Society for Mathematical Biology

MAY 2014
Newsletter
Volume 27, No. 2

IN THIS ISSUE

Society

Recent Conference Reports

Perspectives

SMB Education Highlights

People

The 2014 Joint Annual Meeting of the JSMB & SMB
Osaka, Japan
July 28-August 1, 2014

JSMB SMB 2014

https://sites.google.com/site/jsmbsmbjointmeeting2014osaka/home

Letter from the President

Dear SMB members,

When I was out plucking ruefully at the dandelions in our lawn the other day, I was accosted by my lawyer neighbor who was doing the same, although rather more forcefully. "*What do you teach, anyway?*" he asked, and I said "*math and biology*", which elicited the response we have all become so used to, "*Those seem like two completely unrelated subjects.*" He seemed the wrong person to get into an argument with, so I attacked another dandelion. Perhaps the Society will have succeeded when we don't hear some such response every time we confess to what we do.

As I look through this newsletter and think about the goals of the Society, it is clear that neighbors are just one of the many audiences we have a chance to educate. Schoolchildren, college students, academic colleagues, administrators, and medical researchers need to feel the gathering wave of successful education, research, and application that mark not so much an oncoming flood of mathematical biology as the filling of a waterway.

This mathematical waterway is a conduit of scientific communication. Historically, cities were founded almost invariably near waterways less for water supply and security than for efficient transportation. Even today, floating a ship, perhaps from California to Japan, takes far less energy than any other mode of transport because the buoyancy of the water does most of the work of fighting gravity and friction. And that is precisely the promise of mathematical biology. When the good ship math biology is sailing the intellectual oceans with cargo ranging from cancer delivery strategies and models of ant behavior to ways to combat biofilm-associated diseases, our neighbors of all sorts will know that mathematics belongs in biology because it often provides the most efficient way to solve problems.

The upcoming joint meeting in Osaka with the Japanese Society for Mathematical Biology makes connections across geographic rather than conceptual distance. Even in the era of globalization, the rich traditions of Japanese, Chinese and Korean science are something many of us in Europe and the Americas know only through published work and some lucky encounters. I am looking forward to diving more deeply into that world and expanding my network of friends, colleagues and collaborators.

Sincerely,

Fred Adler

SMB Treasurer Update

Dear SMB members,

It is hard to believe that another fiscal year for SMB has come and gone. Our year runs from April 1 through March 31. Many thanks to Torcom Chorbajian for his multiple years of service to the society and for graciously doing the taxes for 2013! He has been instrumental in keeping the society moving in the financial aspects. As of November 2012, we began a transition period in which I began to learn the ropes, if you will. With Torcom and Heiko Enderling's membership support, we migrated to an online membership system with a connection to PayPal. Heiko has done a fabulous job of keeping in contact with Springer regarding the membership so that the Bulletin of Mathematical Biology can be properly distributed to you, either in print or electronically.

The Travel and World Outreach Committees have worked to provide opportunities for people to host workshops throughout this past year. There have been events in Buenos Aires, Columbia, and Israel, to name a few. An entire programmatic concept related to Models and Methods in Ecology, Epidemiology, and Health created opportunities for workshops throughout this last year. For each sponsored event, documentation is required. A standardized SMB travel form has been developed. Each participant completes the fillable form provided by the workshop organizer or via my email, kfister@murraystate.edu. After the workshop organizer has determined the allocation of the funds and the forms with the receipts have been received, then disbursement has been sent. Please note that if a wire transfer is requested that there is a cost associated with that which is subtracted from the reimbursement funds. For each workshop, the paperwork for all is requested to be returned within a month of the event, if at all possible. A second item related to documentation is an article that is to be sent to the SMB Newsletter concerning the workshop. If you have not done so, please send your articles to Amina Eladdadi at eladdadi@gmail.com.

Some bookkeeping items that have occurred this past year are the use of QuickBooks for all the income and expenses of the society. We are a solid group financially to date. We are working on mechanisms to enhance the growth of our funds. There is a task force that is looking at the cost of membership for the different categories and the benefit for our members. We have also had our Articles of Incorporation updated, and they are now current and in good standing through 2016 as required by the government.

As you are planning for our joint annual meeting hosted by the Japanese Society for Mathematical Biology in Osaka, Japan from July 28-August 1, remember to see if you are eligible for the Landahl-Busenberg awards, http://www.smb.org/meetings/landahl.shtml.

Your support of SMB has given opportunities to researchers to continue their studies in different cultures and interdisciplinary aspects. Thanks for your continued support!

Renée Fister,
SMB Treasurer

The 2014 JSMB/SMB Annual Meeting Announcement

Dear SMB members,

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 joint meetings of the SMB and the JSMB were held first at Hilo, Hawaii in 2001, and second at San Jose, California in 2007. This third joint meeting is the first one held in Japan, and co-sponsored by the Chinese Society for Mathematical Biology and the Korean Society for Mathematical Biology. The themes of the conference will include all areas of mathematical biology at the interface of mathematics and its application to biology. Professor Masayasu Mimura (Meiji University, Tokyo), President of the JSMB, will chair the conference.

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) and two Lee Segel prize lectures.

Seventy one minisymposia (including double sessions) were proposed in the areas of Medicine, Virus, Cancer, Cell Biology, Developmental Biology, Pattern Formation, Biological Movement, Network, Epidemiology, Ecology, Evolution, and Mathematics from USA, Canada, UK, Germany, France, Austria, Poland, Australia, Saudi Arabia, China, Korea, Taiwan, and Japan. The number of minisymposia exceeded the total of numbers of minisymposia and contributed sessions combined at the Tempe meeting. In expectation of numerous presentations at contributed oral and poster sessions, we will be able to welcome many participants from all over the world.

Summer in Osaka is very hot and humid, so although the temperature itself is much lower than that at Tempe, casual wear made of fabric that breathes well is recommended. The local organizing committee (`https://sites.google.com/site/jsmbsmbjointmeeting2014osaka/organizing-committee`) will make every effort to appreciate excellent presentations and productive discussion in a comfortable atmosphere.

Please visit `https://sites.google.com/site/jsmbsmbjointmeeting2014osaka/home` for details.

Minisymposia: `https://sites.google.com/site/jsmbsmbjointmeeting2014osaka/minisymposia` .

Toshiyuki Namba,
On behalf of the Organizing Committees

Advances in Mathematical Biology

Universidad Autónoma de Occidente, Colombia, November 20th, 2013

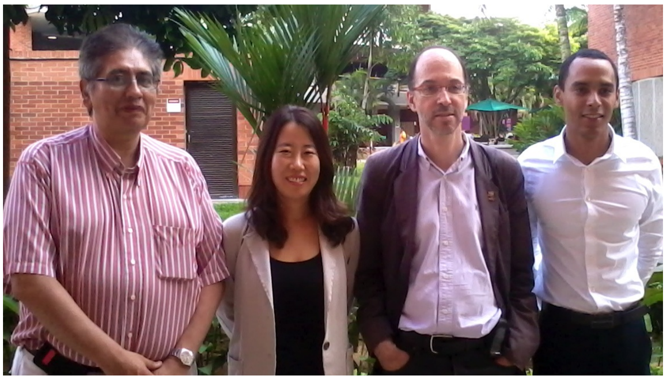
by Paula Gonzalez

Report by an SMB WOC - Grant Recipient

The workshop AMAB 2013 was held at Universidad Autónoma de Occidente in Cali Colombia, on November 20th, 2013. In the previous workshop (2010) we had around 30 participants, while at this time the audience reached about 50 people. There were students and professors from several universities in Colombia: Universidad de Los Andes (Bogotá), Universidad del Quindio (Armenia), Universidad de Pasto (Pasto), Universidad del Valle, Universidad Icesi, and Universidad Autónoma de Occidente (Cali).

These universities represented different geographical regions of Colombia. Also we had researchers coming from United States, France, Korea and Guatemala.

With the SMB world Outreach support we were able to invite Professor Sunmi Lee from Kyung Hee University (Korea), Dr. Reinaldo Sanchez from The University of Texas at El Paso (USA) and Professor William Polanco from Rafael Landivar University (Guatemala). The mission of these enthusiastic young scientists was not only to offer mini-courses and oral presentation, but also to motivate and encourage our students and young researcher into pursuing further academic career in the area of mathematical biology, which we visualize has a promising future in Colombia.



Carlos Castillo-Chavez, Sunmi Lee, Michel De Lara , and Reinaldo Sanchez

Group Photo

During the workshop we had three mini-courses: Optimal Control, Optimization and Applications in Machine Learning, and Neurocomputation. These were offered by Professors Sunmi Lee, and David Ramirez respectively. The Plenary lectures were presented by Professors Carlos Castillo-Chavez from Arizona State University, Vladick Kreinovich from The University of Texas at El Paso and Michel De Lara from Universite Paris-Est France.

There were poster and oral presentations given by students and researchers from the different participant universities from Colombia. It was a great opportunity for both undergraduate and graduate students to get constructive feedback from outstanding researchers; in particular they had great time learning from Carlos Castillo-Chavez a well known mentor and leader in the area. For most of the students it was the first time to attend a workshop with top-notch researchers. Based on all these accomplishments, we truly believe that our main goal, i.e. dissemination of research results among local scholars and seeking of possible collaboration for further research, was reached and we look forward to continue working with the same commitment and professionalism.

We want to thank The Society for Mathematical Biology for their financial support, without it, it would have been more difficult to invite these high quality researchers and reach our goals.

Systems Approaches in Immunology

Santa Fe, NM, January 10-11, 2014

by Vitaly Ganusov

Report by an SMB - Grant Recipient

The third biennial conference on Systems Approaches in Immunology and Infectious Diseases was held in Santa Fe, NM on January 10 - 11, 2014. As with the first two international workshops, this meeting provided a multidisciplinary forum to discuss the latest developments at the boundary of experimental and computational immunology. It was organized under the premise that understanding of immunology will be advanced by the development of theoretical and experimental techniques and models that bring together phenomena at different levels of complexity. Research themes focused on systems-level analysis of immunological processes and spanned the molecular, cellular, population, and organismal levels, both experimentally and theoretically. The meeting included talks, panel discussions and a poster session. It was organized by Vitaly Ganusov (University of Tennessee), Steven Kleinstein (Yale School of Medicine), Alan Perelson (LANL) and Ruy Ribeiro (LANL). The meeting was held under the auspices of the Center for Nonlinear Studies (CNLS) of Los Alamos National Laboratory, with support from the Society for Mathematical Biology and the Army Research Office.

