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IN THIS ISSUE

The Society for Mathematical Biology
Annual Meeting & Conference
June 10-13, 2013
Arizona State University
http://math.asu.edu/SMB2013

Letter from the President

Dear SMB Members,

This letter marks the last time that I write to you as President of the SMB. It has been an honor to serve as President. The last two years have flown by. During that time, we have updated our website, obtained a new logo, migrated to a new membership system, moved to electronic delivery of our newsletter, updated our bylaws, and modernized our financial record keeping. It is my expectation that these changes will sustain the SMB for the next years and allow it to grow its membership and expand its activities in mathematical biology. There still are a few items left on my to-do list, but I still have a year ahead as Past President, and will continue to work on behalf of the SMB during that time.

I would like to welcome Fred Adler into his new role as President. Fred already has been very helpful in his role as President-Elect, so I know that the SMB will be in good hands. I also wish to thank the Officers, Directors, Committee Chairs, and other volunteers for all the work that they do behind the scenes. Their support is much, much appreciated.

On behalf of the SMB, I wish to congratulate Leon Glass, who is the recipient of the 2013 Arthur T. Winfree Prize. This prize honors a theoretician whose research has inspired significant new biology. You can find the full citation of the prize announcement elsewhere in this newsletter.

We are just weeks away from the SMB Annual Meeting and Conference, which will take place June 10-13, 2013, in Tempe, Arizona. The local organizing committee has worked hard to put together an excellent program, filled chock-a-block with an interesting line-up of plenary speakers (including Leon Glass, as well as Rafael Pena-Miller, co-author of the paper that won the 2012 Lee Segel Prize for best paper published in the Bulletin of Mathematical Biology) and mini-symposia. You can find more details about the meeting elsewhere in this newsletter, or at the conference website at math.asu.edu/SMB2013. It promises to be an exciting scientific and educational meeting, and I hope to meet or reconnect with many of you there.

Best wishes for a stimulating and inspiring summer.

Sincerely,

Gerda de Vries

2013 Arthur T. Winfree Prize Announcement

Prof. Leon Glass

The Society for Mathematical Biology is pleased to announce that this year's recipient of the Arthur T. Winfree prize is Prof. Leon Glass of McGill University. Awarded every two years to a scientist whose work has "led to significant new biological understanding affecting observation/experiments," this prize commemorates the creativity, imagination and intellectual breadth of Arthur T. Winfree.

Beginning with simple and brilliantly chosen experiments, Leon launched the study of chaos in biology. Among the applications he and his many collaborators and students pursued was the novel idea of "dynamical disease" and the better understanding of pathologies like Parkinson's disease and cardiac arrhythmias. His elegant work (with Michael Guevara and Alvin Shrier) on periodic stimulation of heart cells demonstrated and explained how the interaction of nonlinearities with oscillations create complex dynamics and chaos. The book "From Clocks to Chaos," which he co-authored with Michael Mackey, was an instant classic that illuminated this difficult subject for a whole generation of mathematical biologists. His combination of imagination, experimental and mathematical insight, and ability to communicate fundamental principles has launched new fields of research and inspired researchers ranging from applied mathematicians to medical researchers.

SMB Annual Meeting & Conference June 10-13, 2013

by Fabio Milner & Hal Smith

The annual meeting of the Society for Mathematical Biology (SMB) will take place at the Mission Palms Hotel and Conference Center in Tempe, Arizona, June 10-13. It is organized through a coordinated effort from Arizona State University and the University of Arizona, and it will bring together hundreds of participants from around the world, at all ranks in the profession: undergraduate students, master's students, doctoral students, post-doctoral scientists, university and community college faculty of all ranks, as well as industry specialists. The themes of the conference are physiology, disease, ecology, and sustainability.

The meeting will feature six plenary lectures, by Dr. Carlos Bustamante (School of Medicine, Stanford University), Dr. Marie Doumic-Jauffret (INRIA, France), Dr. James Lechleiter (School of Medicine, University of Texas Health Science Center, Dr. Rafael Peña-Miller (Department of Zoology, University of Oxford, winner of the Lee Segel Prize), Dr. Shigui Ruan (Department of Mathematics, University of Miami), and Dr. Leon Glass (Centre for Nonlinear Dynamics, McGill University, winner of the Arthur T. Winfree Prize). Complementing this impressive array of diverse plenary speakers will be 32 mini-symposia and 35 contributed sessions with approximately 250 other speakers, as well as a poster session where many students will present results of the ongoing research.

