Society for Mathematical Biology

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Newsletter

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`http://www.smb.org/membership/index.shtml`

Letter from the President

Dear SMB members,

"*Mathematical biology is a field where creativity and logic overlap.*" I found this nicely phrased insight from Kelsey Gasior on page 28 of this newsletter both inspiring and thought-provoking. Unlike what outsiders might think, the logic is not tied to the "mathematical" and the creativity to the "biology". Indeed, it can often be the opposite. Those of us who work closely with molecular biologists know the careful and almost obsessive logic they use to demonstrate the function of particular protein in a pathway. On the flip side, nothing is more creative than, for example, the work of David Sankoff in using combinatorial statistics with classical probability theory.

Nobody reading this newsletter could doubt that this combination of logic and creativity has spread hyphae through the entire corpus of the modern life sciences. But has the approach, as Philip Maini asks in his perspective on page 19, become so successful as to make itself obsolete? Are we in the position of a skin cancer researcher who finds a cure so effective that she puts herself out of work? Obviously I think not. In my view, the challenge of linking mathematics and biology is hardly a disease that needs to be cured, and the integration of mathematicians into Biological departments and societies does not destroy the role of mathematical biology as a separately defined field.

As the biological sciences become more quantitative, and as genetics, imaging, tracing, and informatics provide methods that unify formerly disparate fields, the role of mathematical biology in providing the *principles* that link the whole of biology becomes even more pertinent. Not only are mathematical biologists almost uniquely privileged to share in discoveries ranging from neuroscience and population biology to partial differential equations and statistics, but we are ever more essential in serving as the vectors that can transmit ideas across disciplines. To do so, we do need to rethink the purview of the field, particularly with regard to the role of data analysis and informatics, as Philip Maini argues. I see the more classical dynamical systems approach that I personally pursue as being fully complementary with grappling directly with Big Data, with the rapid advances of Bayesian methods in ecology providing just one direction.

To advance our role in synthesizing modern biology and enhancing mathematical creativity, I am proposing two programs. First, to work with SMB members who are also members of other societies in both the life sciences and mathematics to organize joint sessions that cross disciplines, and which could form the focus for collaboration, working groups, or Special Issues of the Bulletin of Mathematical Biology. Second, to start MCDS, for Mentoring in Cross-Disciplinary Science to help people at all stages of their careers make decisions about education, jobs, tenure, funding and collaboration by establishing links between those with questions and our many members with experience and insight. Expect updates on these initiatives soon, and all the best for a logical and creative New Year!

Sincerely,

Fred Adler

Report on SMB Membership

Dear SMB members,

2013 was an exciting year for the Society for Mathematical Biology. The number of our active members has increased to 750 from 39 countries around the globe. The Society welcomed 170 student members and further fostered our reciprocal memberships with the European Society for Mathematical and Theoretical Biology and the Japanese Society for Mathematical Biology.

Most visibly during Past-President Gerda de Vries' tenure, the SMB made the first steps for the transition of its administration into the 21st century. The membership database has been migrated to WildApricot.com, an independent membership management portal with improved handling for the Society and easy profile maintenance and control for SMB members. The newsletter distribution moved away from costly hardcopy delivery to email distribution and online archiving. We have received a lot of feedback from you and learned from the first year. We are working hard behind the scenes to continuously implement your suggestions and improve the membership experience. We invite you to renew your membership for 2014 and share your experience with the membership committee.

As a Society member you receive a 30% discount of Springer books and have complementary access to the Society's journal, the Bulletin of Mathematical Biology. To access SpringerLink you will need to sign up and create a new user account at `http://link.springer.com`. Click on 'Sign up/Log in' located in the upper right side of the screen to start the registration process. After the registration is completed you can activate your access rights by entering your unique Springer token that you find in your SMB online membership profile. For new members it might take up to 48 hours to get a token assigned.

SMB members continue to receive discounts at the annual meeting, which this year will be held jointly with the Japanese Society for Mathematical Biology in Osaka, Japan, from July 28 through August 1, 2014. We look forward to an exciting meeting hosted by our friends and colleagues in the JSMB together with the Chinese and Korean Societies for Mathematical Biology.

Further emphasizing the SMB facelift is the social media Facebook page at `http://www.facebook.com/smb.org`, where mathematical biology and general science news are shared with over 1500 friends. We invite you to follow us on Facebook, and interested Society members are welcome to send a message and join the Social media team as an administrator and active facebooker.

As the SMB continues to be at the forefront of both mathematical biology research and education, we invite you to renew your membership for the calendar year 2014, encourage you to invite your colleagues and students to become members of the Society, and request your active participation in the SMB to shape the future of mathematical biology. Further information on the SMB membership can be found here: `http://www.smb.org/membership/index.shtml`

Heiko Enderling,
SMB Membership Committee Chair.

The 2014 Lee Segel Prizes for Best Paper Announcement

The Society for Mathematical Biology is proud to announce the winners of the 2014 Lee Segel Prizes for best paper in the Bulletin of Mathematical Biology. The award funded by Springer in partnership with the Society for Mathematical Biology, honors the late Lee A. Segel, past-President of the Society and former Editor of the Bulletin. This year's prize selection considered papers accepted for publication from January 2012 up to the end of September 2013.

The recipients are honored with a cash amount of USD $2000-3000, and are asked to present their work at the SMB annual meeting. This year's annual meeting is held jointly with the Japanese Society for Mathematics in Osaka, Japan from July 28 - August 1.

- **Best Research Paper: S.R. McDougall, M.G. Watson, A.H. Devlin, C.A. Mitchell, M.A.J. Chaplain. A hybrid discrete-continuum mathematical model of pattern prediction Bull Math Biol (2012) 74:2272-2314**

- **Best Student Paper: Stephen O'Malley, Martin A. Bees. The orientation of swimming biflagellates in shear flows Bull Math Biol (2012) 74:232-255**

Mark Lewis,
Chair, Segel Prize Committee
Society for Mathematical Biology

About The Lee Segel Prize

The Lee Segel Prizes were established in memory of Lee Segel, who made great contributions to the Bulletin of Mathematical Biology and the field of mathematical biology as a whole. The prizes honor outstanding contributions to the field of mathematical biology and will help to promote and advance important research findings in this scientific area. There is a Best Paper Prize, as well as a Best Student Paper Prize. Other prizes may be awarded as deemed appropriate by the selection committee, the Society for Mathematical Biology, and Springer. The Lee Segel Prizes are awarded every two years.

Lee A. Segel (1932-2005) was an applied mathematician primarily at the Rensselaer Polytechnic Institute, and a professor at the Weizmann Institute of Science, Rehovot, Israel, where he served as Chairman of Applied Mathematics, Dean of Mathematical Sciences, and Chairman of the Scientific Council. He is particularly known for his work in the spontaneous appearance of order in convection, slime molds and chemotaxis.

Information processing in biological systems: from cells to equations, and back.

Buenos Aires, 15 - 19 July 2013

XV
Giambiagi
Winter School

by Alejandra Ventura

The XV Giambiagi Winter School took place at the Physics Department, University of Buenos Aires, Argentina, from July 15 and 19, 2013. The Physics Department has been organizing the Giambiagi Winter School since 1999, attracting a broad audience not only from the country but from all Latin America. The subjects covered change every year, so as to offer students and young researchers from the region the opportunity to learn the last developments in a given field from very well-known specialists. The central theme of the 2013 meeting was information processing in biological systems.

The meeting was a one week school with several mini-courses, where about 100 young participants were able to interact among themselves and with the lecturers. Courses covered different key aspects of the proposed theme, such as gene regulatory networks, dynamical aspects of signaling pathways, molecular noise, the quantification of information in cellular processes and the physics of the cell.

The school had five mini-courses, including: Small regulatory networks and motifs, by James Ferrell (Stanford); Noise in chemical reaction networks, by Ivo Sbalzarini (Dresden); Transition to multicellularity by Ray Goldstein (Cambridge); Information processing in tissues, by Marcos Gonzalez-Gaitn (Geneva); and Cellular responses to combinations of signals, by Tobias Bollenbach (IST). Each course consisted of three lectures of two hours each, having three lectures per day. These lectures were followed by students poster sessions. The school was organized by Ariel Chernomoretz, Alejandro Colman-Lerner, Hernn E. Grecco, Luis G. Morelli and Alejandra Ventura, and counted with several sponsors, as the Society for Mathematical Biology, the Institute for Complex and Adaptive Mather, the International Center for Theoretical Physics, and local sponsors. Overall the meeting provided students with an accessible and contemporary view of the most interesting questions in the field, and introduced them to the possible experimental and theoretical approaches that are used to answer these questions, and the tools that can be used to comprehend the complex dynamics of cellular behavior. In summary, we think that the school could effectively bring students closer to these themes and to the tools necessary to tackle a variety of questions of great interest.

We feel that the meeting was a very successful event, and that our main objectives were accomplished. The lectures of our invited speakers provided excellent examples of instances of high level interdisciplinary science, where a synergistic flow between cells and equations takes place. Given the general positive feedback we received from lecturers and participants, and that some networking activities among attendants already started to take place, we are confident that the school will have a significant impact on the development of interdisciplinary science at the regional level. Details on past editions of the school can be found at: `http://giambiagi.df.uba.ar/2013/Home.html`.

Participants at the poster session

by Nadia El-Mabrouk

The MAGE conference took place in the Hôtel Château-Bromont, in Québec's beautiful Eastern Townships region on Augsut 23-26, and gave a retrospective and prospective view on comparative genomics by commemorating the 50 years of scientific contribution of David Sankoff.

> *David Sankoff is known as one of the founding fathers of bioinformatics and computational biology. He has been at the origin of numerous fields in bioinformatics, starting with the fundamental problem of sequence alignment . In particular, he contributed to the early introduction of dynamic programming to computational biology.*

This event brought together the most renowned scientists in computational biology as well as the future generation of young researchers and students. For example, Anne Bergeron of UQAM, Montréal, who kicked off the event by putting David Sankoff's early career into perspective, presented an amusing short film depicting a successful live test of David's 1990 music recognition algorithm.

Joseph Felsenstein of U. Washington, appeared via a web video from Seattle, recalling the precursors of bioinformatics and computational biology in David's work at the Centre de Recherches Mathématiques de l'Université de Montréal. He reminded us of Sankoff's collaboration with late Robert Cedergren, and his inspiring personality, which was deeply moving to many audience members who knew Robert.

