The Society for Mathematical Biology

SMB NEWSLETTER

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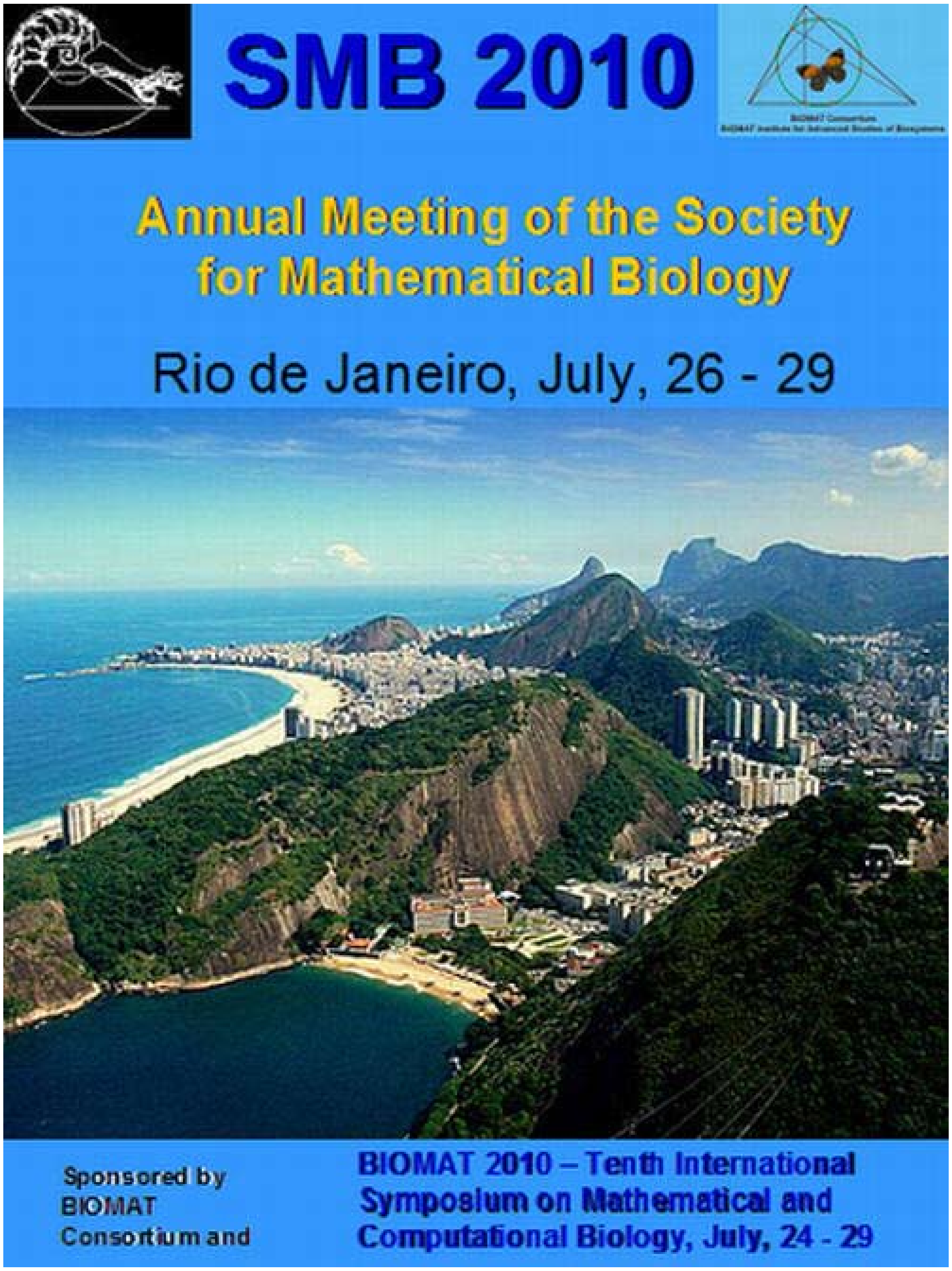
Mark your Calendars for SMB 2010

The 2010 Society for Mathematical Biology annual meeting will be held in Rio de Janeiro, Brazil. The meetings will be July 26-29, 2010. The Plenary Sessions will be held at the School of Naval War while the Parallel Sessions will be held at the Federal University of Rio de Janeiro State - UNIRIO. Check the websites listed below often for all the news about the SMB 2010. Please submit all the suggestions for minisymposia, contributed talks and usual questions about the organization of the conference to smb2010biomat@gmail.com.

Meeting websites:

http://www.biomat.org/smb/smb2010.html

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



Inside this Issue:

Dear SMB Members,

2009 is drawing to a close. The excitement of the impending new academic year many of us felt when the last newsletter came out has been replaced with a somewhat weary resignation as we plow through the last weeks of the semester, grading papers and turning in marks. Such are the vagaries of life!

The last newsletter was written in the heat of Kansas, and this one is taking shape in the chill of a new winter in Montreal (where we have our first snow) and Kansas (pretty darn chilly). The blowing snow (in Montreal) and the bite of the cold reminds me that some lovely snowshoeing and skiing will soon be available.

I have just driven from Wichita to Hutchinson, Kansas. In contrast to my last trip here, the fields are mostly fallow and brown, with a sprinkling of green from those planted with the winter wheat. I stopped in Yoder to buy black jelly beans and fruit slices from the local Amish store for a woman who helps look after my mom (she is a black jelly bean freak like I am) . The Mennonite and Amish farms in the vicinity of Yoder are pristine as always, and the only real sign of life these days are the horses and cows grazing in the fields (slim pickings) and the pigs in their pens. But winter is never an idle time for farmers as there is much to do over the winter months for the coming year. The Arkansas River is very full (maybe Colorado no longer needs water?), and as I detoured off the highway I noticed that Pawley's Gunshop was doing a land office business. The night sky tonight is spectacular with a blaze of stars even more wonderful than in the warmer months because of the clarity of the air. So many stars and galaxies. Is it possible that there is not intelligent life elsewhere? I don't believe it for a minute. And the whistle of the freight trains crossing the prairies whenever they come to a level crossing is just magical. Life here in Kansas where I grew up is much different from life in Montreal where I now live. Better? Worse? The same? Just different. Life is. Deterministic. Not stochastic.

