What are the properties of biological networks? How do they function? How do genes come together to form networks, and how can we use bioinformatics to discover such networks? Can our understanding of the fundamental mathematics inform the design of those bioinformatics methods? How is information transferred in cells? What role can synthetic biology perform in aiding our understanding of real life processes? How can different subjects of biological systems interact together to create effective dynamic systems?

Specific sub-areas of molecular and cellular biology generate their own sets of problems and mathematical challenges, to be addressed by individual workshops throughout the year. For example, how do cells develop, control, and regulate highly-efficient, highly-selective and robust biological transport? What are the algorithms and models that can help elucidate RNA structure and function? What are the basic pathways of cell-to-cell signaling? How can we design genetic regulatory networks with targeted function for synthetic biology? What are the mathematical principles behind DNA-protein interactions and the co-ordinated regulation of gene expression?

The over-arching theme of the workshops bridges multiple scales, from the molecular to the cellular, in pursuit of the fundamental biological principles guiding the structure, evolution, and maintenance of these networks.

A unifying long-term goal of the proposed activities is to develop a unified approach to study the complexity of biological systems within cells. Such a comprehensive view of biology will require an application and development of new mathematical methods. Current approaches include hidden Markov processes, stochastic dynamics, graph theory, partial differential equations, discrete mathematics and other tools of probabilistic modeling, machine learning and computational analysis. As in the past, it is expected that new frontiers in biology will both benefit from and stimulate the development of novel mathematical techniques.

For more information, see: http://www.mbi.osu.edu/2009/scientific2009.html

ORGANIZING COMMITTEE:

- Reka Albert (Department of Physics, Pennsylvania State University)
- Eivind Almaas (Lawrence Livermore National Laboratory, University of California)
- Laszlo Barabasi (Department of Physics, Northeastern University)
- Jeff Hasty (Department of Bioengineering, University of California, San Diego)
- Ian Holmes (Department of Bioengineering, University of California, Berkeley)
- Anatoly Kolomeisky (Department of Chemistry, Rice University)
- Jane Kondev (Department of Physics, Brandeis University)
- Hao Li (Department of Biochemistry and Biophysics, University of California, San Francisco)
- Ron Weiss (Department of Electrical Engineering, Princeton University)
## Events 2009-2010

<table>
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<td>Workshop 5: Mathematical and Experimental Approaches to Dynamics of Protein-DNA Interactions</td>
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<td>Jane Kondev and Hao Li</td>
<td><a href="http://www.mbi.osu.edu/2009/ws5description.html">http://www.mbi.osu.edu/2009/ws5description.html</a></td>
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<td>Events 2009-2010</td>
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<td>Ian Holmes, Anatoly Kolomeisky, Jane Kondev, Hao Li, Ron Weiss</td>
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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.

To learn more about the MBI Institute Partner Program, please visit our website at:

http://www.mbi.osu.edu/about/partners.html

**MBI INSTITUTE PARTNERS:**

Arizona State University  
Boston University  
Case Western Reserve University  
Drexel University  
Duke University  
Florida State University  
Howard University  
Indiana University-Purdue University Indianapolis  
Iowa State University  
Michigan State University  
New Jersey Institute of Technology  
The Ohio State University  
Ohio University  
Princeton University  
University of California at Irvine  
University of Cincinnati  
University of Georgia  
University of Houston  
University of Iowa  
University of Maryland, Baltimore County  
University of Michigan  
University of Minnesota  
University of Notre Dame  
University of Pittsburgh  
University of Southern California  
University of Washington  
Vanderbilt University  
Virginia Tech

**IOWA MATH BIOLOGY GROUP**

In each issue of the MBI newsletter we will feature an article on one of our Institute Partners. This issue the spotlight is on University of Iowa.

Mentoring students is a tradition within the University of Iowa mathematics program. The department currently has an NSF VIGRE award and has recently won the national Presidential Award for Excellence in Science, Mathematics, and Engineering Mentoring and the American Mathematical Society Exemplary Program award for 2008. Additionally, our graduate program was one of two nationally receiving the American Mathematical Society award-Programs that Make a Difference. Our Alliance, GAANN, and VIGRE programs allow us to recruit a diverse group of highly talented mathematics students.

Most mathematical biology students apply to our Applied Mathematics and Computational Sciences (AMCS) program. A student in the AMCS program may choose to have an adviser in the mathematics department and/or an adviser from a different department such as biology or the medical school. In their first year, most math-bio students take three qualifying exam courses such as Analysis, Topology, Differential Equations, and Numerical Analysis. The following summer, students study for their qualifying exams with the help of other graduate students. This includes a few advanced graduate students who have already passed the qualifying exams and have been assigned as teaching assistants to help the new graduate students. In the second year, students will take additional courses while exploring research areas and choosing an adviser(s) in their second or beginning of their third year. AMCS students also normally take courses outside of the mathematics department in their area of application.