The meeting started out on Friday January 10 with a session on Systems Approaches in Humoral Immunity. The first two talks focused on B cell responses in the germinal centers. Mark Shlomchik from the Immunology Department at the Pittsburgh School of Medicine gave a brief history of how modeling has been used to investigate B cell population dynamics and affinity maturation in the germinal center. Next, Rob De Boer from Theoretical Biology and Bioinformatics, Utrecht University proposed a mathematical model for how germinal centers evolve broadly neutralizing antibodies. Arup Chakraborty from the Department of Chemical Engineering, MIT continued on the theme of HIV. He presented a statistical physics approach to designing immunogens that could be used as vaccine components.

Venue of the meeting: beautiful Santa Fe

Following a short break, the next talk was given by Garnett Kelsoe from the Department of Immunology at Duke University School of Medicine.This talk focused on the origin of natural antibodies, antibodies which arise in young individuals in the absence of exposure to any foreign antigen. The final talk in the session was given by Alan Perelson from Los Alamos National Laboratory, who presented a model, developed with Jessica Conway also from Los Alamos, to account for post-treatment control of HIV to undetectable levels using a model that exhibited bistability in the viral set-point of HIV.

On Friday afternoon, the session theme was Systems Approaches in Cellular Immunity and the session consisted of six contributed presentations on this topic. The first four covered issues of T-cell homeostasis. Jose Borghans from the Immunology Department at the University Medical Center in Utrecht, Netherlands, presented experimental and modeling work to understand the maintenance of the lymphocyte pool during healthy ageing. Next, Robin Callard, from the Institute of Child Health at University College London, analyzed T-cell reconstitution in HIV-infected children under antiretroviral therapy. Julia Drylewicz, also from Utrecht, presented kinetic T-cell data from mice and humans to study whether recent thymic emigrants formed a short-lived sub-population of the naive T-cell compartment. Changing the subject slightly, Vitaly Ganusov, from the University of Tennessee, presented detailed analyses of experiments on lymphocyte recirculation, where radioactively labeled lymphocytes were injected in animals and then collected at several times. After a coffee break, Benedict Seddon of the Medical Research Council in the UK presented work on trying to understand CTL killing efficiency from different target types, including different levels of antigen on the target. The final talk of the day was by Victor Garcia of the ETH in Zurich. He re-analyzed data on HIV escape from CD8+ T-cell recognition (timings and rates), re-interpreting the observations in terms genetic interference (and linkage) among HIV escape strains. On Friday afternoon there was an informal poster session, with a reception followed by dinner. There were about 20 posters presented, which generated much discussion. Indeed the posters were on display throughout dinner time until the next morning, and generated much traffic and lively conversation between the authors and the other participants.

The second day of the meeting, January 11, opened with a morning session on System Approaches for Understanding Immune Responses. It was opened by Denise Kirschner, the University of Michigan, who gave a thorough overview of her work over the last decade on using multiscale and systems approaches to uncovering the mechanisms governing immunity to tuberculosis. Her talk was followed by an exciting presentation by John Tsang from the Laboratory of Systems Biology, NIAID and the Tarns-NIH Center on Human Immunology, discussing methods for quantifying the immune response to seasonal influenza vaccination focusing on the variation in response among 63 healthy volunteers. Matthew Krummel from the University of California at San Francisco then discussed his group's intravital imaging studies of T cell motion focusing on the theoretical question of how T cells move to maximize surveillance for foreign material on the surface of antigen-presenting cells. Lastly, Joshua Schiffer, MD from the Fred Hutchison Cancer Research Center and University of Washington in Seattle described work done over the last decade by his lab to understand the spatial-temporal aspects of human simplex virus-2 (HSV-2) infection and immune responses in the human genital track.

On the final session of the meeting (Saturday afternoon) the main theme of presentations was Systems Approaches in Signaling. The session stated with a talk by Lily Chylek, from Cornell, on T cell receptor signaling and the role of SHP-1 in enhancing early signaling events. Next, Jialiang Wu, from the Yale School of Medicine, presented a mathematical model of interferon stimulated gene (ISG) dynamics. The next talk by Chitra Nayak, the University of Toronto, also focused on the interferon response. Rodolphe Thiebaut, INSERM, then presented experimental data from a recent trial of a therapeutic vaccine against HIV involving ex vivo generated dendritic cells loaded with HIV-derived lipopeptides. Daniel Gadala-Maria, from Yale School of Medicine, presented a novel method for detection of novel immunoglobulin (Ig) V segments from next-generation Ig sequencing data (Rep-Seq). The next talk by Grant Lythe, University of Leeds, switched gears to dynamics of T cells in the body with the question of how many different T cell specificities can the body maintain. The session was concluded by the talk of Phillip Johnson, Emory University, discussing the puzzle of T cell receptor repertoires in humans.

The meeting was well attended by junior scientists, and five of these received travel support from the Society for Mathematical Biology. Altogether, this was a very productive meeting, in the lovely setting of "Inn at Loretto" in Santa Fe, which allowed plenty of discussion among the participants. The feedback received by the organizers was in general very positive, with encouragement to hold a fourth installment of these meetings in January 2016.

Discussions did not stop after presentations: Garnett Kelsoe, Alan Perelson, Arup Chakraborty, Rob De Boer, and Mark Schlomchik

Reports from The 2014 Joint Mathematics Meetings

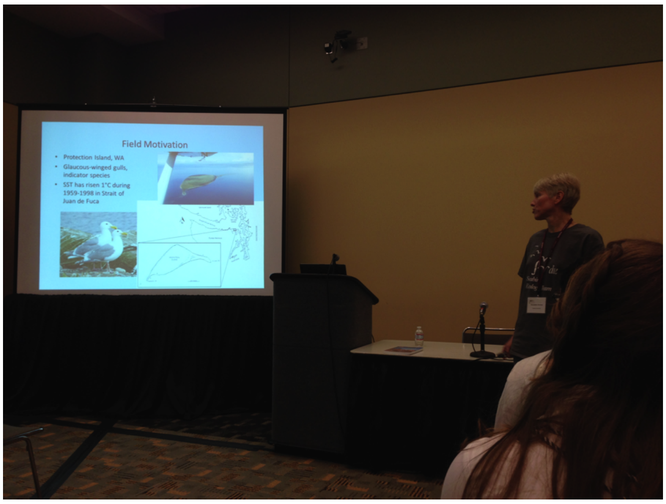
Baltimore, MD, January 17, 2014

Mathematics in Natural Resource Modeling

by Catherine Roberts

The sessions on Mathematics in Natural Resource Modeling at the Joint Mathematics Meeting in Baltimore, MD in January 2014 included a total of 16 talks and were very well-attended. Further information about the talks can be found here: `http://jointmathematicsmeetings.org/meetings/national/jmm2014/2160_program_ss43.html`

Suzanne Lenhart : Optimal control in models of management of forest resources



Shandelle Henson: Reproductive synchrony in populations can ameliorate the effects of adult-on-juvenile cannibalism

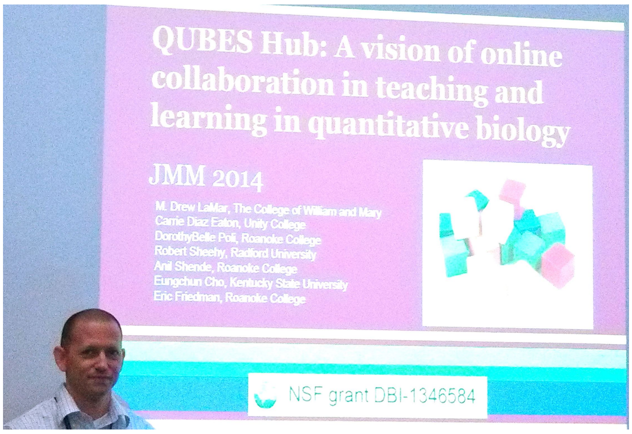
Undergraduate Mathematical Biology Education

by Tim Comar

On Friday, January 1, the MAA Special Interest Group in Mathematical and Computational Biology (BIO SIGMAA) sponsored the MAA Contributed Paper Session, Trends in Undergraduate Mathematical Biology Education at the Joint Mathematics Meetings in Baltimore. The topics of the twelve talks include discussions of Bio-calculus courses, upper level courses, including a presentation of a course on the Mathematics of Cancer at Arizona State University by Eric Kostelich, and undergraduate research projects.

One particular highlight was Drew LaMar's introduction to the currently under development Quantitative Undergraduate Biology Education and Synthesis (QUBES) Hub, which will serve a central resource for educational materials in quantitative biology and a social network. As quantitative tools are recognized as more important to biologists, and biological applications of more interest to mathematicians, an interdisciplinary approach to education in these areas is crucial.

A similar session will occur at the 2015 Joint Mathematics Meetings, and a contributed paper session focusing on undergraduate research projects will occur at Mathfest in 2014 in Portland, OR. Check out the website for abstracts: `http://jointmathematicsmeetings.org/meetings/national/jmm2014/2160_program_friday.html#2160:MCPCOMN5` and


QUBES Hub: A vision of online collaboration in teaching and learning in quantitative biology

JMM 2014

M. Drew LaMar, The College of William and Mary
Carrie Diaz Eaton, Unity College
DorothyBelle Poli, Roanoke College
Robert Sheehy, Radford University
Anil Shende, Roanoke College
Eungchun Cho, Kentucky State University
Eric Friedman, Roanoke College

NSF grant DBI-1346584

Drew LaMar giving his presentation on QUBES

Translating Cancer Data and Models to Clinical Practice

University of California Los Angeles, February 10-14, 2014

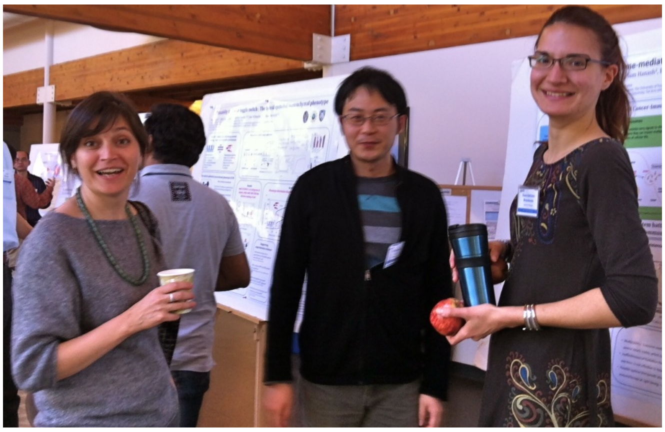
by Dana-Adriana Botesteanu & Geoffrey Clapp

This workshop on understanding cancer dynamics from a multitude of morphological, proteomic, genomic and mathematical perspectives took place at the Institute of Pure and Applied Mathematics (IPAM) at the University of California Los Angeles (UCLA) from February 10-14, 2014. The workshop was organized by Gyan Bhanot (Rutgers University, The Cancer Institute of New Jersey), Tom Chou (UCLA, Mathematics), and Doron Levy (University of Maryland, College Park) and was supported by the National Science Foundation, UCLA and IPAM.

