The Society for Mathematical Biology

SMB Newsletter

Volume 23 #2 - May 2010

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SMB Governance

Do you know your SMB Officers and Directors?

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- Michael Mackey, President, McGill University
- Avner Friedman, Past President, The Ohio State University
- Mary Myerscough, Secretary, University of Sydney
- Torcom Chorbajian, Treasurer

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- Nick Britton, University of Bath
- Renee Fister, Murray State University
- Mary Myerscough, University of Sydney
- Patrick Nelson, University of Michigan
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- Finance - Santiago Schnell
- Mentoring - Caroline Bampfylde
- Publications - Sharon Lubkin
- Travel and Meeting Funding - Meredith Greer
- World Outreach - Abdul-Aziz Yakubu
- Membership - Avner Friedman
- Meeting - Nick Britton
- Landahl/Busenberg Funds - Richard Bertram

New officers will be elected in the next couple of weeks. Watch for your SMB Ballot for the upcoming elections!

Dear SMB Members,

The end of winter has arrived (well, almost, as Montréal had quite a snowstorm a week ago) and spring is well on the way with flowers popping up here and there, leaves budding on the trees, the forsythia and magnolias blooming and birds darting about singing and calling for mates and building nests in which to hatch the eggs that inevitably follow from finding those mates.

And, too, classes have ended or are soon going to do so for most of us in the Northern hemisphere, final exams are being prepared and taken and graded, and college and university campuses gearing up for the round of graduations that will soon take place before the solitude of summer descends.

For many academics summer is a time free of academic responsibilities and a period in which research can be resumed, meetings attended, and one can relax and rejuvenate after the past months of the academic year. This summer, as always, there is no shortage of conferences and workshops and summer schools for mathematical biologists to choose from—something for every taste and interest. To get a sampling of what is available see http://www.smb.org/meetings/other.shtml

Our own summer school here in Montréal (run jointly with the MBI) will start in only two weeks, and though much has been done it feels like much remains to be done. Thankfully there is no shortage of willing hands!

This summer the SMB meeting will be held in Rio de Janeiro, 26-29 July, 2010, and the web site is at http://www.biomat.org/smb/smb2010venue.html I see the registration page is now functional, and a list of suggested hotels for SMB members to choose from is promised to be forthcoming. I hope to be able to greet many of you in Rio. However, do check to make sure about the necessity of a visa because it takes on the order of two weeks for it to be issued if you require one!

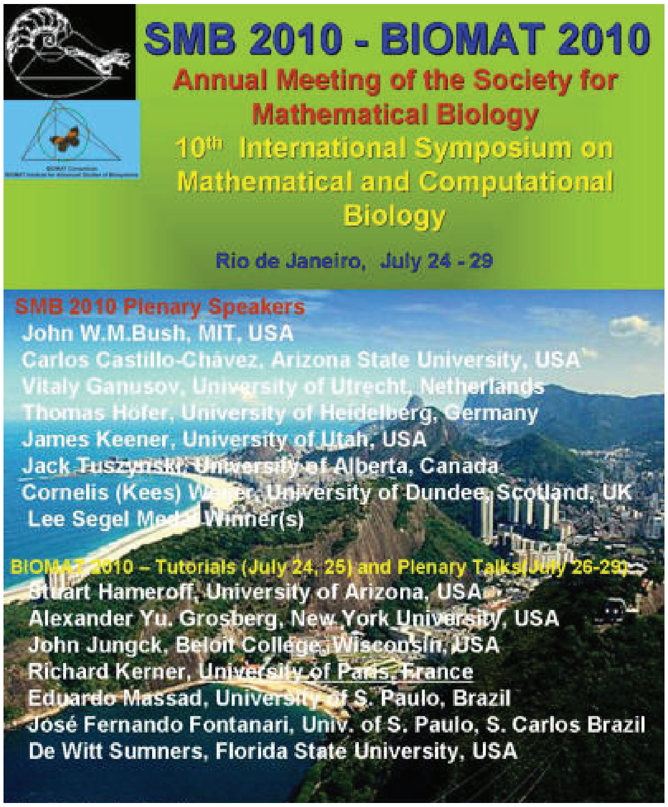
Ryszard Rudnicki, who is the meeting coordinator for the joint ESMTB-SMB meeting in Krakow, Poland, 28 June to 2 July, 2011, writes that plans for that meeting continue to evolve and all seems to be going well. The web site is located at http://www.impan.pl/~ecmtb11/.

Wherever your summer weeks take you and whatever you do with them, I hope that the time you have over the next months is personally and professionally rewarding to you and that you arrive at the end of the summer renewed personally and professionally.

Sincerely,

Michael Mackey

SMB President



SMB 2010 - BIOMAT 2010

Annual Meeting of the Society for Mathematical Biology

10th International Symposium on Mathematical and Computational Biology

Rio de Janeiro, July 24 - 29

SMB 2010 Plenary Speakers

John W.M.Bush, MIT, USA
Carlos Castillo-Chávez, Arizona State University, USA
Vitaly Ganusov, University of Utrecht, Netherlands
Thomas Hofer, University of Heidelberg, Germany
James Keener, University of Utah, USA
Jack Tuszynski, University of Alberta, Canada
Cornelis (Kees) Weijer, University of Dundee, Scotland, UK
Lee Segel Medal Winner(s)

BIOMAT 2010 – Tutorials (July 24, 25) and Plenary Talks(July 26-29)

Stuart Hameroff, University of Arizona, USA
Alexander Yu. Grosberg, New York University, USA
John Jungck, Beloit College, Wisconsin, USA
Richard Kerner, University of Paris, France
Eduardo Massad, University of S. Paulo, Brazil
José Fernando Fontanari, Univ. of S. Paulo, S. Carlos Brazil
De Witt Sumners, Florida State University, USA

2010 SIAM Great Lakes Conference on Modeling and Numerical PDEs in Mathematical Biology

Yangjin Kim

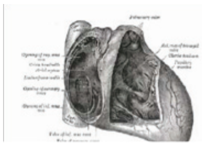
One hundred and fifteen people gathered on the campus of the University of Michigan-Dearborn (UMD) for the SIAM Great Lakes conference on April 17, 2010. The conference showcased cutting edge research in mathematical biology and provided opportunities to explore new areas, build collaborations, and reconnect with colleagues. Conference themes covered cancer, wound healing, mechanics, systems biology, spatial patterns, and industrial applications.

The program included three plenary sessions, each representing a different research area in mathematical biology: Avner Friedman (Ohio State University) on “What is Mathematical Biology and How Useful Is It,” Mark Alber (University of Notre Dame) on “Multiscale Modeling in Biology,” and Leonard Sander (University of Michigan) on “Biomechanics of Cell Motility in Dictyostelium.” David Field, former SIAM Great Lakes section president, served as host, and conference participants were warmly welcomed by UMD’s Chancellor, Daniel Little. In addition to the plenary speakers, there were 29 talks in four special sessions that ran concurrently and a poster session with over 22 participants. To keep the “I” in SIAM, Ed Moylan of Ford Motor Company organized one special session with four speakers that offered insight on applying these models in industry. The abstracts of all presentations and, when possible, the presentations themselves are available online at http://groups.engin.umd.umich.edu/siam.

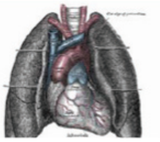
The conference was generously supported by SMB, SIAM, and the University of Michigan-Dearborn, and funding from SMB and SIAM was used to support travel for a number of graduate students, postdocs, and junior faculty while the local expenses were covered by UMD. The co-organizers (Yangjin Kim, Joan Remski and Michael Lachance at UMD) thank all who attended for making the meeting a success despite the unexpected cold weather and long drive. In addition, the co-chairs are grateful to David Field and Ed Moylan for their many thoughtful suggestions and comments.

Plenary speakers for the SIAM Conference were Leonard Sander, Mark Alber and Avner Friedman.

Some of the many participants at the conference.