As life is generally full of surprises, mine is no exception (no, that does not mean that my life is stochastic—just deterministically unpredictable) . My mother has defied all expectations and still survives albeit in a highly diminished state, unable to talk very well as a consequence of a series of strokes but still totally lucid. Her body continues to fight on, refusing to give her the release ("I just want this to be over") that she so badly wanted four months ago. Her apartment has been given up and her worldly goods distributed to family and friends as she mandated. The baby swallows (see the last newsletter) all survived and flew the nest, even the weakling. The fate of the baby rabbits is unknown, but some probably survived and others (the slower or unlucky ones) became part of the hawks' food chain. The hawks, by the way, are doing quite nicely and looking very perky. I counted 9 on my way here today—all looking pretty hungry because these are lean months. We will see how many are looking perky and have survived by spring. Such is life, with a beginning and an end for each individual while the collective whole lives on—for now.

Rubem Mondaini, who is coordinating the meeting in Rio de Janeiro 26-29 July, 2010, reports that "There is a provisional website running at http://www.biomat.org/smb/smb2010venue.html . We have also created an account smb2010biomat@gmail.com for interested people to ask about dates, plenary speakers, mini-symposia, contributed talks, accommodation and so on …". There will soon be a link from the SMB website to the meeting site. Additionally, Ryszard Rudnicki, meeting coordinator for the joint ESMTB-SMB meeting in Krakow, Poland, 28 June to 2 July, 2011, tells us that plans for that meeting are shaping up nicely. If you are interested the web site is located at http://www.impan.pl/~ecmtb11/.

I hope that this period at the end of 2009 and start of 2010 is a good one for each of you reading this, that you feel contented with what you have accomplished in the past year and looking forward to the start of a new one.

Michael Mackey

CAMBAM/MBI Summer School

Summer School 2010 at McGill University in Montreal is jointly sponsored by the Centre for Applied Mathematics in Bioscience and Medicine (CAMBAM)* and the Mathematical Biosciences Institute (MBI)** and will take place under the theme: “ Nonlinear Dynamics in Biological Networks”

The past decade has witnessed a renaissance in the biological sciences with a new and almost insatiable desire for interdisciplinary research with the physical and mathematical sciences. The life sciences have been propelled into the quantitative era. There is a demand in academia, government, and industry for people who speak the languages of the mathematical, physical, and biological sciences. The CAMBAM/MBI summer school is precisely aimed at satisfying this demand by providing the knowledge needed to boost the move from one side of this divide to the other with a special emphasis on the non-linear dynamics of biological networks.

Applicants are encouraged from the mathematical, physical and the life sciences. Though at least one year of calculus is needed, a first course in differential equations is highly desirable. Each day will consist of morning lectures followed by computational lab work in the afternoon. The laboratories are aimed at solidifying the concepts taught in the morning lectures, and additionally student groups will work on a project that they select from a list provided by the organizers and lecturers. The ultimate goal of the new biology, which has been loosely termed Systems Biology, is to produce a computational model of a biological system which allows accurate, experimentally verifiable prediction in the laboratory or field. The CAMBAM/MBI summer school will provide a solid introduction to the fundamental science on which Systems Biology is based. Each lecture will explore the concepts and basic mathematical ideas of a different strand of Systems Biology and will be illustrated with examples from recently published research. Participants will develop a set of tools and a vocabulary which should allow them to discuss and become actively involved in problems in quantitative biology. They will become familiar with the powerful MATLAB programming language as well as the (free) XPPAUT software package.

Topics to be covered will include linear and non-linear systems, chaos, bifurcation theory, stochastic systems, differential delay equations, Boolean models, and cellular automata. Applications will range from the molecular level (e.g., bacterial operon regulation) to the cellular level (e.g., neural signal propagation) to the systems level (e.g., cardiology, neural control, sensory transduction, ecology, epidemiology). Each lecture will be delivered by an expert working in the field and at the end of the course participants will be familiar with several of the research directions available in quantitative Systems Biology.

DEADLINE DATE FOR SUBMISSION OF APPLICATIONS IS MARCH 1, 2010

There is no tuition fee and the Summer School organizers have committed to cover accommodation costs for participants who opt to stay in the McGill Residence for the two weeks (see Accommodation page). However, students are expected to cover the full cost of their travel to and from Montreal as well as their upkeep during the two weeks. In addition, persons who have been selected to participate in the Summer School will be expected to pay a registration fee. After receipt of notification of participation from the Summer School organizers, students will have up to March 15th, 2010 to pay the $150 registration fee. Thereafter and up to April 15th, students will have to pay $200.

* CAMBAM acknowledges support from MITACS

** MBI acknowledges support from the National Science Foundation and the Ohio State University

Advanced Study Institute and Workshop on Economic Epidemiology Makerere University 2009

Nina Fefferman and Fred Roberts

Economic epidemiology deals with the mathematical conceptualization of the interplay among economics, community organization, individual human behavior, and disease ecology to improve our understanding of the emergence, persistence, and spread of infectious agents and of optimal strategies and policy to control that spread. Mathematical models of disease spread already exist to allow the examination of the relative efficacy of particular intervention strategies at curtailing disease spread. However, these models frequently assume unmotivated levels of behavioral compliance, making their results difficult to interpret in real-world scenarios. To correctly evaluate health interventions and alternative public policies, models of disease spread must incorporate both group and individual behaviors (which are often the result of economic, and therefore quantifiable, considerations). Incorporating these behaviors entails important and complex mathematical challenges but is necessary in order to understand which of the theoretically efficient policies could result in the most effective real-world disease control.

To help foster interest and research in the important and expanding interdisciplinary field of economic epidemiology, and made possible by the combined efforts and support of DIMACS, MITACS, SMB, MBI, and Makerere University, students and researchers from Canada, the United States, and from many countries throughout Africa met at Makerere University in Kampala, Uganda, from July 20th to August 5th, 2009. The first two weeks were dedicated to a research-based multidisciplinary learning experience for the nearly 40 graduate student participants, coming from 13 countries (Botswana, Cameroon, Canada, Ethiopia, Kenya, Nigeria, Rwanda, South Africa, Sudan, Tanzania, Uganda, the US, and Zimbabwe). This Advanced Study Institute (ASI) welcomed students from the fields of mathematics, economics, epidemiology, and public health with the purpose of introducing them to novel topics and research methods at the interface of their fields.