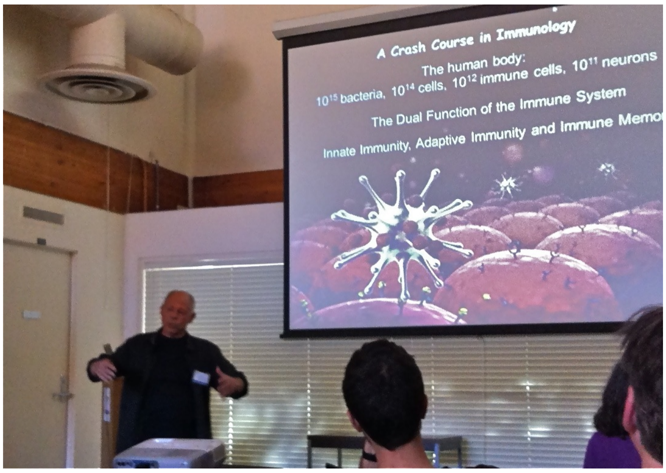
The purpose of this workshop was to discuss current investigative directions in cancer research. The workshop brought together researchers from a variety of backgrounds, including medical doctors, biologists, physicists, mathematicians, and computer scientists, to discuss aspects of cancer initiation, progression, metastasis and treatment. It was fascinating to compare the problems that each group was studying and how their approaches to these problems differed. The presentations given by clinicians were especially useful in identifying areas where mathematical modeling could be applied to better understand a phenomenon.

The first day of the workshop began with a presentation from Robert Gatenby (Moffitt Cancer Center Research Institute), who emphasized that cancer therapy should be adaptive and patient-specific. Moreover, rather than always choosing high-dosage therapy aimed at eradicating cancer, it may be beneficial to consider alternative drug schedules, for instance, administering the minimal effective dose that will maintain manageable levels of cancer. Beatrice Knudsen (Cedars-Sinai) discussed the importance of identifying good predictors in describing the pathology of a cancer, by using growth patterns, nuclear morphology, and immunohistochemical information to measure cancer severity in patients. Linda Liau (UCLA) reported theoretical and empirical results on using immunotherapy in treating glioblastomas, while Edwin Posadas (Cedars-Sinai) discussed the challenges in identifying molecular classifiers and markers in diagnosing prostate cancer, given the peculiar natural history of the disease. Doron Levy (Maryland) closed the afternoon with a mathematical modeling presentation on the role of symmetric and asymmetric division of stem cells in developing drug resistance to cancer, using ordinary differential equations. A poster session and a reception generously hosted by IPAM followed.

On the second day, the first speaker, Joseph Lehar (Novartis), discussed the role of cancer cell lines in drug discovery and the identification of synergistic combinations of existing drugs. Shridar Ganesan (The Cancer Institute of New Jersey) discussed the limitations of existing chemotherapeutic treatments in targeting cancer cells, given the interplay between cell cycle dynamics and DNA repair pathways. Monica Nicolau (Stanford) presented a framework for visualizing genetic changes in tumors via topological clustering. In the afternoon, Eytan Domany (Weizmann Institute of Science) presented an algorithm quantifying pathway deregulation levels in individual tumors based on genetic expression data, in order to illuminate potential pathways associated with cancer survival. Trevor Graham (Barts Cancer Institute) ended the second day of the workshop with a discussion of carcinogenesis viewed as an evolutionary Darwinian process. He suggested that genetic diversity in tumors constitutes a universal biomarker for cancer prognosis and progression.



Inna Brainis , Mingyang Lu, and Dana-Adriana Botesteanu at the poster session



Prof. Eshel Ben-Jacob Lecturing on Exosomes and the Cancer-Immunity Cyberwar

Wednesday began with two more presentations related to tumor initiation. Darryl Shibata (University of Southern California (USC)) introduced a framework for constructing a tumor's ancestral tree based on the spatial distribution of mutations within it. Moreover, the distribution of mutations can be used to distinguish between tumors with abnormal cell motility, and therefore a high risk of invasion and metastasis, and benign tumors, that can potentially go untreated. Tibor Antal (Edinburgh) discussed the application of multi-type branching processes in determining time to appearance of passenger mutations and the probability of tumor relapse after initial therapy. The last morning presentation, given by Hans Sieburg (Sanford-Burnham Medical Research Institute), considered the clonal diversity of hematopoietic stem cells and its implications regarding the mechanisms driving leukemias. In the afternoon, Eshel Ben-Jacob (Tel Aviv University) introduced the concept of exosomes as packages that facilitate long-distance communication between cells. He considered a mathematical model of cancer and immune cell competition that incorporates exosomes. Benjamin Berman (USC) concluded the third day with a presentation of a new method for analyzing epigenomic data, to identify changes in epigenetic state across subpopulations of a tumor.

On Thursday, Sui Huang (Institute for Systems Biology) presented the concept of an epigenetic landscape, where certain attractors represent healthy development while others, which are not usually occupied by any cells, represent cancer. Genetic mutations or therapy can cause changes in the landscape that result in cells falling into cancer wells or developing drug resistance. Peter Jones (USC) focused on epigenetic changes involved in cancer and the combination of epigenetic therapies with other standard techniques. Stefanie Jeffrey (Stanford) pointed out that it is frequently the spread of cancerous cells that leads to the demise of a patient, emphasizing the importance of studying circulating tumor cells as sources of metastatic growth and as prognostic signatures for early diagnosis of cancer recurrence. In the afternoon, Chang Chan (Rutgers) presented the Li-Fraumeni Syndrome, a genetic disorder that causes significantly increased risk of several forms of cancer. A genetic regression model was proposed to explain the observation that average onset of cancer decreases across successive generations. Gabriela Alexe (Harvard) concluded the day's talks with a discussion on metagene projection strategies as a tool for discovering functional annotations of genes and identifying synergistic changes at the micro and quantum levels derived from biological data. The final day featured two presentations, followed by an open-ended discussion of several of the topics presented earlier in the week. First, Kimryn Rathmell (UNC) described how genetic and epigenetic data is used to further classify renal cell carcinoma and distinguish it as a heterogeneous set of diseases. James Glazier (Indiana) concluded the workshop with a presentation of a multi-scale multicell computational modeling platform and its application to age-related macular degeneration.

Lively discussions followed the many excellent talks delivered throughout the week. Frequently, the coffee breaks proved insufficient to conclude the ongoing conversations. The diversity of the attendees' backgrounds and experiences ensured a dynamic and engaging atmosphere, fostering cross-disciplinary connections at all levels. The warm and welcoming atmosphere of IPAM was a definite catalyst to these intellectually challenging conversations.

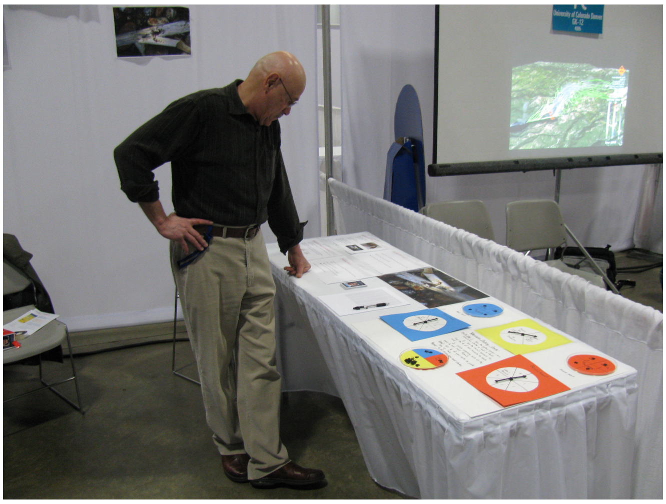
The workshop provided an excellent opportunity for researchers in the physical and mathematical sciences and clinicians to form connections. Such experiences represent a crucial step toward a more integrated approach to cancer research, where scientists and clinicians collaborate regularly and influence one another's approaches. The number of researchers in attendance, and the diversity of institutions and locations throughout the world that they represented suggest that the scientific community is becoming more open to this cross-disciplinary form of research. More info at: `http://www.ipam.ucla.edu/programs/cdm2014/`

SMB at the USA Science & Engineering Festival

Thinking Like Ants!

by ANDREW BASINSKI

The Science and Engineering Festival took place this past April in Washington D.C. The massive event attracted 325,000 people, and featured over 3000 hands-on activities for K-12 kids and their teachers. Space travel, 3D printing, and watershed management were just a few of the panoply of topics represented. SMB's booth showcased the fusion of mathematics, computer simulation, and social insect ecology. The diverse crowd of participants ranged from kindergartners attracted to bright colors, plastic ants and spinners, to high school teachers seeking new ideas in relating the excitement and usefulness of math to their students.



Raymond Mejia at the SMB booth in the Science and Engineering Fair

Our goal was to show how math can be used to understand complex biological processes. Readers of this newsletter no doubt understand how math clarifies the mechanisms that allow cells to function, for example; however, it is easy to forget that the idea of combining math and biology is often downright puzzling to the average student. Indeed, many of our participants were attracted to the booth upon seeing the words "mathematical" and "biology" next to each other. The challenge was to pose questions motivated by biology, but mathematical in nature, and make these questions accessible to an audience with a diverse background in both biology and math. Our booth used social insects (in particular, ants) as a model organism in an attempt to make this idea intuitive and fun for kids and adults of all ages. Participants were asked to think like an ant as they played 3 boardgames demonstrating how ant colonies think, search their environment, and fight.

