Society for Mathematical Biology

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Newsletter
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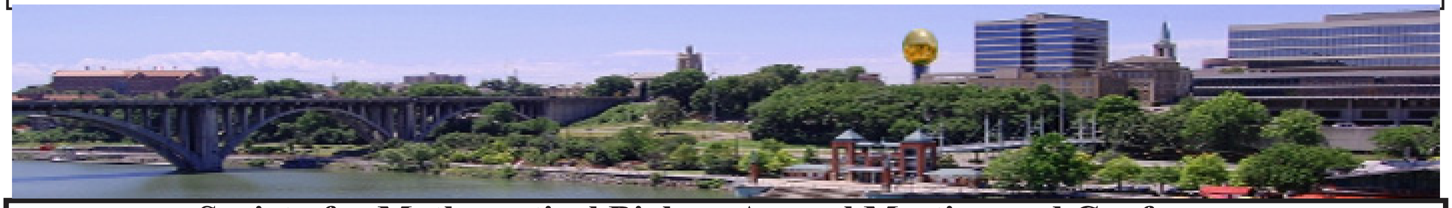
Inside this Issue



Society for Mathematical Biology Annual Meeting and Conference

July 26-28, 2012
Location: Knoxville Convention Center
http://nimbios.org/SMB2012/
Mathematics and Biology: Interdisciplinary Connections and Living Systems

Math Biology at TEDMED

This month's featured Future of Math Biology student, Jacob Scott, presented a talk at the 2012 TEDMED conference. His talk was entitled "Can we stop the imaginectomies?" He used the opportunity to tackle the issue that he sees in biomedical science: that we have too many deeply siloed specialists, and no one capable of connecting the dots. He called for a sea change in medical education to fill this need - a "specialist generalist" if you will. The video of the talk should be out on their website soon. www.tedmed.com. TEDMED is a conference of about 3000 people from across the biomedical industry getting together to talk about big ideas. See page 16, for the full Future of Math Biology interview with Jacob.

Dear SMB Members,

Planning for our Annual Meeting and Conference, July 25-28, hosted by the National Institute for Mathematical and Biological Synthesis (NIMBioS) in Knoxville, is well underway. I am very excited by the slate of plenary speakers, who will present on topics that include protein networks, gene regulation, epidemiology, immunology, evolutionary biology, and population and community ecology. With twenty-five mini-symposia, the return of our popular mentoring program for junior researchers, and a poster session, the meeting promises to be a lively exchange of scientific ideas. Registration for the conference is now open. Also, there is still time (until June 15) to submit an abstract for the poster presentation. You can find details at the conference website: nimbios.org/SMB2012.

I really enjoyed reading the articles contained in this newsletter, and I hope you will too. I particularly enjoyed reports of insightful interviews with two remarkable researchers, and former SMB President Avner Friedman's reflection on his career in mathematical biology. These articles represent inspiring examples of the possibilities in our field. The newsletter also contains reports of past scientific events and announcements of future ones, as well as an interesting article on how to build a supportive student research network.

I wish you a productive summer, and look forward to meeting many of you in Knoxville.

Best wishes,

Gerda de Vries

MBI Emphasis Year on Mathematical Neuroscience, July 2012 – June 2013, www.mbi.osu.edu/2012/scientific2012.html

2012 MBI Undergraduate Summer Research Program, May 29 –August 17, 2012, www.mbi.osu.edu/eduprograms/undergrad2012.html

Joint 2012 MBI-NIMBioS-CAMBAM Summer Graduate Workshop Stochastics Applied to Biological Systems, June 18-29, 2012, www.mbi.osu.edu/eduprograms/graduate2012.html

MBI BioSciences Problem-Solving Workshop, July 16-20, 2012, www.mbi.osu.edu/2012/stgrdescription.html

2012 Workshop for Young Researchers in Mathematical Biology, August 27-30, 2012, www.mbi.osu.edu/wyrmb/wyrmb2012.html

Math Biology: Looking into the Future (MBI's 10th Anniversary meeting), September 19-21, 2012, www.mbi.osu.edu/2012/10thdescription.html

Models and Methods in Ecology, Epidemiology and Public Health: Canada Thematic Year 2013

The planet on which we live and the challenges that we face on this planet become increasingly complex as ecological, economic and social systems are large intertwined networks governed by dynamic processes and feedback loops. Mathematical models are indispensable in understanding and managing such systems since they provide insight into governing processes; they help predict future behavior; and they allow for risk-free evaluation of possible interventions.

The goal of this thematic program is to tackle pressing and emerging challenges in population and ecosystem health, including understanding and controlling major transmissible diseases, optimizing and monitoring vaccination, predicting the impacts of climate change on invasive species, protecting biodiversity and managing ecosystems sustainably

This program will bring together the international community of researchers who work on these topics in a series of 10 workshops to foster exchange and stimulate cross-disciplinary research between all scientific areas involved, to discuss perspectives and directions for future advances in the field, including new models and methods and to foster tighter links between the research community, government agencies and policy makers. Three summer schools will introduce graduate students and postdoctoral fellows to the art of modeling living systems and to the latest tools and techniques to analyze these models. The table below lists all activities.

The activities of the program are distributed across all of Canada, and financial support is provided by all mathematical research institutes in Canada: Atlantic Association for research in the mathematical sciences (AARMS); Banff International Research Station (BIRS); Centre de Recherches Mathématiques in Montréal (CRM); Fields Institute in Toronto (Fields); Pacific Institute for the Mathematical Sciences (PIMS).

The program is organized by Jacques Bélair (Montréal), Mark Lewis (Alberta), Frithjof Lutscher (coordinator - Ottawa), Jianhong Wu (York) and James Watmough (New Brunswick). More information will soon be available online (www.crm.math.ca/M2E2). Please contact the workshop organizers or Frithjof Lutscher (flutsche@uottawa.ca) if you have questions. The program is part of the global thematic year “Mathematics of Planet Earth 2013” (www.mpe2013.org).