Modeling Neural Control of the Cardiovascular and Cardiopulmonary Systems



VCU/NHLBI Spring 2010 Conference

Amina Eladdadi & Jyoti Champanerkar

The Center for the Study of Biological Complexity at The Virginia Commonwealth University (VCU) in the historic and culturally diverse city of Richmond, organized a short course on Modeling Neuromuscular Control of the Cardiovascular and Cardiopulmonary System during a beautiful spring week of March 17-21, 2010. The course was organized by Dr. Tarynn M.Witten, Biological Complexity and Emergency Medicine at VCU, as part of an ongoing NIH-NHLBI T15 grant effort. This workshop was the last in a series of seven workshops dedicated to the study of cardiovascular and cardiopulmonary systems.

The focus of this three-day workshop was on providing participants with an understanding of the theory and modeling of biological and biomedical signals arising in cardiovascular and cardiopulmonary dynamics, with a primary application of studying clinical problems related to the neuromuscular control systems. The workshop incorporated presentations from twelve scientists including mathematicians, statisticians, computer scientists, bioengineers, life scientists, medical clinicians and hybrids of these. The excellent talks varied across experiments, biological modeling, mathematical modeling, computer simulations and biostatistics; and varied on scale from genomics and molecular biology to organs and physiology.

Approximately forty participants from a large and wide-ranging group of graduate and undergraduate students, postdoc, senior and junior faculty, as well as a local high school teacher attended this event. This short course allowed participants to interact directly with skilled researchers in their respective fields which eventually will aid in establishing links between future and current researchers and developing a longer-term collaborative interaction. It provided means for students to interact with faculty in a comfortable environment and encouraged faculty to mix with students. The conference schedule allowed for many informal discussions over breakfast, lunch, dinner and coffee breaks and during the reception on the last evening of the conference. Those fortunate enough to arrive in Richmond early enjoyed a preconference reception at Lewis Ginter Botanical Garden on the evening of March 17th.

Dr. Vera Novak from Harvard Medical School kicked-off the series with a talk on cardio-respiratory locomotor coupling. She described various cardiac couplings such as cardiac-respiratory, cardiac-locomotor and entrainment phenomena as representations of signaling among multiple organ systems. She also presented experiments and data showing how as signaling and processing speed declines with aging, coupling among other systems may be enhanced and their clinical implications for daily living in older adults. The second talk on the first day entitled, "Modeling and model analysis in autonomic regulation of heart rate and autoregulation of cerebral blood flow," was given by Dr. Mette Olufsen from North Carolina State University. Dr. Olufsen described in detail how the parameter space of a general system of ordinary differential equations can be methodically reduced to include the most significant and sensitive ones. She demonstrated this method on a Heart Rate model with 14 parameters reduced to 6 significant parameters while looking at the solutions obtained from both the original and the reduced model. Dr. Ilya Rybak from Drexel University presented the third lecture, "Computational modeling of neural control of respiration." In his talk, Dr. Rybak showed that there are multiple rhythmogenic mechanisms in the CPG and their expression is state-dependent. Dr. Bruce Lindsey from University of South Florida gave a talk entitled, "Brainstem neural circuits for breathing: Connectivity, computational models and cardio-respiratory coordination." Dr. Lindsey described conduction of experiments using micro-electrodes. Dr. J. Andrew Taylor from Harvard Medical School delivered the last talk of the first day, "Observation and Estimation of Human Cardiovascular Autonomic Control: When Does the Physiology Coincide?" He talked about determining the autonomic control of heart rate oscillations as well as the importance of cardiac vagal outflow and the role of cardiac sympathetic outflow.

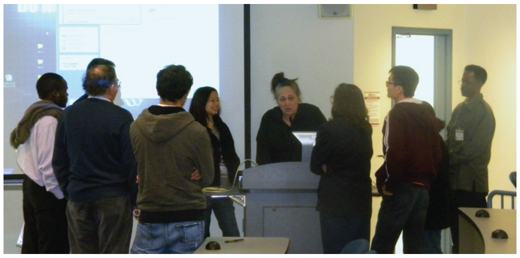
Dr. James Schwabber from Thomas Jefferson University started the second day of the workshop with his talk, "Genomes to Homeostasis (G2H): Central Autonomic Orchestration in Hypertension." The first part of the talk was aimed at graduate students describing the intricate details of Baroreceptor reflexes and their role in hypertension. The second half, was dedicated to a new hypothesis of molecular remodeling of blood pressure neural control system, bridging systems biology to mammalian brain functions, bridging high dimensional datasets and modeling-simulation studies and discussing predictive multi-scale models of molecular processes. Dr. André Diedrich from Vanderbilt University presented the second talk of the day, "Predictive Model of Spontaneous Blood Pressure Fluctuations Using Sympathetic Nerve Traffic." Dr. David Goldstein from the National Institutes of Neurological Strokes and Disorder lectured about "Computer Models of Stress, Allostasis, and Acute and Chronic Diseases." He talked about the evolution of concepts of stress and distress, and the homeostatic definition of stress. Dr. George Billman from the Ohio State University spoke about "Cardiac autonomic remodeling and susceptibility to sudden cardiac death: the effect of exercise training."

The first lecture on the last day was presented by Dr. Kun Hu from the Medical Chronobiological Program, Division of Sleep Medicine, Brigham & Women's Hospital/Harvard Medical School on "Influences of the Circadian System on Fractal Patterns of Heart Rate Fluctuations." In his lecture, Dr. Hu showed how healthy cardiac dynamics exhibit fractal regulatory patterns, and that there is an endogenous circadian rhythm in fractal cardiac control at time scales less than 1 hr which independent of behavioral and environment influences. Dr. Michael Pencina from Boston University spoke about "Development of Framingham cardiovascular risk-prediction algorithms." Dr. Pencina described the Framingham heart study project which started in the 1950s, is still continuing and has been a pioneer of cardiovascular risk prediction. Dr. Jeffrey L. Ardell from Quillen College of Medicine, ETSU talked about "Targeting the Cardiac Nervous System in treatment of heart disease." In his lecture, Dr. Ardell showed that most intrinsic cardiac neurons generate concurrent stochastic activity that is predicated primarily upon local network processing of cardiac chemotransduction, and that these intrinsic cardiac nerve networks exhibit short-term control over regional cardiac function. He added that over longer time scales, interdependent neural coordination of cardiac function is mediated via interganglionic interconnections and descending inputs. Dr. Tarynn M. Witten, the principal organizer of this NIH-NHLBI T15 course series, gave the closing presentation entitled, "Where have we come from and where are we going – Review and looking forward." Dr. Witten outlined her preliminary plans for the final grant workshop which is World Conference on Modeling and Simulation of Cardiovascular Dynamics that will be held next spring of 2011 in Washington, DC. Further details about this conference will be available at the VCU/NIH-NHLBI workshop series website: http://www.vcu.edu/csbc/nhlbi/calendar.html.

We would like to acknowledge and thank Dr. Witten for her dedication and excellent organization of the NIH-NHLBI T15 lecture series, and particularly for the financial support to participate for the third time. On behalf of all the attendees, we would like to thank the organizing committee and the staff at the Center for the Study of Biological Complexity department at VCU Life Sciences for the excellent service.

A detailed description of the conference can be found here: http://www.vcu.edu/csbc/nhlbi/spring10/index.html

Above: Group picture of some conference attendees.
Below: Dr. Tarynn Witten answering audience questions after her closing presentation.
Previous page: Discussions over lunch.



African Society for Biomathematics Inaugural Conference

Asamoah Nkwanta

The First African Society for Biomathematics (ASB) Conference was held on November 23-26, 2009 at Stellenbosch University in Stellenbosch, South Africa. The major themes of the conference were on infectious diseases, ecology, sustainable resource management, and mathematical models of other biological phenomena.

The conference was hosted by the Department of Mathematical Sciences, Stellenbosch University and Department of Mathematics and Applied Mathematics, University of Cape Town, Cape Town, South Africa. Conference sponsors were Stellenbosch University, University of Cape Town, African Institute for Mathematical Sciences (AIMS) of Cape Town, South African Centre of Excellence for Epidemiological Modeling and Analysis (SACEMA) of Stellenbosch, Society for Mathematical Biology (SMB), Institut de Recherche pour le Developpement (IRD) of France, and Embassy of France in South Africa.