The most popular boardgame demonstrated how social insects, like proteins in a cell, collectively produce complex behavior despite relatively simple individual behaviors. The game was based off of the house-hunting ant *Temnothorax* - colonies of which collectively assess and choose a new nestsite after their current nest is destroyed. These ants have very particular preferences when choosing a new nestsite, and are able to collectively choose the best nest when given multiple options. This is incredible when paired with the fact that individual ants do not directly compare nestsites. Instead, this comparison emerges as a result of two key individual behaviors: 1) ants that assess better nests communicate the potential nest location to more naive ants than those that visited lower quality nests; 2) ants spend a time assessing the visited nestsite that is inversely proportional to its quality. Together, these individual behaviors favor the spread of information concerning better nest options for the colony.

We used boardgame-simulations to demonstrate this decentralized decision-making mechanism to participants. Players spun spinners and guided plastic ants through various petri dishes representing nests to directly observe how this decision-making process takes place. Younger participants cheered and booed at the build-up of ants vying for the "good" and "bad" nestsites, while teachers commented on how such a game offers an interesting application in a course on statistics or dynamical systems. After playing the game, we discussed how math could be used to understand the influence of individual ants' behavior on the colony's ability to make the right decision.

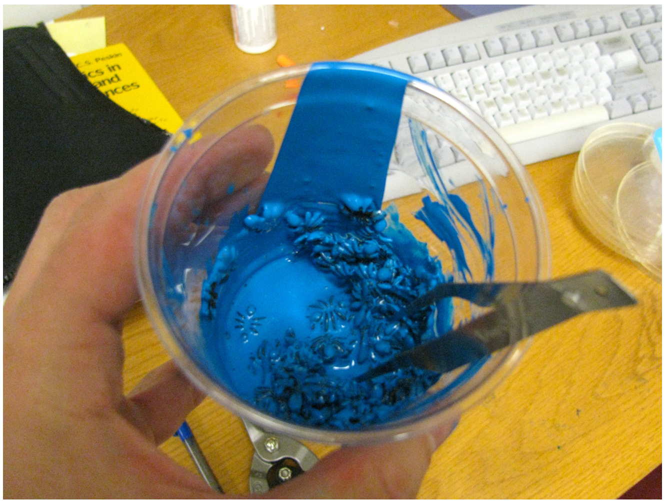
In another game, participants explored the relationship between searching efficiency and movement attributes of ants undergoing a random walk. Players rallied behind ants searching a checkerboard with 1 of 4 different random walks, and recorded the ability of the different ants to find baits (Hershey's Kisses) distributed across the board. This game was extremely entertaining for groups of children, as well as for the people running the booth. After moving several turns, kids were asked to hypothesize how the ability of finding food would differ for each type of ant, and what implications this has for real ants foraging their environment.

Finally, a strategy game representing battles of the pavement ant, *Tetramorium caespitum* was built. Pavement ants are commonly seen on sidewalks in huge aggregations during territorial disputes of neighbors. To represent a colony-wide strategy during a dispute, players moved ants representing two neighboring colonies. At each turn, players chose to either advance their ants, or recruit ants to the battlefront in a risk-like strategy game. Here, the question was how the outcome of a battle could be traced back to the fighting strategies of individual ants.

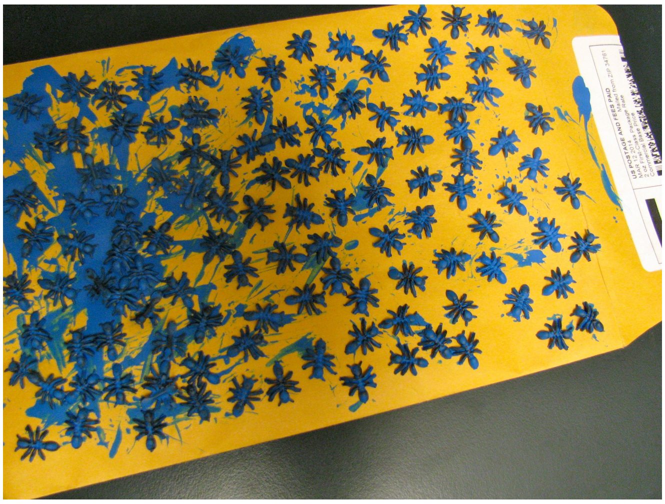
The wealth of curiosity and wonder, especially of K-12 students, was absolutely inspiring. Interestingly, the most common reason people stopped at our booth was to ask how math and biology could possibly be studied together. Our focus was not in presenting mathematical models or solutions to biological processes, but instead to give insight into the types of questions that demand mathematical modeling. Social insects provided a fun, insightful way to show youth how math is used to better understand how complicated biological systems work.

For further information on The Science and Engineering Festival check out their webpage: `http://www.usasciencefestival.org/2014-festival.html`

Andrew Basinski at the Science & Engineering Fair



Preparation for the science festival involved the mass painting of plastic ants to be used in boardgame simulations.



The finished product! These ants were used to simulate colony decision making, searching, and fighting

Computational Neuroscience Workshop

McGill University, Montréal, April 29, 2014

by FRÉDÉRIC SIMARD, RICHARD GREG STACEY & LENNART HILBERT

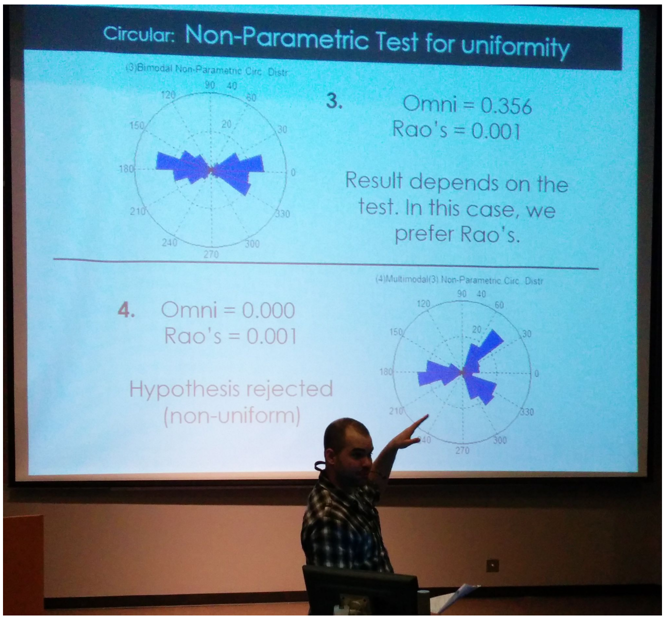
Thursday April 29th was the second edition of our CAMBAM (Center for Applied Mathematics in Bioscience And Medicine) student's computational neuroscience workshop. For a second year, several graduate students have grouped together to offer a series of talks covering various tools and techniques in computational neuroscience.

This year, rather than chasing after speakers, we were delighted to see many of last year's speakers come back. Given that this was a voluntary workshop and students have many competing interests, we were happy to see people choose to return. Moreover, members of the audience from last year now wanted to give talks. This drive toward active participation didn't limit itself to the speakers, as we observed a significant increase in the number of attendees, even though advertising for the event was small. Our fears were eased. Because we see many seminars struggling to increase attendance we decided to share, through this newsletter, what we think is our recipe for success.

From the beginning our goal has been to create an event that links students through a common factor other than their research topics: computational tools and techniques. We all do research in extraordinarily specialized topics, and often even our lab mates aren't aware of what we're really up to. When asked to participate in a local seminar, either as an attendee or a speaker, most of us know the slim chances that the topic will relate to our research. Our research questions are often too specific. To correct this we took a different direction. Rather than speaking about their research projects, the speakers were asked to talk about their method of investigation. How do I analyze my data? What kind of models are available? What's the appropriate stats test? Our workshop aimed to offer information about data analysis tools common to many research questions. From what we saw, interest in exchanging ideas about the fast-changing tools of the trade was very high.

A second feature of our workshop is that each talk is shot and uploaded to YouTube. Speakers leave our event with something lasting that shows their hard work. One of last year's speakers told us that he had been thanked by several people that had seen his video and he was happy to have given the talk. Not only that, but he went as far as to include the link to the video in his resume. Through this online supplemental our workshop can offer continuing benefits to both the speakers and future students interested in the topics.

And finally, unlike several other seminars, we do not measure the success of the event by counting the number of participants, and in fact we're biased toward keeping it small. As a student workshop, we aimed to be as convivial as possible, and provide a space where speakers and attendees merge together during the coffee breaks and everyone has the time to express their thoughts and discuss their opinions. During the workshop, beginners, intermediates and experts all find the time to express themselves and this is something we are not ready to sell out for the price of a few more attendees. For more information, you can find a blog post of this year's workshop by following the link here: `http://blogs.mcgill.ca/cambam/2014/04/07/computational-neuroscience-workshop-2014/`



Circular: Non-Parametric Test for uniformity

3. Omni = 0.356
Rao's = 0.001

Result depends on the test. In this case, we prefer Rao's.

4. Omni = 0.000
Rao's = 0.001

Hypothesis rejected (non-uniform)

Frédéric Simard discussing the non-parametric aspects of circular statistics.

Perspective on "*New and Less New Opportunities For Mathematical Biology as Applied To Biological and Clinical Medicine*"

by JEAN CLAIRAMBAULT

*A*nother conception that makes applications of mathematics quite different from applications of mathematics to sole biology resides in the interventionist nature of medicine ...

This perspective, bouncing from Philip Maini's "*Perspective on The Changing Face of Mathematical Biology*" [1], focuses on the specific case of mathematics as applied to medicine. Philip Maini acknowledges the pioneering work of James D. Murray in Oxford: for sure, this immense founding enterprise with no equivalent worldwide has led, through his stimulating teaching and research, to the training of scores of students, from pure to very applied mathematicians, many of whom have themselves become leading scientists in different fields of mathematical biology.