Workshops planned:
1. Models and methods in ecology and epidemiology, J. Bélair and J. Wu, CRM, February 2013
2. Establishing the scientific foundation for quantitative public health decision-making: Linking surveillance, disease modeling and simulation, D. Buckeridge, C. Dean and J. Wu, Fields, March 2013
3. Climate Change and Ecology of Vector-borne Diseases, N. Ogden and H. Zhu, Fields, July 5-8, 2013
4. Mathematical Modeling of Indigenous Populations Health, S. Moghadas, J. Wu, M. Li and B. Sanders, BIRS, September 28-29, 2013
5. Major and Neglected Diseases in Africa, J. Heffernan and J. Arino, CRM Ottawa, May 5-9, 2013
6. Disease Dynamics 2012: Immunization, a true multi-scale problem, J. M. Conway, D. Coombs and R. Meza, PIMS Vancouver, January 17-19, 2013
7. Biodiversity in a changing world, F. Guichard and F. Lutscher, CRM CAMBAM, July 22-26, 2013
8. Sustainability of aquatic ecosystems networks, F. Lutscher and J. Watmough, AARMS Fredericton October 2013
9. Impact of climate change on biological invasions and population distributions, M. Lewis, H. Berestycki, A. Hastings, P. Molnar, BIRS, May 12-17, 2013
10. Current Challenges for Mathematical Modelling of Cyclic Populations, R. Tyson, J. Sherratt and H. Wang, BIRS, November 10-15, 2013
11. Summer school: Mathematics of infectious diseases, J. Wu, FIELDS/CDM, May 19-27, 2013
12. Summer school: Mathematics behind biological invasions, M. Lewis, PIMS/IGTC Alberta, Spring 2013
13. AARMS summer school: Dynamical Systems and Mathematical Biology, X.-Q. Zhao, AARMS/MUN, July 2013

NEW COLUMN: Research Interviews

Math Biology in Industry: Robert Phair

Robert Phair talks with Santiago Schnell about mathematical biology in industry and the challenges scientists face.

What inspired you to become a mathematical biologist? As far back as high school I knew that I wanted to combine mathematics and biology. At MIT, I concluded that the best way to do this was to study electrical engineering. I was inspired by Don Howell who taught me high school chemistry and biology, by Les DeGroot at MIT, by Mihajlo Mesarovic's book *Systems Theory and Biology*, by Richard Jones at Northwestern, Mones Berman at the NIH, and John Jacquez and Harvey Sparks during my PhD in physiology at Michigan. Actually, I'm much more an engineer than a mathematician; I like my numbers to have three significant digits and physical units. John Jacquez once told a mutual friend that I was a good applied modeler, but not much of a theoretician. I took this as high praise.

Why did you decide to build your own company and work in industry? There are two answers to this question. The first is that I think it's impossible to solve the remaining major diseases without teamwork. Working as independent consultants has allowed our company, Integrative Bioinformatics, Inc., to become the modeling team for multiple world-class academic laboratories. In some sense, I never left academia; I just have a new business model. Thoru Peterson, a distinguished cell biologist, says I'm a freelance scientist. The second reason is access to professional software developers. Steve Jobs said that the dynamic range between the average software engineer and the best software engineer is at least factor of 25. In our view, scientific teams need PI-level expertise at every position. Professional software engineers just build better systems.

What are you working on? We're working on computational biology that spans the scale from molecular cell biology to physiology and disease. Much of systems biology is purely statistical, yet most experimental biologists think mechanistically. Our software tool, ProcessDB, is intended to support teams of experimentalists and modelers who share a common goal – mechanistic understanding of some particular disease. Disease modeling is beginning to gain a foothold in the pharmaceutical industry and we plan to be there when decision makers finally realize that modeling is the only way to make complex hypotheses testable.

In what ways has your research made an impact? From my perspective, our impact has been to convince just a few very highly respected experimental laboratories that modeling is a powerful tool that can answer really hard biological questions. Like many of our SMB colleagues, we think modeling must become a mainstream tool in molecular biology, cell biology, biochemistry, and physiology, and in our experience the best way to advance this goal is one investigator at a time.

What is the state of mathematical biology in industry? Modeling is well established in the pharmaceutical industry, but not in the sense of mechanistic disease modeling. The statistical and pattern-recognition approaches that you see in "-omics" work are widely used, but dynamic ODE-based modeling is largely restricted to pharmacokinetics and pharmacodynamics. There's more and more talk about disease modeling, and some companies have active programs in this area. This is, in my view, where the opportunities lie.

What's the next big challenge? We haven't yet convinced the mainstream of biomedical research that modeling is more than "nice to have." The 21st century should be about integrative biology – putting the reductionist pieces together. Every advanced civilization supports what Jacob Bronowski called the "ascent of humankind," but the level of funding provided for biomedical research is orders of magnitude greater than funding for the arts. In return for this investment, the public expects diseases to become treatable or even curable. The natural challenge for a computational biologist is the same as it is for all of biomedical research – show us how to improve the quality of life for us and our kids.

What would your message to a young and aspiring mathematical biologist be? Aim to speak the language of experimental biology as well as an expert experimentalist. For our company, I tell job applicants they have to be able to hold their own in a scientific conversation with a world-class experimental biologist. One of the best ways to learn this is to do experiments yourself. Join an appropriate professional society devoted to experimental biology; go to their annual meetings and spend all your time at posters asking questions. Form a collaborative team with an experimental biologist. As a team, you can write twice as many grant proposals as you would alone. Prove the value of modeling to that collaborator, then, together, solve a really important problem.

If you weren't a scientist, what would you be? A mapmaker. My dad inspired me with his love of maps; on a summer beach he'd draw several highways coming together and challenge me to draw a successful and efficient interchange. A great map conveys a huge amount of information and is, at the same time, a work of art. Perhaps this is why diagrams are the primary user interface for our ProcessDB software.

If you have any spare time, what do you do when you're not working? I meditate. I read philosophy, history of science, novels and mysteries. When I was a kid, my hero was Sherlock Holmes. In the winter, though, reading takes a back seat to snowboarding. Meditators train to stay in the present and riding a snowboard is, for me, the very best way to stay in the moment while surrounded by the grandeur of nature.