The conference organizers consisted of Henri Laurie of University of Cape Town; Joseph Mugisha of Makerere University in Kampala, Uganda; Ingrid Rewitzky of Stellenbosch University; Aziz Ouhinou and Clovis Oukouomi Noutchie of AIMS; Rachid Ouifki and Farai Nyabadza of SACEMA; and Nicolas Florsch and Edith Perrier of IRD. Conference participants came from various African countries (Algeria, Botswana, Ghana, Kenya, Morocco, Senegal, South Africa, Sudan, and Tanzania), France, Poland, and the United States.

The conference consisted of four plenary talks, a series of contributed talks, a poster session, and an ASB meeting. The plenary talks were given by Edward Lungu (University of Botswana), "The Status of Biomaths in Africa: Is it a Relevant Tool for Solving Africa's Epidemiological and Ecological Problems;" Doug Butterworth (University of Cape Town), "An Overview of the Management Procedure Approach to Fisheries Management;" Joseph Mugisha, "The State of Biomathematics and Its Immediate Future;" and Abdul-Aziz Yakubu (Howard University, USA), "The Impact of Periodic Harvesting Policies on TAC-regulated Fishery Systems." Eleven sessions for contributed talks were presented by students and researchers while sessions were given on topics involving the epidemiology of infectious diseases; differential equations and population dynamics; ecology; fractals and ecology; HIV-AIDS dynamics under strategies; and other topics on biomathematics. There were a variety of interesting talks given in the sessions. For instance, Bewketu Teshale Bekele's (SACEMA, Stellenbosch University) talk was entitled "Modelling Tuberculosis Transmission Dynamics in Children and Adults in the Presence of Vaccination;" Dan Jacobson (Stellenbosch University) "Metabolomics of Wine and Wine Organisms;" Helene Brettschneider (University of Pretoria, Pretoria, South Africa) "A Mathematical Epidemiological Model of Bartonella Infection in the Invasive Rattus rattus in South Africa;" and Aziz Ouhinou (AIMS) "Stability Analysis of the Observed Pattern in Avascular Solid Tumour Growth." The

contributed and plenary talks generated much discussion and potential for future collaborations.

The African Society for Biomathematics was developed and organized at the January 3-8, 2008 International Conference on Biomathematics that was held at Cadi Ayyad University, Marrakech-Morocco. Some objectives of the society are to stimulate research and teaching in Biomathematics, to disseminate research information on Biomathematics, and foster interdisciplinary research. The meeting held in Stellenbosch was the first official meeting of the newly formed society. SMB members from the United States and other countries were present at this historic meeting of the society. Amendments to the constitution, initiation of the society's journal, student and faculty memberships, and standing committees were all formed and initiated at the meeting. In addition, elections were held for officers of the society and Joseph Mugisha was elected as the first president. Regional vice presidents were also elected as follows: Hassan Hbid (North African region), Henri Laurie (South African region), and Isaac Dontwi (West African region). The east and central African regions have not yet been determined. The African Society for Biomathematics Conference is a bi-annual conference and there was discussion on future sites for hosting the conference. The next conference will be in 2011 and interest was expressed at the meeting for having the conference in Ghana, Botswana, Kenya, or again in South Africa. For more details and information on the 2009 conference visit the website http://conf2009.afsocbio.com/web/. For information on the 2011 conference and ASB membership information contact Henri Laurie at henri.laurie@uct.ac.za.

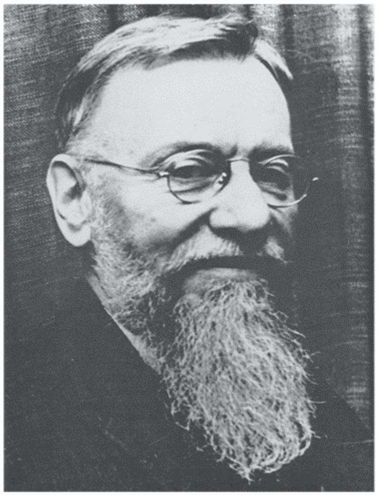
On the final day of the ASB conference, Abdul-Aziz Yakubu, chairman of the SMB World Outreach Committee, was invited to give a talk at the African Institute for Mathematical Sciences. This institute is an educational research center located in Muizenberg, South Africa, a small seaside suburb of Cape Town. The students are entirely from the African continent and a number of them participated in the ASB conference. Visiting lecturers come from African universities as well as other universities throughout the world. For more information on AIMS visit the website http://www.aims.ac.za/.

Above: Abdul-Aziz Yakubu, Aziz Ouhinou, Asamoah Nkwanta
Previous page: Participants at Inaugural Conference

Nicolas Rashevsky

Paul Cull

As some of you know, our society's journal the Bulletin of Mathematical Biology was founded by Nicolas Rashevsky, but you may not know much more about him. I have recently published a brief review of his career: The Mathematical Biophysics of Nicolas Rashevsky. BioSystems 88 pp 178-184. {Paul Cull. 2007.} Reprints are available on my website: http://eecs.oregonstate.edu/research/members/cull/pubs.html



Systems approaches in immunology: advances and challenges in multi-scale modeling

Santa Fe, NM – Jan 10 & 11, 2010

Vitaly Ganusov

In the last several decades, immunology has grown from a science of antibodies to diverse fields of research dealing with molecular, cellular, population and organismal details of immunological processes. Our understanding of how the immune system controls growth of infectious diseases is increasing dramatically due to the development of techniques of molecular biology and in vivo imaging of T and B cell responses. These new techniques have led to the generation of vast amounts of data and there is a rapidly increasing number of studies applying methods of mathematical modeling aimed at analysis of these data and at a deeper understanding of immunological processes. However, most experimental and theoretical work thus far has focused on questions generally relating only to one level of organization, for example, on understanding signal processing in cells or on the population dynamics of T cell responses to viruses. Further understanding of immunology will be advanced by the development of theoretical and experimental techniques and models that bring together phenomena at different levels of complexity to study mechanisms arising at the systems level. This was the main goal of the international workshop "Systems approaches in immunology: advances and challenges in multi-scale modeling" that was held in Santa Fe, New Mexico on January 10-11, 2010. The workshop was organized by Vitaly Ganusov (LANL), Steven Kleinstein (Yale), Ruy Ribeiro (LANL) and Alan Perelson (LANL) under the auspices of the Center for Nonlinear Studies (CNLS) at Los Alamos National Laboratory (see http://cnls.lanl.gov/immunology/ for oral and poster presentations and other details). Financial support for the meeting was provided by CNLS, the New Mexico Consortium, The Society for Mathematical Biology, The Program for Research on Immune Modeling and Experimentation (PRIME, NIAID) and the Theoretical Division at LANL.

More than 70 participants from 7 countries attended this 2-day meeting, with over 15 oral and 20 poster presentations. Two invited talks focused on understanding how B cell responses are generated. Aaron Dinner (University of Chicago) discussed how B cells make cell fate decisions with implications for how memory B cells are formed during initial programming of the response. The transcription factor IRF-4 was proposed to be a master regulator of B cell fate determining when cells are to become antibody-secreting cells (high IRF-4) or memory B cells (low IRF-4). In the next talk, Phil Hodgkin (Walter and Eliza Hall Institute of Medical Research, Australia) argued that cell differentiation, at least when assessed in vitro, is tightly linked to the number of divisions cells have undergone. This sparked an interesting discussion related to the previous talk on whether the decision to become a memory cell or an antibody-secreting cell was dependent on the time since stimulation or was explicitly programmed via the number cellular divisions. Phil presented several new results on filming division of B cell stimulated with CpG where the division history of all dividing and dying cells could be followed. It was found that division of daughter cells was highly correlated. Furthermore, there was a division destiny reflected in the number of divisions cells originating from a single founder would undergo, with most progeny of a given cell ceasing their division at a given division number. A strong correlation between division destiny and the initial size of the founder cell at division was also noted. To explain these findings, Phil proposed a model where division of cells is determined by a factor that is diluted following cell division.