Guest researchers working in the field of economic epidemiology (see list below) provided an initial series of brief, introductory lectures in model building, mircoeconomics, game theory, meaningful data analysis, epidemiological modeling, operations research, decision and control theory, applied statistics, health economics, evolutionary epidemiology, and the epidemiology of infectious diseases of Africa. Each of these lectures was meant to establish a common background among the students, and to cover the full breadth of the various fields pertinent to research into questions in economic epidemiology. After only a few days, the students formed 7 small groups in which they defined, and then pursued research into, open problems of economic epidemiology relevant to questions of infectious disease in Africa. Selection of projects and the course of the research were guided carefully by the Institute Co-organizers (Matthew H. Bonds, Harvard University, and Jan Medlock, Clemson University) to encourage a diversity of concepts and ability of the

outcome to inform real-world policy decisions once the research was accomplished.

The ASI student research groups made two presentations during the two weeks of the ASI: once in the first week to present their chosen research topics for feedback from their colleagues and the ASI organizers, and once at the end of the second week to present their initial results and plans for continuation of the work for the future. All participants committed to continuing their research after the formal close of the ASI, working towards the production of a manuscript to be submitted for publication. In this way, the structure of the research experience not only expanded the students' understanding and capability within the field of economic epidemiology, but also continues to foster ongoing intercontinental collaborations with fellow students in hopes of generating a truly global cohort of life-long colleagues.

As a capstone event to the ASI, the students were then able to participate in a workshop, involving a broader diversity of researchers from North America, South America, and Africa. The workshop program was co-chaired by Nina Fefferman (Rutgers University) and Ramanan Laxminararayan (Resources for the Future). In addition to Bonds, Medlock, Fefferman, and Laxminararayan, the organizing committee consisted of Alison Galvani (Yale), Wayne Getz (UC Berkeley), Abba Gumel (U. of Manitoba), Simon Levin (Princeton), Joseph Mugisha (U. of Kampala), Fred Roberts (Rutgers), and Dave Smith (U. of Florida). Mugisha was in charge of local arrangements.

The organizers are very grateful to the Center for Discrete Mathematics and Theoretical Computer Science (DIMACS), the International Development Research Centre (IDRC), the Mathematical Biosciences Institute at Ohio State University (MBI), the Mathematics of Information Technology and Complex Systems (MITACS), the Society for Mathematical Biology (SMB), South African Centre for Epidemiological Modelling and Analysis (SACEMA), the US National Science Foundation, the London Mathematical Society, and Makerere University for their generosity in supporting these efforts.

Further details about both the ASI and Workshop in Economic Epidemiology are available at the website: <http://dimacs.rutgers.edu/Workshops/ASIEconEpi/>.

List of ASI Guest Researchers: Nelly Biondi, SACEMA; Nina H. Fefferman, Rutgers University; Patricia Geli, Resources for the Future; Wayne Getz, Berkeley; Abba Gumel, U. of Manitoba; Senelani Dorothy Hove-Musekwa, NUST; Joseph Mugisha, Makerere University; Fred Roberts, DIMACS, Rutgers University; Michael Washington, U.S. Centers for Disease Control

Building Capacity for Meaningful Modeling: A first step

Juliet Pulliam, Steve Bellan, John Hargrove, Brian Williams, Fred Roberts, and Jonathan Dushoff

In May 2009, 41 researchers and students from across Africa and North America met for 9 days at the African Institute for Mathematical Sciences (AIMS) in Muizenburg, South Africa for the first annual Clinic on the Meaningful Modeling of Epidemiological Data. The Clinic brought together mathematicians, statisticians, ecologists, and epidemiologists at different stages in their careers to engage with meaningful questions about infectious disease dynamics by integrating mathematical models with epidemiological data.

The program developed out of the observation that many mathematicians, particularly in Africa, are highly motivated to apply their analytical skills to pressing public health problems but often have trouble bridging the gap between theory and real-world applications. In particular, they lack the skills necessary to analyze data and use it to develop and test their models. The primary focus of the Clinic was accordingly to illustrate techniques for bridging the gap between models and data, using a series of interactive lectures and computer tutorials, moving gradually from canned exercises to independent exploration of novel research ideas.

In many ways, this Clinic was an experiment. The diverse academic backgrounds and life experiences of the participants meant that everyone had unique insights to contribute, and the line between organizers and other participants was intentionally blurred to encourage a collaborative atmosphere. Most of the participants were graduate students, pursuing Master's degrees or doctorates in mathematics or epidemiology, and the Clinic provided an atmosphere for students to develop their own research projects with an emphasis on linking theoretical work to available data sets. Participants were asked to bring posters on current or previous work, and poster sessions during the first days of the Clinic as a time for both social interaction and intellectual engagement.

The organizers aimed to link lectures closely with computer exercises that would help participants internalize the power of a data-driven approach to modeling. Participants began computer practicals on the first day, working through a set of exercises that illustrated how to fit a simple mathematical model of HIV transmission to prevalence data from Uganda. They were asked to think about why the simplest possible model did not satisfactorily explain observed trends and to progressively modify the model, building up an understanding of which assumptions were necessary to produce the observed patterns. Although this first exercise was a worked example, on the second day, students were asked to engage with new data sets not previously explored with the tools they were using, interpret differences between the initial data set they had explored and the new data, and present their work-in-progress to the group.

As the Clinic moved forward, the problems posed became more complex, and eventually participants were presented with active research problems. In particular, participants were given HIV testing data from antenatal clinics in Harare, Zimbabwe and were asked to think creatively about how the age structure of the testing data could be used to infer incidence from prevalence data and about how antenatal clinic data can best be used as a surrogate for prevalence in the whole population.

The approach to unifying models and data also progressed as the Clinic moved forward. Initially, participants were instructed to take a simple approach to model fitting by choosing parameters that produced the best visual fit to data or by using canned optimization functions. Later on, participants received introductory lectures on statistical methods and philosophy, building on their generally strong background in probability theory. Several discussions were also held to introduce participants to the importance of bias in generating data as well as logistical issues associated with acquiring epidemiological data in a public health setting. While emphasizing that the goal of the Clinic was not to provide a thorough training in statistical techniques, students were guided towards freely available resources and encouraged to spend time learning these skills after the Clinic.

While participants spent much of the Clinic engaging with data and models, the greatest challenge for the Clinic's organizers was to achieve an appropriate balance between teaching the technical aspects of data-driven modeling and imparting the philosophy that motivates this type of work. With the latter goal in mind, a substantial amount of time was spent asking participants to simply look at data, describe what they saw, and discuss potential drivers of observed patterns -- based not on formal mathematical models but on their intuition and real-world knowledge. In essence, the goal was to help the participants develop a knack for asking meaningful questions based on their observations and realize that once a meaningful question was formed, a model could become a tool for formulating and testing hypotheses.