NIMBioS
National Institute for Mathematical
and Biological Synthesis

Curriculum Development Faculty Workshop, Jan. 12-14, 2012. NIMBioS, along with the University of Tennessee and the SCALE-IT, co-hosted a workshop to assist faculty in developing interdisciplinary computational biology courses that engage students and provide practical, hands-on experience. http://bioquest.org/scaleit2012/

NIMBioS Investigative Workshop: Modeling Social Complexity, Feb. 6-8, 2012. The great majority of humans today live in complex societies, which can exist only on a basis of extensive cooperation among large numbers of individuals. This workshop, jointly sponsored by NIMBioS and the National Evolutionary Synthesis Center, brought together a diverse group of modelers with anthropologists, archaeologists, and other social scientists to synthesize the state of knowledge in formal models of the evolution of social complexity. www.nimbios.org/workshops/WS_social_complexity

NIMBioS Investigative Workshop: Disturbance Regimes and Climate-Carbon Feedback, Feb. 13-15. This investigative workshop brought together disturbance ecologists, biogeochemists, mathematicians, statisticians, and computer scientists to discuss various issues related to integration of disturbance ecology with biogeochemistry using mathematical and statistical approaches. The goal was to develop mathematical models that integrate disturbance ecology with biogeochemistry so as to predict future changes in disturbance regimes and their influences on carbon-climate feedback. www.nimbios.org/workshops/WS_carbon

Requests for Support. September 1 is the deadline for submitting proposals for new scientific and educational activities at NIMBioS. 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. Application information is also available for Postdoctoral Fellows, Sabbaticals and Short-term Visitors. www.nimbios.org/research/

Modern Math Workshop The eight NSF math institutes and NIMBioS will offer three concurrent sessions immediately preceding the Society for Advancement of Chicanos and Native Americans in Science (SACNAS) annual meeting, Oct. 11-14, 2012, in Seattle, WA. The sessions – one for graduate students and recent PhDs, and two for undergraduate students – aim to invigorate the research careers of minority mathematicians and mathematics faculty at minority-serving institutions. Application deadline: July 1, 2012. www.nimbios.org/education/modern_math_ws.

Undergraduate Research Conference at the Interface of Biology and Mathematics The fourth annual undergraduate research conference to be held Nov. 17-18, 2012, in Knoxville, TN, provides opportunities for undergraduates to present their research at the interface of biology and mathematics. Student talks and posters are featured as well as a panel discussion on career opportunities. Faculty and students are invited to attend. Middle and high school teachers are also invited to attend. www.nimbios.org/education/undergrad_conf2012

Systems Approaches to Drug Discovery and Development in Oncology

Amina Eladdadi

The workshop on systems approaches to drug discovery and development in oncology was held at the American Institute of Mathematics (AIM), at Palo Alto, California on February 6-10, 2012. It was organized by Gianne Derks from the University of Surrey, Bart Hendriks from Merrimack Pharmaceuticals, Hien Tran from North Carolina State University, and Michael Zager from Pfizer. The workshop was sponsored by AIM and NSF.

The workshop brought together twenty-seven leading experts and junior scientists in applied mathematics, as well as experimental, computational and systems biology from pharmaceutical industry and academia. All with a strong interest in the application of systems biology approaches to target identification and validation in drug discovery in oncology. The purpose of this workshop was three fold: (1) to initiate a forum for the participants working on various aspect of cancer to exchange ideas and share their perspectives on current progress and problems in cancer drug discovery and development; (2) to provide a platform for academia and pharmaceutical researchers to explore opportunities for collaboration across disciplinary boundaries, and to propose and solve problems in cancer drug discovery and development, and (3) to identify and discuss key areas in modeling, computing, laboratory experimentation, and clinical diagnosis that are critical in the success of cancer drug discovery and development.

The organizers put together a great program for the week, which included two lectures in the morning followed by a panel discussion, breakout discussion sessions, then general discussion sessions for conclusions and recommendations. Speakers at the workshop did a wonderful job in providing the participants with the background material leading up to specific problems. These lectures covered topics in signaling networks, mathematical modeling of tumor growth and immune system, sensitivity analysis of signaling pathways, and mathematical modeling techniques such as filtering and control methods. Each day, the participants formed four parallel working sessions to discuss problems that arose during the lectures and the panel discussion.

Brian Conrey, executive director of AIM kicked off the workshop by welcoming the participants. He gave a short historical introduction on AIM, and talked about the research activities that take place at AIM. He also introduced the friendly and hospitable AIM staff that helped with the organization of the workshop, to the participants.

Mike Zager welcomed the participants and thanked them for taking precious workweek time to attend the workshop. He gave a brief summary of the events that led up to this workshop and outlined the plan for the whole week. Zager reiterated the main goals of the meeting, which were: to facilitate discussion between experimentalists, modelers, and computationalists, and between industrial and academic researchers; to identify sources of the challenges in systems biology in oncology; and to offer some solutions to the suggested problems. He then stressed that the success of this workshop depended on full participation from the audience by leading topic-focused discussions, and offering recommendations.

The focus of the first day was on the collective understanding of the state of the field of systems biology in drug discovery and development in oncology. Zager opened the lecture series of the workshop with his presentation on “Why Are We Here?” He talked about the motivation behind organizing this workshop, and shared the organizers’ vision for the meeting with the participants. Zager discussed the challenges facing the pharmaceutical companies in their pursuit to bring effective new drugs to market. He also added that the need for collaboration between academics and pharmaceutical industries in systems approaches to cancer drug discovery and development is greater than ever, and how this partnership could hold the key to enhancing drug discovery and development for cancer. Zager highlighted that there are opportunities for

Lisette de Pillis presenting her talk

Mary Spilker answering participants' questions

partnerships and consortia between pharmaceutical industry and academia, and that collectively all the parties would bring in their own expertise and resources into dealing with the challenges of drug discovery and development in oncology. Points raised in discussion following Zager's lecture were mainly about sharing data on model parameter and how to break the hurdle of confidentiality, which impedes the collaboration between academia and pharmaceutical industry. These questions led to the first round table of the workshop "Ask the Experts," where industrial researchers fielded questions from the participants about the drug discovery and development process and the main challenges drug companies face.

The second lecture was given by Matt Onsum from Merrimack Pharmaceuticals, " Math Bends to Biology: A Perspective of Systems Biology in Drug Discovery in Oncology." Onsum talked about how Merrimack uses mathematical models of cancer signaling pathways to design novel therapeutics, identify predictive biomarkers, and guide clinical development plans. He also discussed how these mathematical models are used to assess other targeted oncology drugs and determine which of these drugs should be combined with their therapies. Onsum presented the case from of the MM-121, a bi-specific antibody against ErbB3 that uses an ErbB2 targeting arm to enhance avidity and inhibitor potency.

Halut Resat from Pacific Northwest National Laboratories gave the third lecture of the workshop on "Computational Analysis of Cell Signaling." In this presentation, Resat presented an overview of many aspects of HER signaling network, and explained how the body of knowledge on HER signaling has been constructed from in vitro studies that used different cell lines and treatment conditions. He also described how the conceptual model for HER receptor mediated signaling in HME cells models provided the starting network topology for detailed mechanistic models. In his elaborate presentation, Resat pointed out that the lack of consistent and reliable, quantitative data for parameter estimation was a major hurdle in mathematical model building efforts. He also stated how mining kinetic parameters out of the experimental data could be difficult and not always straightforward. The discussion surrounding to Resat's presentation focused on the use of multiple cell lines to derive kinetic parameters, and their estimates. This resulted in a topic of discussion for one of the afternoon's breakout sessions.