The local organizers were able to secure generous donations by the Department of Mathematics at the University of Arizona, the Institute for Mathematics and its Applications (IMA) at the University of Minnesota, the Mathematical Biosciences Institute (MBI) at Ohio State University, the Mathematical, Computational & Modeling Sciences Institute and the School of Mathematical and Statistical Sciences at Arizona State University, and Pfizer, Inc. Part of these funds were use to fund in part or in full the cost of participation of 67 students and young investigators. SMB provides separate awards directly through the Landahl Travel Award Program.

Disease Dynamics, 2013-UBC-Vancouver

by DANIEL COOMBS

Disease Dynamics 2013 was the first event in the Canadian series of conferences and summer schools on Methods and Models in Ecology, Epidemiology and Public Health, itself part of Mathematics of Planet Earth 2013. The event was held at UBC-Vancouver from January 17-19, 2013, and was financially supported by generous grants from the Pacific Institute for Mathematical Sciences, Mitacs, and the Society for Mathematical Biology. The main organizers were Jessica Conway (Los Alamos), Rafael Meza (Michigan) and Daniel Coombs (UBC).

The idea of the meeting was to bring together experts in mathematical modeling at multiple levels, from global aspects of epidemiology, to the microscopic details of infection at the individual level. The mathematical modeling of infectious diseases also covers a wide range of mathematical techniques, from deterministic systems of ODEs, to stochastic models of disease transmission over dynamic contact networks, to individual-level simulation and game-theoretic models for the evolution of disease. Our goal was to build on previous successful models at the between- and within- host levels, and to reflect on how new modeling tools might allow multiscale modeling of infectious diseases to have a real impact on population health and disease control. We were particularly lucky to hear two fascinating reflective talks given by David Patrick and David Wilson, both public health scientists who use interdisciplinary and modeling tools to study infectious

Joshua Havumaki (Michigan) explains his poster to Pauline van den Driessche (Victoria) and Dennis Chao (Fred Hutchinson)

The Koelle group in Vancouver. From left, Katia Koelle, Ashley Sobel, Shishi Luo and Stacy Scholle (Duke University)

disease and give policy advice. In the first talk of the meeting, David Patrick (BC Centre for Disease Control and UBC) stressed the importance of understanding transmission networks in two different epidemics in Vancouver - H1N1 flu, and sexually transmitted infections. He also asked a pointed question: why was the SARS epidemic more serious in Toronto than in Vancouver? His answer showed the importance of understanding chance events early in an epidemic situation. David finished his talk with a list of possible challenges for mathematical modellers to consider: models for endemic disease elimination, prioritization of vaccine development, and questions about climate change and the spread of vector-borne diseases into temperate areas of the globe.

On Friday afternoon, David Wilson (Kirby Institute at UNSW in Sydney, Australia), drew from his research on HIV epidemiology in Australia, Asia and Africa, to discuss the interface between mathematical modeling and public health policy. His talk emphasized the importance of linking modeling to the quasi-experimental data (e.g. randomized controlled trials) and cautioned against speculative models. This talk was immediately followed by a lively discussion on the values and pitfalls of mathematical modeling in studying infectious disease epidemiology.

Also at the epidemic scale, Dennis Chao (Fred Hutchison) presented results from massive individual-scale simulation models of epidemics, capturing temporal and spatial variations in the in-

cidence and prevalence of influenza, cholera and dengue. Compartmental epidemic modeling was represented by Jan Medlock (Oregon State) talking on optimizing influenza vaccine allocation over 17 age-classes, leading to complex nonlinear constrained optimization problems, Elamin Elbasha (Merck, Inc) on modelling hepatitis C epidemics in the presence of treatment, and Anuj Mubayi (NE Illinois University) on visceral leishmaniasis in India.

Meanwhile, down at the within-host and cellular scale, Alan Perelson (Los Alamos) showed how multiscale models of systemic and cellular infection were needed to understand particular aspects of hepatitis C treatment - leading to the adoption of "2-day clinical trials" to assay for fast kinetics. Libin Rong (Oakland University) showed how careful modeling could elucidate the importance of CD8+ T cells in controlling SIV infection in macaques, while Stanca Ciupe (Virginia Tech) analyzed hepatitis B infection with a virus dynamics model.