Sunday was another eventful day. David Sankoff talked about his most recent work with Chunfang Zheng of U. Ottawa, on the evolution of plants through cycles of polyploidization and fractionation, follow by presentations on modeling (inference of ancestral genomes and of evolutionary distances) and applications (to the genome evolution of tomato, coffee, Utricularia and other core eudicots).

Following Sankoff's talk, a couple of participants presented their more biologically oriented talks (participants were: Joseph Nadeau, Aoife McLysaght, Eric Lyons, Victor Albert). Later during the day, another group of participants (Tao Jiang, Pavel Pevzner, Dannie Durand, Meidanis and Yancopoulos, Binhai Zhu) gave talks on more methodological and algorithmic aspects of their research.

The three-day conference closed on Monday morning with presentations on future research directions. For example, Ron Shamir of U. Tel Aviv presented his work on the massive theoretical and empirical study of rearrangements in cancer cells.

This event was a unique opportunity to come together, to trace the developments that had led to the discipline of bioinformatics and computational biology, and to discuss the challenges that lied ahead. It was also a great occasion for the publication of a volume consisting of fourteen chapters by participants in MAGE, in the Springer series "Computational Biology". This book was highly anticipated by the community. For my part, some chapters are already serving as reading material for my graduate courses in bioinformatics!

For more detail on the MAGE conference, please check out their website:
`http://www.iro.umontreal.ca/~mabrouk/MAGE2013/index.php`

Participants at the MAGE meeting

Models in Population Dynamics and Ecology

Osnabrück University, Germany, August 26 - 29, 2013

by Horst Malchow

Since 2007, the series of Models in Population Dynamics and Ecology (MPDE) conferences attracted more attention of the international community. The MPDE conferences focus on the ecosystem dynamics at all scales using various mathematical, computational and interdisciplinary methods. The 2013 meeting held from August 26 - 29, 2013, at Osnabrück University focussed on the mathematical aspect of population dynamics and ecosystem. It also explored the corresponding processes and mechanisms from the micro-scale of individual growth and evolutionary dynamics to the macro-scale of population interactions and dispersal with applications to metapopulations, regional dynamics and geographical invasions.

The meeting also explored similarities between modeling techniques traditionally applied in ecology and those used in physics, systems biology and other life sciences with the purpose to enhance interdisciplinary approaches and to stimulate further advances in mathematical ecology and population dynamics. Themes of this meeting included: bioinvasions and epidemic spread, biological and ecological networks,biological flows, dynamic energy budget modeling, pattern formation, epidemiology and ecoepidemiology, evolutionary dynamics, individual and collective dynamics, noise in bio- and ecodynamics as well as scaling and aggregation.

Alan Hastings, Flora Cordoleani and the MIO group from Marseille behind

The organizer Horst Malchow and Nanako Shigesada after her Honorary Lecture

The meeting was generously funded by the German Science Foundation (DFG) and the Lower Saxony Ministry for Science and Culture (MWK). SMB and ESMTB had supported the travel of a couple of young members. Almost 200 scientists, graduates and PhD students from all continents attended the conference. Nanako Shigesada (Kyoto, JPN) and Masayasu Mimura (Tokyo, JPN) were honorary speakers. Both are pioneers of the mathematical theory of ecological pattern formation and biological invasions. SMB and JSMB have just announced that the 2013 Akira Okubo Prize will be awarded to Nanako Shigesada.

Further invited plenary speakers were Ulrike Feudel (Oldenburg, Germany), Volker Grimm (Potsdam/Leipzig, Germany), Mats Gyllenberg (Helsinki, Finland), Alan Hastings (Davis, USA), Emilio Hernández-García (Palma d. M., Spain), Jean-Christophe Poggiale (Marseille, France), Bas Kooijman (Amsterdam, The Nederlands), Michel Langlais (Bordeaux, France), Ran Nathan (Jerusalem, Isreal), Roger Nisbet (Santa Barbara, USA) and Sergei V. Petrovskii (Leicester, UK). The program, abstracts of talks, posters and other informations can be found at `http://www.mathebios.net/Conferences/mpde13`.

The 2014 conference will be organized by Ezio Venturino at the University of Torino, Italy.

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Models in Population Dynamics and Ecology

Osnabrück University, Germany

26-29 August 2013

Report By an SMB Travel Grant Recipient

by Iyare Egberanmwen Barry

The MPDE'13 has finally come and gone but the memories linger on. Although I missed the opening ceremony due to flight delays in Lagos, Nigeria, it was nevertheless a worthwhile experience attending MPDE'13 in Osnabrück Germany.

The conference took place at the prestigious university of Osnabrück, Germany. It was well organized throughout, especially the coffee/tea break, which provided an informal atmosphere for scientific discussions and exchange of ideas. This was followed by three parallel sessions. In one of the parallel sessions I attended, the talk presented by Ramona Marguta from Portugal on "*Spread of Infectious Diseases in Large Geographical Area*" and that of Surabhi Pandey from India, who presented a talk on "*Modeling and Analysis of Biological Control of Malaria*" were the most beneficial to me because it is my area of research. The posters session was lively; it was a colorful display of many interesting and original ideas. This was the session where I displayed my research work on "*A Model for Vector - Transmitted and Transfusion Transmitted Malaria Disease.*"

Iyare Egberanmwen Barry, Horst Malchow, Sansao Pedro & Peter Mwamtobe

Iyare Egberanmwen Barry and a participant at the poster session

The event coincided with the 60th Birthday of Horst Malchow, a co-organizer of the conference. His friends and former students gave a vivid account of his accomplishments in the field of mathematical ecology. The day ended with a conference dinner in his honor at a brewpub in the city of Osnabrück. It was a wonderful experience for everybody present. We were treated to a variety of food and the traditional German beer for those who knew how to drink.

I would like to thank the organizers especially Dr. Horst Malchow for his prompt response to my questions before and during the conference. I would also like to acknowledge the financial support from the Society for Mathematical Biology that helped make this trip possible for me. I look forward to the next MPDE'14!

Banff International Research Station
for Mathematical Innovation and Discovery

Mathematical Modeling of Indigenous Populations Health

Banff, Canada, September 27-29, 2013,

by Katya Richardson & Seyed Moghadas

The *Mathematical Modeling of Indigenous Populations Health* workshop was held at the Banff International Research Station (BIRS) from September 27-29, 2013. It was financially supported by the BIRS, the Canadian Institutes of Health Research (CIHR), and the Society for Mathematical Biology (SMB). The workshop was organized by Michael Li (University of Alberta), Seyed Moghadas (York University), Beate Sander (Public Health Ontario), and Jianhong Wu (York University), and professionally coordinated by Katya Richardson (York University).

The purpose of the meeting was to bring together public health professionals, researchers, and trainee students and postdoctoral fellows from diverse backgrounds, including disease epidemiology and modeling, biology and microbiology, and the social sciences, in an effort to identify and prioritize areas of Aboriginal health research that have yet to be addressed. The main idea is that through interdisciplinary dialogues we can begin to recognize gaps in knowledge and develop a more comprehensive understanding of Aboriginal health that can be incorporated into disease models both quantitatively and qualitatively. The meeting also sought to present outcomes of post-pandemic 2009 research findings, and demonstrate their relevance to public health policy for improving health outcomes and equality for Indigenous populations. Finally, the workshop aimed to enhance collaboration with Aboriginal health organizations and communities within territorial, provincial, and federal jurisdictions, and to establish a national network that would advance Aboriginal health objectives.

This workshop unfolded as a continuation of a previous meeting organized by the "Pandemic Influenza Outbreak Research Modeling" (Pan-InfORM) team, held at York University in May 2012. In that meeting, a wealth of knowledge and information were shared and important recommendations for research were established. The intention for the follow-up meeting in BIRS was to build on this Canadian initiative in plausible ways that would move us from evidence to action. Opening the workshop in BIRS, Katya Richardson (York University) provided a brief summary of the previous workshop and presented the main findings from the published report "*Indigenous Populations Health Protection: A Canadian Perspective,*" in BMC Public Health in 2012.

There were several presentations from disease modelers. The first presentation was given by Marek Laskowski (York University) with an evaluation of the impact of age-specific cross-reactive antibody protection levels on the outcomes of a pandemic outbreak of a novel influenza A (H3N2v). This was followed by a presentation from Kathryn Morrison (McGill University) who discussed the impact of geographical location of residence on disease outcomes among Canadian First Nations populations during the 2009 influenza A(H1N1) pandemic.

There were also presentations from health researchers currently working on new vaccine candidates. Marina Ulanova (Northern Ontario School of Medicine) presented her work on Haemophilus influenza serotype a (Hia), a disease that has reached alarming incidence rates within Indigenous populations in Canada, particularly in northern latitudes. It is unknown whether any specific biological or environmental factors are responsible for an increased susceptibility of Indigenous populations to this invasive disease. However, the presentation provided a compelling argument that developing a vaccine against Hia is a realistic and important goal and all necessary efforts should be taken to prevent this serious infection in susceptible populations. Eleonora Altman (National Research Council Canada) spoke about *Helicobacter pyroli*, a disease that has been associated with chronic gastritis and increased risk of ulcers and gastric cancer in adults. It is particularly common among developing countries but only seems to be prevalent within Indigenous populations in Canada. This presentation explained methods for developing a conjugate vaccine based on lipopolysaccharide.

Janet Smylie (University of Toronto) brought important perspectives to the meeting with her talk on data quality, coverage, and governance issues. She raised key concerns about the availability of reliable Indigenous health data sets, and explained that data sets have limited linkages between registries. It is common for Indigenous events to be misclassified as non-Indigenous, resulting in an underreporting of Indigenous mortality and morbidity rates. She therefore cautioned disease modelers to only draw on data that have undergone rigorous examination for quality, coverage, and governance. Michelle Driedger (University of Manitoba) ended the first day of the workshop with a presentation on risk communication. In a two-hour focused session, she discussed lessons learned from communicating risk to Indigenous peoples during the H1N1 outbreak. Through these experiences, we have learned that the ability to communicate risk effectively is critically dependent on having built relationships of trust.

On the second day of the workshop, Donald Sutherland (Global Public Health Consultant) shared his life experiences working as a physician abroad. He reminded us of the need for research projects that are ethical in terms of ‘good’ science. That is, projects are guided by the needs of the communities for which they are designed. He also stressed the importance of engaging indigenous students who will develop technical and professional expertise that can be shared with their communities. The final presentations were given by disease modelers. Betsy Varughese (University of Alberta) presented her work on modeling tuberculosis transmission and David Fisman (University of Toronto) theorized about the disease dynamic mechanisms that could have produced an elevated incidence of the 2009 influenza A (H1N1) pandemic virus in remote and isolated Canadian communities.