Jason Haugh, from North Carolina State University, presented a lecture on "Signaling transduction network: where and when to go from here." He talked about modeling the integration of biochemical and biophysical processes across multiple scales of abstraction, and the challenges of going from molecular structure and function to protein activation and localization of the state, to biochemical signaling pathways, to cell behavior and function, to integrated tissue-level response. Jason also highlighted some of the benefits of mathematical modeling such as quantifying contributions of multiple pathways in dynamic systems, and the magnitude and mechanism of negative feedback, and the power of predicting and evaluating differences between normal and transformed networks. The discussion during Haugh's presentation focused on linking the signaling network models to tumor growth, and the multi-scale modeling from pathway to cell to whole cell tissue. This resulted in a further discussion at one of the afternoon's breakout sessions.

Mary Spilker from Pfizer talked about "Modeling Tumor Growth to Assess Exposure-Response Relationships." Her lecture centered on the question: "Are preclinical experimental models for oncology predictive of human response?" The answer is that we do not currently know. One (perhaps the only feasible) way to address this question is through a precompetitive consortium between industry, academia, and the NIH to run definitive studies to begin chipping away at the answer.

Ami Radunskaya from Pomona College presented a lecture on "Mathematical Models of Tumor Growth and Immune Response". Radunskaya started her presentation with a brief introduction on how she became interested in tumor modeling, and then gave a "big tour", as she put it, on different mathematical models that describe tumor growth in tissue, the immune response, and the administration of different therapies. Radunskaya also talked about the complexity of the immune system and the spatial heterogeneity of human tissue, and the challenges that they bring to mathematical models. This includes modeling behavior over vastly different time scales, fitting large sets of dependent parameters to data, incorporating delays into the model, and, optimization in high-dimensional spaces. She also explained how tumor cells are sensitive to their microenvironment, and briefly talked about cancer vaccines.

Lisette de Pillis from Harvey Mudd College gave an overview on "Modeling Cancer Growth and Immunological Interactions." de Pillis used the question, "Why might a tumor grow when it is treated, and shrink when it is not?" as a motivation for her lecture, referring to the challenge of the response of the immune system to a tumor. She gave examples of the immunotherapies alone and in combination with chemotherapy treatments and discussed how the regulatory T-cells affect the renal carcinoma treatment with sunitinib.

Hien Tran from North Carolina State University presented "Modeling Techniques for Complex Biological Systems Sensitivity, Identifiability, Filtering and Optimal Control." Tran gave a nice introduction using simple mathematical models for the concentration of a drug in a biological system and explained the issue with the simple model. That is, the effect of certain parameters on the measured output may be "linearly" dependent. He used this model to introduce the concepts of identifiability and sensitivity. In addition, Tran outlined the Kalman filter-based estimation and some control techniques. The discussion following Tran's lectures led to the topic of "mathematical tools for model verification and validation", which generated a lively debate on parameters estimates tools.

The highlight of this workshop was the breakout sessions after the lectures. Discussion topics varied from day to day, and followed the trend of the day's lectures. For example, in the second day, the focus of the breakout sessions was limited to four issues in order to guide the discussion: academic-industrial collaboration, modeling complexity, uncertainty in model structure, and parameter estimation. Each topic came with its own set of questions. Participants formed groups according to their common interest in these topics. Through a series of informal presentations and elaborate discussions, these interactive parallel working sessions focused on finding ways/techniques/methods to answer the open questions proposed by participants. There was plenty of time devoted to the parallel breakout sessions every day. All participants actively engaged in cross-disciplinary discussions on various aspects of systems approaches to drug discovery and development in oncology. They were very enthusiastic to learn about current experimental, clinical and computational techniques in the field of systems biology. Additionally, they spiritedly contributed their expertise to the breakout discussions. At the end of the working sessions, participants held a general discussion panel for summaries, conclusions and recommendations. Certain recommendations were made as a result of the discussions. These included the needs of interdisciplinary collaborations between the academics and the pharmaceutical industry, and the need to identify models and methods for enhancing drug discovery and development for cancer amongst others.

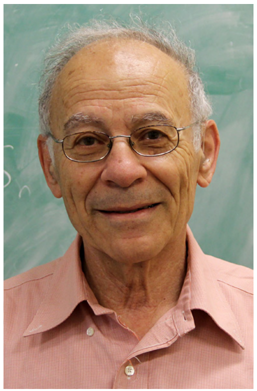
In summary, the workshop on systems approaches to drug discovery and development in oncology was very unique in a sense that it allowed participants to suggest open problems and questions in cancer drug discovery and development, and be able to provide answers and recommendations. The workshop was very stimulating and engaging with a lot of opportunities of interactions. It has provided a great and informal forum for academics and pharmaceutical researchers to discuss their work, encourage collaboration and promote a sense of community in this very active, and growing area of systems biology applied to drug discovery and development in oncology.

Finally, on behalf of all the participants, I would like to thank the organizers for their hard and splendid work of organizing such a great and stimulating workshop. We sincerely thank the staff of AIM for their kindness and hospitality. We also acknowledge the financial support from NSF and AIM. See www.aimath.org.

Workshop participants in front of AIM building

My Career in Mathematical Biology

Avner Friedman



I began my academic career as a theorem proving mathematician. For the next 30 years I have worked in the field of partial differential equations with some diversions into stochastic differential equations and control theory, but had little contact with engineers and physical scientists. Then, in 1985, I was invited from Northwestern University to Purdue University to build a center for applied mathematics. This was when I first moved from my "comfort zone" of pure mathematics to new zones where one first raises a scientific question and only then tries to develop whatever mathematical models and mathematical ideas that will address that question. I began to talk to engineers, and discovered for the first time the excitement of doing interdisciplinary research.

Two years later I assumed the directorship of the Institute for Mathematics and its Applications (IMA) at the University of Minnesota. Here again I had the opportunity to learn about many scientific disciplines which mathematics can advance as well as benefit from. In particular, we ran several programs in mathematical biology: cardiac rhythm and the role of calcium, medical imaging, genomics/proteomics, and statistics in the health sciences. I became convinced that great opportunities are awaiting for mathematicians interfacing with biologists.