Importantly, the Clinic relied entirely on open access software – including the Open Office spreadsheet program Calc and the statistical programming language R – allowing all participants to continue projects started at the workshop. Most of the data used were also from publicly available sources. A major goal of future Clinics will be developing an interactive online research community that will facilitate long-term international collaborations between workshop participants. By posting links to publicly available data and creating forums for their discussion and analysis, this community will also stimulate the development of new collaborations between researchers on open problems in infectious disease dynamics.

Several important lessons were learned during the Clinic. First, many African participants, despite their experience building dynamic disease models, had taken hardly any university level coursework in the life sciences and clearly lacked exposure to fundamental biological concepts. The week-long duration of the Clinic did not allow sufficient time to include an overview of infectious disease biology, but short discussions were held to introduce how biological disciplines such as microbiology, immunology, and clinical epidemiology provide the knowledge underpinning transmission models and why participants should seek future coursework and collaborations in these fields. The two week duration of the 2010 Clinic will allow extra time to be dedicated to these topics and additional focus on development of student research projects.

We also found a lack of familiarity with traditional approaches in epidemiology and biostatistics sometimes prevented participants from choosing the best method to answer a given question. During the 2010 Clinic, participants will be presented with lectures and engaged in discussions regarding basic epidemiological concepts including measurements of disease, bias, study design, and types of epidemiological analyses. The Clinic will emphasize what types of questions require dynamic analyses, which do not, and what are the fundamental differences between the types of insight gained from statistical and dynamical models.

While a learning process for all participants, including the organizers, the interactive pedagogical approach emphasized during the 2009 Clinic was in large part successful. Despite the many changes to be made for future Clinics, participants still stated that the Clinic had changed the way they thought about infectious disease modeling and redirected their careers. Many participants felt that while they still were not adequately trained to perform the caliber of data-driven modeling work they would like to, they now felt knowledgeable enough about where their weaknesses were and in what directions they must head to achieve that quality of research. We anticipate that improvements between 2009 and 2010 will make this year's Clinic an even better opportunity for participants to learn how to engage their quantitative skills in addressing applied public health problems.

The second Clinic on the Meaningful Modeling of Epidemiological Data will be held at AIMS on May 24 – June 4, 2010. For up-to-date information on the program and how to apply, please visit http://lalashan.mcmaster.ca/theobio/mmed.

Acknowledgements

The Clinic was part of an African Biomathematics Initiative organized by the Center for Discrete Mathematics and Theoretical Computer Science (DIMACS) at Rutgers University and the Mathematical Biosciences Center (MBI) at Ohio State University, in collaboration with the South African Centre for Epidemiological Modelling and Analysis (SACEMA) and the African Institute for Mathematical Sciences (AIMS). It was funded primarily by an NSF grant to DIMACS and support from SACEMA and AIMS. The authors thank US National Science Foundation grant 0829652 to Rutgers University for support of the Clinic. JP was supported in part by the Research and Policy in Infectious Disease Dynamics (RAPIDD) Program of the Science and Technology Directorate, Department of Homeland Security, and Fogarty International Center, National Institutes of Health. The Clinic organizers would like to thank the DIMACS, AIMS, and SACEMA staff for logistical support and Gavin Hitchcock for valuable feedback on the Clinic and useful suggestions for future improvement.

Participants in the 2009 Clinic on the Meaningful Modeling of Epidemiological Data, outside the African Institute for Mathematical Sciences in Muizenberg, South Africa. Photo courtesy of Travis Porco.

My Career in Mathematical Biology
A Personal Journey

John Milton

Baby Boomer to Biomathematician

In 1967, at age 17, I arrived at McGill University to face introductory classes that bulged with thousands of Boomers students--classes that were many orders of magnitude larger than my entire home town of Port Williams, Nova Scotia. No matter about the cramped quarters, for us enthusiastic Baby Boomers, it was an exciting time to be in Montreal. The town blossomed during Expo ’67, and McGill was still the magnet that attracted the best students from Canada and the British Commonwealth.

It is said that universities tear down the dreams of boys and then rebuild them as the careers of men. With my high school dream of a marine biology career washed away because of my inability to swim, I found myself enrolled in a Cell and Molecular program in the Department of Botany under the supervision of Ronald Poole and Gordon A. Maclachlan. Brian C. Goodwin (Temporal Organization of Cells) had studied in this department a few years prior, and I was intrigued that someone had actually been able to develop mathematical descriptions of biological systems. McGill already had a long history of biologists studying mathematics, and thus I was able to include lots of math courses in my honors program — the most influential being courses in probability theory and qualitative theory of differential equations.

In 1971, choosing a graduate school was problematic since there were no mathematical biology programs of the type that are widespread today. By chance I met William C. Galley, a biophysical chemist at McGill, who excelled in my two scientific loves, thermodynamics and simple mathematical models that described experimental observations. Thus, I found myself developing excited state spectroscopic techniques to study the movements of solvent molecules on the surface of macromolecules, such as DNA.

It was during this time that I read Robert Rosen’s *Dynamical System Theory in Biology* as part of my qualifying examination on periodic chemical reactions and their role in biology. On completing my PhD in physical chemistry, I was awarded a Japan Society for the Promotion of Science award to work on oxygenases in the laboratory of Osamu Hayaishi at Kyoto University. I was pretty miserable scraping rabbit intestine to purify these enzymes, and hence Professor Hayaishi suggested that I look around campus and see if I could locate another suitable lab. Armed with only a Japanese-English dictionary, I eventually discovered the laboratory of two pioneer Japanese bio-mathematicians, Ei Teramoto and Nanako Shigesada. To my amazement, their laboratory had just completed translating Rosen’s book into Japanese!

I had a wonderful time in Kyoto studying mathematical ecology. However, it was in Japan that I began to understand the downside of the “baby boomer” generation—there were no jobs in academia. In their efforts to cope with high student numbers, universities had greatly increased the size of their faculties. All these new young faculty members effectively eliminated job opportunities for the next generation of graduates, especially in new fields such as mathematical biology.

My rallying cry became that old adage “any port in a storm”. Fortunately, S. G. Mason, a rheologist, had a position available for a post-doc in the Pulp and Paper Institute at McGill University — and you guessed it, I was back to McGill after a two year absence. Professor Mason quickly recognized that I was much more interested in biology than pulp wood and suggested that I work on blood platelets in the lab of his colleague, Mony M. Frojmovic, in the Department of Physiology.