Participants were enthusiastic about the goals set forth in the meeting, and a consensus opinion supported the idea of establishing a national network to advance Aboriginal health objectives. This network would achieve its objectives by drawing on existing resources and expertise in Canada pertaining to the fields of disease modeling and public health, and would seek guidance from Aboriginal organizations in all stages of its operation. A number of participants agreed to take leading roles in establishing the network including Seyed Moghadas, Joel Kettner (National Collaborating Centre for Infectious Diseases), Janet Smylie, Isaac Sobol (First Nations Health Authority) and Michael Li, forming the executive board of this Canadian research network. Further information:
`http://www.birs.ca/events/2013/2-day-workshops/13w2111`

PDEs and Dynamical Systems in Biology

Bar-Ilan University, Israel, Sept. 30-Oct. 3, 2013

by Leonid Berlyand & Avner Friedman

The last two decades have seen rapid progress in mathematical biology. Applied mathematics programs at most major research universities around the world have developed a substantial biological component. While the 20th century witnessed tremendous achievements in mathematics originating from physics, in the 21st century biology has become a great source of novel mathematical problems. In particular, emerging biological models are raising new mathematical challenges in PDEs and Dynamical Systems.

A conference on “PDEs and Dynamical systems in biology” took place on September 30 - October 3, 2013 hosted by the Department of Mathematics, Bar Ilan University, Israel. The conference was primarily supported by NSF and it also received support from the Society of Mathematical Biology and Bar Ilan University. While majority of the participants were applied mathematicians, some speakers presented their results of biological experiments and highlight the connections with mathematical modeling.

The main purpose of the conference was to attract researchers working on PDEs and Dynamical Systems to problems in biology. Modeling and mathematical analysis in the areas of Cell Biology, Collective Motion, Biomedical problems and Population Biology were emphasized in the talks at this conference. The talks also identified biological problems where PDEs and Dynamical systems could provide novel insight. A significant presence of young scientists was the key feature of this event and the primary focus was on the facilitation of interactions between young and senior researchers working in the exciting and rapidly developing field of mathematical biology. The conference was organized by Gil Ariel (Chair of organizing committee), L. Berlyand (Chair of scientific committee), Suncica Canic, Avner Friedman, Yoram Louzoun, and Vered Rom-Kedar. The conference consisted of 14 invited talks, 4 contributed talks, and 15 talks by junior researchers as well as a dedicated two hour poster session with a discussion.

The plenary lectures were given by Igor Aranson (Argonne National Lab) "*Modeling crawling cell movement on soft engineered substrates*", Leonid Berlyand (Penn State University) "*PDE/ODE models of motility in active biosystems*", Avner Friedman (Ohio State University) "*Free Boundary Problems with Stokes Equations Arising in Mathematical Biology*", Celine Grandmont (INRIA) "*Mathematical and numerical modelling of the respiratory system*", Miguel Herrero (Universidad Complutense, Madrid) "*Some Modelling Problems in Radiotherapy*", Jim Keener (University of Utah) "*The dynamics of fibrin gel formation*", David Kessler (Bar-Ilan University) "*Logistic Growth in Spatial Systems: From Stochastic ’Reality’ to PDEs*", Doron Levy (University of Maryland) "*The Dynamics of Drug Resistance in Cancer*", Yuan Lou (Ohio State University) "*Dispersal in heterogeneous environments*", Michael Reed (Duke University) "*Big Data and Networks Are Not Enough*", Vered Rom-Kedar (Weizmann Institute) "*The innate immune system: some theory, some experiments and some medical implications*", Sorin Solomon (Hebrew University) "*Generic Emergence of complex collective adaptive behavior in stochastic systems with simple proliferating agents*", Angela Stevens (University of Münster) "*A free boundary value problem for cell motion*", and Richard Tsai "*Boundary integral methods using signed distance function and the closest point mapping*" (University of Texas at Austin).

The conference provided an excellent opportunity for initiating new contacts between young and senior researcher; it also strengthened scientific interactions between American, Israeli and European researchers. These will surely bear fruits in the coming years.

International Symposium on Biomathematics and Ecology Education and Research

Marymount University, VA, October 11-13, 2013

by Hannah Callender

Bigger is not always better; but when it comes to BEER, this is usually the case. The 7th annual Symposium on Biomathematics and Ecology: Education and Research (BEER) began with a bang this year with a record numbers of over 120 attendees and over 100 oral presentations. The meeting took place in our nation's capital, on the campus of Marymount University. While many of the city's attractions stood silent due to the government shutdown, the BEER meeting was livelier than ever.

The weekend began with a keynote address by Avner Friedman titled, "*Are Macrophages Our Friends or Enemies,*" and was followed by our traditional opening reception which was full of tasty treats including, as always, complimentary beer. Undergraduate and graduate students wishing to participate in either the poster or the oral presentation competition were asked to submit a publication-quality manuscript prior to the meeting. A team of judges graded the papers and attended the presentations. The top combined scores (paper combined with poster or paper combined with oral presentation) received monetary awards, thanks to the support from Marymount University, in addition to the support from NSF, which provided travel grants to nearly 30 participants.

First place for undergraduate poster went to Cara Sulyok of Ursinus College; Second place went to Abbiana Arenas of NOVA Southeastern University. For the undergraduate oral presentations, Catherine King from the College of William and Mary won first place; Jim Crowder of Rhodes College received second place. Bradford Taylor from Georgia Institute of Technology was awarded first place in graduate presentations; Michael Crone of George Mason University placed second.

Participants enjoying a soccer game

In typical BEER fashion, there was a wide assortment of talks: some more mathematical, others more focused on ecology or biology; some were exclusively research-oriented, others focused instead on enhancing education of undergraduates in biomathematics, biology and ecology. This variety was reflected both in the contributed talks as well as the invited speakers. Plenary talks were given by Jeremy Wojdak of Radford University who spoke on "*Horizontal and vertical integration of mathematics and statistics across the biology curriculum*", and Rebecca Segal of Virginia Commonwealth University who presented an "*Overview of Modeling Techniques for Wound Healing*".

In addition to contributed and invited talks, John Jungck from the University of Delaware demonstrated active learning at its best with a hands-on workshop on "*Applications of Graph Theory to Biology.*" Two panel sessions later discussed graduate programs and careers in biomathematics. One session was designed specifically for students and the other for faculty. Yet another new addition to this year's meeting will be the publication of conference proceedings by McGraw Hill.

The organizers would like to thank all of this year's attendees for our best meeting yet. A special thanks goes out to our local organizer, Elsa Schaefer, and her amazing team of students and staff from Marymount University. Their hard work and participation assured a successful meeting. We look forward to seeing both old and new faces alike for our next meeting at Claremont Colleges, Claremont, CA on October 10-12, 2014.

by Frithjof Lutscher

This workshop on sustainability of aquatic ecosystem networks took place in Fredericton, New Brunswick, on October 22 - 25, 2013. It was one of ten workshops within the pan-Canadian thematic year on "Models and Methods in Ecology, Epidemiology and Public Health (`http://www.crm.umontreal.ca/M2E2/`). The workshop was organized by Frithjof Lutscher (Ottawa) and James Watmough (University of New Brunswick) and was supported by AARMS, CRM, NSF and SMB.

Aquatic ecosystems, freshwater and marine, supply tremendously important ecosystem functions from food supply to transportation and recreation. These ecosystems are imperiled due to changing climate and human activities. The goal of this workshop was to bring together researchers from mathematical modeling and quantitative biology to exchange recent empirical results, novel ideas and modeling frameworks on the topics of sustainability in aquatic system with focus on spatially distributed systems.

Participants ranged from mathematicians and modelers to theoretical and empirical biologists as well as government scientists, and topics spanned a wide range of temporal and spatial scales. Connectivity was a recurring theme, characteristic length scales were discussed frequently, and invasive species as well as intended re-introduction of extirpated species were discussed.

The opening talk by Kurt Anderson (UC Riverside) introduced the question of scales in a single river or stream. How far downstream will a point-disturbance in the benthic community be felt? He presented a simple model for this response length and used the theory of transfer functions to explore responses to more complex disturbances. He pointed out the frequent mismatch in scales between management actions and management goals.

Jonathan Sarhad (UC Riverside) presented ideas of ecological dynamics on river networks and their connection to quantum graphs. A reaction-advection-diffusion equation describes the population dynamics within each reach, and the equations are coupled at confluences. Yasmine Samia (Ottawa) continued the topic of persistence on a river network comparing topological measures (the dentritic connectivity index) with ecological quantities (the population growth rate) under various conditions.

Les Stanfield (Ontario Ministry of Natural Resources) presented his vision of a unified ecohealth network, based on standardized protocols and open access data bases, as well as a transparent adaptive management cycle. He reported his success with the SMART regional monitoring program of wadeable streams in Ontario. Andrew Paul (Fish and Wildlife, Alberta) reported on monitoring and assessing fish stocks in Alberta where a rapidly growing population and industrial demands for freshwater put multiple pressures on wildlife and cumulative effects are often difficult to assess. In addition, management action such as the closure of fisheries may infringe on first nations treaty rights and are difficult to negotiate.

Daniel Boiclair (Montreal, HydroNet) began the second day with a study on the impact of hydropower on fisheries. While fisheries are in decline hydropower is expected to increase massively; both tap into renewable resources. The question is how to reconcile the two. Pierre Girard (UFMT, Brazil) continued the topic of the effect of dams on fish populations with a case study from Brazil in the Pantanal wetland (world heritage) in the Upper Paraguay Basin. Qihua Huang (Alberta) presented a study on how homing fidelity of migratory fish can affect their persistence in a river network.

The afternoon focused on more mathematical aspects again. Gunog Seo (Colgate) presented a model for the Asian clam invasion in North America, with five coupled delayed reaction-advection diffusion. Olga Vasilyeva (Christopher Newport University) presented an impulsive reaction-diffusion model for stream insects with a winged adult stage. Frithjof Lutscher (Ottawa) modeled transport and uptake of nutrients from the water column in heterogeneous conditions.

For Thursday and Friday, the focus of the workshop shifted from freshwater systems to marine systems. The opening speaker was Alan Hastings (UC Davis) who talked about connectivity and persistence in marine systems. His metapopulation setup led to some nice applications of matrix theory. Inclusion of stochasticity gives rise to some very hard problems about products of random matrices. Myriam Barbeau (UNB) presented exciting empirical results about connectivity of communities of Corophium volutator in the mud flats of the Bay of Fundy. Michael Neubert (WHOI) and Holly Moeller (Stanford) presented various models for fisheries management using bioeconomic models and optimal control. Some of these models included the damage that bottom trawling does to fish habitat.