In other parts of the world, such pioneers were scarce, but little by little, by the virtue of example, scientists coming either from the engineering world or from pure and applied mathematics learnt to know that non-trivial mathematics had been written by some of them, starting from open biology questions, often by transposing methods from physics or chemistry. For instance, reaction-diffusion equations have been studied as providing a theoretical basis for traveling waves of physical phenomena by Kolmogorov, Petrovsky and Piskunov and independently by Fisher (for the spread of a gene in a population), all in 1937, and later a basis for morphogenesis by Turing in 1952. However, James Murray reports (Mathematical Biology 3rd ed., vol. 1, 13.2) that the first discovery of the so-called KPP-Fisher equation is due to the German chemist Luther in 1906, but also that his publication soon sank into oblivion, to be rediscovered later, much later than 1937. The scientific audience likely was not ripe then to catch the scope of this discovery and its potential applications to biology, even though Fick (1855) in the same country had already presented his law of diffusion 50 years earlier. The now classical examples of Hodgkin-Huxley (1952) and later FitzHugh-Nagumo models of action potential propagation (1961, 1962) or Turing instability (1952) came later, on apparently more favorable ground.

What had changed? Maybe the fact that biological phenomena that were until then considered as just being there - the propagation of nerve impulse or the spots on a leopard - were investigated by advanced scientists - physicists or mathematicians - as having in fact a physical basis and hence a mathematical expression. Maybe in about the same way as in the Greek antiquity, presocratic philosophers and the mathematicians among them tried to organize a corpus of pre-existing observations (in particular from Babylon and Egypt) according to rules, some of which could be shown to be more than rules.

The situation in which we are now is indeed somewhat different. In a world where scientists of different disciplines regularly meet in conferences and workshops, and publish jointly in journals in which attention is given to both mathematical modeling and experimental results, it is less likely that breakthrough discoveries may be lost. Furthermore, centers for mathematical biology, and as regards oncology, centers for integrated research on cancer (essentially in the US for the latter) now exist and offer institutional opportunities to exchange knowledge between disciplines, including mathematics and clinical medicine. In the UK, the Mathematics in Medicine Study Group (MMSG) organizes meetings in different locations to model and tackle during 2-3 days problems coming from requests by biologists or physicians. Even in places where such institutions are not yet present, grants coming from international and national calls more and more allow constituting coherent teams of applied mathematicians working in close contact with teams of biologists and - less frequently - physicians.

As Philip Maini stresses, data coming from biological experiments are most often static, i.e., snapshot-like, when we need movie-like data to identify the dynamics of the biological systems under study. Furthermore, a frequent and simplifying underlying assumption is that tissues are homoge-

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[1] `http://www.smb.org/publications/newsletter/vol27no1.pdf`

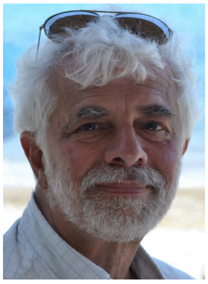
neous, genetically and phenotypically, when for instance multilocular samples in the same tumor show that this is frequently not the case, at least in cancer. In biological and medical research teams, people are keen on identifying intracellular signaling pathways - or cell membrane targets upstream of them - searching for so-called *“druggable targets*" to block or enhance them. But the dynamic viewpoint that mathematicians are fond of "*where does this lead to? i.e., what is the asymptotic behavior of the system, controlled or not?*", is seldom present. However, such a dynamic perspective has always been present in the mind of biologists dealing with evolution, and recently - remembering that, as stated by Theodosius Dobzhansky in 1973, *“Nothing in biology makes sense except in the light of evolution”* - it has also become clear at least for some *cancer* biologists. Some indeed consider cancer as an evolutionary disease, in the sense that cell populations evolve, partly with prescribed rules, partly due to random events and partly under the influence of tissue environmental factors, towards diseased states as populations of multicellular organisms do. In my opinion, this view is about to deeply change our conception of diseases, and in particular of cancer.

Another conception that makes applications of mathematics quite different from applications of mathematics to sole biology resides in the interventionist nature of medicine, that is absolutely irreducible to an applicative branch of biology. Whereas the physicist describes the evolution with time of natural phenomena, and in particular of diseases, the physician is expected to correct them or prevent them, otherwise said to control them. This leads to the idea, not only to apply optimization and optimal control principles to therapeutics, but also to design models of health and disease in tissues and organisms as dynamical systems under physiological control mechanisms that can be corrected when they fail. In this respect, firstly it is necessary to reintroduce physiology at the era of genetics at all levels where physiological regulations occur: intracellular gene regulatory networks, equilibria between competing populations of cells, whole body hormonal regulations, and also between these levels; and secondly, setting such physiological controls and the correction of their disruptions as optimization problems (physiologically solved or to be solved by therapeutic intervention) should foster much more work between physicians and mathematicians specialists of optimal control. This is another opportunity that I see for the future, and it will make all the more sense as the biological control mechanisms will be more known. Even if they are not known in detail to perform quantitative predictions, qualitative results about optimized therapeutic strategies to combine drugs should prove helpful to clinicians.

Of course, the continuous progress of imagery techniques, at all possible biological levels of observation, from intracellular signaling pathways to whole-body recordings, in a more and more dynamic way, i.e. with space and time resolutions that are driving us from a scenery of poorly defined snapshots to another one of high precision movies, will never exclude the fact that important variables of the dynamic systems under study will remain hidden. This naturally calls for other new mathematical developments, which resort to statistical theory and to inverse problem methods.

Such perspectives, some of them rather recent, together with a growing open-mindedness of biologists and physicians towards mathematics open new tracks to follow for the growing number of mathematicians interested in doing "*mathematics for medicine*". There are hard problems - and less hard ones - to solve, that will be a source of inspiration for mathematicians and a help to physicians - be it only to provide new ways to ask questions - provided that the initial question is of biological and medical nature, transposable in mathematical settings, and that a collaborative work is performed interactively between members of the two disciplines towards advances in solving them.

About The Author:



Dr. Jean Clairambault, PhD, MD, trained - in that order - in mathematics and medicine, is presently a senior scientist (“directeur de recherche”) at INRIA and Laboratoire Jacques-Louis Lions, Pierre et Marie Curie University in Paris. His current research interests are the emergence of drug resistance in cancer and the evolution from premalignant cell populations to tumors, together with therapeutic optimization methods using combined drug delivery strategies to overcome such evolutions at the cell population level. Website: `http://www.rocq.inria.fr/bang/JC/Jean_Clairambault_en.html`.

SMB Education Highlights New Guidelines for Programs in Mathematical Biology

by Elsa Schaefer

> *.. The report was intended to generate discussion and to address the challenges for mathematics departments of all shapes and sizes to create biology-inspired curricula for mathematics majors, ...*

As many institutions are starting to consider the development or refinement of concentrations in mathematical biology, our community has been eager to discuss best practices for these new programs, and to share ideas that make such program creation feasible for departments of varied sizes and research expectations. Perhaps all biomathematics programs should include two key foundational courses that build competencies in modeling and in data analysis. A good program would also include a biomathematics capstone course or undergraduate research opportunity, something already offered by most departments. It is likely that other specific competencies needed for undergraduate students in mathematics can be fulfilled with courses already offered at most institutions, and thus new programs in mathematical biology can be realistically established at a wide variety of institutions. These are the main ideas presented in a thoughtful new report that was unveiled at the 2014 Joint Mathematics meetings by a working group serving on behalf of the committee on the Undergraduate Program in Mathematics (CUPM) of the Mathematical Association of America.

The first foundational biomathematics course suggested by the working group focuses on the importance of modeling and multiple mathematical points of view (discrete, continuous, stochastic), including, of course, meaningful interaction with the biological subject matter. The second suggested foundational course would focus on data analysis, in particular, the ability to implement a statistical comparison between data sets. This course should include regression analysis and fluency in at least one programming language, and an introduction to the biological databases.

The working group lists a basic set of mathematical competencies that a concentration in biomathematics should include, one that many mathematicians might largely duplicate without looking. They also include a list of biological competencies that a biomathematics concentration could include, and I suspect that list may be a particularly helpful asset to mathematics programs interested in developing a biomathematics concentration.

The report was intended to generate discussion and to address the challenges for mathematics departments of all shapes and sizes to create biology-inspired curricula for mathematics majors. The authors note that there has been much focus on and success in establishing recommendations for a mathematics curriculum for life sciences majors, but they note that uniform recommendations for the incorporation of biology into mathematics is likely inappropriate given the tremendous diversity of the biomathematics field.

The undergraduate mathematical biology report outlines some of the challenges that face successful program implementation, and its recommendations are intended to allow small departments to succeed in creating such programs. One specific challenge for biomathematics programs has been discussed in our community for years: the institutional obstacles to the hiring and support of truly interdisciplinary faculty, especially at non-research institutions.

Other obstacles described are more typical of all curricular efforts in mathematics, and perhaps the most daunting concern for small programs is the potential fragmentation of a small number of majors.

.. The mathematical biology guide provides a solid starting point for programs from multiple points of view without making the mistake of over-prescribing for this widely varied and emerging field, ...

The study group's gentle and generic advice is for departments to start small - with modules in existing courses, for example, and they additionally list resources to help faculty learn more about biomathematics. The group was hesitant to pigeonhole this broad field of biomathematics with specific recommendations, and its report notes that there are "*many paths to success.*" Of course, collaboration between science and mathematics departments is advocated, and the report has some good suggestions about how to engage the administration and to encourage their support of biomathematics efforts.

The report also includes an institutional list of contacts for biomathematics (listed by institution type), as well as links to biomathematics resources maintained by multiple societies and an impressive list of textbooks that are now available.