The next 13 years in the Department of Physiology was a great stroke of luck and changed my life in unforeseen ways. First, I met two young professors, Michael C. Mackey and Leon Glass, who were just beginning their collaboration that led to the now famous Mackey-Glass equations. One day I suggested to Mike that there were lots of interesting problems in hematology, and this started a friendship and collaboration that has lasted over thirty years. Second, the Canadian Heart Foundation launched a program to send PhDs back to medical school. I was fortunate to be awarded one of these fellowships and in 1978 began life as a McGill medical student. I then completed a neurology residency and fellowship in epilepsy at the Montreal Neurological Institute. During this time I met a young physics student, Andre Longtin. Together with Mike Mackey, we studied the pupil light reflex — an investigation that was helped by my experience with cinematographic techniques created while studying platelet shape change and by the support of the Hamamatsu Corporation who loaned us a pupillometer.

In 1989, it was time to finally leave McGill. I was recruited to the Department of Neurology at The University of Chicago by Barry G. W. Arnason. There I ran the clinical epilepsy program with my good friends Jean-Paul Spire and V Leo Towle and conducted basic research in computational neuroscience. At the U of C, my research focused on whether it might be possible to develop feedback control devices to treat neurological diseases such as epilepsy. Although I didn't get far on this project, thanks to great graduate students (Jennifer Foss and John D. Hunter), wonderful post-doctoral fellows (Juan Luis Cabrera and Christian D. Eurich), and shared students with Jack D Cowan (Toru Ohira and Trevor Mundel), I was able to greatly expand my research on the dynamics of neural populations including the formation of travelling waves, multistability, and spike timing reliability.

Perhaps not surprisingly, the expressive baby boomer generation had still more to say about my career. Many of my baby boomer patients with chronic neurological disease sorely missed playing golf. The deceptively simple research question was, "Could rehabilitation strategies be improved by making them more fun?" To answer it, I approached the Ladies Professional Golf Association (LPGA) and with the help of Betsy Clark, research director, and Rosey Bartlett, golf professional and 2005 national teacher of the year, was able to complete golf professionals' instructional programs with an emphasis on teaching disabled golfers. This, in turn, led to the creation of a short-lived golf neurology clinic-- an idea that was picked up nearly ten years later by the American Heart/American Stroke Associations in their "Saving Strokes" programs. Even more important, I was intrigued to discover that the LPGA emphasized educational science not simply teaching golf skill. This led me to ask how the nervous system learns a skill and becomes expert in its performance. These questions have formed the basis of my mathematical and experimental research for the last 10 years.

In 2003, Mike Mackey drew my attention to a sabbatical position advertised by Dr. Lisette de Pillis at Harvey Mudd College in southern California. At Mudd, I soon found myself teaching a course on the mathematics of toys and play. One thing led to another, and I became the William R. Kenan, Jr Chair in Computational Neuroscience for all five Claremont Colleges.

In this liberal arts college environment, I find it very rewarding to work with undergraduates and help them appreciate the value of mathematics in biological research. Not only has my students' enthusiasm kept me young, but by teaching them, I have the opportunity to repay the kindness and understanding I received from the many mentors that shaped my Baby Boomer's career.

Students today are dismayed by the effects of the global economic downturn on their future. However, the "booms and busts" of society have always affected the dreams of its youth. Here's my advice: My career happened not by conscious design, but through chance encounters and coincidences shaped by demographic forces. It was true that I was lucky enough to meet key mentors along the way, but more importantly I never turned down an opportunity, always did the best I could, and above all, I had fun!

Selected Publications:

John Milton's publications can be obtained from the website http://faculty.jsd.claremont.edu/jmilton/.

Math Bio Education

Thoughts, trends and topics

Editor's Note:
John Jungck served as Chair of the SMB Education Committee from 1995-2009. The Society wishes to thank John for his service. This article is his tribute to those who helped bring math biology education to where it is today.

But is it mathematics or biology or education?

John R. Jungck

Students in Carlos Castillo-Chavez's Mathematical and Theoretical Biology Institute held at Los Alamos National Laboratory (more recently at Arizona State University) in a workshop led by John R. Jungck (on the far right) on knot theory and DNA with his beloved mathematical manipulatives and engaging students interactively.

How do you thank a community for thirty-three years of collaboration, mutual support, and incredible stimulation? The mentoring tradition of the mathematical biology community has been tremendous throughout my career. While I became interested in mathematical biology in the sixties and had written a thesis on what would now be considered part of bioinformatics, the term was not used then and there was no extended community. Also, while I have much to be thankful for such as the help of the famous University of Wisconsin population geneticist Jim Crow, my greatest debt is for something he didn't do – namely when he couldn't make it as a speaker at the 1976 Gordon Research Conference on Theoretical Biology and Mathematics, I substituted as a speaker on "Random Processes in Evolution" and presented my contribution to the neutralism-selectionism debate. But I was totally unprepared for entering such a supportive community. Myron Hood from Occidential College stayed up half the night upon my arrival helping me revise my talk for better appreciation by mathematicians, Carla Wofsy, in transition from Berkeley to New Mexico, helped me develop the confidence to give up my wet lab and move my career completely to mathematical biology and education, and three senior scholars: Lee Segel, Sol Rubinow, and Frank Stewart welcomed me into the larger community. They shared their zeal for bringing in new people to the field and welcomed a biologist who was interested in collaborating with mathematicians.

After attending an international NATO Advanced Study Institute at the Weizman Institute and the Technion and the Aspen Center for Physics Conference on Sequence Databases, I was asked by Editor Hugo Martinez to review mathematical tools in computational and mathematical molecular biology in the Bulletin of Mathematical Biology which appeared in 1984 and served as a basis for a series of workshops that we have been offering ever since for faculty around the world in bioinformatics and later through our BioQUEST Curriculum Consortium's BEDROCK project: Bioinformatics Education Dissemination: Reaching Out, Connecting, and Knitting-together (http://bioquest.org/bedrock). I don't think that I would have moved in this direction if it hadn't been for the support and encouragement of Hugo, Walter Goad at the Los Alamos National Lab, Rosemarie Swanson at Texas A &M, and John Devereaux at the University of Wisconsin Genetics Computer Group.

The highly international aspect of the mathematical biology community was extremely important to me from the start. My early work in graph theory and molecular biology was initially influenced by Shkurba and Volkenstein in Russia with rich development later with colleagues such as Penny, Lockhart, Hendy, and Steele in New Zealand, my genetic coding work was picked up profitably by Jimenez-Montano in Mexico, and my work in computational geometry was deeply influenced by Honda and Tannemura in Japan, Aurenhammer in Austria, and Gold in Hong Kong – all of which led to long and productive collaborations with Noppadon Khiripet's group at NECTEC in Thailand. Thus, I greatly appreciate the opportunities that these intellectual networks have led to workshops, talks, and research collaborations at over forty countries including Ukraine for a Voronoi celebration, Portugal for art, mathematics, and biology at an art museum, and Brazil for Biomat 2008. This year the International Union of Biological Sciences celebrated the 200th anniversary of Charles Darwin's birth on February 12th in Christchurch, New Zealand and the 150th anniversary of the publication of Charles Darwin's publication of the Origin of Species in Capetown, South Africa this fall.