We have several faculty who work in the area of mathematical biology, many of whom collaborate with faculty in the UI medical school and other departments outside of mathematics. Bruce
Ayati applies numerical mathematics and computational science to understand multicellular systems such as biofilm and tumors. Rodica Curtu applies methods from nonlinear dynamical systems, pattern formation and bifurcation theory to study how the dynamics of neuronal networks contributes to neural information processing. Her current projects include computational models of learning and memory formation, models of buffered calcium diffusion near multiple sources and modeling of the unfolded protein response to ER stress. She has collaborators from the Psychology department and Anatomy and Cell Biology department, and she is an affiliate member of the Delta Center (Developing and Learning from Theory to Application; www.uiowa.edu/delta-center/). Isabel Darcy works on applications of knot theory to biology. She studies the shape of DNA bound by protein. For more information on her research, check out the cover article of the June 2008 issue 11 of Nucleic Acids Research (http://nar.oxfordjournals.org/content/voi36/issue11/cover.dtl). Tong Li's research area is nonlinear parabolic and hyperbolic partial differential equations and their applications. Her research interests span the areas of shock wave theory, combustion theory, mathematical modeling of traffic flow, mathematical biology and numerical analysis. Yi Li's research interests are in partial differential equations, and their applications in medical imaging, epidemiology, and cell motility. He is also the chair of the mathematics department. Colleen Mitchell works on applications of analysis, probability and dynamical systems to physiology. Her current projects include cardiac electrophysiology, timing in the auditory brainstem, language acquisition in children and stochastic modeling of synaptic vesicles. She has collaborators from the departments of Biology, Psychology, Cellular Physiology and Biophysics, and Internal Medicine and is an affiliate member of the Delta Center. Keith Stroyan is working on visual depth perception with Mark Nawrot at North Dakota State University. They have shown mathematically that the ratio of retinal motion over smooth eye pursuit determines relative depth and have done psychophysical experiments that suggest that people use this ratio to perceive depth.

Our math-bio group has a weekly seminar and a weekly lunch group. In the seminar, students and professors (from mathematics and other departments) present their research or a paper of interest. In Fall 2006, Colleen Mitchell started the Mathematical Biology Journal Club Lunch in order to provide mentoring to graduate and undergraduate students interested in mathematical biology. This lunch seminar has been an excellent way to introduce students to mathematical biology and for undergraduates, beginning and advanced graduate students, and faculty to interact. Math-Bio Lunch now regularly has 10-20 participants each week (see picture). The following are a few quotes from our graduate students about our program:

Jeannine Abiva: “I really enjoy being part of the math biology program. It offers many opportunities to be exposed to different topics in math biology through weekly readings for Math Bio Lunches and talks at seminars. It also provides a source of great mentorship through faculty and fellow students. It’s a great program.”

Candice Price: “I really like the Math Bio program here at Iowa. It feels more like a family than anything. We really support each other, especially during our Math Bio lunches where we present papers to one another.”

Kamuela (Wela) Yong: “The UI MathBio group has given me experience in reading papers and giving presentations. They have exposed me to the math bio world. As a result of this group, I am applying to a math bio research program this summer.”

For further information, please check the following web pages:

- Mathematics Department: http://www.math.uiowa.edu/
- AMCS: http://www.amcs.uiowa.edu/
- Mathematical Biology (under development): http://math.uiowa.edu/Research/MathematicalComputationalBiologyFaculty.shtml.
- VIGRE: http://www.uiowa.edu/~vigre/
LECTURES AND AWARDS:

Professor Martin Golubitsky, Director of MBI, has been selected to deliver the Jurgen Moser Lecture at the SIAM Conference on Applications of Dynamical Systems (DS09) to be held May 17-21, 2009 at Snowbird Ski and Summer Resort in Snowbird, Utah. Previous winners of the award have included Professors Sinai, Ruelle, Smale, and Swinney.

Professor Chiu-Yen Kao, a long-term visitor at MBI, is one of the 2009 Sloan Fellowship recipients. Dr. Kao is currently an assistant professor at The Ohio State University. Her research expertise lies in level set methods, Hamilton-Jacobi equations, computational anatomy, and inverse problems. For biological applications, she is working on the structural study of human brains, automatic numerical extraction of ciliary muscle, and general image processing techniques based on partial differential equations.