David Drolet (UPEI, for Andrea Locke, DFO) presented a novel tool for managers to evaluate potential success of eradication programs against invasive species. This tool is based on a statistical analysis of published case studies and can be updated as new studies emerge. Jessica Hearns (Central Florida) reported on recent efforts to re-introduce sea urchins in the coral reef systems in Florida.

On the final day, Ali Gharoumi (UNB) proposed a model to describe the spread of Green Crab along the Eastern Coast of North America. David Drolet (UPEI) answered the question of whether a single introduction of many potential invaders or several introductions of fewer invaders causes a higher probability of establishment. James Watmough (UNB) presented two models for invasive tunicate species and their dispersal patterns around mussel aquaculture sites on PEI. As the final speaker, Emily Moberg (MIT/WHOI) presented a new stochastic method to detect poleward movement of a species distribution in response to climate change.

The workshop gave participants ample time for individual or small group discussions during coffee and lunch breaks. Those opportunities were used widely, and many inspiring insights appeared. The final discussion summarized many of the challenges that emerge for the modeling and management of these aquatic systems.

Banff International Research Station
for Mathematical Innovation and Discovery

Current Challenges for Mathematical Modeling of Cyclic Populations

Banff, Canada, November 10 - 15, 2013

by Rebecca Tyson & Frithjof Lutscher

Population cycling is a ubiquitous phenomenon that occurs across a number of animal, insect and bird populations in a wide variety of ecosystems. The dynamics of cyclic populations generate events of significant management and economic concern. For example, important cyclic events include periodic insect outbreaks, population lows in economically valuable fish stocks, closure of grouse moors during troughs in population cycles and cycles in the observed effectiveness of biocontrol agents. Our ability to anticipate, manage, and mitigate the effects of these cyclic populations rests heavily on our mathematical understanding of the processes that generate or drive the observed cyclicity. The workshop brought together 21 ecologists and mathematicians in the beautiful setting of the Banff International Research Station for Mathematical Innovation and Discovery (BIRS) to share ideas and discuss recent progress and new ideas. The workshop was organized by Rebecca Tyson (UBC Okanagan), Jonathan Sherratt (Heriot Watt) and Hao Wang (Alberta) under the umbrella of the pan-Canadian thematic year ‘Models and Methods in Ecology, Epidemiology and Public Health’ as part of MPE 2013.

Invariably, the classic examples of population cycles, the Canadian lynx and hare system and the vole system in Fennoscandia, played a prominent role throughout the workshop. Other experimental systems ranged from parasites and diseases to salmon. More theoretical presentations included the effects of stochasticity on cycles and statistical methods for parameter estimation.

Frédéric Barraquand laid out several critical questions about mechanisms of population cycles and thereby set the stage for the entire workshop. He began with a short history on modeling cyclic populations, that began in the 1920s with Charles Elton and the arctic lemming cycles as well as the Canadian hare lynx cycles. He reported on the relative importance of specialist and generalist predation in initiating cycles. He then considered the importance of resource (mosses, plants) depletion for lemming cycles. More recently, cycles seemed to disappear, and in the search of mechanisms the link to climate change emerged. In the end, Barraquand advocated new research that considers the interaction of all these different factors.

Gail Wolkowicz (McMaster) presented a simplified model of phytoplankton populations and explored model predictions for algal bloom development. She raised the philosophical question about how to identify mechanisms for complex patterns if simple models can already produce a wealth of complicated behavior, such as a period-doubling cascades in her three-dimensional autonomous model.

Dennis Murray (Trent) presented detailed data on lynx-hare cycles in North America, including stable isotope studies of lynx diet. The percent of hares in the lynx diet closely correlated with the likelihood of the population to cycle, as well as lynx juvenile recruitment. Frithjof Lutscher (Ottawa) considered a model for predator-prey interactions when predation behavior changes from generalist in the summer when alternative prey is abundant and specialist in the winter when alternative prey is scarce. Karen Abbott (Case Western) explored how stochasticity can produce large qualitative changes to ecological dynamics when the underlying deterministic skeleton has alternative stable states.

Jeremy Fox (Calgary) talked about his work on spatial synchrony, motivated particularly by cyclic systems. He began by presenting a theoretical model, a two-patch predator-prey model with environmental and demographic stochasticity. He then reported corresponding empirical results on a microcosm experiment. The major conclusion was that population interaction, driving population cycles, is a crucial amplifier of dispersal induced synchrony.

Frank Hilker (Bath) asked the question of how to control chaotic behavior. Frank gave a comprehensive overview of several different methods and discussed management implications. Don DeAngelis (Miami) added a novel perspective to the hare-lynx cycle by including plant-herbivore interactions. Bret Eldert (Louisiana State) talked about the importance of pathogens for population cycles in insect populations such as gypsy moth. Field experiments revealed that induced plant defenses can decrease population heterogeneity in disease transmission, and the decreased variability can cause the system to cycle.

Jude Kong (Alberta) showed with a model for an indirectly transmitted disease that a bacteria-phage system that cycles in a reservoir can entrain a human susceptible-infected system and cause it to cycle, or a joint annual cycle can emerge. Kelsey Vitense (U of Washington) explored the effects on habitat fragmentation and generalist predation on population cycles. Cindy Greenwood (UBC) gave an introduction on stochastic differential equations, specifically about how adding stochastic components to an ODE system with damped oscillations can sustain the oscillation. Stilianos Louca (UBC) developed a method to distinguish intrinsic causes of limit cycles (e.g. arising from a Hopf bifurcation in a deterministic ODE) from extrinsic periodic forcing (e.g. annual variation or El Nino effects). Chris Stieha (Cornell) presented models to explore the effects of constitutive or induced plant defenses on plant-herbivore cycles.

David Campbell (SFU) talked about a method for probabilistically solving a differential equation in the presence of chaos and outlined the advantages in using these ideas in parameter estimation. Rachel Taylor (Heriot-Watt) included seasonal forcing into vole-weasel models to explore the effect of seasonally varying breeding season length on the cycle length of the system. Flora Cordoleani presented a model for cyclic salmon dynamics and its relation to the Pacific Decadal Oscillation. Christina Cobbold (Glasgow) investigated the effects of landscape configuration on the dynamics of forest insects and their parasitoids in two model systems using integrodifference equations and various nonspatial approximations. Huaiping Zhu (York) gave an overview of mathematical mechanisms that lead to periodic solutions in two-species predator-prey models, including global bifurcations and relaxation oscillation. Rebecca Tyson (UBC Okanagan) closed the workshop by presenting several predator-prey models and compared and contrasted their behavior under habitat fragmentation.

The schedule of the workshop gave ample time for unstructured discussion, and participants made good use of all the opportunities to network and learn from one another. In addition, in several carefully organized break-out groups, participants identified current challenges in cyclic population modeling. Website: `https://www.birs.ca/events/2013/5-day-workshops/13w5151`

NIMBioS
National Institute for Mathematical
and Biological Synthesis

5th Annual Undergraduate Research Conference at the Interface of Biology and Mathematics

Knoxville, November 16-17, 2013

by Hannah Lily Postman [1]

The weekend of November 16th and 17th, I joined undergraduates from around the country for my first experience at an undergraduate research conference. We gathered in Knoxville at the University of Tennessee Conference Center, where my peers presented their research on topics ranging from invasive shellfish in Lake Michigan to mathematical applications in human healthcare. This conference, organized by NIMBioS brought together aspiring mathematicians and biologists to explore how the skill-sets (and perhaps mindsets) of each field may complement each other. Of 159 registered participants, 131 of us were undergraduates, and many of us were from backgrounds underrepresented in STEM fields[2]. The conference also brought a number of wonderful professional researchers, who were featured at various points in the program.

The keynote speaker, Dr. Mariel Vazquez, Associate Professor of Mathematics at San Francisco State University, delivered the lecture "*DNA Unlinking by Xer Recombination,*" giving students a peak into her research as a highly accomplished mathematician . In particular, this lecture exposed students to the powerful potential of advanced thinking in knot theory and tangles, insightfully applied to biological problems.

Dr. Andrew Liebhold, research entomologist from the USDA forest service, giving his plenary talk.

Dr. Louis Gross speaking to students about the NIMBioS Summer REU & Graduate Programs at the UT

In part of her presentation, Dr. Vazquez played a video made using a software called KnotPlot (developed by Robert Scharein), which showed rotating perspectives of animated models that resembled the tiny structures that are the focus of her research. To hear a researcher who has presented at Oxford and is a recent recipient of the Presidential Early Career Award for Scientists and Engineers relate topology to human health was truly a treat for me.

The plenary lecture was well complemented by an address from the featured speaker, Dr. Andrew Liebhold, Research Entomologist for the USDA Forest Service. Dr. Liebhold gave students another perspective on the potential for problem solving in fields that use both math and biology. Dr.

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[1] Hannah Lily is an undergraduate student from Oberlin College double-majoring in Comparative Literature & Mathematics.

[2] Undergraduate and total registration figures provided by NIMBioS.

Liebhold's presentation, "*Forest Insect Outbreaks: A Never-Ending Puzzle,*" showcased ecology interacting with math. He introduced the concepts of periodicity and spatial synchrony as they relate to insect populations. In his presentation, students had the opportunity to see research that had taken Dr. Liebhold both into the forest for data collection, and into mathematical thinking in order to model findings and questions. This was another illuminating session.

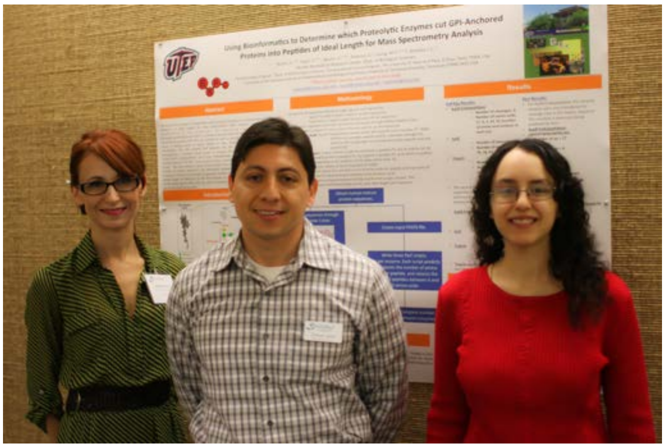
Undergraduates attending the conference presented 34 posters, and 42 fifteen minute talks. Topics ranged widely, some focusing more on math theory, some more on biological bases, and often united the two fields in discussions of mathematical models developed to describe biological findings: viruses, muscle function, and hunger were just a few topics of research supported by mathematical models. I was taken with the great variety of topics on which students presented. It was exciting to see both students and professional researchers combine math and biology in different ways. I appreciated that Dr. Vazquez and Dr. Liebhold together exemplified this breadth, using innovative statistical or mathematical thinking to advance biology research in very different areas.