As I became more involved with the Society for Mathematical Biology, with the encouragement of Lee Segel, then Editor of the Bulletin for Mathematical Biology, Rick Cooper of Trinity University in Texas and I formed a discussion group in 1995 which led to the Society endorsing us to start up the Education Committee again. With the wonderful leadership of SMB presidents, executive committee members, and established scholars like Leah Edelstein-Keshet, Lou Gross, Gerda DeVries, Claudia Neuhauser, etc., the education community within SMB grew substantially. SMB made a commitment that every year's meeting would have a standing symposium and contributed paper session as well as poster possibilities. What became exceedingly rewarding was that the membership of SMB grew by attracting many math bio educators and mathematical biologists who primarily conducted their research with undergraduates as their collaborators. Furthermore, the interest was sustained in meetings outside the USA; for example, symposia and contributed paper sessions in Dresden, Germany, Dundee, Scotland, and both Toronto and Vancouver, Canada were very well attended. The development of prizes for both undergraduate and graduate student posters has helped to attract many more young students to our conferences and has served the NSF UBM community of funded institutions very well.

These involvements led to participation in discussions that led to NRC's publication of *Bio 2010* and HHMI's publication of *Beyond Bio 101*, both of which sounded an alarm of the need for more mathematics in biology education. The MAA hosted our co-sponsored conference that led to the publication *Math & Bio2010: Linking Undergraduate Disciplines* and, on the biology side, AIBS, NESCent, BSCS, and NABT hosted our co-sponsored conference that led to the publication of *Evolutionary Science and Society: Educating a New Generation*. Exciting projects like Claudia Neuhauser's NUMB3R5 COUNT: Numerical Undergraduate Mathematical Biology Education, Anton Weisstein's Biological ESTEEM Project: Excel Simulations and Tools for Exploratory, Experiential Mathematics, Eric Marland's and Rene Salinas's annual TIMBER conference, HHMI's annual quantitative biology education institutes, and MAA's BioSIGMAA have been great developments. Thus, during this past decade, my interests in mathematics, biology, and education have come together and I have benefited greatly from a new generation of kindred spirits. Recently, two articles from our community in mathematics, biology, and education have been accepted for publication in the Bulletin of Mathematical Biology. What lies ahead? I encourage authors to contact me because we are seeking manuscripts for three journals that will be producing special issues on mathematics, biology, and education: cbe Life Sciences Education, Mathematical Modeling of Natural Phenomena, and the International Union of Biological Sciences' Biology International.

Call for Papers for Special Math-Bio Issue

To celebrate progress made toward achieving some of the aspirations announced in the National Research Council's publication, Bio2010, for a more quantitatively rigorous undergraduate curriculum in biology and to lay a stronger foundation for future reform of biology education, CBE—Life Sciences Education (<http://www.lifescied.org/>) will publish a special issue on mathematics in biology education in 2010.

Especially welcome are manuscripts describing the impact of innovations such as NSF-supported undergraduate research programs in mathematical biology with mentors in both biology and mathematics; HHMI-sponsored initiatives in developing quantitative curricular materials for classroom usage; NIH-supported programs at traditional minority-serving institutions; AAAS HBCU-UP programs; new majors in mathematical biology, computational biology, or bioinformatics; and faculty development efforts to promote the use of more mathematics in biology.

Manuscripts submitted in response to this call by Monday March 15th, 2010, will be guaranteed consideration for the special issue. Please contact one of the guest editors for this volume (John R. Jungck, jungck@beloit.edu, and Pat Marsteller, PMARS@learnlink.emory.edu) if you have questions.

The Second International Conference on Mathematical Modeling and Analysis of Populations in Biological Systems

Amina Eladdadi

The Second International Conference on Mathematical Modeling and Analysis of Populations in Biological Systems was held at the University of Alabama in Huntsville (UAH) from October 9-11, 2009. The conference was organized by Professors Jia Li, Jim Cushing and Saber Elaydi, and sponsored by NSF, the Journal of Difference Equations and its Applications, the Journal of Biological Dynamics, and UAH.

The meeting focused on mathematical theory, model analysis and modeling of quantitative data of the temporal dynamics of biological populations. Since the outbreak of the H1N1 virus, mathematical modeling of epidemics has received much attention from the scientific community and more so from the news and the media. A special emphasis at this second conference was on the modeling of epidemics. The conference brought together national and international mathematicians, computer scientists, physicists and biologists interested in mathematical modeling of population dynamics and epidemics. There was a handful of talks and poster presentation on epidemic modeling, of which three talks were on H1N1 outbreak.

The conference program included plenary talks, three sessions of invited talks, and poster presentations. In addition, there was a special session about the NSF programs and funding opportunities related to mathematical and computational biology. There were a total of 96 participants in the conference, of which 5 were plenary speakers, 58 were invited speakers, and 15 were poster presenters. The plenary talks included known mathematicians in the field of population dynamics and epidemics.

Following the opening remarks by President Williams from UAH, the first plenary talk, “Population Persistence without a Compact Attractor,” was delivered by Dr. Horst R. Thieme from Arizona State University. In his talk, Dr. Thieme described and showed how persistence theory gives mathematically rigorous answers to the epidemic modeling questions such as if a disease will drive a host population to extinction and if a disease remains endemic in a population.

The second plenary talk of the day was given by Dr. Hans Heesterbeek from the University of Utrecht. Dr. Heesterbeek presented a detailed method of constructing the next-generation matrix (NGM) for compartmental epidemic systems. He also showed several applications of next-generation matrices for epidemiological systems, particularly the possible insights that can be achieved from sensitivity analysis using the NGM.

The second day of the conference opened with the plenary talk by Dr. Louis Gross, the director of NIMBioS. Dr. Gross introduced the National Institute for Mathematical and Biological Synthesis (NIMBioS) to the audience, and discussed the role that the institute plays in the interface between mathematics and biology. Surprisingly, a good number of the participants (including myself) were not aware of NIMBioS. Dr. Gross also talked about how increased funding in this area by agencies such as the NSF is necessary in order to enhance research across the biological sciences –something we all agreed upon! This created a very lively debate among the attendees.