Many talks were well attended with plenty of time for questions

Three invited talks tried to link the behavior of T-cells at multiple scales. Dan Coombs (University of British Columbia, Canada) presented a new model for T-cell signalling initiation. Current ideas for T-cell signalling are based on serial engagement and kinetic proof reading. Still some theories and experimental data seem to indicate that affinity is the main determinant of activation, whereas other data and theoretical interpretation seem to favour activation determined by the dissociation constant alone. Dan demonstrated that a theory based on the local confinement of the TCR and peptide:MHC complexes includes both explanations and, thus, can interpret both types of data. The next topic covered was the modeling of exhaustion during T-cell responses, presented by Rustom Antia (Emory University, Atlanta). In particular, he discussed recently published results on adoptive transfer experiments of LCMV-specific naïve CD8+ T cells into mice followed by LCMV (clone 13) challenge. They found that persistence of LCMV infection and exhaustion of the response depended on the number of CD8+ T cells transferred. In his new model, Rustom includes an immune response that depends on antigen load via a saturation function and allowed for the virus to escape from the T cell response. The model was able to explain the data on persistence of the virus at low numbers of cells transferred and increase in mortality at intermediate levels of virus-specific CD8 T cells. The model also led to a new proposal for the exhaustion of cross-reactive responses in recurring infections, such as malaria. This would explain why cross-reactive responses are short-lived, without making a priori assumptions. Next, Miles Davenport (University of New South Wales, Australia) presented work trying to relate how fast a pathogen replicates and the probability that it will lead to a chronic infection. The idea is that even though immunity is often seen as a race between pathogens and the immune responses, some pathogens could “win” by replicating sufficiently slowly that the immune response initially does not see them. Miles presented data on the dynamics of antigen presenting cells in support of this idea.

Several presentations covered state-of-the-art in vivo imaging of lymphocytes and their migration. Data from the formation of germinal centers, anti-tumor immune responses and the FRC network was discussed. These talks highlighted the power of these new techniques to shed light into spatial processes during immune responses, but also made clear that modelling will increasingly be necessary to make sense of these observations and link them with other experimental modes.

Poster presentations provided time to meet new colleagues and discuss research.

At the end of the first day, we had a plenary lecture by Bali Pulendran (Emory University, Atlanta) where he presented his work to dissect the immune response and long-term immunity following yellow fever vaccination of human volunteers. His approach was to measure gene expression profiles, multiplex analysis of cytokines and chemokines, and multiparameter flow cytometry in 15 healthy volunteers vaccinated for yellow fever. Their results showed that vaccination induced regulatory genes of the innate immune response and of type I interferon production. They found early genes that correlated with the CD8+ T-cell response and predicted it with 90% accuracy.

Overall this meeting struck an excellent balance between structured presentations and enough time for meaningful discussion and interactions between more senior and junior scientists. The organizers got very positive feedback from the participants, and the strong suggestions to repeat the format and the theme in one or two years.

My Career in Mathematical Biology
A Personal Journey

Leon Glass

When I was a young boy, I used to spend hours watching the shenanigans of my ovoviviparous guppies and rearranging my fish tanks. On one notable occasion I siphoned the water from a 10 gallon tank into a 5 gallon tank, much to the dismay of the downstairs neighbor.

After graduating from high school I headed to Brooklyn College as a pre-med major. An encounter with comparative vertebrate anatomy (What is the gestation period of an aardvark?) led me to change my major to psychology. But I ran into problems in both normal psychology (What are the three characteristics of a normal personality?) and abnormal psychology (How do you interpret a dream of a girl riding a horse?). So I switched to chemistry.

After graduating from college in 1963 I went to graduate school in Chemistry at the University of Chicago. I worked with Stuart Rice, an extraordinary scientist who himself had gone to Brooklyn College a decade earlier. My first project dealt with spectroscopy and energy transfer in compounds with multiple benzene rings. But after ruining several high quality UV cuvettes, I switched to statistical mechanics of liquids. During the last year of my thesis work, I attended seminars that were organized by Jack Cowan, who had just been hired to revitalize the Committee of Mathematical Biology at Chicago.

When I finished my PhD in 1968, I obtained an NIH fellowship to work in the newly formed Department of Machine Intelligence and Perception in Edinburgh. My mentor, Christopher Longuet-Higgins suggested that I study geometric illusions. Since I knew nothing about illusions, I started reading, but this was discouraged since “reading rots the mind”. A decisive step took place when Longuet-Higgins showed me a demonstration discovered by physicist Erich Harth in Syracuse. Take a blank paper and make a copy of it using a Xerox machine. Then keep iterating, always taking a copy of the last copy. Soon a stable dot pattern emerges (Beware - it no longer works!). To study the spatial autocorrelations of the dot pattern, I made a transparency to project on a bull’s eye pattern. In the process, I superimposed the copy with the original and discovered striking circular images when the two images were slightly rotated with respect to each other. Under Longuet-Higgins’ guidance, I managed to write up the description before leaving Edinburgh.

Jack Cowan had invited me to return to Chicago when I was done in Edinburgh. Although I had initially planned to keep working on vision, I was intrigued by results from Stuart Kauffman, one of Cowan’s new recruits. Kauffman had shown that randomly constructed Boolean switching networks could fall into a small number of asymptotic behaviors. This was Kauffman’s picture of how lots of genes could lead to a much smaller number of cell types. But I was bothered by the fact that Kauffman’s models called for discrete states and discrete updating, and I worked to develop nonlinear equations that embodied the logical structure of the discrete time systems. This was my first contact with nonlinear dynamics, and I greatly appreciated the geometric approach. During my time in Chicago, I also had the good fortune to be inspired by seminal studies that were being carried out by other Chicagoans including Art Winfree, John Tyson, Hugh Wilson, Stuart Newman, and Jack Feldman.

In 1972 I migrated to Elliot Montroll’s group in Institute for Fundamental Studies at the Department of Physics and Astronomy at the University of Rochester. In Rochester I followed up on several projects that emerged from my earlier studies on vision, pattern formation, and dynamics in model gene networks in collaboration with Ronald Shymko, Rafael Perez Pascual, and Joel Pasternack

While in Rochester, I realized that it was essential to have more contact with experimentalists. I had met Michael Mackey at Gordon Conferences in Mathematical Biology in the early 1970s. Mackey was a young faculty member in the Department of Physiology at McGill and was searching for someone to build up mathematical physiology with him. This was the opportunity I had been seeking and I accepted the job enthusiastically.

At about that time in the summer of 1975, I attended a workshop in Aspen where I learned about "chaos", i.e., aperiodic dynamics in deterministic systems. Returning back to Montreal, Mackey and I posed the question, "Could physiological systems display chaotic dynamics." We wrote a team grant to the Natural Sciences and Engineering Council of Canada, which was funded for the remarkable sum of $7000/year. We developed time delay differential equations for physiological control including one that displayed chaos. We also used the term "dynamical disease" to refer to abnormal pathological dynamics arising as a consequence of a bifurcation in the underlying physiological control system. This work set the theme for the rest of my career.

Was it possible that complex dynamics in physiological systems could be identified with chaotic dynamics? Early mathematical studies showed that chaotic dynamics could be found by periodically forcing nonlinear oscillators. Translating this to physiological experiments, graduate student Gino Petrillo studied mechanically ventilated cats in collaboration with respiratory physiologist Teresa Trippenbach. This was shortly followed by graduate student Michael Guevara who suggested searching for chaos by carrying out periodic pacing of the heart. This became feasible when the cardiac electrophysiologist Alvin Shrier was recruited to McGill. Guevara's massive thesis carried out extensive analysis on the resetting and entrainment of periodically forced chick heart aggregates and demonstrated (to my satisfaction at least) chaotic dynamics over limited ranges of stimulation amplitude and phase.

Guevara's enthusiasm for cardiac arrhythmias was contagious, and a major part of my work has continued with the analysis of mechanisms of cardiac arrhythmias in biological and mathematical models as well as in people. But I have also managed to continue studies in dynamics in other biological systems including genetic networks, vision, and motor systems. Throughout I have had the great fortune to collaborate with a remarkably talented group of colleagues and students including Alvin Shrier, Jacques Bélair, Daniel Kaplan, Jim Keener, Anne Beuter, Jim Collins, Ary Goldberger, Rod Edwards, Ted Perkins and many, many more (apologies for not naming all).

I am struck by how convoluted my path has been, and how much it has been affected by what appears to me to be chance decisions. Although, I am now honored to be the Isadore Rosenfeld Chair in Cardiology at McGill, during my PhD and the following seven year period, it was not clear if I would be able to find a job.