Two sessions were held for students to learn about career and graduate school opportunities. In one, Dr. Talitha Washington, Associate Professor of Mathematics at Howard University, and Dr. Joe Bailey, Assistant Professor of Ecology and Evolutionary Biology at the University of Tennessee, Knoxville, joined Dr. Vazquez and Dr. Liebhold in a panel discussion. Each shared the narrative of their career trajectory, and then answered audience questions about what an undergraduate might anticipate in following an interest in math and biology. The other event in which students explored future prospects was a small forum, where graduate school representatives were available to answer questions about specific programs, and where many representatives were excited to discuss graduate school and career choices in general with students individually. These career and graduate school sessions were a particularly valuable aspect of the weekend for me.

One attendee commented that this conference was unique in its effort to help students get to know each other in networking activities. The conference was welcoming as well in its thoughtful catering, and the staff of NIMBioS were warm and enthusiastic. I had a wonderful weekend, meeting new people and new ideas. I came away from the conference with an appreciation for the breadth of math's applications to the biological sciences. The number of reasons to like math started to look uncountable. I hope to learn more about the interconnection of biology and math. I feel lucky to have attended this fifth annual Undergraduate Research Conference at the Interface of Biology and Mathematics, and I am looking forward to another very full weekend next year!

For more information about the meeting check out NIMBioS website: `http://www.nimbios.org/education/undergrad_conf2013` .

Photos in this article are courtesy of NIMBioS: (`http://www.flickr.com/photos/nimbios/sets/72157637887884765/`)



Andrea Wurm of UTEP, Dr. Clemente Aguilar of NIMBioS, and Sara Yazdi of UTEP.

Participants at the poster session

Perspective on "*The Changing Face of Mathematical Biology*"

by Philip Maini

There are many positives regarding mathematical biology. In more and more talks, it is becoming difficult to spot where the mathematics ends and the biology begins; such is the close integration ...

This year marks the 30th anniversary of the founding of the Oxford Centre for Mathematical Biology (now renamed the Wolfson Centre for Mathematical Biology). Such landmark birthdays naturally make one pause for thought. The Centre was founded by Professor James Dickson Murray, FRS. He was awarded a grant from the Science and Engineering Research Council (SERC) to set up a Centre to promote mathematical biology in the UK.

Thirty years on and the Engineering and Physical Sciences Research Council (EPSRC - which is what SERC became) announced a new model for funding graduate studies in the UK, called Centres for Doctoral Training (CDT), with over 60 theme areas. The only one that contained the words "mathematics" and "biology" was "*New mathematics in biology and medicine*". To my mind, this totally misses the point as mathematics should be used to discover new biology and medicine and, in the process, inevitably new mathematics arises. More importantly, however, is that we are entering the era of validated mathematical models, an era where the application of these approaches is what is new. The "winners" were announced in November, and of the over 70 CDTs awarded, not one was for mathematical biology. So, is this a bad time for mathematical biology in the UK? One can argue both ways - several of the CDTs will implicitly use mathematical biology for applications in industry and healthcare, so does this mean that mathematical biology is now such an integral part of science that it does not need special treatment, or that it is having to be slipped in under the radar? Only time will tell, but the fact is that, just as the subject area is growing at its fastest rate, so the number of UK graduates in the subject will fall.

Both mathematics and biology have changed enormously over the past 30 years. For example, computing power has increased so much that one can do in seconds what would previously have taken months. At the same time, advances in biotechnology have led to huge amounts of data, and "big data" is the phrase everyone uses nowadays [3]. However, mathematical biology has not kept pace with these advances. Why? I would argue that most data that are being generated are not appropriate for the sort of mathematical biology practiced by the SMB community. We focus on mechanism and develop models that are typically spatiotemporal in nature, yet most data are static. This, I feel, is one reason why we have been overtaken by bioinformatics where the methodology can use the data presently being generated and great advances have been made in this field. However, I feel that we are now on the threshold of very exciting times in mathematical biology, as advances in imaging and staining etc. now mean that, for the very first time, there is the chance that we will acquire the data that our models need.

To take full advantage of this new opportunity will, in many cases, involve us having to go back to go forward. Certainly in my area of mathematical biology (developmental biology, wound healing and cancer) many of the models proposed over the past 30 years were way beyond what could be verified experimentally and therefore they could not be validated. Now that they will, in principle, be verifiable, we must revisit them. This poses a challenge, as we are always under pressure to move "forward" in developing new mathematics, new models and collect new data. Under this system, funding to revisit old models would not be granted. However, we are the system, and we must do something about this!

There are many positives regarding mathematical biology. In more and more talks, it is becoming difficult to spot where the mathematics ends and the biology begins; such is the close integration. We also publish more in scientific journals, so that our work reaches the application areas. Certainly, in many mathematics departments, this is very unusual, even for "applied" mathematics. The journal

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[3] See Perspective on "*Big Data*" in the previous issue, p20. `http://www.smb.org/publications/newsletter/vol26no3.pdf`

> *... I see a further exciting era of more pure mathematicians getting involved in mathematical biology. One of our responsibilities is to find a way to make this community aware of these exciting opportunities ...*

Cancer Research has several mathematical biologists on its Editorial Board. The Moffitt Cancer Center in Tampa has, within it, the Integrated Mathematical Oncology Department, chaired by Dr Sandy Anderson, a mathematician. Then there is the recent appoint of Dr Kristin Swanson (a mathematician) as Professor in Neurological Surgery and Vice Chair of Research for Neurosurgery at the Northwestern School of Medicine. These are just two examples of the growing number of mathematical research groups embedded in medical schools/institutes, adding to the numbers embedded already in the more traditional haunts of physiology, zoology, ecology and epidemiology departments. In Europe, BIOMS in Heidelberg is just one of the growing numbers of institutes in which mathematicians and experimentalists work side by side. The subject is informing government strategies on epidemiology and general ecological management. Mathematical biologists are beginning to be invited to present at biology/medical/healthcare conferences and departments.

Then, of course, there is NIMBioS and the MBI, two centers that have greatly contributed to the growth of mathematical biology. I remember when I started as a graduate student in 1982, my supervisor, Professor Jim Murray, handed me a small number of papers and told me that I should be able to read them by Christmas and then I would basically be able to start research as I would know all the important literature. In those days, one was aware of everything going on in the subject. Now, it is impossible to keep up even in one's own very specialized part of mathematical biology.

As well as being interdisciplinary, mathematical biology is becoming more intradisciplinary. For example, understanding networks requires ideas from graph theory; work on viral capsids requires group theory; fitting models to data requires ideas from algebra (not to mention control theory, probability and statistics). Therefore, I see a further exciting era of more pure mathematicians getting involved in mathematical biology. One of our responsibilities is to find a way to make this community aware of these exciting opportunities. As the subject area continues to grow in breadth and depth there are inevitable questions about training. Should there be undergraduate degrees in mathematical biology, or is it at the graduate level, or postdoctoral level that a student should broaden out. I would say that for interdisciplinary research one should have at least a discipline and so it is at graduate level that one should start interdisciplinary research, but I know many people who disagree with that, arguing that this is too late or, indeed, too early.

Then there is the question of at what level can the sort of mathematics we do be applied. My own approach more recently has been, largely, to focus on a particular biological question that cannot be answered purely by experiment and then work closely with experimentalists in a predict-test-refine-predict iterative cycle. I have tried to resist the temptation to include too many things in the model as I feel that such models are difficult to parameterize and that it is also difficult to learn a great deal from them.

I think that the new generation of scientists is more open and, while there undoubtedly are challenges in the immediate future (particularly of a financial kind faced by all of society, and caused by another field of mathematics), the fact is that the number of people in the non-mathematical sciences who feel mathematics is important is growing. I hope that this means that the very narrow, small-minded view of some departments as to what constitutes good research will eventually disappear, and that we will enter a new era of truly interdisciplinary science.

About The Author:

Prof. Philip Maini is a professor and director of the Wolfson Centre for Mathematical Biology in Oxford. He is currently on the editorial boards of a large number of journals, including serving as the Editor-in-Chief of the Bulletin of Mathematical Biology. He has also been an elected member of the Boards of the Society for Mathematical Biology (SMB) and European Society for Mathematical and Theoretical Biology (ESMBTB). His website: `http://people.maths.ox.ac.uk/maini/`

SMB Education Highlights

UNIVERSITY OF RICHMOND
INTEGRATED QUANTITATIVE SCIENCE

by ELSA SCHAEFER

Welcome to the SMB Education Column! We will be exploring some innovative projects in Mathematical Biology education over the next few issues. I would love to hear your ideas for topics that you would like to read more about, or that you think could be helpful to others. Please send me a note: elsa[at]marymount.edu.

This issue's column reflects a recent conversation I had with Lester Caudill, who is currently coordinating the University of Richmond's (UR) innovative Integrated Quantitative Science (IQS) project. The information and quotes are from Lester. This project, funded by a $1.4 million grant from Howard Hughes Medical Institute (HHMI), integrates freshman chemistry, mathematics, biology, computer science, and physics in a truly interdisciplinary effort. Lester explained that the IQS initiative was developed by UR faculty who "*wanted to give students the experience where they learned the science in the context of the relationships between the different sciences, and particularly how they align their different strengths to address big problems.*" The curriculum was introduced at the freshman level, with the hope that as students continued in disciplinary courses they would bring with them "*the ability to at least think and recognize potential connections,*" as Lester noted, and, of course, these students would be ideally suited to participate in the great number of interdisciplinary research opportunities that are available on the UR campus.

The IQS sequence counts as double-credit (in comparison to other courses offered) for a full year, and pulls together the five disciplines mentioned above. Lester shared the two overarching principles guiding the IQS development. The first principle is the cool part: IQS focuses on big problems through the lenses of five disciplines. The hope is that while students may not "*become experts in using all five disciplines,*", as Lester said, they would at least be familiar with "*the strengths of each (discipline), so that even if they are working on, say, a biology problem, they would recognize where a consult with a physicist would be useful to address some aspect of the problem,*" he added.