The fourth plenary talk of the conference by Dr. Jianhong Wu from York University took place in the afternoon. In his talk, Dr. Wu talked about the roles of migratory and wild birds in the highly pathogenic avian influenza (H5N1) transmission dynamics. He introduced the different factors implicated in the spatial spread of H5N1 virus in Asia and presented the results of a few models of seasonal migration linking the local dynamics during migratory stopovers to the larger-scale migratory routes.

The last plenary talk of the conference was given by Dr. Alun Lloyd from North Carolina State University on modeling genetic strategies for controlling mosquito borne diseases, especially malaria and dengue. In his talk, Dr. Lloyd talked about an original method of attack involving the production and release of mosquitoes that have been manipulated or genetically engineered to be less able or even unable, to transmit infection. He also presented the biology of some of the approaches and the accompanying modeling work.

The invited talks' sessions included a wide range of topics on mathematical modeling of population dynamics at various levels, including cellular, molecular, and genetic, and other topics of population biology, epidemiology and ecology. For example, Holly Gaff talked about human monocytic ehrlichiosis (HME), which is tick transmitted disease, with serious consequences in the USA. She presented a deterministic model for HME to study the underlying dynamics of prevalence in tick populations. Baojun Song presented a discrete model to study the role of a migratory bird population in the transmission of the highly pathogenic strain of avian influenza (H5N1). Suzanne Lenhart talked about optimal control of treatments in a cholera model. Abdessamad Tridane introduced mathematical models of the dynamics of killer T cells and the differential expansion of antigen-specific CD8+ cell in the influenza infection. Azmy Ackleh described a discrete-time stage-structured population model which depicts the competition of two similar species. Abdul-Aziz Yakubu presented an extension of the TAC regulated fish population model of Ang et al. to include stock under compensatory and over-compensatory dynamics with and without the Allee effect. Jim Cushing illustrated how the Fundamental Bifurcation Theorem can be extended to Darwinian matrix models and how the basic properties of the bifurcation can be described equivalently by means of the inherent net reproductive number. Hal Smith showed in his talk how Lyapunov exponents can be employed in establishing persistence of discrete and continuous-time finite dimensional dynamical systems. Khalid Boushaba presented a talk on mathematical feasibility for the use of aptamers in chemotherapy and imaging. John Burns talked about sensitivity analysis of cancer models with proliferating and quiescent cells and how these sensitivities can be used to help predict the long term behavior of the model with and without drug treatment.

There were many other equally interesting contributed talks (concurrent sessions that I was not able to attend) that dealt with notably broad topics, including cancer modeling, genetics, and ecology. The talks were consistently excellent and engaged a great deal of discussion among the audience, allowing students, post-docs and junior researchers to interact with reputable researchers in the field of population dynamics.

The conference schedule allowed for many informal discussions over lunch, dinner and during the reception on the second evening of the conference. Between talks, attendees were able to revitalize at coffee and tea breaks, and also to check out the latest in the mathematical biology publications and books that Dr. Torcom Chorbajian showcased during the two and half day-conference.

On behalf of all the attendees, I would like to thank the organizing committee and the staff of the math department at UAH for the excellent organization; even when the power went out for almost 30 minutes during the thunder storm, they made sure that the conference went on with the help of the generators and relying on the laptop batteries!

I would like to acknowledge and thank Prof. Saber Elaydi for inviting me to present my research in this conference, which also allowed me to collaborate with other members of the mathematical biology community.

A detailed description of the conference could be found here: http://brisk.math.uah.edu/~conf/

The meeting went on despite the power outage! Suzanne Lenhart holding the laptop while Abdul-Aziz Yakubu is presenting.

Jim Cushing, Saber Elaydi and Jia Li at the reception.

Positions Available

Postdoc: Cleveland Clinic

An exciting position has become available in the Department of Infectious Diseases / Quantitative Health Sciences, Cleveland Clinic Foundation & Lerner Research Institute, to study the impact of antiretrovirals on the spread of human immunodeficiency virus (HIV) and drug resistance using mathematical and computational models. The successful applicant will hold a Ph.D. in mathematics, physics, engineering, operations research, computer science, or related field. Expertise in advanced programming languages such as C++ and Java is essential. Strong methodological background in stochastic modeling (including Markov modeling, individual-based modeling, and Monte Carlo simulation), dynamical systems, and numerical techniques is required. Excellent communication skills are necessary. Experience in statistical analysis and working knowledge of mathematical, statistical and simulation software are desirable. Please submit your curriculum vitae, a brief statement of research interests and goals and contact information for three references to Ume L. Abbas, MD via email at abbasu@ccf.org.

PhD Studentships: Maths & Stat in Biomedical Problems, Nottingham

The Centre for Mathematical Medicine and Biology invites applications for fully-funded PhD Studentships, starting September 2010. Potential projects involve the application of mathematics and/or statistics to problems in a range of areas, including physiology, tumour growth, regenerative medicine, neuroscience and population health. Students should have, or expect to obtain, a first or upper second class degree in mathematics, statistics or a closely related subject. The studentships available include MRC-funded ones that carry an enhanced stipend and are subject to residence requirements. Informal enquiries may be addressed to Mrs Cathie Shipley (email: cathie.shipley@nottingham.ac.uk). Further details of the projects and application procedure are available at: http://www.maths.nottingham.ac.uk/cmmb/.

Postdoc Positions: Comp / Math Modelling, Univ Western Ontario

Candidates with expertise in (i) Mathematical Biology, specifically biomechanics, disease dynamics or evolutionary theory, or (ii) Condensed Matter Physics, specifically soft and biological matter, and/or multi-scale modelling are invited for several post-doctoral positions in the Department of Applied Mathematics at the University of Western Ontario. These positions are not tied to specific research projects, thus successful candidates will have considerable latitude in their choice of research topic in consultation with their supervisor(s). Potential supervisors for this call are: Rob Corless, Colin Denniston, Mikko Karttunen, Lindi Wahl, Geoff Wild, Pei Yu, Xingfu Zou and Mair Zamir. Candidates must provide a cover letter which explains which of these potential supervisors would be appropriate for the proposed research program. Successful candidates will have completed a Ph.D. degree, and will have an active research program in mathematical modelling. The appointments will be for 1+1 years with flexible starting dates. Salary will be commensurate with experience and qualifications. Applicants should apply via mathjobs.org (position ID: Western-PDF), including a curriculum vitae and a research statement, as well as two or three letters of reference. Applications and letters of reference should be received by February 28, 2010. This competition is open to all qualified candidates, regardless of citizenship.