It is a rare privilege to be a scientist and to have the opportunity to think about interesting problems every day and to teach students about ideas I find fascinating. Through the community of scientists I have met fascinating people and have made many lifelong friends. I have been honored by colleagues in three different professional societies (APS, SIAM and SMB) to have been elected to serve in executive positions or committees.

For those at an early stage of their careers I have two suggestions: "Have confidence that what you are doing now will work out, and the tenacity to make sure that it does," and "Look at the data!"

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First International Workshop “Mathematical Methods in Systems Biology”

Urszula Ledzewicz

It is my privilege to write the report of another successful event co-sponsored by the Society for Mathematical Biology, the First International Workshop “Mathematical Methods in Systems Biology,” that took place at Tel Aviv University in Israel on January 4-7, 2010. The workshop goal was to bring together applied mathematicians and researchers working in various fields of systems biology in order to exchange ideas and initiate and promote collaborations. We invited researchers from various areas in applied mathematics (e.g., mathematical modeling, computer simulation, optimal control theory, numerical methods), engineering (e.g., medical imaging, computer assisted diagnosis) and systems biology (e.g., cancer systems biology, cancer modeling, detection and treatment, epidemiology and infectious diseases, signaling pathways) to participate in an effort to create an interdisciplinary setting for the exchange of ideas, methods and methodologies used by the different groups. The aim was to advance the development of a mathematical toolbox of procedures that would be useful in the solution of concrete practical problems of interest to the medical field.

The workshop was originally planned as a US-Israel meeting and the Office of the International Science and Engineering of the NSF awarded us a generous grant to support the travel of US participants, mostly junior faculty and graduate students. Support from the Vice-President for Research and Development of the Faculty of Exact Sciences and the School of Mathematical Sciences of Tel Aviv University helped us with local expenses. The interest in the workshop by far exceeded our expectations and also experts from Canada and several European countries expressed interest. We had a dedicated international Organizing Committee consisting of researchers from the US, Israel and Europe with whom we worked closely on scientific and other issues of the meeting. The workshop was a great success with 170 registered participants and 100 talks and posters presented. It was the largest meeting in this field in Israel. Our host, the Dean of the Faculty of Exact Science of Tel Aviv University, Prof. Haim Wolfson, gave the opening lecture presenting the work of his group in bioinformatics. We had many excellent plenary lectures oriented for a general audience and interesting parallel sessions focused on specific mathematical tools applied to biology or medicine. One particular success of the meeting consisted in attracting a good mixture of mathematicians, biologists and medical doctors from the US, Israel, Canada and Europe. Thanks to Prof. Lewi Stone from the Faculty of Life Sciences of Tel Aviv University, we had a special session in theoretical biology that ran in parallel with the more mathematically oriented sessions throughout most of the workshop. Dr. Zvia Agur, from the Institute of Medical Biomathematics, Israel, successfully moderated a panel “Current Directions and Mathematical Challenges in Medical Research” consisting of medical doctors attending the workshop and presenting open problems for possible medical-mathematical collaboration.

We are most proud of a huge participation of junior researchers, graduate students and postdoctoral fellows, from the US, Israel and Europe. Originally we had planned a small poster session with one “Best Poster Award” sponsored by the Society for Mathematical Biology, but we ended up with two poster sessions full of excellent poster presentations with a total of 24 posters. We therefore decided to extend our award with three additional “Outstanding Poster Awards”! On the attached photo you see the happy winners from Israel, US and Germany. Taking advantage of such a large participation of young scientists, we organized a Junior Scientist Luncheon “Career Opportunities in Mathematical Biology” also sponsored by the Society for Mathematical Biology during which some of the senior faculty from the US, Israel and Europe shared their experiences with graduate students and junior researchers.

Our hosts, the Faculty of Exact Sciences and School of Mathematical Sciences of Tel Aviv University, co-sponsored the workshop, providing us with comfortable classrooms for parallel sessions and all the technical support as well as a spacious auditorium, which, to our surprise, was located in the architecturally beautiful Cymbalista Synagogue (designed by the world famous Swiss architect Mario Botta). They also arranged for an amazing banquet in the Jewish Diaspora Museum with delicious food and live music. We were not even short of performances: one of our plenary speakers turned out to be a professional tango dancer and his tango with the workshop secretary provided an artistic touch to the very successful evening. Of course, when it came to the dancing floor nobody could really compete with past President of the SMB, Prof. Avner Friedman, whose presence at the workshop, both scientific and social, contributed significantly to its overall atmosphere and success. The other SMB “official” Prof. Abdul-Aziz Yakubu made sure his field of epidemiology was well represented and has been a tremendous help in many organizational issues before and during the workshop. Other social events included a half-day trip to Jerusalem. Our tour guides did an amazing job and in one afternoon and evening we got such a great overview of what Jerusalem has to offer that it left us enchanted by this wonderful city with the wish to return for a longer visit. The “icing on the cake” of the workshop was the weather. Having been warned before of often rainy conditions at this time of the year, we had beautiful sunshine with growing temperatures, which on the last days made us (unnecessarily) worry how to keep participants in the classrooms and away from the beach. Anyway, the workshop ended still with quite a high participation that is attested to by the group photo, which was taken on the steps of the Faculty of Exact Sciences building on the last day. For people who stayed in Israel an extra day the hosts organized a beautiful walk along the sea to the Old Jaffa and the historical part of Tel Aviv. Everybody left carrying a lovely conference bag (we got a lot of compliments on these and I use it till today to carry notes for my classes) and a T-shirt with the workshop and the SMB logo. I should add that we even started and ended our event in the grand style of expensive large conferences: we had both welcome and farewell receptions with wine and appetizers. All of this happened with a very modest registration fee (of which students were exempt) thanks to our wonderful local sponsors and the great bargaining skills of our local organizers, Dr. Eugene Kashdan and Prof. Nir Sochen from Tel Aviv University and, not to forget, their secretary, Sonya Hasday. Many participants complimented us on both the scientific and social parts of the workshop and I believe Eugene, Nir and Sonya deserve a lot of credit for that.

For us the work is not over yet and we are now preparing a volume of the workshop proceedings, which will appear as a special issue of the journal “Mathematical Biosciences and Engineering”.

As for all the people asking about when and where the Second Workshop “Mathematical Methods in Systems in Biology” will take place, we are open to suggestions. We will also be happy to pass on all of our expertise grown from this one to a team with a vision for the new meeting and the energy to put it together. For those interested, the official workshop website is http://www.math.tau.ac.il/~mmsb and a photo-album telling the story of our successful workshop and surrounding events can be found on the Internet at http://picasaweb.google.com/mmsb012010/MMSBWorkshop.

Above: The winners of the best and outstanding poster awards (from left to right): Yoav Ram (Tel Aviv University), Jan Kelkel (Stuttgart University), Uri Roll (Tel Aviv University), Horia-Mihail Teodorescu (Harvard University) and Oren Barnea (Tel Aviv University)
Below: Workshop participants in front of the building of the Faculty of Exact Sciences, Tel Aviv University

Center and Institute Updates

Editor's Note: This is a new section for the SMB Newsletter to highlight activities at Research Centers and Institutes of interest to Math Biology. If your Center or Institute would like to contribute a column, please contact us. editor@smb.org

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DIMACS

Center for Discrete Mathematics & Theoretical Computer Science
Founded as a National Science Foundation Science and Technology Center

Upcoming Programs

Advanced Study Institute and Workshop in Conservation Biology. DIMACS and MBI are sponsoring an Advanced Study Institute and workshop in Conservation Biology to be held July 28-August 13, 2010 at the Kenya Wildlife Services Training Institute in Naivasha, Kenya. During the 3-day workshop (August 11–13) interdisciplinary researchers will discuss their work with graduate students and assist the graduate students in developing research projects. A 2-week advanced study institute (July 18–August 10) will prepare the graduate students to participate in the workshop. Topics to be covered include population viability analysis, conservation genetics, reserve design, GIS and remotely sensed data, plant and animal disease, and global change including climate change. To contribute a paper or poster, please send a title and abstract by June 1, 2010 to Christine Spassione at sapssion@dimacs.rutgers.edu. http://dimacs.rutgers.edu/Workshops/ASIConsBio/