The second principle that guided the IQS program's development was the "*do no harm*" principle: the IQS coursework needed to fit within the current curriculum, and students needed to perform well in subsequent disciplinary courses. This meant that certain disciplinary topics simply had to be covered, even if they didn't fit particularly well into the theme of the IQS course. The IQS curriculum replaces, for the purposes of prerequisites, the first courses in the calculus, biology, chemistry, physics, and computer science introductory sequences. The IQS course has not been expected to cover everything from those courses, but it must prepare the students for subsequent disciplinary courses. I asked Lester how the students did in the second semester in the various disciplines, given that they had missed some of the material in the first semester. He said, "*They are prized.*" IQS students are thriving within later disciplinary courses.

In the original instantiation of IQS, five faculty members taught every class of twenty students, which makes IQS an un-sustainable effort from a faculty-resource standpoint. UR is working to redesign IQS with cost and sustainability as parameters, and is piloting a more cost-efficient version during this academic year. Lester notes that while the economic version makes some sacrifices in comparison to the original IQS, on the whole it simply makes more sense. This new incarnation of IQS divides each semester into three modules, followed by an integrative experience at the end of each semester.

> *.. while students may not become experts in using all five disciplines, they would at least be familiar with the strengths of each (discipline), so that even if they are working on, say, a biology problem, they would recognize where a consult with a physicist would be useful to address some aspect of the problem, ...*

"*Each of the modules consists of various subsets of the five disciplines. One of the things we learned from IQS is that having all five disciplines going at once is more overwhelming to the students than we had originally anticipated. The second thing we learned in this regard is that (IQS) is much more demanding on faculty time than anticipated,*" Lester added. For faculty workload, the difference in teaching the same material in concentrated bursts versus scattered throughout the year is significant. Additionally, in the past, one team of five faculty taught IQS in the fall, and a new team of five taught in the spring. Now the same team of five teaches the entire year, which Lester says makes more sense to him from a continuity standpoint. Each faculty member is "*on*" for three of the six modules, and the faculty member can focus efforts elsewhere when "*off.*"

Lester shared another lesson learned from the original IQS. "*While we talk about big themes, and while all five disciplines have ways of contributing to those, it turns out that when you start looking at specific sub-problems, which you must do ultimately, then usually it's not all five (disciplines) involved ... it's two, maybe three, not more.*" Thus, the move to modules that focus on fewer disciplines at once is more synergistic with the needs of the problems at hand. "*For example, this semester, our first module was math, biology and computer science. The second one was physics, biology, and computer science. And the third one was math, chemistry, and computer science.* " All of the computer science is front-loaded into the Fall semester, to address the students' need for frequent exposure when learning a programming language, as with students learning any new language. In the spring semester, there will be a module with math and physics, one with chemistry and physics, and one with biology and chemistry.

Although economics drove the IQS redesign, Lester thinks this new approach is more natural, and so far, he thinks it has been great. "*The down-side, for me, is that I was on for the first module, but I was out for the second module, so I don't have nearly as good a feel for what went on there. That's kind of strange. But on the whole, I think it's a big step forward, and also it helps another consideration that we had, making it feasible at other institutions,*" Lester explains.

Lester says that while the first version of IQS was important from a historical perspective, and for the many lessons learned, it's very unlikely that another institution would have the huge cross-disciplinary support and financial resources needed for its implementation. On the other hand, the idea that an institution would have a subset of the five disciplines that wanted to create a smaller interdisciplinary experience seems quite realistic. Thus, once fully developed, the dissemination of the organization and materials in the individual modules can provide good resources to our broader community. The IQS faculty are still refining the materials, but have clear plans to share the IQS modules with the bio-mathematics community once they are developed.

Those in our community who are in charge of any assessment efforts will appreciate that one of the biggest challenges in the IQS effort that we have not discussed above is how to measure interdisciplinary growth. Lester asks, "*how can you tell if a student is better at thinking in an interdisciplinary way than he/she was on their first day in IQS?*" This is certainly the reason for the IQS initiative, and while we may have intuitive beliefs that this goal is accomplished, it's quite difficult to demonstrate. But the IQS team is working hard on this. Learn more about IQS: `http://iqscience.richmond.edu/why/index.html`.

About The Author:

Dr. Elsa Schaefer is a Professor of Mathematics at Marymount University. Her current research interests are in modeling disease spread, and particularly cholera and tick-borne diseases, and in seeking optimal intervention strategies. She is the SMB Chair of Education. Her website: `http://muweb.marymount.edu/~eschaefe/`

My Voyage into Mathematical Genomics

David Sankoff

In the late 1950s, science students graduating from my high school were led to believe, whether because of Sputnik or simply the charisma of the physics teacher, that the only respectable university degree at McGill University was honors mathematics and physics. An easily influenced 16-year-old, I went along and actually felt vaguely guilty about having been more interested in my 10th grade biology course. Or at least the botany parts, being less attracted to bugs, reptiles and rodents than to flowers and trees. Fortunately, while struggling through my undergraduate years, being kicked out of the honors program along the way and twice failing my Statics and Dynamics course, I spent the summers acquiring and applying tissue culture and virology skills and learning about DNA, the ongoing deciphering of the genetic code, and the discovery of mRNA, as a nepotic summer student in the lab of my uncle Lou Siminovitch at the Ontario Cancer Institute.

I made it through my mathematics Ph.D. thanks to tolerant comprehensive examiners and the encouragement of my supervisor, Don Dawson. He not only taught an advanced course on Brownian motion that I actually understood, and turned one of my weird ideas into a paper on the so-called Dawson-Sankoff inequality, but also told me to write a thesis on whatever interested me, which at the time was the phylogeny of language families, and the stochastic processes generating language divergence. I also benefitted from the large contingent of statisticians in the department, particularly Michael Stephens, who was a generous mentor to many students and who got me involved in his research on the distribution of goodness-of-fit statistics.

My first academic appointment in 1969 was at the Centre de recherches mathématiques at the Université de Montréal, and while I was continuing my work on phylogeny, my friend the late Robert J. Cedergren, a biochemist, posed a series of questions having to do with the comparison of RNA sequences. Over a period of five years, we published a series of algorithms and analyses for nucleic acid sequence comparison, multiple alignment and secondary structure prediction, along with mathematicians such as Peter H. Sellers and Vaclav Chvátal. I have written in detail about this period in the journal Bioinformatics (2000). A small number of other mathematicians, including Michael Waterman, were doing this kind of work at about the same time, but we did not fit in with any established community. I had the impression some of my colleagues thought we were crackpots and many biologists thought we were turning easy procedures (on short sequences) into unnecessary, complicated, algorithms. I did participate in mathematical biology meetings, but felt out of place with researchers in differential equations and statistics. I finally edited a collection of articles, including five of my own, with the late Joseph Kruskal in 1983. For lack of any alternatives, this volume eventually became somewhat of a classic.

At about the same time a growing number of mathematicians and computer scientists, motivated by the increasing number and length of DNA and protein sequences, joined us in this problem area, many molecular biologists became knowledgeable about algorithms, and we began to organize small meetings. By the end of the 1980s the newly named field of bioinformatics was quite busy, and we crackpots suddenly became pioneers. At about the same time, the term "genomics" came into usage, and not long after "computational biology" was used to refer to the more mathematical aspects of bioinformatics.

In 1987, the Canadian Institute for Advanced Research set up a network of scholars across Canada in the field of Evolutionary Biology, and Cedergren and I were among the nine or ten Fellows appointed. Later on, Joseph Felsenstein and Michael Waterman became Associates of the program. At the first annual Fellows' meeting, I was listening to a talk by Monique Turmel, a biologist from Laval University comparing the order of markers on the chloroplast genomes of two algae. One of her diagrams, with lines connecting the marker positions on the two genomes, immediately suggested an interesting combinatorial statistics problem to me, which was easily solved with the help of my colleague Martin Goldstein, and indeed was well-known, as the late Sam Karlin later pointed out to me. Nevertheless this led to my 25-year preoccupation with chromosomal rearrangement and other gene order problems.

I soon expanded my statistical approach to combinatorial algorithmics. Fortunately, during the 1990s a good number of (but not all) the brilliant students and postdocs working with me found this problem area as attractive as I did. Whatever I know about algorithms, they taught me, while we formulated and solved, or almost solved, a number of comparative genomics problems, inversion distance for signed and unsigned genomes, more general genomic distances, the median problem and rearrangement phylogeny, genome halving, and the exemplar problem. These people are now all prominent figures in the field: John Kececioglu at Arizona, Mathieu Blanchette and Guillaume Bourque at McGill, Nadia El-Mabrouk at the Université de Montréal, Vincent Ferretti at the University of Toronto and David Bryant at Otago in New Zealand. Many other scholars joined us in this research endeavor, notably Pavel Pevzner and his students in California, who achieved a number of striking results.

At the same time I continued my gene-order modeling work, collaborating with Joseph Nadeau, who was briefly at McGill and Dannie Durand at Carnegie-Mellon.

When I left Montreal for the University of Ottawa in 2002, it did not take long for a number of other students and postdocs to get involved in my mathematical genomics projects. In a series of separate projects, Wei Xu and Chunfang Zheng made great strides in the median problem, including work with Eric Tannier in Lyon. Zheng also introduced guided genome halving, and developed a suite of techniques for ancestral gene order reconstruction. We became increasingly interested in flowering plants, because most of them descend from processes of genome duplication or triplication followed by massive loss of many of the extra genes. We developed consolidation algorithms, with Katherine Jahn of Bielefeld, and practical halving methods and applied them to detailed study of the grape, poplar, cereal, tomato, coffee, turnip and lotus genomes. Our biologist colleagues appreciate our ability to objectively deconstruct the processes of evolution, and I find myself finally able to indulge my high-school fascination with the botanical world!