Postdoctoral Position: Computational Neuroscience & Neuroinformatics

Computational models based on detailed neuroanatomical and electrophysiological data have been used for many years as an aid for understanding of the function of the nervous system. NeuroML is an international, collaborative initiative to develop standards for describing models of neural systems. The NeuroML model specifications facilitate the exchange of complex neural models, allow for greater transparency and accessibility of models, enhance interoperability between simulators and other tools, and support the development of new software and databases. NeuroML is a free and open community effort developed with input from many contributors. We are seeking a postdoctoral researcher to contribute to further development of NeuroML. The position is somewhat flexible and can include NeuroML schema design and implementation, tool development and testing, website development and maintenance, and model database design and implementation. The position also provides opportunities for involvement in computational modeling studies. The postdoc will be located in the computational laboratory of Dr. Sharon Crook (http://math.asu.edu/~crook) at Arizona State University in Tempe, Arizona (http://www.asu.edu). Prior extensive programming experience is required, and experience with XML, website and database development, and computational neuroscience research would be beneficial. The candidate also must be able to demonstrate excellent communication skills and the ability to work as part of a team. Some international travel is required. Locally, the postdoctoral researcher will interact with faculty, students and other postdoctoral researchers in the Center for Adaptive Neural Systems (http://ans.asu.edu) at ASU. ASU has vibrant, interdisciplinary research communities in neuroscience, biomedical informatics, and high-performance computing. Candidates should send a curriculum vitae, a short summary of research experience and interests, and the contact information (name, address, phone number and email) for three references to: Dr. Sharon Crook at sharon.crook@asu.edu.

Postdoc: Center for Biodynamics, Boston University

Postdoctoral position available immediately at Boston University to work with N. Kopell and M. Whittington (Newcastle) on biophysical modeling of rhythms in the auditory cortex. Interested applicants should contact Kopell directly (nk@bu.edu). http://cbd.bu.edu/

Postdoc Position: Mathematical and Computational Immunology, Bar-Ilan

The Computational Immunology Lab of Prof. Ramit Mehr (http://repertoire.os.biu.ac.il/) at Bar-Ilan University, Israel (http://www1.biu.ac.il/) is seeking a Post-Doctoral Trainee in Mathematical and Computational Immunology The Computational Immunology (CIL) in Bar-Ilan University is seeking a recent PhD graduate for a post-doctoral position in the field of Mathematical and Computational Immunology. This is an emerging field bridging theoretical and applied research directions in immunology, currently attracting immense interest within the research community. The position focuses on creating models of interacting populations of cells and molecules in the immune system. The ideal candidate is expected to have expertise in mathematical modeling in biology, preferably in immunology; familiarity with software's such as Matlab and at least basic programming; and excellent English. Job Starting Date is as soon as possible - funding is already in place. Application Deadline: open. Salary: Standard BIU post-doc fellowship. How To Apply: Send CV, LP and statement of interest to: Prof. Ramit Mehr at mehrra@mail.biu.ac.il. Please also provide names of people who will be willing to recommend you - e.g., advisors from previous studies, projects or jobs (please give names + phone numbers and/or email addresses of these).

Postdoc Position: Viral Evolutionary Genetics, University of Utah

The Departments of Mathematics and Biology at the University of Utah are seeking a post-doc to work on the Ecology and Evolution of rhinoviruses, the primary cause of common colds. This two year position will focus on analyzing the evolutionary genetics of both archived and newly collected rhinovirus samples, using mathematical models to link population dynamics, viral biodiversity, immunology and evolution. Experience with genetic data analysis is preferred, but not required. Funding is in place, and the position could begin any time before September 2010, salary competitive based on qualifications and experience. Send a curriculum vitae, a statement of research interests, and contact information for three references to
adler@math.utah.edu Please any questions to Fred Adler at this same address. http://www.biology.utah.edu/adler/ http://www.jsmf.org/grants/d.php?id=2007010

Positions Available (Continued)

Graduate Assistantship Program in Life Sciences - Transdisciplinary Team Science

The Virginia Bioinformatics Institute (VBI) at Virginia Tech, in collaboration with Virginia Tech's Ph.D. program in Genetics, Bioinformatics, and Computational Biology (GBCB), is providing substantial assistantships in support of graduate work in transdisciplinary team science. The Transdisciplinary Team Science Assistantship Program for the Life Sciences was developed for students interested in joining the Virginia Tech GBCB Ph.D. program. With the goal of connecting students with accomplished researchers working in a team science environment, these assistantships cover the costs of the students' first two years in the GBCB program ($29,679 per year) plus tuition and fees. After completion of the first two years of study, students will be supported by a research grant from their selected mentor professor. The program is open to students with bachelor's degrees, while master's students, in particular, are encouraged to apply for the assistantships. For more details, and information, please visit our website at: https://www.vbi.vt.edu/tts/. For more information please contact: Dr. Kristy DiVittorio, Graduate & Post-Graduate Education Program Manager, Email: kdivitto@vbi.vt.edu; Phone: (540) 231-1389

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

Remember to renew your SMB membership for 2010 now!

I am pleased to invite you to join/renew membership in the Society for Mathematical Biology membership for 2010 using our on-line membership process. We are continuing to work with the Botanical Society of America on this so the page is listed through their site. As a reminder, here is how it works.

Go to: https://payments.botany.org/joinsmb/index.php
To renew: If you used the on-line system previously, choose "Renew your membership with the Society" and then simply fill in your username and password. There is the "Forgot your login details" if you can't remember your password. If you have not used the on-line system, you may still be in the system if have been a SMB member in the past and you provided us with your email address. Try this first, simply fill in your email in the "Forgot your login details" section and push "Send reset details". If we have your email in the database, this will send you an automatically generated email with a link to login. You will be prompted to change your password and led through the renewal process. If your email is not in the database, please follow the join for the first time option.

To join for the very first time: Select this button, continue, and you will be led through the process.

You can pay on-line using a credit card, or you can opt to send a check by mail. We encourage you to use the on-line process either way as it will allow you to fill in your address accurately, specify interests and other options, and will expedite the membership process.

Please let me know if you have any troubles. One quick troubleshooting trick to try is to clear your internet browser cache if you get an error and then try again. Also, if you happen to enter an incorrect expiration date for your credit card, you will need to wait at least fifteen minutes to prevent the duplicate charges prevention system from causing you problems.

Thanks,
Holly Gaff (hgaff@odu.edu)