Advanced Study Institute and Workshop in Genetics and Disease Control. DIMACS and MBI are sponsoring a four-day Advanced Study Institute and workshop in Genetics and Disease Control to be held August 8–12, 2011, at the University of Antananarivo in Antananarivo, Madagascar. The four-day event will bring together U.S. and African graduate students introducing them to the present state of research in pathogen genetics, host genetics, and vector genetics. The interdisciplinary workshop will also feature several sessions devoted to the special biological/health/agricultural problems of Madagascar. To contribute a paper or poster, please send a title and abstract by April 15, 2011 to Christine Spassione at sapssion@dimacs.rutgers.edu. Graduate student applications are now being accepted for the ASI/Workshop. http://dimacs.rutgers.edu/Workshops/ASIDisControl/

One-Year Research Opportunities in Biomathematics for African Graduate Students. The Africa-US Student Research Initiative (ASRI), funded by a grant from the National Science Foundation, is offering two outstanding African students who are currently studying for a Ph.D. degree in Africa an opportunity to spend one year at the Center for Discrete Mathematics and Theoretical Computer Science (DIMACS) of Rutgers University, working on research projects that enhance their dissertation and prepare them for an independent research career in biomathematics. DIMACS has had extensive programs in biomathematics for many years and offers the opportunity to participate in workshops and tutorials and to work one on one with a faculty mentor. The students will receive a stipend and housing allowance of $30,000 for 12 months, airfare from Africa to the US, and health insurance. The visits will start in the spring or summer semester 2010. In some cases, visits starting in the fall will be considered. Some biomathematical areas of particular interest include, but are not limited to, mathematical epidemiology, mathematical models in ecology, bioinformatics, and mathematical population biology. Applications are also being accepted in other areas that have relevance to biomathematics. The application process for ASRI awards is highly competitive, and we urge students to submit their nomination packets as early as possible. For more information see the web pages at: http://dimacs.rutgers.edu/Workshops/ASRI2009/.

Mathematical Biosciences Institute

Summer Undergraduate Program in Mathematical Biology, June 21 – July 2, 2010
Current Topic Workshop: Mathematical Neuroendocrinology, August 9-13, 2010
Workshop for Young Researchers in Mathematical Biology, August 30 – September 1, 2010
Workshop 1: Mathematical Modeling of Plant Development, September 27 – October 1, 2010
Workshop 2: Circadian Clocks in Plants and Fungi, October 25-29, 2010
Current Topic Workshop: Blackwell-Tapia Conference, November 5-6, 2010

News from the National Institute for Mathematical and Biological Synthesis

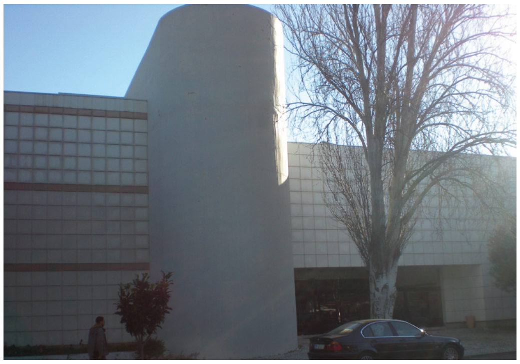
As NIMBioS is inherently an interdisciplinary institute with crosscutting activities involving mainly biology and mathematics, researchers from a wide variety of disciplines have met at the institute in recent months to address key biological questions using appropriate mathematical methods. Some of the activities in recent months have included the NIMBioS Tutorial on Optimal Control and Optimization in which a variety of individuals with mainly separate backgrounds in biology or mathematics learned the conceptual foundations and skills to utilize optimal control approaches in various areas of application to the life sciences. A continuing NIMBioS Working Group on Binary Matrices brought together ecologists working on food webs, network biologists, and conservation biologists with statisticians who have expertise in applying emerging statistical methods to field data. A Workshop on Bovine Tuberculosis brought together mathematical modelers, veterinarians, geographers and epidemiologists to consider methods to utilize USDA data to estimate potential likelihoods and impacts of this disease in the US. Also, NIMBioS sponsored the first gathering of mathematical modelers and epidemiologists to consider models for the spread of white-nosed syndrome in bats across the US.

Numerous outreach activities focused on providing information on how mathematics contributes to biology to various audiences. This included perhaps the largest gathering of undergraduates carrying out research at the interface of mathematics and biology sponsored through the NSF UBM program; a summer program providing research experiences for an interacting group of undergraduates from biology and mathematics, high school science teachers and graduate students in veterinary medicine; collaboration with high school teachers in addition of mathematics curricular components to the Biology in a Box program; and numerous talks to undergraduate and graduate student audiences about what NIMBioS is and how the interface between math and biology is important in developing new techniques for significant societal problems as well as investigating basic biology.

Upcoming events and opportunities at NIMBioS include several Tutorials and Investigative Workshops. NIMBioS is now accepting applications for the NIMBioS Tutorial: Computational Biology Curriculum Development to be held July 6-9, 2010. This tutorial focuses on strategies for including computational biology and cyber-learning in the development of interdisciplinary modules for teaching undergraduate biology. NIMBioS is also accepting applications for the NIMBioS Tutorial: Graph Theory and Biological Networks to be held August 16-18, 2010. This tutorial is designed to teach participants how graph theory can inform their understanding of many common biological patterns that are graphs. In May and July, respectively, NIMBioS will host the Investigative Workshop on Modeling Toxoplasma Gondii and the Investigative Workshop on Modeling Reef Ecosystems. Upcoming outreach activities include the summer Research Experience for Undergraduates and Veterinary Students. Seventeen students and two high school teachers from 17 different institutions across the United States have been chosen to participate in this year's eight-week program in June and July. NIMBioS also welcomes four new postdoctoral fellows whose research topics include the evolution of speciation in coevolving system; dispersal and dynamic occupancy models for the spread of white-nose syndrome; evolution of social-ecological networks; and local adaptation and gene flow under climate change.

September 1, 2010 is the deadline for requests for NIMBioS support for Working Groups, Investigative Workshops, Postdoctoral Fellows and Sabbatical Fellows for activities beginning Winter/Spring 2011. Applications for Short-term Visits are considered four times a year, with deadlines on March 1, June 1, September 1, and December 1. All areas of research at the interface of biology and mathematics are considered, but we are especially interested in activities expanding beyond the areas of research supported to date. Potential organizers of activities in areas of molecular biology, cell biology, network biology, immunology and systems biology are particularly encouraged to submit requests for support of Working Groups or Investigative Workshops.

For more information about NIMBioS and how to apply, visit our website at www.nimbios.org <http://www.nimbios.org>



Dynamical Systems Applied to Biology and Natural Science

Andrea Gregory

The First Workshop on Dynamical Systems Applied to Biology and Natural Sciences, sponsored by The Centro de Matemática e Aplições Fundamentais (CMAF), was hosted at Lisbon University, February 1-3, 2010. The workshop brought scholars together from across the globe to foster research development within the international community through the presentations of studies on various subjects, all centered on dynamical systems. In addition to the stimulating lectures, the conference offered participants the opportunity to network with scientists with mutual research interests and to create lasting relationships in an open and friendly atmosphere. This objective was originally achieved through regular coffee break sessions held within the university and was furthered through touristic endeavors. The city of Lisbon created a prime location for the event, greeting the participants with beautiful weather, historic sights, and a fun ambiance for the duration of the workshop.

Immediately upon arriving, it became evident that the organizers had gone to extreme lengths to accommodate the presenters and to maximize the experience. These efforts optimized the program, setting it apart from previous workshops that I have attended and created a lasting positive memory.