So when the NSF, in 2000, solicited proposals for new mathematical institutes, I saw my calling in the creation of a mathematical institute that will build bridges to biology. In 2001 I moved to The Ohio State University, where we developed a proposal for a Mathematical Biosciences Institute. When the proposal was funded and I became the director of the MBI, I immersed myself in learning biology. I began to read books and book chapters (several times), talk to biologists, and sit down with postdocs to work on building mathematical models that can predict experimental results. This has been an exciting life changing experience.

Although it does take time and effort for a mathematically educated researcher to delve into biology to the extent that he/she can then work with biologists on joint projects, the rewards are tremendous. You can easily identify interesting questions that are highly motivated, and some of them may even lead to new mathematics, even pure mathematics. Choosing "good" problems is an acquired skill. I have been working on projects that deal with cancer and cancer therapy, wound healing, and immune response to infection. Moving into mathematical biology has been a most rewarding and enriching journey in my later life, and I am still going.

Selected Publications

1. (with J.J.L. Velazquez) A free boundary problem associated with crystallization of polymers in a temperature field, Indiana Univ. Math. J., Vol. 50 (2001), 1609-1649.
2. (with F. Reitich) Quasi-static motion of a capillary drop, II: the three-dimensional case, J. Diff. Eqs., Vol. 186 (2002), 509-557.
3. (with M.A. Fontelos) Symmetry-breaking bifurcations of free boundary problems in three dimensions, Asymptotic Analysis, Vol. 35 (2003), 187-206.
4. (with X. Chen) A free boundary problem for an elliptic-hyperbolic system: An application to tumor growth, SIAM J. Math. Analysis, Vol. 35 (2003), 974-986.
5. (with B. Hu) Bifurcation from stability to instability for a free boundary problem arising in a tumor model, Archive Rat. Mech. & Anal, 180 (2006), 293-330.
6. A free boundary problem for a coupled system of elliptic, hyperbolic, and Stokes equations modeling tumor growth, Interface and Free Boundaries, Vol. 8 (2006), 247-261.
7. (with B. Hu) Uniform convergence for approximate traveling waves in linear reaction-hyperbolic system, Indiana Univ. Math. J., Vol. 56 (2007), 2133-2158.
8. (with J. Day and L. Schlesinger) Modeling the immune rheostat of macrophages in the lung in response to infection, PNAS, Vol. 106 (2009), 11246-11251.
9. (with C. Xue and C. Sen) A Mathematical model of ischemic cutaneous wounds, PNAS, Vol 106 (2009) 16782-16787.
10. (with H. Jain, S. Clinton, A. Bhinder) Modeling mutation acquisition in prostate cancer undergoing androgen ablation therapy, PNAS, Vol. 108 (2011), 19701-19706.

CAMBAM – Community building in Applied Mathematics for Bioscience And Medicine

Lennart Hilbert, Morgan Craig, Thomas Quail, Frédéric Simard

A quick comparison of this piece's title and our affiliation indicates CAMBAM both as a young research centre in Canada and a sprouting community. CAMBAM – the Centre – is an interuniversity, interdisciplinary research network for the application of mathematics to address challenges in bioscience and medicine through partnership with industry, government and other stakeholders in society. We established the CAMBAM student chapter a little over one year ago to foster the community aspect. Initially two, then three, now four started to actively build a student community inside CAMBAM. Since our debut, we have a surprising resonance, have built a great momentum throughout the year, and have gained a couple of insights about starting and running a student chapter in CAMBAM's specific environment. We would like to share these insights, hoping that they can serve as inspiration for other student initiatives and as a reflection on how to improve interdisciplinary research through student organization.

One of CAMBAM's aims as a research center is to bridge the gap between academe and industry, governance, and communities. With this in mind, we realized the following general objectives for building a student community: (I) Give students opportunities to connect, forming a vital and powerful community that can effectively respond to requests made to CAMBAM's various quantitative skills inside and outside of our network. (II) Use modern "marketing" methods to allow shareholders, potential partners, and future students an insider perspective on CAMBAM.

Before doing any work on the ground, the two initial organizers (TQ and LH) identified a few strategic points that we believe could, in general, apply to (potential) initiatives in other interdisciplinary centers: (1) As we do this outside of our own research and studies, our time is limited. While the student initiative has a small allowance, finances are nonetheless tight. (2) We had the names of CAMBAM's Principal Investigators (PIs); however, we needed to make a contact list from scratch as no student contact list or student database existed. (3) Almost all CAMBAM research groups are situated in Montréal. However, integrating students from the different departments of McGill University, Concordia University, l'Université de Québec à Montréal, and l'Université de Montréal poses a major infrastructural challenge. (4) In our view, if we wanted to be relevant, we needed to offer something new, something that matters to a student in CAMBAM!

Here are our answers to these strategic points: (1&2) Limitations in time and money forced us to travel light and cheap, and to integrate our community work with the rest of our lives in an enjoyable way. We integrated new teamwork tools (Dropbox, Trello) in addition to e-mail. Team meetings take place in labs, cafés, and (unsurprisingly) bars. Google groups and Facebook were indispensable for communicating with the CAMBAM community through a mailing list, discussion forums, and for general member management. Finally, for outside marketing, the McGill IT did an outstanding job giving us a super-flexible Wordpress blog. (3) To unite the disparate parts of CAMBAM – not only on paper but in reality – we realized we actually had to bring the CAMBAM community right to the different geographical locations of CAMBAM. We made a point of holding events located in the home department of the speaker. It was interesting to see new laboratories and work environments, and, more importantly, it further exposed the student chapter to CAMBAM students. Also, we were proactive in terms of making contacts and turning those contacts into active participants. Fostering other students' participation allows them to become multipliers who look out for potential new students and communicate events to their respective research environments. Some even became fully active organizers (FS and MC) bringing large doses of fun, new ideas and drive to our initiative. At the risk of pointing out the obvious – this approach also sets all the parameters for a snowball effect.