The rest of the speakers endeavored to link the within-host and between-host levels in their presented research. Joshua Schiffer (Fred Hutchison) presented clinical data for herpes simplex virus 2 in the genital mucosa, leading to a spatial model of the dynamics of ulcers with implications for transmission and control. In a related talk, Jane Heffernan (York) questioned how a vaccination program against this virus should be implemented. Rustom Antia (Emory) updated our knowledge of vaccination by presenting a broad framework, with the particular example of experimental LCMV infections of mice. Tim Reluga (Penn State) talked about how including immune responses into models can alter the calculations in population-scale analysis. Jamie Scott (Simon Fraser) discussed antibodies to HIV,

Ben Holder (Rhodes College) explains his poster to Joshua Schiffer (Fred Hutchinson)

A krill's-eye view of the poster session at the Beaty biodiversity museum

and issues with the development of strain-specific HIV vaccines, while Jessica Conway (Los Alamos) presented stochastic models of the earliest stages of HIV infection. Katia Koelle explained how vaccination can be expected to change the evolutionary dynamics of influenza and (in the last talk of the meeting), Miles Davenport (University of New South Wales) reinvigorated the audience with his demonstration of combining within- and between- host information to understand how malaria re-infection is linked to within-host parameters..

Undoubtedly the highlight of the meeting was the reception and poster session held under the newly installed blue whale skeleton at the Beaty biodiversity museum. There were 21 posters, all of a very high standard. Our team of judges had a difficult job in picking four winning poster presenters: Florence Debarre (UBC): "Auto-immunization: how spatial structure influences the evolution of host defense strategies", Shishi Luo (Duke): " Understanding Viral Immune Escape: A Multiscale Problem", Stephanie Peacock (Alberta): "From farm to wild: sea lice control and transmission dynamics" and Bernhard Konrad (UBC): "Mathematical models that predict the length of the window period for HIV infection". Congratulations to the winners and thanks to all the participants for a wonderful meeting!

Many of the talks from the meeting are available for viewing online:
http://www.mathtube.org/conference/disease-dynamics-2013

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Mathematics in Natural Resource Modeling

by Catherine A. Roberts

Shandelle Henson, Professor and Chair of Mathematics at Andrews University in Berrien Springs MI, and Catherine A. Roberts, Professor and Chair of Mathematics and Computer Science at College of the Holy Cross in Worcester MA, co-organized a special session at the Joint Mathematics Meetings in San Diego CA in January 2013 on the topic of Mathematics in Natural Resource Modeling. This was part of the launch of Mathematics of Planet Earth 2013+ (http://www.mpe2013.org), a worldwide initiative where over 100 scientific societies, universities, research institutes, and organizations have dedicated 2013 as a special year for the Mathematics of Planet Earth. Visit their website for a comprehensive list of events planned for the next three years.

In their session at the JMM, Shandelle and Catherine asked speakers to address all aspects of mathematical modeling of natural resources, for example fisheries, forestry, threatened and endangered species, ecological implications of climate change, community dynamics, ecological invasions and range limits, disease vectors, and management of natural resources. They asked speakers to provide practical suggestions for establishing fruitful communication between mathematicians, applied scientists, and natural resource managers. Speakers included applied mathematicians, ecologists, biologists, foresters, and others. This report will describe just a few of the biological talks.

Donald L. DeAngelis, a biologist from the University of Miami, described his mathematical analysis of ecotone resilience for two vegetation types existing along a gradual gradient of groundwater salinity, from highly saline at the coast to lower salinity values inland. He and his collaborators identified the existence of two alternative equilibria on which they conducted a sensitivity analysis. Grey Dwyer, an ecologist from the University of Chicago, described his work discerning the reasons for outbreaks of defoliating insects that damage forests and exacerbate climate change. Using the gypsy moth as his case study, Greg and his collaborators showed how induced hydrolysable tannins strongly reduce variability in infection risk among gypsy-moth larvae to a virus widely believed to be driving the gypsy moth cycles.