The mathematical biology guide provides a solid starting point for programs from multiple points of view without making the mistake of over-prescribing for this widely varied and emerging field. This mathematical biology program report was one of multiple reports by Program Area Study Groups serving on behalf of the committee on the Undergraduate Program in Mathematics (CUPM) of the Mathematical Association of America. The mathematical biology report was authored by Jennifer Galovich (St. John's University and chair of this committee), Fred Adler (University of Utah, SMB President), Lou Gross (University of Tennessee and Director of NIMBioS), (Andrew Kerkhoff (Kenyon College), and Joe Mahaffy (San Diego State University). The January 2014 CUPM reports can be accessed online at: `http://www2.kenyon.edu/Depts/Math/schumacherc/public_html/Professional/CUPM/Birds_feather.html#Programs`

About The Author:

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 past Secretary and current Electronic Communications Coordinator of the MAA's BioSIG-MAA, a red-dot and consultant for Project NExT, a member of the MAA textbook committee, and the SMB Chair of Education. She was also the local organizer for the most recent BEER (Symposium on Biomathematics and Ecology Education and Research) conference which was held at Marymount in October 2013, and she has served as a program officer for the National Science Foundation's Mathematical Biology program within the Division of Mathematical Sciences.

Her website: `http://muweb.marymount.edu/~eschaefe/`

In the next SMB Education column, I'd like to celebrate graduate school admission season with an overview of some PhD programs in mathematical biology. I'd like to share some modest information about the variety of programs available, and I am hoping to pull out some key program differences so that faculty in small programs like those being encouraged above can successfully steer our best students to the best-fitting program. I would love to hear from graduate directors about their advice to college seniors seeking further biomathematics studies. Please send me a note at elsa@marymount.edu.

"*How The Leopard Gets Its Spots*" The Catalyst of My Mathematical Biology Journey!

Trachette L. Jackson

"*How The Leopard Gets Its Spots*" flyers were peppered all over the walls of the mathematics department at Arizona State University in the fall of 1992. They were advertising an upcoming lecture by Jim Murray. I was an undergraduate mathematics major beginning my junior year of study in classical analysis. I walked by this flyer every day for about a week and was simply perplexed as to why this lecture was being advertised in the Mathematics department. Finally, I read a bit of the abstract, which said something about how a single mechanism could underlie the wide variety of animal coat markings found in nature and that results from mathematical models are opening lines of inquiry for developmental biologists. I had never been exposed to mathematical efforts aimed at the biological sciences, so I decided to attend my first-ever departmental colloquium to hear Jim Murray speak.

William Butler Yeats said that education is not the filling of a pail, but the lighting of a fire. The day I heard Jim Murray speak sparked the fire for mathematical biology that has been burning in me ever since. At that time, I did not understand much of the underlying theory that Jim presented, but I walked away from that seminar with the belief that mathematics could profoundly impact the biological and biomedical sciences. That day, I made a promise to myself that I would do everything in my power to eventually become one of Jim Murray's students. Those were pretty big thoughts from a sheltered 20 year-old math major. It was, after all, rather late in my undergraduate training. It would be difficult for me to completely switch gears and embark on learning a science that I was very unfamiliar with, while still trying to take a few graduate level mathematics courses that would help me get into a PhD program. So, I had a steep hill to climb. My first step was a Research Experience for Undergraduates (REU) with Professor Betty Tang, an Applied Mathematician, working in mathematical biology, which led to my first publication. I also participated in the NIH-funded Minority Access to Research Careers (MARC) program, which gave me a crash course in biological research.

These experiences helped me to be admitted into the PhD program in Applied Mathematics at the University of Washington and to achieve my goal of working under the direction of Jim Murray - the person who unknowingly started me on this path. Jim provided an atmosphere for his students that I have never seen recreated. It was honestly the best possible place for me to learn to become a steward of the discipline. My PhD thesis was based on a problem presented to our Applied Math Clinic, where researchers brought their scientific problems to a group of motivated graduate students to work on. At that time, considerable research was being aimed at improving the efficacy of chemotherapeutic agents for cancer therapy. Dr. Peter Senter, a Biochemist working for Bristol Myers Squibb Pharmaceutical Research Institute, was pioneering a promising two-step approach designed to minimize systemic drug toxicity while maximizing activity in tumors by employing monoclonal antibody (mAb)-enzyme conjugates for the activation of anticancer prodrugs. Their research questions were ideal for mathematical modeling. By combining theory and experiment, were able to quantify the biodistribution, pharmacokinetics and localization properties of mAb-enzyme conjugates in tumor tissue and in the bloodstream. This was the first time I experienced the satisfaction and sense of accomplishment that working at the interface of mathematics and biology now brings me everyday. My four years of graduate school, where I was able to work closely with experimentalists, taught me the power of collaboration and to communicate mathematics to biological audiences. It also opened my eyes to the potential for applied mathematics to become an integral part of cancer research.

When I earned my PhD in 1998, mathematical biology was a booming and exciting field that had gained international attention. Although I had a tenure-track job offer, I decided that I needed time to explore and expand my research portfolio in order to become a productive and independent mathematical biologist. Fortuitously, the Institute for Mathematics and Its Applications at the University of Minnesota was hosting its first annual thematic program on Mathematics and Biology. I spent one amazing year there as a Postdoctoral Associate. Many of the international leaders in Mathematical Biology - Lee Segal, Alan Perelson, Lisa Fauci, Zvia Agur and many others - rotated through the IMA that year, which gave me the opportunity to see the many different configurations that a successful career could take.

My year at the IMA was an excellent introduction to the worldwide community to which I wanted to belong. I had the good fortune to share an office with Helen Byrne, who took me under her wing and became a long-time mentor and collaborator. The following year I moved to a second post-doc at Duke University. There I came to know Mike Reed who, together with Jim Murray and Peter Senter, is one of the three greatest influences on my career as a Mathematical Biologist. Mike facilitated research connections and collaborations and allowed me the space to become an independent researcher. While at Duke, I was first introduced to the angiogenesis research that has been become a major emphasis in my research program.

During my first year at Duke, I applied to just five places to test the waters for the potential of tenure-track positions. I accepted an offer from the University of Michigan in the fall of 2000. To date, I have had the opportunity to work with an outstanding group of collaborators, graduate students, and postdocs. Together, we have developed a variety of cell-based and hybrid mathematical models of tumor angiogenesis designed to untangle some of the complexities associated with vascular tumor growth, in the hopes of manipulating new knowledge for therapeutic gain.

As an educator, I have always been interested in the training and education of the next generation of interdisciplinary mathematical scientists. Therefore, I quickly began developing courses and educational experiences in Mathematical Biology when I arrived at the University of Michigan. Previously, there had been no institutional mechanism for faculty and students interested in quantitative methods in biology. To change this, Patrick Nelson and I co-founded the Mathematical Biology Research Group (MBRG) at the University of Michigan, which was a campus wide initiative to foster interdisciplinary research at the interface of Mathematics and Biology. We also developed the SUBMERGE (Supplying Undergraduate Biology and Mathematics Education and Research Group Experiences) program, which aimed to merge the subjects of mathematics and biology for undergraduate students by exposing them to mentored, team-based research on real problems in mathematical biology.

Currently, I am coordinating a new Applied and Interdisciplinary Mathematics Bridge to the PhD program at the University of Michigan in order to address the national challenge of educating and training a diverse scientific workforce capable of unifying the fields of mathematics and the natural sciences. The program aims to impart on the next generation of under-represented minority (URM) scholars the foundational skills required to combine a deep knowledge of applied science with the mathematical, computational, and physical sophistication needed to address the increasingly complex problems that are on the international horizon.

It is hard for me to believe that I have been in this field for 16 years, but I know I would not be where I am today if it were not for my biggest academic and research supporters, especially, Jim Murray, Peter. Senter, and Mike Reed I met each of them at a different, yet critical, juncture in my career and have benefited greatly from knowing and working with them. After all this time, it still energizes me to know that many of the various sub-disciplines of mathematical biology are on the verge of critical scientific advances. I am excited to see what the future holds and am proud to call myself a Mathematical Biologist.

Related Links: My home page:
http://www.math.lsa.umich.edu/ tjacks/

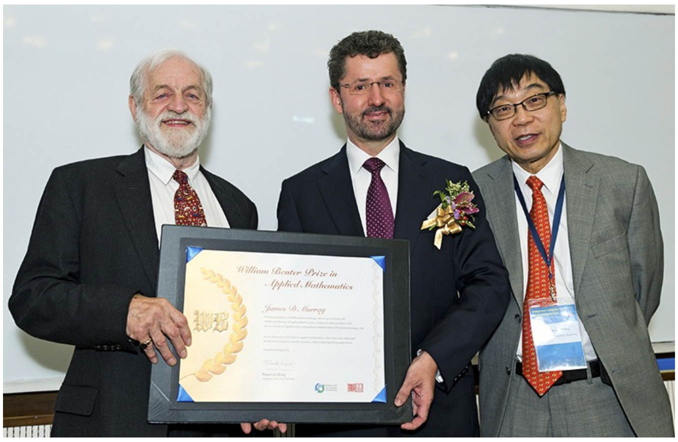
James D. Murray Talks About His Benter Prize

by James D. Murray

To be awarded the 2012 William Benter Prize was a particular honor, which gave me enormous pleasure since it not only recognized applied mathematics as an important part of the mathematical sciences but also that it recognized the importance of our field of mathematical biology [2]

Prizes in Mathematics and Mathematical Sciences universally mean pure mathematics irrespective of the prize description. The William Benter Prize in Applied Mathematics, awarded every two years, is the first that I know of to single out Applied Mathematics. Bill Benter, who funded the prize, is, himself, a real applied mathematician whose practical mathematical and computing skills are the basis of his phenomenal betting business' success in the Hong Kong horse racing market. Among other things, he supports a large number of charities. Professor Roderick Wong was responsible for the prize being associated with the City University of Hong Kong where the conferences are held. To be awarded the 2012 William Benter Prize was a particular honor, which gave me enormous pleasure since it, not only recognized applied mathematics as an important part of the mathematical sciences but also that it recognized the importance of our field of mathematical biology.

Prof. James D. Murray delivering his lecture following the Benter prize presentation ceremony



Prof. James D. Murray with Bill Benter and Prof. Roderick Wong

The atmosphere of the conference was incredibly warm, friendly and welcoming and was among the nicest I have ever been at. The warm atmosphere was in large part due to the university administrator organizer Sophie Xi, and Roderick Wong. The meeting went without the slightest hitch with the student helpers genuinely helpful and very thoughtful.