Perhaps the most significant decision was to frankly address point (4). We intentionally eschewed the regular seminar series format – seminars have their place in academia, but there are enough of them. They also do not really support the growth of connections between people in the audience – most of the time, there is one person speaking, and with luck, the two to five usual suspects get a word in. An important question we ask ourselves each time we host an event is "Will it allow participants to connect based on their research interests?" To address this point, we decided on different event formats. At our challenge seminars, speakers bring difficult data sets, modeling challenges or project ideas to discuss. After an initial period of 20-30 minutes, the audience enters a moderated discussion with the speaker, giving comments, suggestions or asking "the important questions". Method sessions allow sharing of mathematical or computational methods amongst CAMBAM students. We've also implemented on-site visits, in the spirit of "field trips", in which we visit laboratories that use quantitative methods for biomedical research, allowing participants to explore new environments for the application of quantitative methods and have a great group experience. "Interaction" is our guiding principle, down to the details: we book rooms for an extra 30 minutes, which allows people to chat and sketch ideas on the whiteboard following the session. We also incorporate a lunch break into our events so that people have the chance to discuss over pizza and/or coffee. We extensively prepare and moderate many of our sessions – the moderator plays a particularly important role during the challenge seminar format, encouraging everyone to avoid slipping into the standard seminar format that we have internalized during years of careful academic schooling.

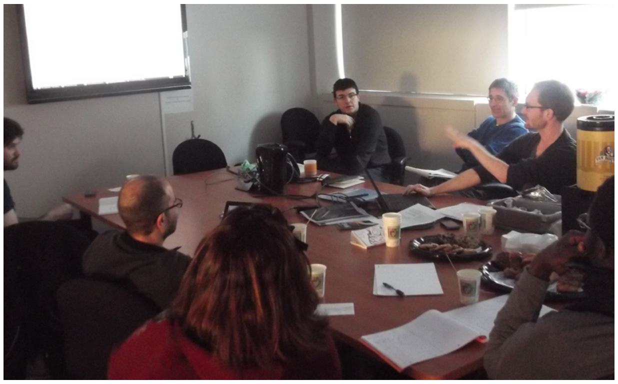
One last strategic decision suggested by CAMBAM's founding director Michael C. Mackey: No faculty allowed! The resulting change of atmosphere from formal to colloquial is hard to believe – time and time again.

So, what have we accomplished since March 2011? 5 Challenge seminars, 5 method sessions, 3 whole day events, two of which were on-site visits (Montreal Clinical Research Institute and Montreal Laboratory for Ultrasonography and Biorheology), and 1 student session with a guest from industry. After a recent competition for CAMBAM student funding, a conservative estimate of the number of currently active members is around 30, all contacts number around 60. Students from all levels of study – from Undergraduates to PostDocs – participate.

A note to PIs: while we are experiencing great moral and material support from CAMBAM's directors, small but crucial contributions from PIs often make a difference. Relaying e-mails to students or giving the e-mail addresses of new students takes two to four minutes of time. For a PI's students, such simple acts can determine whether they are involved in a community or not, so taking that little time makes a great difference to a community such as ours.

Some wisdom from along the way:

- Build the community on something that is relevant for its members – a well-posed problem will get more people involved than bowling alley and pitchers.
- Do not control people, but support the development of their ideas. Some ideas seem a little strange at first. Try to understand them and give them space – if you add constructively to them, you will go somewhere. If you suppress them, you stop the train.
- Align your activities with your goals. Your time and force is limited. Especially in the beginning, you have to avoid frustration from doing stuff that does not push your goals.
- Do what works now, don't build a general solution. Do not build an online forum that can handle >100 users if only 5 people come to your events. Work on your events instead.
- Create opportunities for others: a major motivation of our initiative is to put people in the best position to realize their tools, training, and talents for their success. This success will feed back to the overall community.
- One case to be forceful is when you want to do something different from the way it is usually done. In our case, in every session again, we have to enforce interactivity by moderation – otherwise our sessions degrade into "yet another seminar series".



Lively discussion at a CAMBAM student chapter workshop, L'Université de Montréal, February 8, 2012

Edward Lungu giving the opening lecture

The US-SA Workshop: Mathematical Methods in Systems Biology and Population Dynamics

Amina Eladdadi and Urszula Ledzewicz

It is our privilege to write the report of another interesting scientific event made possible by the co-sponsorship of the Society for Mathematical Biology, the US-SA Workshop on Mathematical Methods in Systems Biology and Population Dynamics. The meeting was held at the African Institute for Mathematical Sciences (AIMS) in Muizenberg, South Africa during a gorgeous early summer week on January 4-7, 2012 (Yes, it is summer down there!). The choice of the location was motivated by the unique character of AIMS as an institute for postgraduate studies with a large enrollment of students from all over Africa and particular groups interested and specializing in mathematical biology. The main sponsors of the workshop were the National Science Foundation and the Society for Mathematical Biology World Outreach Committee, the National Research Foundation of South Africa with some institutional support of AIMS, the University of Kwazulu-Natal, Durban and Southern Illinois University Edwardsville. We are very grateful to all the sponsors for making this event possible.

The purpose of this four-day meeting was to bring together international and African experts in the field of mathematical and systems biology and populations dynamics to exchange ideas, to advance the knowledge of research in the field and explore opportunities for collaborative exchange and education between the African, European, and North American countries. Topics addressed at the workshop included the spread of infectious diseases or the growing need for robust and reliable models in ecology, both of special importance in the host country of South Africa where research naturally has focused on fighting diseases like HIV/AIDS, malaria and others. In the US, on the other hand, a strong emphasis exists on Systems Biology and on its aspects related to cancer. Therefore a second focus area of the workshop was about improved and more realistic models for the dynamic progression and treatment of various types of cancer, a truly globally challenging problem. Given mathematical methods and techniques from various disciplines that apply to both major areas, there was a platform for interactions of both groups as well as between applied mathematicians on one side and biological and biomedical researchers on the other side that facilitate the establishment of prolonged relationships between US and African research groups.

The co-chairs, Urszula Ledzewicz, Southern Illinois University Edwardsville, and Jacek Banasiak, University of KwaZulu-Natal, opened the workshop by giving an overview of the meeting. After that, the director of AIMS, Barry Green, welcomed all the attendees to AIMS, to the world's most beautiful city of Cape Town, and of course to Muizenberg's magnificent beach. The workshop was originally planned as a small US-SA meeting, but with the growing interest approximately 60 participants, representing 16 countries from Europe, Africa, Asia and Australia, attended this workshop.

The program included ten plenary talks by African and internationally renowned mathematicians and scientists active in the field of mathematical biology. The program comprised two concurrent sessions of forty invited and contributed talks, a very well attended poster session, and two panel discussions: one on "Career and Funding Opportunities in Mathematical Biology", and the

Urszula Ledzewicz (left) and Holly Gaff (right) with the winners of the Best and Outstanding Poster Awards: Siewe Nourridine, Jillian Stupiansky, Karly Jacobsen and Moussa Doumbia (from left to right) other one on "Challenges and Future Directions for Mathematics in Systems Biology and Population Dynamics." The presentations covered topics as diverse as cancer modeling and treatment, epidemiology, population dynamics, modeling of biochemical processes, and signaling pathways. The modeling approaches ranged from novel variations on classic ODE and PDE models to stochastic and agent-based models to control and hybrid systems, as well as network modeling. The contributed talks and the poster session provided an opportunity for the young researchers to showcase their research, and more importantly, for the locals to interact directly with international researchers.