Holly V. Moeller, a biologist at Stanford University, described some joint work with Michael G. Neubert, a biologist at Woods Hole Oceanographic Institute. She described how tree species form mutualistic partnerships with the group of belowground fungi known as ectomycorrhizae and the rather surprising fact that an individual tree may host dozens of species of the fungi simultaneously. She described how to explain this diversity in terms of niche differences among the fungi and the influence and importance of temporal variation to the maintenance of fungal diversity. For a complete list of speakers at these sessions, including links to their abstracts, please visit: http://jointmathematicsmeetings.org/

Shandelle and Catherine have proposed to organize another special session on mathematics in natural resource modeling at the next Joint Mathematics Meeting to be held in Baltimore MD in January 2014. If you are interested in speaking or attending the special session, please contact Catherine at croberts@holycross.edu for more information.

The International Symposium on B.E.E.R 2012 St. Louis, Missouri

by Hannah Callender

This past November over 60 mathematical and biological researchers and educators convened for the 5th annual International Symposium on Biomathematics and Ecology: Education and Research, which took place in the historic St. Louis Union Station Hotel. Though the symposium would have been equally as successfully in any other location, one could not help but be impressed by the ornate scenery. The Union Station Hotel dates back to 1894 and at its height handled 100,000 rail passengers a day. The weight of its history was inspiring to all.

The meeting began with a bang as Dr. Jim Cushing from the University of Arizona delivered a riveting presentation on "Population and Evolutionary Dynamics of Semelparity: a Dynamic Dichotomy." Following Dr. Cushing's talk, the three sets of parallel sessions throughout the weekend provided a range of exciting topics, including Differential and Difference Equations With Applications To Biology, Epidemic Models, Education, Ecology, Mathematical Models of Complex Biological Systems, Statistical Modeling, and several sessions on general models of biological systems.

As is customary at B.E.E.R, plenary talks were presented by two individuals, one an authority in the field of biology and one in mathematics. The former was presented by Dr. John D. Reeve from Southern Illinois University, Carbondale's Department of Zoology. Dr. Reeve spoke on "Applying diffusion models to insect movement in natural landscape tales from two systems." Dr. Suzanne Lenhart of University of Tennessee, Knoxville's Department of Mathematics presented the latter talk on "Exploring the effects of order of events in population models with discrete time."

In addition to the invited talks and parallel sessions, the meeting included a lively panel discussion on "New Directions and Career Opportunities for Biomathematics and Ecology," moderated by Urszula Ledzewicz from Southern Illinois University, Edwardsville, a poster session for undergraduates, and two workshops focused on enhancing education in mathematical biology. Dmitry Kondrashov from the University of Chicago led the first workshop, entitled "On proteins and vibrating springs, or teaching modeling through normal mode analysis of molecular structures." Christopher Hay-Jahans from the University of Alaska Southeast gave the second workshop on "A Practical Introduction to Using R."

From the first time I attended this conference in Izmir, Turkey in 2010, it has been my favorite of all mathematical biology conferences. As a mathematical biologist who has a strong desire for both contributing directly to the field of mathematical biology through my own research and also enhancing the educational experiences of the next generation of researchers in this field, I place tremendous value on meetings where I can speak with and learn from others with similar visions.

Some participants in the Symposium on BEER 2012

Keynote presentation by Jim Cushing

The B.E.E.R. conference, more than any other conference I have attended, meets both of these needs. It provides high quality talks in areas of research and education, from both mathematicians and biologists. In my brief ten years of conference attendance, this forum has provided some of the best opportunities for networking and future collaboration, for conference organizational involvement, for sparking new ideas in research and education, and for developing life-long friends and mentors in the field.

The organizers, Olcay Akman-Illinois State University, Hannah Callender, University of Portland, Tim Comar-Benedictine University, and Elsa Schaefer-Marymount University have planned yet another star lineup, with a keynote presentation to be delivered by Dr. Avner Friedman, Distinguished Professor of Mathematics and Physical Sciences at The Ohio State University, and plenary presentations to be given by Dr. Rebecca Segal of the Virginia Commonwealth University, Department of Mathematics and Dr. Jeremy M. Wojdak of Radford University's Department of Biology. Graduate and undergraduate student research competitions will be some of the new and exciting highlights of this year's meeting. Fully refereed proceedings of this year's meeting will be published by McGraw Hill. For more information on 2013 meeting, please see the conference webpage: http://cas.illinoisstate.edu/sites/beer/. We look forward to seeing you in October 2013, and remember to pack your soccer gear for our traditional friendly game of soccer!