The conference opened with welcoming remarks from one of the organizers, Nico Stollenwerk, who invited the attendees to take advantage of the casual forum of intellectual exchange. From this point on, the conference hosted various talks spanning 10AM- 6PM. Plenary lectures were dispersed across the entirety of the conference, signifying both the beginning and ending of the scholarly presentations. While other talks ran concurrently, plenary lectures were attended by all workshop participants. Frank Hilker's discussion of Controlling Chaotic Population Dynamics started the program with the first plenary talk. Carlos Braumann presented his plenary presentation on Stochastic Models of Growth and Extinction of Populations. This was followed by Ezio Venturino's lecture on Models for Biological Control of Crops, concluding the lecture presentations for the first day. Immediately following, was the poster session, which enabled graduate and undergraduate researchers to defend their work along side other honorary scholars. The workshop community critiqued potential issues of the studies, offered alternative suggestions, and provided constructive feedback for poster presenters. For some, this was an unprecedented opportunity to learn and challenge their own conceptions in an attempt to perfect their own research initiatives.

The second day of the conference focused on the application of dynamical systems on epidemiological studies. It began with two consecutive plenary talks by Gabriela Gomes and Mario Recker, on Integrative Epidemiology and Competing Evolutionary Pressures Shape the Pattern of Antigenic Switching in Malaria, respectively. Following graduate researcher Sebastian Ballesteros' presentation on Immune Boosting and Influenza A Phylodynamics, the workshop warmly welcomed three more plenary lectures. Eduardo Massad shared a new perspective on the Estimation of R0 from

the Initial Phase of An Outbreak of a Vector-Borne Infection. Yves Dumont spoke on Vector Control for the Chikungunya Disease and Cláudio Struchiner added discourse On the Distribution of Mosquito Susceptibility to Malaria. The day concluded with a social dinner at the Sana Metropolitan Hotel.

On the last day of the conference, Nico Stollenwerk delivered his speech on Rich Dynamics in Multi-Strain Epidemiological Models. After lunch, Bob Kooi discussed an Analysis of Torus Bifurcations in Epidemiological and Ecological Models. Simone Bianco concluded the event and the plenary talks with his presentation on Diseases with Multistrain Interactions, focusing on cross-immunity and antibody-dependent enhancement. This lecture sparked heated deliberation on dengue fever dynamics and the appropriate parameter values in its modeling from various schools of thought, bringing the workshop to a fitting end.

In conclusion, the conference succeeded in encouraging scholarly debate. Perhaps most interestingly, it was able to bring people, young and old, from a variety of specialized backgrounds together. Gaining experienced from established scholars and a new perspective from the fresh ideas of the younger researchers, the workshop facilitated increased bio-mathematical understanding, which was mutually beneficial for all participants.

Previous page top and above: Photos of the beautiful buildings in Lisbon.

Previous page bottom: Some of the attendees of the Workshop.

Positions Available

Postdoc: College of William and Mary

A postdoctoral position is available in Leah Shaw's group (http://lbshaw.people.wm.edu/), Department of Applied Science, College of William and Mary. The topic is stochastic population modeling, including epidemic spread in adaptive social networks and stochastic extinction in complex populations. Details can be found at http://jobs.wm.edu for position number G0116W.

Postdoc: Georgia Tech

A postdoctoral position in computational molecular biology is available with an interdisciplinary RNA research group at Georgia Tech under the direction of Dr. David Bader (Computing), Dr. Steve Harvey (Biology) and Dr. Christine Heitsch (Mathematics). The postdoc will lead efforts to develop new mathematical approaches and innovative computational methods in RNA structural biology, with a particular emphasis on algorithms for the analysis, prediction, and design of folded RNA viral genomes. The research position, to begin in fall 2010, is supported by an NIH R01 grant and will provide a competitive 12 month salary with standard benefits. The appointment is expected to be for three years, with annual renewal subject to satisfactory progress and mutual agreement. Requirements include: (1) PhD in computer science, mathematics, biology, physics or other closely related field; (2) Demonstrated research excellence; (3) Strong oral and written communication skills. Prior interdisciplinary experience is preferred, but outstanding applicants looking to broaden their field of interest will also be considered. Applications should be emailed to <appRNApostdoc@math.gatech.edu> and consist of a cover letter describing your interest in the position, the names and contact information for at least three references, a curriculum vita, and a short research summary written for a general scientific audience. Applications will be reviewed starting from May 15, 2010, and continue until the position is filled.

Postdoc: The University of Toronto

Applications are invited for a research associate/postdoctoral researcher position on transmission modeling of hepatitis C and HIV, and economic evaluation of the impact of hepatitis C treatment strategies on individuals co-infected with hepatitis C and HIV in Canadian settings. Successful applicants will be expected to have a strong background in programming large-scale simulation models, such as agent-based models, network models, and/or large systems of differential equations. Previous experience in infectious disease transmission modeling, and a graduate-level degree (MSc/PhD) is a plus. Individuals with at least a Bachelor's degree in computer sciences, physics, mathematics, health economics, and epidemiology with the above skills are encouraged to apply. Experience in writing scientific papers is a plus. Individuals should be ready to work in an exciting, interdisciplinary environment as part of a team of experts from various health-related and quantitative fields. Individuals will be appointed at the research associate level or postdoctoral researcher level, according to their background preparation and degree level. The successful applicant will be based at the Toronto Health Economics and Technology Assessment Collaborative, housed in the School of Pharmacy at the University of Toronto. The initial appointment is for one year, with renewal for an additional year subject to satisfactory performance. To apply, please send a CV, cover letter, representative publications (if available), and the names and contact details of three references to Dr. Rosie Thein (rthein@nchecr.unsw.edu.au) and Dr. Chris Bauch (cbauch@uoguelph.ca). Applications will be considered as they are received up until June 30, 2010. Only successful applicants will be notified.

Postdoc: IUPUI

The Department of Mathematical Sciences and the Center for Mathematical Biosciences at Indiana University-Purdue University Indianapolis (IUPUI) invite applications for a postdoctoral position in the area of mathematical biology and computational neuroscience. The position is with a collaborative group of scholars from the Department of Mathematical Sciences at IUPUI and the Department of Neurosurgery of the Indiana University School of Medicine. The current research project is aimed at understanding the properties, origin and function of basal ganglia rhythmic activity, oscillations and synchronization at health and in Parkinson's disease. The postdoctoral fellow will perform data analysis and dynamical systems modeling and will have the opportunity to contribute to other aspects of the project. The position offers excellent interdisciplinary training possibilities in mathematical biology and computational neuroscience. Qualifications: Applicants are expected to have a Ph.D. in mathematics, physics, neuroscience, biomedical engineering, computer science or other related field. Applicants should have strong quantitative skills in data analysis and modeling and a strong interest in neuroscience applications. Experience in applied dynamical systems/nonlinear time-series analysis/neuroscience is a plus. How to apply: Send your CV with a list of publications, research statement, and arrange two-three recommendation letters to be sent to Dr. Leonid Rubchinsky via e-mail: leo@math.iupui.edu. Address all your inquiries to the same e-mail. Alternatively send your application by regular mail to: Dr. Leonid Rubchinsky, Department of Mathematical Sciences, IUPUI, 402 N. Blackford Street, LD 270, Indianapolis, IN 46202. Screening of applications will continue until position is filled.

Postdoc: University of Nevada

A postdoctoral fellow position is open in the Mechanical Engineering department at the University of Nevada, Reno. The theoretical/computational postdoc will focus on complex biomaterials and low Reynolds-number hydrodynamics. The postdoc will apply analytical and numerical techniques to topics including the behavior of chiral particles in flows and the locomotion of microorganisms, especially locomotion in non-Newtonian fluids and gels.

The position has a preferred start date in September 2010. Experience with scientific computing and/or low-Reynolds number hydrodynamics is preferred. Interest in interacting with experimentalists is a plus. Candidates should have a recent Ph.D. in engineering, physics, applied mathematics, or a related field. To apply, email a CV (including contact information for references) and a statement of research interests and experience to Henry Fu at fu.henry.c@gmail.com. More details available at http://sites.google.com/site/henrychienfu.

Postdoc: University of Guelph

Applications are invited for a postdoctoral researcher position on developing simulation models for mitigation of emerging infectious diseases. The position is funded under the Ontario Ministry of Research and Innovation Postdoctoral Fellowship program. Successful applicants will be expected to have a PhD in mathematics and several years of programming experience in the private or public sector. Applicants with experience in infectious disease modelling will be strongly preferred. Experience in writing scientific papers is a plus. Individuals should be ready to work in an exciting, interdisciplinary environment as part of a team of experts from various health-related and quantitative fields. The successful applicant will be based in the Department of Mathematics and Statistics at the University of Guelph. The initial appointment is for one year, with renewal for an additional year subject to satisfactory performance. To apply, please send a CV, cover letter, representative publications (if available), and the names and contact details of three references to Dr. Chris Bauch (cbauch@uoguelph.ca). References will be sought from short-listed applicants only. The closing date for applications is May 17, 2010.