Those of us who started working in biological and medical applications many, many years ago came in for quite a lot of criticism and ridicule. When I decided that I did not want to do any more traditional applied mathematics research (in my case fluid dynamics) a colleague lectured me not to waste my time on "that rubbish". There were also lots of biologists who thought we could be of no use whatsoever but there were others, even in the early days, who were keen on interdisciplinary collaboration. Genuine interdisciplinary mathematics and biomedical research has been a pleasure to me practically all my academic career. In the early days in the 1960s you could almost count those in the field in one hand whereas now they number in the thousands with centers and societies all over the world.

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[2] Read more about Prof. James D. Murray's City U's 2nd William Benter Prize: `http://wikisites.cityu.edu.hk/sites/newscentre/en/Pages/201205281139.aspx`

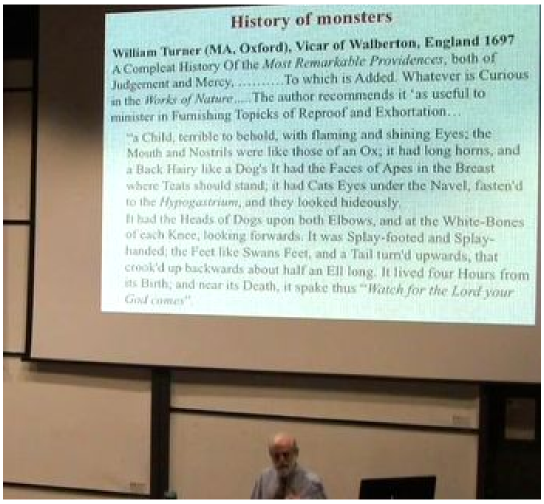
Oxford Mathematics Interviews: *Jim Murray - Reflections on a Life in Academia*

by PHILIP MAINI

Philip Maini interviewing Jim Murray

Jim Murray is one of the leading mathematical biologists of our times and the Inaugural Hooke Lecturer here in Oxford. In this wide-ranging interview with Philip Maini, Professor of Mathematical Biology in Oxford, Jim talks about his career, the range of his work, his successes and failures and his hopes and expectations for a subject that is the pointing the way for the future of applied mathematics. Watch the full interview here: `http://www.maths.ox.ac.uk/node/25330`

Professor Jim Murray, gave the first Hooke Lecture here in Oxford on 4th March 2014, entitled "*Why there are no 3-headed monsters, resolving some problems with brain tumors, divorce prediction and how to save marriages,*" Jim described three very different problems: the development of the mechanical theory of morphogenesis and how it was used to move evolution backwards; a model for quantifying the growth of brain tumors and individual patient treatments: and an example from the social sciences that is used to predict marital stability and divorce. The Hooke lectures are part of a series of Public Lectures intended to display the power and beauty of mathematics to a wider audience. The lecture attracted over 300 people and can be viewed at `http://www.maths.ox.ac.uk/node/25270`



History of monsters

William Turner (MA, Oxford), Vicar of Walberton, England 1697

A Compleat History Of the *Most Remarkable Providences*, both of Judgement and Mercy, ……….To which is Added. Whatever is Curious in the *Works of Nature*…..The author recommends it 'as useful to minister in Furnishing Topicks of Reproof and Exhortation…

"a Child, terrible to behold, with flaming and shining Eyes; the Mouth and Nostrils were like those of an Ox; it had long horns, and a Back Hairy like a Dog's It had the Faces of Apes in the Breast where Teats should stand; it had Cats Eyes under the Navel, fasten'd to the *Hypogastrium*, and they looked hideously.
It had the Heads of Dogs upon both Elbows, and at the White-Bones of each Knee, looking forwards. It was Splay-footed and Splay-handed; the Feet like Swans Feet, and a Tail turn'd upwards, that crook'd up backwards about half an Ell long. It lived four Hours from its Birth; and near its Death, it spake thus "*Watch for the Lord your God comes*".

Jim Murray Giving his Hooke Lecture at Oxford

Research Interview

Beyond Boundaries

Nick Cogan talks with Mark Whidden about his journey into mathematical biology and research on biofilms

Who or what inspired you to become a mathematical biologist? When I was an undergraduate I was fortunate to have a senior faculty member in the math department ask if I was interested in doing an honors thesis with him. At the time I knew that I wanted to do applied math, but I was thinking more along the lines of working on some aspect of the space program. Dr. M. was collaborating with a forensic scientist looking at ways to determine the time of death for a body that was exposed to the elements for several weeks. We looked at a model of insect dynamics for bugs that typically colonize carcasses in the area. You can compare the predicted life-stage populations with the observational data and get a decent range for the time of death. I found this a fascinating problem because it directly connected mathematics to a practical need but with an interesting twist.

Tell us about your research. What are you working on? My focus is on bacterial biofilms which are aggregates of bacteria enmeshed in a self-produced polymer gel that form very distinct structures. Biofilms are everywhere in natural, industrial, and medical environments. I am particularly interested in understanding why it is so difficult to eradicate a biofilm infection. The bacteria within the biofilm are not genetically resistant to antibiotics, but the biofilm provides several protective mechanisms. Understanding why it is so difficult to kill the biofilms will help develop new treatment methods which has practical usefulness. Right now I am looking at biofilm-associated diseases within plants (specifically wine grape vines), bones, and in industrial filtration settings – all very important applications.

Why study bacterial dynamics and disinfection with applied mathematics? Why Not! It is cheaper than most experiments, more transparent (in that you can see things that are not visible to experimentalists), often more insightful than intuitive experiments can be. The connections that are made by applied mathematicians are often broader than are available to other scientists: mathematicians can see the similarities between forest fires and heart beats; bacterial swimming and soda pop bubbles; bacterial population dynamics and human disease dynamics; etc. I think mathematical scientists are able to introduce lines of thought that experimentalists/clinicians can use to jump start their research and, at the same time, help validate certain lines of study.

Which aspect of your research are you most excited about? I have been supervising numerous students and one of the things that I am finding is that they can lead me in directions that I would not have moved myself. I have always believed that one of the gaps in biofilm research, from a clinical standpoint, is the lack of models that included interaction between the biofilm pathogen and the host immune response. Even though there are many examples of the immune response to a bacterial challenge, almost none are aimed at bacteria within a biofilm with all the multilayered protection that comes from the biofilm lifestyle. I really love that all of my current projects include direct collaboration with experimentalists or clinicians. I think that the interplay between the biology and the mathematics is much more interesting and forward moving when the biologist can help point to interesting questions that the mathematical analysis can shed light on.

What's the next big thing in mathematical biology? That is a big question – there are lots of things that need to be addressed. One part that I am particularly keen on is how to understand the role of uncertainty in the models. This means being able to quantify both the importance of particular parameters, but also some understanding of what uncertainty is inherent in the problem and what uncertainty can be reduced by experimental data. This topic has been approached in other disciplines for quite some time, but seems to be less well developed in mathematical biology.

What are the most significant challenges you've faced as an interdisciplinary scientist? As always, I think it is the language gap between the mathematician and the experimentalists. It takes a lot of time for the two research approaches (mathematical versus experimental) to get on the same page. I think it used to be mainly the mathematicians job to learn enough biology language to bridge the gap but I am finding that more and more experimentalists and data people are eager to learn the why and how of applied mathematics. Sometimes this is almost impossible, but the challenge is to make the mathematics approachable so that, together, the team can find a common direction.

Have you ever found the complexity of biological systems daunting? Almost always – it is quite scary to move into a new area. There is so much to learn and so much that you might be missing. Things like the immune system have been studied by so many really smart people – it is hard not to think that you can't make a new contribution. But I know people who feel that way about bacterial dynamics, which I am more at home with. So I think it is a matter of time and effort.

What would your message to a young and aspiring mathematical biologist be? I think that there are so many aspects of biology that are not understood and can be explored using mathematical tools. However, it is not very clear what tools are most suited to an application. That means that, even more than traditional applied mathematicians, mathematical biologists need to know a little bit about all sorts of mathematics. That way you can ask questions about temporal dynamics, spatial dynamics, optimal control, topological constraints, special solutions, perturbations, dynamical systems (discrete and continuous), and on and on. You never know what tools will be useful, so stock up on as many as possible. Also, whenever possible, find a friendly biologist and ask all the dumb questions that you can.

What attracted you to a career in academia? Both my parents were faculty members and I essentially grew up on a college campus. It is an environment where everyone was learning, discussing, arguing and generally being academics, and it feels like home. As I went to college and grad school I really liked being around interesting people who were interested in the world around them. Staying up late and talking about some particularly interesting topic was way more fun than putting on a suit and tie and going to work. I also really like the freedom that comes in academia.

How does your career influence your personal life? I view myself as a scientist and I take my work home with me. We homeschool our children and they often ask leading questions. I encourage them to look for answers on the own – experiment, observe, make bold hypotheses. Then look again in a different way. Last year we collected data about whether toast really lands peanut butter side down – over the summer we will look at the descriptive statistics and see what the answer is. The only downside is that I am never allowed to be right based on authority – I have to have some justification.

If you were not a scientist, what would you be? Most likely a dishwasher. I used to work in kitchens before grad school and dishwashers have it pretty easy. Sometimes you get a freebie from a cook or bartender, you usually get your own music to listen to, if you show up and do a decent job they think you are something amazing. Either that or a long-haul truck driver.

If you have any spare time, what do you do when you are not working? My family travels quite a bit – we are always up for a road trip to somewhere new. Mostly we just hang out and work on the house, garden, and family life.

About Nick G. Cogan

Dr. Nick Cogan is Associate Professor in the Department of Mathematics at Florida State University. His research focuses on biofilm dynamics and host-pathogen interactions. For more info, please visit: `http://www.math.fsu.edu/~cogan/`

The Future of Mathematical Biology

Russell C. Rockne, Ph.D, Research Fellow
Department of Neurological Surgery at Northwestern University
Former PhD Student & Post-doc of Dr. Kristin Swanson

What attracted you to mathematical biology?
Mostly, I was curious about what kind of mathematics would be required to describe biology. I quickly realized that there is no master equation or single technique for biology–how could there be? The mathematics depends on the driving scientific hypothesis, the biological situation, and the data. I had my first research experience in math bio investigating a model for radiation therapy in glioblastoma brain tumors. I was a Master's student working under the supervision of Dr. Kristin Swanson, whose mentorship and vision for how mathematics can be used to study cancer inspired me to pursue a Ph.D. and continue in research.