Recent Publications:

- Phase change for the accuracy of the median value in estimating divergence time (A. Jamshidpey & D. Sankoff) BMC Bioinformatics 14, S15:S7 (2013)
- Ancient eudicot hexaploidy meets ancestral eurosid gene order (C. Zheng, E. Chen, V. A. Albert, E. Lyons & D. Sankoff) BMC Genomics 14, S7:S3 (2013)
- A consolidation algorithm for genomes fractionated after higher order polyploidization (K. Jahn, C. Zheng, Jakub Kovac & D. Sankoff) BMC Bioinformatics 13, S19:S8 (2012)
- Medians seek the corners, and other conjectures (M. Haghighi & D. Sankoff) BMC Bioinformatics 13, S19:S5 (2012)
- Listing all sorting reversals in quadratic time (K.M. Swenson, G. Badr & D. Sankoff) Algorithms for Molecular Biology 6, Doi: 10.1186/1748-7188-6-11 (2011)
- Multichromosomal median and halving problems under different genomic distances (E. Tannier, E., C. Zheng & D. Sankoff) BMC Bioinformatics 10, 120 (2009)

Books:

- Models and algorithms for genome evolution (C. Chauve, N El-Mabrouk & E. Tannier eds.), Springer, 2013
- Comparative Genomics: Empirical and Analytical Approaches to Gene Order Dynamics, Map Alignment and Evolution of Gene Families (D. Sankoff & J.H. Nadeau, eds), Kluwer, 2000

Related Links:

- My home page: http://albuquerque.bioinformatics.uottawa.ca

Honoring Carlos Castillo-Chavez' 60th Birthday!

by Melissa Castillo-Garsow

From Rock Star Researcher to Selfless Mentor: A Daughter's Perspective [4]

Looking back now, I recognize how lucky I am to have Carlos Castillo-Chavez as my father. His example taught me the value of hard work, the importance of community, the significance of mentorship...

I can still remember the year life changed for us all in the Castillo family. It was in 1996 and the phenomenon that did it was The Mathematical and Theoretical Biology Institute (MTBI). I was only 12 at the time, but the energy and excitement as my dad planned that first summer institute is unforgettable. Originally, established by Carlos Castillo Chavez at Cornell University, the intensive summer research experience for undergraduates, MTBI, is designed to provide the best quality support and research based education to individuals from nonselective universities that are underrepresented in the mathematical sciences. Since 1996, my father has thrown himself wholeheartedly into this and other similar programs with the goal of increasing the number of U.S. educated students, particularly members of underrepresented minority groups and women pursuing advanced degrees in the mathematical sciences through mentorship, cooperative learning and leadership training. He decided that advancing the careers of minorities and women was more important than continuing to advance his own already remarkable and distinguished career. As he once commented, "No matter how many papers you publish, you have to realize that your contributions to knowledge are really minimal. But changing the life of a young person is something very visible. What could be more rewarding than that?"


Prof. Carlos Castillo-Chavez

My father came to the United States in 1974, where he worked a number of odd jobs including a brief stint as a material handler at a cheese factory in Wisconsin. "Fortunately, the cheese factory was an eye opener, " he says. "I saw some people that had been there 20 or 30 years, and I knew that I had to do something else.

I decided I had to go to college." Initially unsure of what to study, my father, graduated in just two years in 1976 with dual degrees in Mathematics and Spanish literature. This always amazes me, because, so early on in a new country he already overcame so many barriers to success - language, a new country, and being just one of just two Latinos on the entire campus - yet was never deterred to stop.

He completed his master's degree in Mathematics at the University of Wisconsin-Milwaukee followed by a Ph.D. in Mathematics in 1984 (also then with two small children, my brother age 4 and me,

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[4] This article first appeared in the Mathematical Biosciences and Engineering (MBE) (V.10, Number: 5/6 October/December 2013) Special Issue in Honor of Carlos Castillo-Chavez 60th Birthday. For more articles please check out the Journal's website: `http://aimsciences.org/journals/contentsListnew.jsp?pubID=619`

just about to be born). After teaching for a year at the University of Tulsa in Oklahoma, he accepted a postdoctoral position in the Section of Ecology and Systematics and the Center for Applied Mathematics at Cornell University in 1985. Under the mentorship of Simon Levin, he began making a name for himself working on HIV and influenza research. He introduced the concepts of cross immunity in influenza epidemics and HIV and wrote more than 20 papers in just a few short years. Not surprisingly, he became incredibly sought after, accepting the offer to join the Cornell biometrics department in 1988 where he was promoted to associate professor in 1991 and to a full professorship in 1997. Over his 18-year tenure at Cornell, Castillo-Chavez would became one of the most prominent mathematicians in the country.

A few years ago, my father remarked to me that as a scientist he could have advanced his research and publications much more if it wasn't for his focus on mentorship and the increasingly large administrative duties he has taken on at Arizona State University (ASU) as executive director of not just MTBI, and the Institute for Strengthening Understanding of Mathematics and Sciences (SUMS), but also of The Mathematical, Computational and Modeling Sciences Center (MCMSC) and the graduate field in Applied Mathematics in the Life and Social Sciences (AMLSS) which he established at ASU in 2008 and which graduated 19 PhD students in 2011- 2012 (including 13 URMs, 11 Latinos/as and 2 African Americans). But that was a choice he doesn't regret, and by pretty much any one else's standards but his own, his research is at the top of the field.

I'm proud to say, my father, Carlos Castillo-Chavez is a force. He is someone who keeps tabs on not just his 27 PhD students and 23 postdoctoral students, but on hundreds of MTBI alumni - following, supporting, and motivating students from undergraduate studies through professorships, in some cases even from high school. Not only is he a mentor, he is a community maker. And like in Ithaca, he continues to be involved in the larger community through his work with high school students in Arizona through The Joaquin Bustoz Math-Science Honors Program, which has now existed more then 26 years.

So at least for me, it came as no surprise that MTBI was recognized by a second president (although this was my father's third trip to the White House), this time by President Barak Obama who honored the program with the Presidential Award for Excellence in Science, Mathematics and Engineering Mentoring in 2011. His mentoring efforts have also been recognized with the 2007 AAAS Mentor Award, as the 12th recipient of the American Mathematical Society Distinguished Public Service Award (2010); and well as ASU's Outstanding Doctoral Mentor Award. MTBI was also honored as a "Mathematics Program that Makes a Difference" by the American Mathematical Society in 2007.

Today, Carlos Castillo-Chavez is a Regents Professor, a Joaquin Bustoz Jr. Professor of Mathematical Biology, and a Distinguished Sustainability Scientist at ASU. And so despite his focus on mentorship, the accolades for research keep coming. Most recently, President Obama re-appointed him to the President's Committee on the National Medal of Science through 2015 (he was first appointed for the period 2010-2012) and SIAM recently honored his lifetime achievement at their 2012 meeting this past summer, and he just joined the Founding Class of Fellows of the American Mathematical Society.

Looking back now, I recognize how lucky I am to have Carlos Castillo-Chavez as my father. His example taught me the value of hard work, the importance of community, the significance of mentorship. His dedication to minorities inspires me to uncover unwritten histories of Latina women as a doctoral student at Yale, and to teach Latino writings in the future. And when a mathematician's work and example can inspire work in humanities - that is one very long reach.

About The Author:

Melissa Castillo-Garsow is a Mexican-American writer, journalist, and scholar currently pursuing a PhD in American Studies and African American Studies at Yale University. Her short stories, articles and poetry have been published or are forthcoming in numerous journals including Acentos Review, Hispanic Culture Review, Off The Coast, El Diario/La Prensa, The Bilingual Review, Women's Studies, PORTAL: The Journal of Multidisciplinary International Studies and Words. Beats. Life: The Global Journal of Hip-Hop Culture. Melissa's new novel "Pure Bronx" is just out: http://www.melissacastillogarsow.com

Research Interview

Protecting the Environment with Mathematical Models

Caroline Bampfylde talks with Santiago Schnell about her work on ecosystem and risk assessment modeling for the Alberta Government

Would you briefly explain what your work for the Alberta government consists of?
I research environmental issues related to Oil Sands development where the abiotic environment interacts with biodiversity, e.g., how industry affects water, land and air and what the impact is on fish, wildlife and vegetation.

Tell us about your academic background and research training.
My undergrad and masters are in mathematics, while my PhD is in plant sciences/mathematical biology. I spent 4 years as a postdoc with Mark Lewis working on applied ecological modeling problems.

Who or what inspired you to become a scientist in the first place?
A science expedition in the Queensland rainforest inspired me towards science. But I decided to pursue a career in science after graduate school when I met interesting people doing fascinating applied work at SMB and other conferences.

What does it mean to you, on a personal level, to be a mathematical biologist in a government agency?
I love that I can use my science skills to work on issues of importance to me and the Alberta public while influencing environmental policy. I also feel lucky to work with very smart people both within government and outside in academia, industry, NGOs and communities.

Have you been surprised by anything during your tenure with the Alberta government?
The pace of work: fast and slow at the same time. We work intensely on a file for a short period of time and then it will seemingly languish for months. While in reality it may be working its way through a political process over my head. Only for the file to return for another rapid turnaround.

What do you classify as your most important contribution as mathematical biologist in a government agency?
Making science and modeling understandable to non-scientists and management to enable sound decision making

What would your message to a young and aspiring mathematical biologist be?
Work on something that interests you. Never stop learning and challenging yourself. Listen to your mentors.

If you were not a scientist, what would you be?
A landscape gardener.

If you have any spare time, what do you do when you are not working?
Ideally, having fun with my daughter, being in the outdoors and traveling, but often renovating.

About Caroline Bampfylde

Dr. Caroline Bampfylde is an ecosystem and risk assessment modeler with the provincial government of Alberta's department of Environment and Sustainable Resource Development in Edmonton, Canada. Her focus is on environmental management in the Oil Sands regions of northern Alberta. Caroline is the chair of Society for Mathematical Biology's mentoring committee. She bicycle-commutes in the snow free months. For more info: `http://www.math.ualberta.ca/~cbampfylde/`

The Future of Mathematical Biology

Kelsey Gasior, PhD Student in the Biomathematics Program at North Carolina State University, Student of Dr. Sudin Bhattacharya of The Hamner Institutes for Health Sciences and Dr. Marlene Hauck of The North Carolina State University College of Veterinary Science

What attracted you to mathematical biology?
During my undergraduate work at the University of Michigan, I enrolled in a mathematical biology course and, after about a week, I knew I wanted to explore mathematical biology further. To this day, I find it fascinating how these two fields come together and influence each other. Also, I love that mathematical biology is a field where creativity and logic overlap. Every model created must be motivated biologically, but how each model crafted is unique to both the subject, as well as the scientist.

What is your current research project?
I am building a mathematical and simulation-based model to examine the relationship between intracellular signaling pathways and the cellular behavior associated with the Epithelial-Mesenchymal Transition (EMT) in solid tumors- a crucial step in the metastasis of cancerous cells.

What specific areas are you interested in investigating?
In addition to my current research, I am very interested in the tumor-immune system dynamics, as well pharmacology and pharmacokinetics. I am interested in how the immune system and the solid tumor influence each other, as well as the positive and negative effects drug therapy can have when introduced to this system.