SPECIAL EVENTS:

**US-Africa Clinic on Meaningful Modeling of Biological Data: A joint effort with DIMACS**

The Center for Discrete Mathematics and Theoretical Computer Science (DIMACS), in collaboration with the Mathematical Biosciences Institute (MBI), the South African Centre for Epidemiological Modeling and Analysis (SACEMA), and the African Institute for Mathematical Sciences (AIMS) is holding a 5-day biomathematics modeling clinic that will emphasize data analysis. The clinic will bring together graduate students, post doctoral students, and researchers from the United States and Africa, with the goal of engaging the participants in epidemiological modeling projects that use real biological data to grapple with practical questions in a meaningful way. The clinic will be preceded by an international conference entitled “Can We Treat Our Way Out of the HIV Epidemic?” which participants are encouraged to attend.

The clinic will consist of a series of discussions and tutorials that will guide participants through the process of databased epidemiological modeling. The participants will then apply what they have learned using similar techniques to additional data sets. While the organizers will be prepared with their own analyses of the data sets, it is hoped and expected that the process will be open-ended and interactive and that the participants’ models will not exactly match the organizers’ expectations. Participants are encouraged to bring data sets and questions to the clinic, and to start collaborative projects with each other or the organizers. Students and researchers with prior exposure to mathematical epidemiology are encouraged to apply. Various statistical and modeling paradigms will be discussed, and there will be a number of hands-on and computer exercises together with group projects to reinforce and extend the various concepts covered. Participants are expected to continue research projects begun during the clinic when they return to their home institution.
Through funds provided by the US National Science Foundation and SACEMA, funding is available through DIMACS, MBI, AIMS and SACEMA to help cover the travel, housing, and registration costs of the clinic participants. The application process for the clinic is highly competitive; applicants are urged to submit their application materials as early as possible.

MBI LONG-TERM VISITORS AND STUDENTS

**Khalid Boushaba, Department of Mathematics, Iowa State University**

Dr. Boushaba has a long-term interest in the mathematical modeling of spatially-extended processes in cell biology. His recent work includes analyzing developmental processes in living zebrafish embryos. His current interests in MBI revolve around specific aspects of tumor immunology, with a special emphasis on the interplay between E2F3, cytokines and tumor immune response.

**Chirove Faraimunashe, Department of Mathematics, University of Botswana**

Faraimunashe is a PhD student with the Dept. of Applied Mathematics, University of Botswana in Botswana. He is focusing his research on applying nonlinear ordinary differential equations in the modeling of HIV infections, HIV mutations and the role of specific immune response to the HIV infection at immunology level. He employs various intervention strategies (e.g. treatment with Antiretroviral drugs) to investigate their benefits on the progression of HIV infection. Currently, he is a long term visitor at MBI from February 2009 to January 2010. At MBI he is extending his research to incorporate the effects of Malaria disease as a co-infection with HIV infection within the host.

**Edward Lungu, Department of Mathematics, University of Botswana**

Dr. Edward Lungu is a professor of mathematics at the University of Botswana, who is visiting the MBI, Ohio State University for one year from August 2008 to July 2009. Botswana is a country in Southern Africa, which is 80% dessert. Its economy is based on diamonds and beef exports. Dr Edward Lungu is an applied mathematician specializing in Fluid Mechanics, Epidemiological and Immunological modeling of diseases and Stochastic Analysis. In the area of Epidemiological and Immunological modeling, he has focused attention on HIV, HIV/TB and HIV/Malaria the three diseases, either as a single infection or as co-infection, that have affected Sub-Sahara Africa adversely causing a total of about three million deaths annually. In this area, Dr. Lungu is currently supervising seven PhD students working on various aspects of the three diseases. In the application of Stochastic Analysis, Dr. Lungu has one PhD student who is applying Stochastic Analysis to modelling the value of investments in various currencies with the exchange rate evolving as a semi-martingale.

Since arriving at the MBI, Dr. Lungu has collaborated with Dr Avner Friedman in studies investigating treatment of malaria with natural immune boosters produced by the body as part of the current treatment regimen or as a replacement for one of the drugs. He has also collaborated with Barbara Szomolay in a study investigating the development of HIV induced Kaposi’s Sarcoma.

**Najat Ziyadi, Cadi Ayyad University, Morocco**

Najat is a long term visitor at the Mathematical Biosciences Institute (MBI), Ohio state University, USA. She completed her PhD in 2008 at Cadi Ayyad University, Marrakesh, Morocco. Her thesis work was about modelling and studying of mathematical and computer models in epidemiology, with a particular application: scrapie spread within a sheep flock. Her research area is studying mathematical and computer models in epidemiology. Currently at MBI, she is working on modelling the drug resistant in hospitals.
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.

If you would like us to include information on upcoming meetings/programs or employment opportunities, please contact Yuan Lou at lou@math.osu.edu.