Philip Maini's Visit to NIMBioS

Bulletin of Mathematical Biology editor Philip Maini visited the National Institute for Mathematical and Biological Synthesis in Knoxville in February 2013. In addition to meetings with many researchers at NIMBioS, Professor Maini met with NIMBioS Postdoctoral Fellows and graduate students to provide an overview of professional positions in math biology in the UK and Europe, discuss the differences between the systems for providing funding support and evaluating institutions in different countries, and gave his perspective on some challenging new areas in math biology. Philip and several NIMBioS researchers visiting Great Smokies National Park, hiking to one of the few remaining groves of virgin forest remaining in the National Park. He is pictured here along with NIMBioS Director and SMB past-President Lou Gross.

Philip Maini with Louis Gross Visiting the Great Smokies National Park

NIMBioS Partnership with Mathematics of Planet Earth 2013 Initiative

Mathematics of Planet Earth 2013 (MPE2013) is an initiative of mathematical sciences organizations around the world designed to showcase the ways in which the mathematical sciences can be useful in tackling our world's problems. This initiative has led to plans for many events to take place in 2013, including more than 10 long term programs at institutes around the world, and more than 50 workshops. NIMBioS is a partner organization of MPE2013. More information can be found here: http://www.nimbios.org/mpe

Perspective on "*More Is Not Necessarily Better:*" Metronomic Chemotherapy

by Eddy Pasquier & Urszula Ledzewicz

In recent years, there is growing medical evidence that it is not only *w*hat anticancer drugs are administered to a patient but *h*ow it is done in the sense of the dosage, timing and sequencing that makes a significant difference in the treatment outcome. Thus in the war against cancer in addition to the ongoing quest for new drugs, there is also a search for new ways of administering existing ones. Benefits of the well-established MTD (maximum tolerable dose) protocol are being questioned since it has become evident that for some cancers "*more is not necessarily better*". In 2000, two founding papers by G. Klement et al. [1] and T. Browder et al. [2] gave birth to the field of metronomic chemotherapy, a term coined by D. Hanahan in an accompanying editorial, whose title started with the words "*less is more*" [3]. Originally, it was defined as "The frequent administration of chemotherapy drugs at relatively low, non-toxic doses, without prolonged drug-free breaks". But perhaps more appropriately, it has been recently redefined as "the minimum biologically effective dose of a chemotherapeutic agent, which, when given at a regular dosing regimen with no prolonged drug-free breaks, leads to antitumor activity" [4]. By relying on frequent administration of low doses of commonly used chemotherapy drugs, like Taxol or CPA, metronomic treatment can kill cancer cells while reducing toxicity to healthy tissues and positively impacting on the tumor microenvironment: it prevents the formation of the new blood vessels and boosts the immune system. In a way, "we kill three birds with one stone", and it is an inexpensive stone indeed! The common assumption supporting MTD chemotherapy was that lower doses would kill less cancer cells and prompt the development of drug resistance. This view has however been challenged recently since the opposite effect of re-sensitization was observed with metronomic chemotherapy.

There is mounting medical evidence in support of metronomics in certain tumor types and some patient populations such as elderly patients and/or those with poor performance status [5]. Furthermore, because of its affordability and lack of toxicity, metronomic chemotherapy provides a viable option for the treatment of cancer in underdeveloped countries where new expensive drugs are simply not available [6]. Recent successes in early phase clinical studies have led to the development of larger-scale randomized phase III clinical trials, especially for the treatment of advanced and drug-refractory breast and colorectal cancers. Results of these clinical trials where the effectiveness of metronomic chemotherapy regimens is compared for the first time head-to-head with standard of care MTD chemotherapy are highly anticipated in the field and expected to be communicated later this year.