The panel discussion on "Career and Funding Opportunities in Mathematical Biology" was an excellent open forum that engaged a great deal of debate among the panelists and audience, creating lively and constructive dialogues. The panelists made excellent points about how the collaboration and exchange programs for graduate students need to be increased between the European, North American and African countries. Edward Lungu of the University of Botswana suggested creating and fostering PhD programs in mathematical biology locally in Africa. The workshop co-chairs praised the role that US NSF financial support plays in catalyzing collaboration between the US and African countries. The closing discussion on "The Challenges and Future Directions for Mathematics in Systems Biology and Population Dynamics" was a very dynamic and animated debate between the panelists and the audience. Many of the comments emphasized the importance of the cross-disciplinary talks and making mathematical models relevant and understandable to the biological and clinical community. John Hargrove of SACEMA, South Africa, commented on the main challenges and difficulties that hinder research in Africa which are the "inaccessibility" to the experimental, medical and clinical data about the diseases.

The participants were treated to a half-day tour around Cape Town that included a visit to the penguins' colony at the National Table Mountains Boulders Park and a visit to the center of Cape Town. The scenic drives along the beautiful beaches in the Cape were mesmerizing and breath-taking. The participants also liked the short and sweet Zulu dance during the banquet. While the audience was treated to a nice dinner with local South African cuisine, Urszula Ledzewicz and Holly Gaff presented three lucky winners, students from the US and Africa, with their Best and Outstanding Poster Awards sponsored by the SMB. The last treat of the meeting was a typical South African barbecue party with roasted lamb and local wines.

The workshop was a perfect size and was impeccably timed to fit with some beautiful sunny summer days, which set the scene for many outside discussions during the coffee/tea breaks, lunch and dinner, and walks on the Muizenberg famous white sands. The program structure of this US-SA workshop was evidently beneficial for stimulating interdisciplinary dialog and providing participants with an understanding of the mathematical methods in systems biology and population dynamics. The organizers got very positive feedback from the participants who expressed interest in similar meetings in the near future.

On behalf of the attendees we would like to thank all the members of the Organizing Committee for their efforts in putting together this successful scientific event. Special thanks are due to Rene January of AIMS and Shirley Lodes of SIUE for doing a great job coordinating the workshop from both the SA and the US side. On the other hand, the Organizers would like to thank all of the speakers and participants for their exceptional talks and presentations, and the local committee from AIMS for their kindheartedness and hospitality. Finally, we would like to acknowledge once again the sponsorship of NSF and SMB. Mary Ann Horn from the NSF and Aziz-Abdul Yakubu from the SMB could not attend the meetings, but fully understood its importance for catalyzing new collaborations between two countries and both organizers and participants would like to express their gratitude for their support of this event. For more see: http://www.siue.edu/CAS/AIMS/

Positions Available

Postdoc - Quantitative Human Ecology
Quantitative Human Ecology Center at Utah State University seeks a postdoctoral associate for research aimed at better understanding the roles of people in ecosystem dynamics through explicit integration of people into models of ecological interactions and dynamics. Data available for such analyses include archaeological, paleoecological, historical, and contemporary data from the North Pacific and Intermountain West. Position is available for one year. Information and application instructions are available at: http://jobs.usu.edu/applicants/Central?quickFind=57127

Postdoc - Epidemiology
The BioMathematics Unit of the Faculty of Life Sciences at Tel Aviv University invites applications for a theoretical Postdoc Fellowship, ideally beginning as soon as July, 2012. The Fellow will work on mathematical modeling and computer simulations mostly related to epidemiology. The appointment is initially for one year, and is renewable for up to 3 years. Any inquiries should be addressed to Prof. Lewi Stone (lewi@post.tau.ac.il) or Dr. Jacob Bock-Axelson (jacob.bock@gmail.com). The application should contain an updated CV, a short research statement with at a least two letters of reference. The deadline for application is May 21, 2012, but review of applications will continue until the position is filled.

Postdoc - Computational Biological Oceanography
A postdoctoral position in computational biological oceanography is available under the mentorship of Dr. Caz Taylor (Center for Computational Science and Department of Ecology and Evolutionary Biology, Tulane University, New Orleans). The successful candidate will further develop existing computational particle-tracking models that use underlying oceanographic data to simulate larval movement in the Gulf of Mexico for research on the movements and population connectivity of blue crabs in the Northern Gulf of Mexico. The one year position, to start July 2012, is supported by grant funding with possible extension to a second year if funding can be secured. To apply, send a cover letter and CV electronically to: Dr. Caz Taylor, caz@tulane.edu.

PhD Position: Nonlinear Dynamics/Atrial Electrophysics

Four year position studying nonlinear dynamics and control of the electrophysiology of atrial fibrillation at the School of Mathematics and Statistics, University of Glasgow, Glasgow, UK. Supervisors: Dr. R. Simitev (lead, Mathematics), Dr. A. Workman (Cardiovascular and Medical Sciences), Prof. A. Rankin (Medicine), Prof. M. Cartmell (external collaborator, Engineering, Sheffield). Please, send a current CV, an Academic Transcripts from your University studies, evidence of your knowledge of English (if a non-native speaker), a statement of relevant experience and research interests including undergraduate and postgraduate project work, dissertations or any publications you might have written, the names and emails of two referees who can be contacted in case you are shortlisted for the Scholarship, to Radostin.Simitev@glasgow.ac.uk. Deadline: 2012-07-31.

Postdoc: Mathematical modeling in ecology
The Biology Centre, Laboratory of Theoretical Ecology at Ceske Budejovice, Czech Republic, invites applications from outstanding candidates for a Postdoctoral Research position available, to contribute to ongoing research in mathematical modeling in ecology. You can read more about the Laboratory of Theoretical Ecology on http://www.entu.cas.cz/dtb/. If interested contact Prof. Vlastimil Krivan, vlastimil.krivan@gmail.com.