What do you hope to do after graduation?
After completing my PhD, I hope to go on to a post-doc where I can continue researching and modeling different aspects of cancer biology. I would like to extend my current research of EMT and further explore the dynamics of cancer metastasis, as well as how to combat it. I would like to research therapeutic techniques that do not induce negative side effects for the patient but will still help slow and prevent metastasis.

What advice will you give to an undergraduate interested in a mathematical biology career?
Network, network, network! Get to know the other people in your department, both your peers and your professors. Maybe their research topics will inspire you to investigate a new area of biology, to try different modeling techniques, or to examine a problem from a new angle. You never know where you are going to find inspiration for a future research topic or someone you want to work with.

What inspires you scientifically?
My biggest inspiration comes from my advisors, Dr. Hauck and Dr. Bhattacharya because they are constantly challenging me to step outside of my comfort zone. As a result of their guidance, I have learned to ask more questions and push myself to dig deeper and explore our research through different perspectives.

Why did you join the Society for Mathematical Biology?
I thought that being a part of SMB would be a great

way to keep up on the current research in mathematical biology and network with other scientists. Also, I would like to thank the Society of Mathematical Biology for graciously funding my trip to Sydney, Australia to attend the US-Sydney Workshop on Mathematical Models of Tumor-Immune System Dynamics.

Kelsey Gasior's PhD advisor, Dr. Sudin Bhattacharya says:

Kelsey started working with me two years ago while still a Master's student in biomathematics at NC State University. She showed great enthusiasm in taking on a difficult project, modeling the epithelial-to-mesenchymal transition (EMT) in solid tumors using a multi-scale approach. She is combining an ODE-based kinetic model to represent intracellular signaling events triggered during EMT with a spatial agent-based model of the tumor and its microenvironment. I have been particularly impressed by her ability and willingness to pick up ideas from cellular and cancer biology to which she had not been previously exposed. Since joining the PhD program at NC State, Kelsey has delved more deeply into the project. She has also eagerly accepted the opportunity to do experimental work in the laboratory of Dr. Marlene Hauck with cancer cell lines to generate data that can be directly applied to calibrate her model. Kelsey is developing exactly into the kind of scientist, conversant both in the languages of mathematics and biology, that the field of mathematical and computational biology urgently needs.

"The Future of Mathematical Biology" is a new column intended to highlight graduate students and postdocs in Mathematical Biology. Do you want to nominate a student or a postdoc from your research group? Please send your nomination to Santiago Schnell: schnells@umich.edu.

The 2014 Joint Annual Meeting of the JSMB & SMB, Osaka, Japan

Call for Contributed Oral Talks and Poster Presentations

by Toshiyuki Namba

The joint annual meeting of the Japanese Society for Mathematical Biology (JSMB) and the Society for Mathematical Biology (SMB) will take place at Osaka International Conference Center in Osaka, Japan, from July 28-August 1, 2014.

The meeting will feature nine plenary lectures, by Dr. Nanako Shigesada (2013 Akira Okubo Prize Awardee, Professor Emeritus of Nara Women's University, Japan), Carson C. Chow (NIH, USA), Dr. Iain D. Couzin (Princeton University, USA), Dr. Steve A. Frank (Univ. California at Irvine, USA), Dr. Hawoong Jeong (KAIST, Korea), Dr. Laura Miller (University of North Carolina, USA), Dr. Akiko Satake (Hokkaido University, Japan), Dr. Tatsuo Shibata (Center for Developmental Biology, RIKEN Kobe, Japan), and Dr. Yanni Xiao (Xi'an Jiaotong University, China).

Now, call for contributed oral talks and poster presentations are open. The deadline for contributed oral talks is *April 15, 2014*, and the deadline for poster presentations is *May 15, 2014*. Please visit http://www.jsmb.jp for details.

Questions regarding the conference can be directed to Toshiyuki Namba at: tnamba@b.s.osakafu-u.ac.jp.

Positions Available

Masters in Systems & Synthetic Biology, France: A limited number of stipends may be proposed to two foreign students in the Masters in Systems & Synthetic Biology, mSSB (http://www.mSSB.fr) on the basis of academic excellence. Interested students must send before February 5, 2014, to Cécile Gasse (cecile.gasse@issb.genopole.fr), a CV in English or French, including diplomas, dates of obtention, class ranks, marks, languages spoken, university transcripts from the last 4 years of higher education, two recommendation letters or the names of two reference teachers, and their motivation letter in English or French (one or two pages).

PhD in Mathematical Immunology, Heidelberg, Germany: Applicants should send a cover letter stating their interest of research and their previous work, a detailed CV and contact information for two or three academic references to frederik.graw@bioquant.uni-heidelberg.de. Web: `www.bioquant.uni-heidelberg.de/research/junior-research-groups.html`

Postdoc in Multi-scale modeling of the CD8 immune response, Inria Lyon, France: Applications are invited for a one-year post-doc position available in the interdisciplinary team "Dracula" at Inria (http://dracula.univ-lyon1.fr/), Lyon, France. Experience in Gene networks, Cell population dynamics, Analysis of systems of ODEs or PDEs, Numerical computation, will be a plus. Please send your CV, your list of publications, a motivation letter, and the names of two referees to Dr. Fabien Crauste (crauste@math.univ-lyon1.fr)

Postdoc in Modeling Virus Dynamics & Evolution, UCSF: The postdoctoral position will be for 1 year initially and can be extended contingent upon mutual agreement and available funding. Interested individuals are requested to send their CV, publication list, PDF files of two-three publications, and names and electronic addresses of two references to Dr. Igor Rouzine, igor.rouzine@gladstone.ucsf.edu.

PhD & Postdoc in Collaborative Mathematics at CRM: The Centre de Recerca Matematica (Barcelona, Spain) offers PhD and postdoc positions within the Collaborative Mathematics Program funded by Obra Social La Caixa. Ph.D. candidates are expected to have an M. Sc in mathematics, physics or an area relevant to the subject of the project. Candidates for the postdoc positions are expected to have a recent PhD in mathematics, physics or a related area as well as an outstanding research track record. The deadline for submitting an application is January 10th 2014. There will be a second call later in 2014. For more details please go to: `http://www.crm.cat/en/ResearchTraining/CollabMathResearch/Pages/Description.aspx`

Postdoc in Mathematical Biology, Oregon State University: A Postdoc. position in Mathematical Biology is available at the Oregon State University to work with Prof. Patrick De Leenheer. Requirements are: 1. PhD in Mathematics, Applied Mathematics or a related field. 2. Strong analytical skills in ODEs, PDEs, discrete dynamics or dynamical systems. 3. Highly motivated to pursue interdisciplinary research. The position starts in fall of 2014, but the start date is negotiable. Applicants must submit the following: 1. American Mathematical Society cover sheet 2. Curriculum Vitae 3. One page statement explaining research interests and research plans 4. Copies of up to 3 selected publications or manuscripts 5. At least 3 letters of reference. For full consideration all application materials must be submitted via mathjobs.org and received by January 15, 2014.

Four Postdoc Positions: Conservation Science, U. of Queensland: We have four well-funded quantitative postdoc. positions available at The U. of Queensland in the broad field of conservation science. *Two positions* are available until 30 December 2018 with the Centre for Biodiversity and Conservation Science. The fellows will work closely with Professor Hugh Possingham who is in both the mathematics and ecology departments Reference No. 495300. Applications close 10 January 2014. More Information: `http://uqjobs.uq.edu.au/jobDetails.asp?sJobIDs=495300&stp=AW`. *Two postdoctoral fellowships* are available for three years with the Centre of Excellence for Environmental Decisions. The fellows will work closely with Chief Investigators of our ARC Centre for Excellence - `http://ceed.edu.au/`. Reference No. 495304. Applications close 17 January 2014 More Information: `http://uqjobs.uq.edu.au/jobDetails.asp?sJobIDs=495304&stp=AW`

Institute Events

NIMBioS

Upcoming Events & Opportunities at NIMBioS

Spring Opportunities Workshop for Women in the Mathematical Sciences April 9-11: This workshop will familiarize women in the mathematical sciences with professional opportunities in academics, industry and government labs and help them thrive in mathematics-related fields. Application deadline: January 20, 2013. For more information about the workshop and how to apply: `http://www.nimbios.org/education/WS_opportunities`

Investigative Workshop: Modeling Contamination of Fresh Produce, April 24-25: NIMBioS is now accepting applications. Application deadline: January 20, 2014. For more information about the workshop and how to apply: `http://www.nimbios.org/workshops/WS_produce`

Tutorial Parameter Estimation for Dynamic Biological Models, May 19-21: This tutorial is for biologists interested in doing statistics with more complex non-linear models of their data and for mathematicians interested in learning how to apply their modeling skills to the unique demands of real dynamic biological data. Application deadline: January 31, 2014. For more information about the tutorial and how to apply: `http://www.nimbios.org/tutorials/TT_data`

Investigative Workshop: Leptospirosis Modeling, June 3-5: Leptospirosis is a zoonotic disease of global public health importance with complex transmission dynamics. This workshop will explore mathematical tools for describing within-host dynamics of Leptospira infection and immunity in reservoir and incidental hosts, multi-host, multi-species Leptospira transmission dynamics in urban and rural settings; and environmental drivers of leptospirosis transmission in animals and people. Application deadline: February 10, 2014. For more information about the workshop and how to apply: `http://www.nimbios.org/workshops/WS_leptospirosis`

DIMACS

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

MPE 2013+ Workshop on Sustainable Human Environments, April 23 - 25: Location: DIMACS Center, CoRE Building, Rutgers University Organizers: Midge Cozzens, DIMACS, Rutgers University (Education Chair), Lou Gross, University of Tennessee, Fred S. Roberts, DIMACS, Rutgers University, Alexis Tsoukias, LAMSADE, Universite Paris Dauphine, and Laura Wynter, IBM. Deadline to apply for travel support: February 1, 2014. More info: `http://dimacs.rutgers.edu/Workshops/HumanEnvironments/announcement.html`

MPE 2013+ Workshop on Global Change, May 19 - 21: Location: University of California, Berkeley. Organizers: Holly Gaff, Old Dominion University (Education Chair), Virginia, Wayne Getz, UC Berkeley, Hans Kaper, Georgetown University, and Steve Sain, National Center for Atmospheric Research (NCAR). Deadline to apply for travel support: March 1, 2014. For more info: `http://dimacs.rutgers.edu/Workshops/GlobalChange/`

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 website: http://www.smb.org for more information.

Editors: Holly Gaff, Srividhya Jeyaraman, & Amina Eladdadi email: editor(at)smb(dot)org