With a lot of experimental data already available, a lot is still not known or understood, so there is an opportunity for researchers from various fields, certainly mathematical biology among them, to contribute here. There are many open questions as of how to construct mathematical models for metronomic chemotherapy to capture all the complexity of its actions which, hopefully, could provide some insights into how exactly such a treatment protocol should look like in terms of dose rates, frequency and also sequencing since usually multiple drugs are involved. Currently, it is only agreed upon that metronomic chemotherapy should be given at a properly calibrated, so called biologically optimal dose, BOD, which should lie somewhere between 10% and 80% of the MTD, and it is not even clear whether it should vary or remain constant throughout the treatment duration and whether breaks are beneficial or unnecessary. How metronomic chemotherapy affects the different compartments of the tumor (i.e. tumor cells, vasculature, immune cells, tumor microenvironmentÉ) remains to be modeled and validated. Similarly, the best combination to use and optimal sequencing between metronomic chemotherapy, MTD chemotherapy and targeted agents for a given tumor type still needs to be determined.

Many of these questions were addressed at the workshop "Tumor Metronomics: Timing and Dose Level Dynamics" organized by Philip Hahnfeldt and his MD collaborator Giannoula Klement at Tufts University's Center for Cancer Systems Biology in July 2012, which both of us attended as instructors. On a

larger scale, we would like to direct everyone to the website of the "Metronomics Global Health Initiative" founded by Nicolas Andre and Eddy Pasquier, http://metronomics.newethicalbusiness.org/Eddy-Pasquier where current news and upcoming events concerning metronomics are being published. Anybody, who would like to join forces with this group of enthusiastic biologists, MDs and mathematicians and participate in any way in this initiative, is welcome to join. Even small events, like a discussion panel on metronomics we coordinated in Sydney this January at the Workshop on Tumor Immune System Dynamics organized by Amina Eladdadi, Peter Kim and Dan Mallet contribute to the overall awareness of this exciting multidisciplinary challenge where we could say "*there are still many more questions than answers*". As it is stated in [4], it is still "*terra incognita*" ....

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About The Authors:

Dr. Eddy Pasquier is a Senior Research Officer at the Children's Cancer Institute Australia for Medical Research. Over the past 10 years, Dr. Pasquier has made significant contributions to the fields of tumor angiogenesis and innovative cancer therapies. His work on metronomic chemotherapy in particular contributed to elucidate some of the underlying molecular and cellular mechanisms of action of this multi-faceted therapy. Through his long-standing collaboration with Metronomics Global Health Initiative co-founder, Dr Nicolas Andre, Dr Pasquier also helped in the development of more effective metronomic protocols to be used in childhood cancer patients living in both high-income and low- to middle-income countries. More info: http://metronomics.newethicalbusiness.org/Eddy-Pasquier

Prof. Urszula Ledzewicz holds a rank of the Distinguished Research Professor at the Department of Mathematics and Statistics, Southern Illinois University Edwardsville. She is an author and co-author of over 140 research publications in the field of optimal control, particularly with applications to biomedical problems like finding optimal protocols for various anti-cancer therapies. In the most recent years she developed research interests in mathematical aspects of metronomics chemotherapy. She most recently joined the Metronomics Global Health Initiative and tries to promote the awareness of this scientific challenge among mathematicians in her field. More info: `http://www.siue.edu/~uledzew/`

Research Interview

Keeping Academics In The Family

Edmund Crampin talks to Santiago Schnell about his work in mathematical biology, and the family that inspired him to become a scientist

I understand your father is a mathematician and your grandfather won the Nobel Prize for Physics in 1977. How does it affect you having two successful career scientists in your family?

Science was always around, as part of family discussions; a normal activity. As was academia. In fact I think that if I had announced as a child that I wanted to be a banker or an accountant this would have caused much more alarm.

What inspired you to become a mathematical biologist?

Well, certainly not the British education system of the late 1980s in which I was obliged to give up studying biology in order to pursue mathematics and physics ... I gauged my scientific interests as a child by the books I read. For a time these were mainly popular science books about physics - cosmology and relativity in particular. But as I entered university (to read Physics) I found that I had switched to books on evolution and brain sciences. I have had many wonderful teachers, lecturers and mentors, who have also influenced the path I have followed. At Imperial College I was fortunate to be taught by many great lecturers, and in particular three who fostered my interest in biology. Two gave courses in biophysics: Peter Brick in molecular biophysics, and Keith Ruddock, who died tragically just after I left Imperial, on the biophysics of nerve cells and networks. Both emphasized the critical role of mathematical modeling and quantitative analysis in uncovering some of the fundamental properties of biological molecules and cells. The third was Frank Berkshire, whose course on dynamical systems and chaos was the stuff of legend, complete with lecture-theatrical demonstrations of some of the finer points of classical mechanics and dynamical systems from the man himself. Frank was probably the most responsible of all of them for me seeking a PhD in which I could combine my interest in the mathematics of dynamical systems and my interests in biology, which ultimately led me to the Centre for Mathematical Biology in Oxford.