What is your current research project?
I am currently working on applications of patient-specific modeling in cancer. Generally speaking, I am interested in tailoring models to individual data through patient-specific (PS) parameter estimation. Ideally, these methods would only require data that is available as part of a patient's medical care.

What specific areas are you investigating?
My dissertation work at the University of Washington with my advisor Dr. Swanson focused on modeling the biological effects of radiation therapy with applications to glioblastoma brain tumors. I am continuing to investigate patient-specific parameterizations of growth and response models and the use of PS models in clinical research. I am also interested in using PS modeling to interpret the outcomes of clinical trials.

What do you hope to do after your postdoctoral work?
I want to hold a research faculty position that is closely aligned with a clinical department. I want to develop scientific collaborations with clinicians to connect data-driven modeling to clinical research. To achieve this goal, I am applying for early career and training grants from the NIH–and some private funding agencies–that focus on clinical applications of PS modeling. These awards would support my transition to junior faculty.

What advice would you give to an undergraduate interested in a mathematical biology career?
My advice would be to get a dual major in mathematics and another field, although not necessarily biology. You may not need a full bachelor's degree in biology to be successful in math bio. For example, my research focuses on knowledge of cancer at a clinical scale, which is different than the molecular or cellular biology that might be the focus of an undergraduate degree. I would encourage taking biology courses, but more generally to diversify your academic background. This will broaden your toolset and inform your scientific creativity, which is an often overlooked skill. Personally, I pursued two majors: mathematics and fine art. The further I get into research, the more I appreciate the interplay between my mathematical and artistic backgrounds.

What inspires you scientifically?
I am inspired by the vision of mathematics as a tool in an armamentarium for personalized medicine. Imagine a future where doctors take measurements and use quantitative principles and mathematical models to make scientific decisions about which treatment option would be best for you as a patient. This is a big dream that might not happen in my career, but I am determined to contribute to advancing towards it.

Why did you join the Society for Mathematical Biology?
I joined SMB because there is strength in numbers. As the society grows, so does the field and therefore our future careers. Membership also has benefits: student members are eligible for travel awards to support their attendance at annual meetings of the SMB, in addition to other SMB-sponsored workshops and conferences. I have personally benefited from this support, as I recently received the Landhal travel award to participate in the SMB annual meeting in Arizona last year. I would like to take this opportunity to thank the society for this support and for encouraging young scientists and graduate students to take active roles in the society. I also joined so I could help design t-shirts. ;)

Dr. Kristin Swanson, Russell's former PhD and Postdoctoral advisor, says:

I first met Russ in 2006 when I was looking for a master's student for a research project. Amongst the plethora of applicants, Russ rose to the top. In short order he completed the research project and with it, his master's thesis. Based on this incredible work ethic, combined with his excellent research and managerial insights, I offered him a job as a research scientist and lab manager once he graduated. His personality combined with his experience teaching made him a perfect fit for my research group which is heavily focused on mentorship and student involvement. Russ has been instrumental in the overall success of the lab through aiding the growth of both staffing and science. The lab has grown from essentially 1 staff scientist and a few students to 30 at its largest, composed of a diverse mix of junior faculty, staff scientists, post-doctoral fellows, research techs, medical students, graduate students and undergraduate students with the occasional high school student. All the while Russ has served the role of "*senior scientist.*"

Russ is a natural leader while also accepting delegation of responsibilities with eagerness and finesse. Russ' growth as an independent thinker, scientist and senior manager has been exponential in preparation for an independent research role. Staff and peers alike frequently/often comment to me on how approachable and responsive Russ is for scientific discourse/parlance and educational needs as well as lab managerial issues. This reputation extends to the broader scientific community of mathematicians and clinicians alike who have already begun to recognize Russ' contributions to the field. Of particular note, data from Russ' master thesis served as preliminary data for our NIH R01 grant that ultimately funded his PhD and his lab management (research scientist) position. In addition, Russ put forth scientific propositions to further investigate tools for understanding radiation response to treatment. In summary, Russ is an excellent example of the burgeoning community of scientists truly at the scientific interface of mathematics and cancer who, I believe, will lead the field forward.

"The Future of Math Biology" is a column intended to highlight graduate students and postdoc in Mathematical Biology. Do you want to nominate a student or a postdoc from your research group? Please send your nomination to Amina Eladdadi: eladdadi(at)gmail.com

Positions Available

Master in Systems and Synthetic Biology: U d'Evry-Val-d'Essonne. Online applications to the Master in Systems and Synthetic Biology (mSSB) are open until 9 June 2014 (second round of applications). To find out more about mSSB, please visit our website http://www.mssb.fr Applicants may come from Universities or from Engineering schools after a first year of master (M1), or an equivalent qualification, in Life Sciences, Computer Sciences, Mathematics, Engineering, Chemistry and Physical Sciences. Bi-disciplinary courses including Biology is favored, but highly-achieving and motivated students in any of the cited disciplines can apply. Following this M2 Master, several PhD programs are possible on site. Research trainings are also proposed in Europe (England, Germany, Switzerland, Spain) and in the US.

PhD Positions: Basque Center for Applied Mathematics, Spain BCAM, the Basque Center for Applied Mathematics whose mission is to develop high quality interdisciplinary research in the frontiers of Applied Mathematics, has opened an International Call offering up to 7 PhD positions. Applications must be submitted on-line at: `http://www.bcamath.org/en/research/job` Deadline for submission: June 2nd 2014, 17:00 CET

Post-doc: Ecology, U Federal de Vicosa, Brazil The Post-graduate Program in Ecology, at the Universidade Federal de Vicosa, in Vicosa, Minas Gerais State, Brazil, is selecting a postdoc researcher to join the Ecology Team of professionals to work teaching and researching in Theoretical Ecology, using mathematical modeling and computational tools to investigate pattern and processes structuring population and biological communities. Other information about the scholarships for post-doctoral, can be found at: `http://www.capes.gov.br/images/stories/download/legislacao/Portaria_86_2013_Regulamento_PNPD.pdf`

Post-doc: Modeling Protein Metabolism, Paris. A 2-year postdoc position in computational biology is available, in the domain of modeling and simulation of nutritional and metabolic systems (mechanistic and compartmental models, dynamical systems with ODE, numerical analysis, parameter estimation and optimization). Interested applicants should email the following material to Helene Fouillet (helene.fouillet@agroparistech.fr) with subject line "ModProtMetab Postdoc application": i) a cover letter describing their background, research interests and motivation for the position, ii) a detailed CV with research experience, scientific and technical skills, publication list and the contact information of at least two references, iii) copies of some of their best or most relevant papers. The starting date is negotiable and the evaluation of candidates will begin immediately and continue until the position is filled.

Scientific Programmer/Researcher: CSDE, U Washington. The University of Washington Center for Studies in Demography and Ecology (CSDE) and the UW Department of Microbiology invite applications for a Scientific Programmer/Researcher (Research Scientist/Engineer 3) to integrate within-host models for viral dynamics into social network models for the spread of HIV within populations. To apply, go to `https://uwhires.admin.washington.edu/eng/candidates` and enter requisition number 107046 in the required field. If you have questions about this position, you may contact Josh Herbeck (jherbeck@uw.edu), Steve Goodreau (goodreau@uw.edu), or John Mittler (jmittler@uw.edu).

Tenure Track in Mathematics: Risk Analysis, Umea U, Sweden. We are seeking to fill a tenure-track position as associate senior lecturer in mathematics with specialization in risk analysis. The employment as associate senior lecturer (bitradande universitetslektor in Swedish) is permanent consisting of predominantly research during the first four-year period, and with a possibility to build tutoring and pedagogical merits with up to 20% of the employment. At the end of this employment period, an associate senior lecturer owns the right to be examined for a permanent position as senior lecturer at UmeŇ University. For further details and instructions on how to apply, see `http://www8.umu.se/umu/aktuellt/arkiv/lediga_tjanster/2-534-14.html` Your application should be received by May 28, 2014.

Institute Events

Upcoming Events & Opportunities at NIMBioS

Biology By Numbers, July 23-25: Apply now for the NIMBioS/BioQUEST Workshop: Biology by Numbers: Bringing Math to the High School Biology Classroom, July 23-25, 2014, at NIMBioS. Application deadline: June 6, 2014. Visit `http://nimbios.org/tutorials/TT_curriculum_dev2014`

Requests for Support, Sept. 1 : September 1 is the deadline for submitting proposals for new scientific and educational activities at NIMBioS. Potential organizers of activities in areas of molecular biology, cell biology, network biology, immunology and systems biology are particularly encouraged to submit requests for support of Working Groups or Investigative Workshops. Visit `http://www.nimbios.org/research/`

Postdoctoral Fellowships, Sept. 1: September 1, 2014, is the next deadline for submitting applications for postdoctoral fellowships at NIMBioS. NIMBioS is particularly interested in requests to support research that integrates diverse fields, requires synthesis at multiple scales, and/or makes use of or requires development of new mathematical/computational approaches. Fellowships are for two years. Apply at `http://www.nimbios.org/postdocs/`

Requests for Visits to NIMBioS: NIMBioS hosts short-term supported visitors and self-supported visitors. Visit requests are considered at any time, but applications should be submitted a minimum of 6 weeks prior to the proposed visit date. Visit `http://nimbios.org/visitors/`

Visiting Graduate Student Fellowship: NIMBioS offers fellowships for visits to NIMBioS for up to several months by graduate students interested in pursuing research with NIMBioS senior personnel, postdoctoral fellows or working group participants. The program is designed to facilitate graduate student training while fostering research at the interface of mathematics and biology. Visit `http://www.nimbios.org/education/grad_fellowships`

Mathematical Biosciences Institute
at The Ohio State University

Emphasis Program for 2014-2015 is on Cancer and Its Environment:

Workshop 1: Ecology and Evolution of Cancer - September 15 - 19
Boot Camp: How to Simulate and Analyze Your Cancer Models with COPASI - September 29 - October 01
Workshop 2: Metastasis and Angiogenesis - October 13 - 17
CTW: Axonal Transport and Neuronal Mechanics- November 03 - 07
Workshop 3: Cancer and the Immune System - November 17 - 21
More info:
`http://mbi.osu.edu/programs/emphasis-programs/future-programs/cancer-and-its-environment-2014-2015`

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.

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