PhD student position in Ecology

We are looking for an aquatic microbial ecologist with a keen interest to understand how variation in river run-off influences marine ecosystem drivers, e.g. bio-optics and CNP concentrations, and microbial communities and productivity. The project will involve both comparative studies as well as experimental studies along a north-south gradient in the Baltic Sea to elucidate the effect of river inflow on phytoplankton and bacterial productivity and community compositions. See: http://www8.umu.se/umu/aktuellt/arkiv/lediga_tjanster/313-288-10.html

PhD student position in Environmental Chemistry

We are looking for a chemist with good competence in environmental science and mathematics/statistics. The project is focused on finding methods for tracing significant pollution sources to the Baltic Sea. Chemical analyses of Baltic air and sediment cores will be conducted, and the data will be evaluated using various multivariate modeling techniques. The aim is to identify and apportion pollution sources and to increase knowledge and understanding on spatial and temporal trends. See: http://www8.umu.se/umu/aktuellt/arkiv/lediga_tjanster/313-299-10.html

PhD student position in Environmental Chemistry

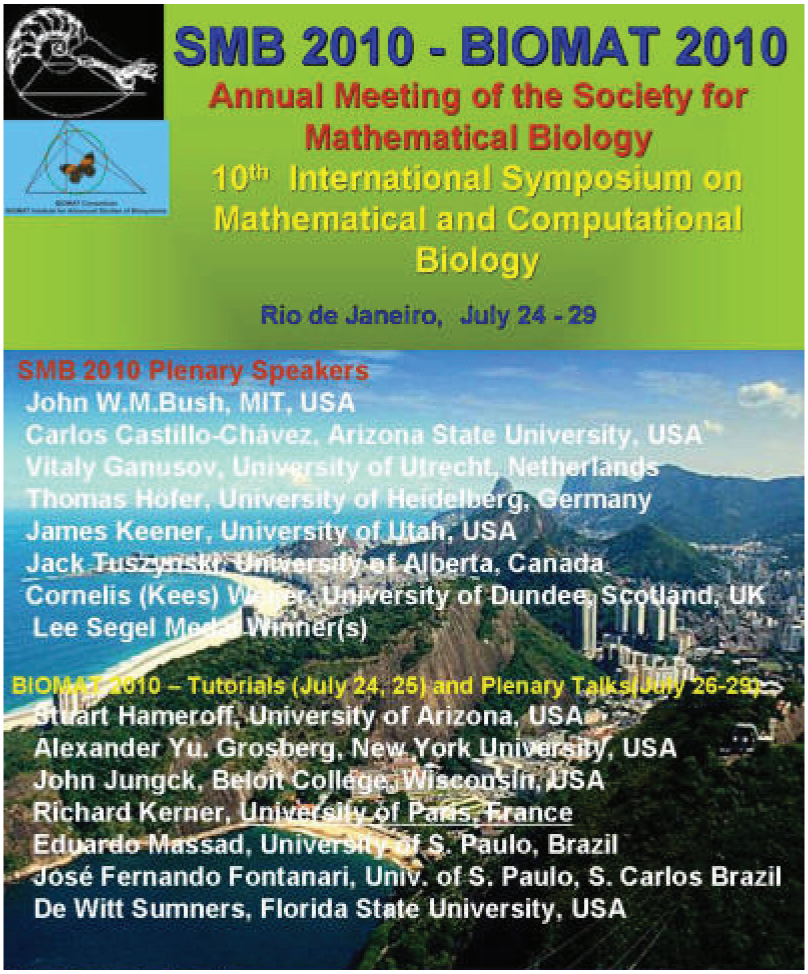
We are looking for a chemist with good environmental and/or analytical chemistry competence. The project is focused on climate-induced changes on the bioavailability of pollutants and related ecosystem functions at lower trophic levels. Studied chemicals will be biologically active environmental pollutants, e.g. health drugs and biocides. Persistent organic pollutants (POPs) will be used as reference substances. See: http://www8.umu.se/umu/aktuellt/arkiv/lediga_tjanster/313-297-10.html

PhD student position in Ecology

We are looking for a candidate in ecology, natural geography or similar with some background in statistics. Focus will be to evaluate common sensors to estimate biomass and activity in the planktonic food web. This includes statistical evaluations of environmental data from historic time series, and extensive measurements in the lab and in contrasting environments, from estuaries to the open sea. The achieved knowledge will be used to design monitoring programs in different time scales with automatic sensors. See: http://www8.umu.se/umu/aktuellt/arkiv/lediga_tjanster/313-291-10.html

PhD student position in Ecology

We are looking for a person with a mathematical, and/or microbiological alignment, who is interested in food web modeling. The long-term goal of this project is to develop a model to predict the complex effects of climate change on the production at lower trophic levels in the Baltic Sea. Work tools will, for example, be compilation of results from experiments to reveal complex mechanisms, available field data to elucidate environmental changes in the Baltic Sea, and to execute modeling simulations to make future predictions. See: http://www8.umu.se/umu/aktuellt/arkiv/lediga_tjanster/313-287-10.html



SMB 2010 - BIOMAT 2010

Annual Meeting of the Society for Mathematical Biology

10th International Symposium on Mathematical and Computational Biology

Rio de Janeiro, July 24 - 29

SMB 2010 Plenary Speakers

John W.M.Bush, MIT, USA
Carlos Castillo-Chávez, Arizona State University, USA
Vitaly Ganusov, University of Utrecht, Netherlands
Thomas Hofer, University of Heidelberg, Germany
James Keener, University of Utah, USA
Jack Tuszynski, University of Alberta, Canada
Cornelis (Kees) Weijer, University of Dundee, Scotland, UK
Lee Segel Medal Winner(s)

BIOMAT 2010 – Tutorials (July 24, 25) and Plenary Talks(July 26-29)

Stuart Hameroff, University of Arizona, USA
Alexander Yu. Grosberg, New York University, USA
John Jungck, Beloit College, Wisconsin, USA
Richard Kerner, University of Paris, France
Eduardo Massad, University of S. Paulo, Brazil
José Fernando Fontanari, Univ. of S. Paulo, S. Carlos Brazil
De Witt Sumners, Florida State University, USA

SMB 2010 Updates

The 2010 Society for Mathematical Biology annual meeting will be held in Rio de Janeiro, Brazil, July 26-29, 2010.

Plenary speakers will include: John W.M.Bush, MIT, USA; Carlos Castillo-Chávez, Tempe, Arizona, USA; Vitaly Ganusov, Utrecht, Netherlands; Thomas Höfer, Heidelberg, Germany; James Keener, Salt Lake City, Utah, USA; Jack Tuszynski, Alberta, Canada; Cornelis (Kees) Weijer, Dundee, Scotland, UK.

On behalf of the Scientific Advisory Committee of SMB 2010 Annual Meeting and due to many requests from participants worldwide , we now announce the Last Call for Abstracts of Contributed Talks. Please check the website for the **NEW** deadline. Application forms are available at http://www.biomat.org/smb/contributedtalk.htm.

Registration is now open. Please find the corresponding form at http://www.coppeteccongressos.org.br/script/FctCadFisica.asp?pStrIdioma=US&CodCongresso=70

For more information see:
http://www.biomat.org/smb/smb2010.html

http://www.biomat.org/smb/smb2010venue.html

Editor's Notes:

We invite submissions including summaries of previous mathematical biology meetings, invitations to upcoming conferences, commentaries, book reviews or suggestions for other future columns. The deadline is the 15th of the month prior to publication.

The SMB Newsletter is published in January, May and September by the Society for Mathematical Biology for its members. The Society for Mathematical Biology is an international society which exists to promote and foster interactions between the mathematical and biological sciences communities through membership, journal publications, travel support and conferences. Please visit our website: http://www.smb.org for more information.

Holly Gaff, Editor, editor@smb.org