You have had something of an interesting career trajectory. Can you tell us a little more about this?

I have moved around a little, both in geographical terms and with respect to the departments in which I have been based. This has allowed me to study in some wonderful places and has informed my approach to mathematical biology, although it certainly wasn't planned this way. Physics in London (and a year as an experimentalist in Paris) led to a DPhil in mathematical sciences with Philip Maini and a Junior Research Fellowship in physiology at Oxford. I was determined to find problems in which there were more data to model, and this led me to work with Denis Noble on some problems in cardiac cell physiology. At this point I met Peter Hunter, a long time collaborator with Denis, who invited me to visit the Bioengineering Institute in Auckland. I ended up staying there for 10 wonderful years with many wonderful colleagues. This year I moved to the University of Melbourne to take up an appointment across three faculties (engineering, science and medicine). Looking at this makes me realize how important meeting the right people at the right time has been for my career to date. Long may this continue!

Tell us about your research. What are you working on?

I am interested in a broad range of problems in modeling regulatory pathways and cellular processes, in particular relating to disease. Most of the prob-

lems we work on involve aspects of computational cell biology. Some of our current projects include using mathematical models of heart cells to understand the development of heart disease; developing computational approaches to study the networks of molecular interactions underlying breast and skin cancers; and modeling the signaling pathways that regulate cellular processes in epithelial tissues. In general I would say that our projects are focused on bringing a more mechanistic understanding of cellular processes to the systems biology approach to understanding disease.

Which aspect of your research are you most excited about?

I have just moved from Auckland to the University of Melbourne to take up a new position as Chair of Systems and Computational Biology. The University of Melbourne, and more broadly the city of Melbourne, is home to a huge amount of activity and expertise in life sciences research. The University also has great strengths across engineering, physics, mathematics and computer science, including the Victorian lab of the National ICT Australia research centre (NICTA). I am very excited at the opportunity and potential that there is here to help to establish Melbourne as a centre for systems and computational biology.

Have you never found the complexity of biological systems daunting?

In a word, yes. I prefer to characterize biological systems as complicated, rather than complex, which is a rather loaded word for physicists. Let me explain what I mean. Statistical physics deals with the interactions of large populations of particles that are, or are treated as being, identical. Typically one looks for emergent properties that arise from these interactions. This type of thinking also leads towards ideas such as self organization, order out of chaos and so forth, often with complexity as the catch word. I don't think cell biology is like this. I am more sympathetic to the view, following Schrchrödinger's discussion in his book What is Life?, that it is more like an exquisitely complicated piece of machinery, he made the comparison to clockwork, in which lots of non-identical components interact to coordinate cellular processes.

What is the next big challenge? What is hot in mathematical biology? I think that a key challenge is better integration of data from a range of different measurement modalities, using modeling to bring together what we have learned about a system from these different vantage points. Secondly, systems biology needs to move towards more tissue and condition-specific data sets and models. Thirdly, we must demonstrate the value of modeling to a rightly skeptical audience and demonstrate real clinical impact arising from quantitative and predictive approaches to biology and medicine.

What would your message to a young and aspiring mathematical biologist be?

My advice would be to learn some physics and chemistry, because this should underpin your mathematical models, and then go and spend some time in the lab and learn the language of biology. During my career I have seen a change from people like me, mathematicians or physicists who have learned how to communicate across the disciplines, to a new type of scientist who is equally at home in the lab with a pipette or in front of a computer. I am fortunate enough to work with some of these people in my group.

If you were not a scientist, what would you be?

There are lots of things I would love to have been musician is at the top of that list. But the only other career I have seriously considered would be related to policy work-I am interested in how research activity is organized, and how governments and societies view and fund research. I was very fortunate in New Zealand to be invited to join a group of scientists who regularly met up at what was then the Ministry for Science and Innovation. But the early retirement plan is still to open a bike shop somewhere.