Post-docs: Plankton Ecology
Three postdoctoral research positions are available in the labs of Elena Litchman and Chris Klausmeier to develop mathematical and statistical models in plankton ecology. 1) Modeling community dynamics in Lake Baikal and analyzing long-term plankton data (job #6136). 2) Using trait-based and community models to optimize algal biofuel polycultures (job #6137). 3) Investigating community dynamics in spatially and temporally varying environments (job #6138). The postdocs will be based at Michigan State University's Kellogg Biological Station <http://www.kbs.msu.edu>. Each position is for one year, with a possibility of renewal, given satisfactory performance. To apply, search for the job numbers above at <https://jobs.msu.edu>. Applications should include a cover letter describing

your research interests and experience and your CV. Also, email the contact information of two references to Chris Klausmeier (klausme1@msu.edu). Review will begin June 1, 2012. For more information, visit <http://preston.kbs.msu.edu> or email Chris Klausmeier (klausme1@msu.edu).

Post-doc: Computational Oncology, U Trento, Italy
The Computational Oncology Laboratory at the Center for Integrative Biology (CIBIO) at the University of Trento is seeking a postdoctoral fellow (http://www.unitn.it/en/cibio/18721/laboratory-computational-oncology). The successful candidate will participate in the development of integrative analysis methods of orthogonal high-throughput data for the characterization of the functional impact of somatic mutations in cancer patients, using high density and Next Generation Sequencing data generated from human samples and cell lines. Applicants should contact the laboratory PI, Dr. Francesca Demichelis (demichelis@science.unitn.it). Application guidelines are posted at the following web-page http://www.unitn.it/en/cibio.

Post-doc: Math Biology
The Department of Mathematical Sciences at the New Jersey Institute of Technology has an opening for a post-doctoral appointment beginning September 1, 2012. The ideal candidate would share research interests with our large group of math biologists, but would also be capable of pursuing their own independent research projects. Details on how to apply for the position may be found at: http://math.njit.edu/about/math_jobs.php. Review of applications will begin immediately.

Post-doc: Control Engineering
We are seeking a Postdoctoral Research Assistant to join the Control Engineering group at the Department of Engineering Science at the University of Oxford. The position is fixed-term for up to 29 months with a start date of 1 July 2012. This post will involve working in Synthetic Biology from a Control Engineering perspective and will be collaborative with two other postdoctoral researchers at the partner institutions. Informal enquiries may be addressed to Dr Antonis Papachristodoulou, antonis@eng.ox.ac.uk. To apply: https://www.recruit.ox.ac.uk/pls/hrisliverecruit/erq_jobspec_version_4.jobspec?p_id=102815. Only applications received before midday

SMB Gets a Makeover

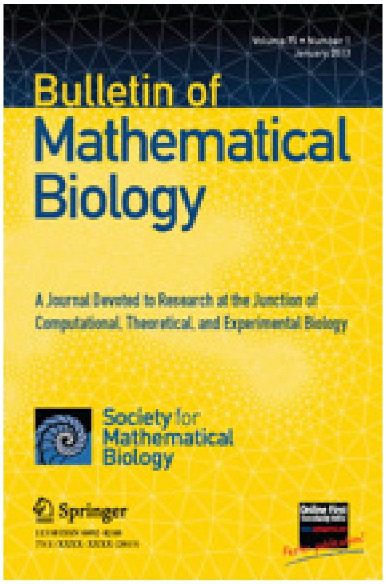
Sharon Lubkin, Publications Chair

Society for
Mathematical
Biology

In the society equivalent of a fresh coat of paint, the SMB has in recent months revised its logo, its website, and the cover of the Bulletin of Mathematical Biology.

The process has actually been a few years in the making. Before circa 2000, the SMB did not have an official logo. Then one conference poster was so elegant that its deconstructed nautilus gradually became the visual identity of the Society. Over time, too many automatic file conversions left us with a coarsely pixelated and barely recognizable deconstructed nautilus. Here we present our new logo, which references the old one, while updating it and tying it to a uniform text identity. The logo is based on vector graphics and an embedded font. Please discontinue use of the old SMB logo, except for historical purposes. For instructions on proper use of the logo, see http://www.smb.org/images/logo/logo.html In particular, the 3-line name of the society is part of the logo.

Our website was also due for an update, and thanks to Heiko Enderling, Holly Gaff, Will Heuett, and others, we have a very functional and elegant webpage: http://www.smb.org/index.html



As happens when you paint one room in the house, the other rooms immediately start to look like they need painting too. We have also worked with Springer to revise the cover of the Bulletin of Mathematical Biology. Look for it in print starting with the next issue.

The Future of Math Biology

Jacob Scott, M.D.
University of Oxford/Moffitt Cancer Center

Mentors: Philip K Maini/Alexander R. A. Anderson

What attracted you to mathematical biology?
The otherwise intractable questions that I faced in my previous life as a cancer physician.

What is your current research project?
My thesis project is modeling the spread of a brain tumor called glioblastoma assuming a hierarchical organization (stem cell hypothesis) using coupled reaction diffusion equations.

What specific areas are you interested investigating?
Cancer initiation, evolution and progression - especially as they can enlighten our therapeutic paradigms.

What do you hope to do after graduation?
Continue my cancer research whilst returning to the clinic as a neuro radiation oncologist.

What advice will you give to an undergraduate interested in a mathematical biology career?
Spend some time in a lab or in the field working on some problems in biology – even if only as a 'tourist' – the key to advancing our field is communication between the mathematicians and the biologists, and any time you spend with 'them' will help immeasurably.

What inspires you scientifically?
My patients.

Why did you join the Society for Mathematical Biology?
It is the flagship organization for my 'new' field and provides access for students to the leaders in the field.

Philip K. Maini and Alexander R.A. Anderson, Jacob Scott's DPhil advisors, say:
"Jacob (Jake) Scott is a very unusual student; he has a background in engineering and physics but is primarily a Medical Doctor and thus brings a fresh clinically focussed perspective to his research. As a radiation oncology resident he treated patients with radiation on a daily basis with advanced stages of cancer progression. Currently Jake's main specialty is brain tumours and he feels strongly that the alternative insights provided by mathematically modelling should help him in the clinic. He is in the first year of his doctorate and continues to write grants (which pay his bills) and publish papers on other work. He has also started a number of collaborations already in the few months he has been at Oxford."

Nominate your student!

"The Future of Math Biology" is a new column intended to highlight graduate students in mathematical biology. Do you want to nominate a student from your research group? Please send your nomination to: schnells@umich.edu.

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 that exists to promote and foster interactions between the mathematical and biological sciences communities through membership, journal publications, travel support and conferences. Please visit our web site: http://www.smb.org for more information.

Holly Gaff, Editor, editor@smb.org