If you have any spare time, what do you do when you are not working?

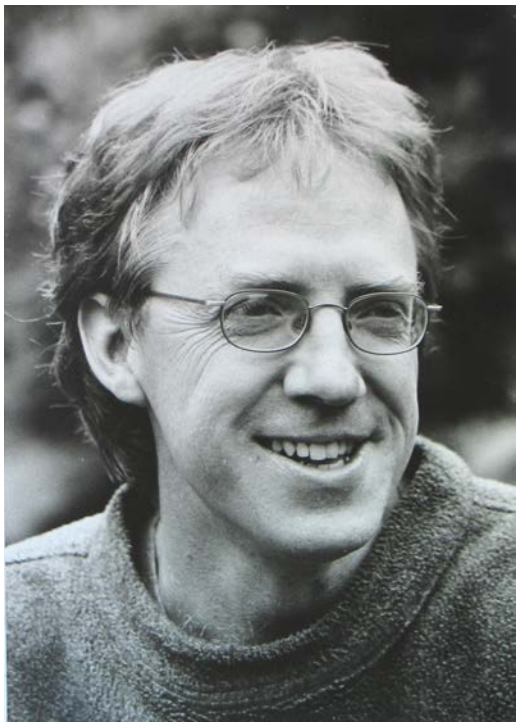
It's all about the bike ...

About Edmund J. Crampin

Edmund J. Crampin is a Professor and Rowden White Chair of Systems & Computational Biology at the University of Melbourne, Australia. Before joining the University of Melbourne, he was an Associate Professor and leader of the Systems Biology Group at Auckland Bioengineering Institute. For more info: http://sites.bioeng.auckland.ac.nz/crampin/

Mathematical Biology: My Personal Journey

James Sneyd



When I first started doing mathematics (in 1981) the field of mathematical biology was very small. I had no idea it even existed. For me, it was all topology and graph theory and group theory and number theory, and all kinds of theories I've never used again. Then, one afternoon in the university library, I remember browsing along the shelves and picking up a little black book, published in some cheap and nasty font, called (I think) Nonlinear Differential Equations in Biology. By some guy called James Murray whom I'd never heard of. Well, when I read that book I knew that was it. That was the stuff I wanted to do. So I did. When I finished my undergraduate degree (at the University of Otago in New Zealand), I looked around for a place to do a PhD. My first choice, unsurprisingly, was Oxford, where James Murray was. But I have it on very good authority that Jim read my application, thought to himself "Sneyd? That's a funny name.", and threw it in the rubbish.

Oxford being unavailable, I started looking at places in the USA. I soon discovered that New York University offered courses on chemical kinetics, neuroscience, biological fluids, the visual system, and a number of other cool things. That decided me, and a few months later, I trundled off to Manhattan. Small town New Zealand to New York City. It was a change, I can tell you.

At NYU I learned my very first real live Mathematical Biology. I did all the usual fluid mechanics - to this day I have only a vague understanding of fluids - but my real love, the stuff that motivated and inspired me, remained biology. I remember consulting with Charlie Peskin about the oral examination, the one you do after two years, before you start real research. Each student had to propose a list of topics to be presented to the examining committee, and I went to town on this. No sense of perspective, that's me. Charlie took one look at my proposed list, chuckled a bit, and said, in his usual kind and gentle way, "James, I'm not entirely sure it would be wise to cover ALL of these topics". At any rate, I ended up doing my PhD with Dan Tranchina on light adaptation in turtle cones. It's difficult to put into words the debt I owe to Dan and to Charlie. Their teaching, their mentorship, still forms the foundations of how I think today. I am standing on the shoulders of giants, but still don't see as far as they do. But I get to see very much further than ever I would if I was standing on my own.

The third major influence on my thinking was, as you might have guessed already, James Murray. After finishing my PhD, I went to Oxford for a year, to spend time with Jim and his group. We talked about patterns and morphogens, about honeybees, ants and termites, about alligator teeth, about infectious diseases, noninfectious diseases, forest fires, bugs, and cells. We argued about asymptotics and the value of nondimensionalization and whether we should prove things (not hard to guess which side I took). It was a wonderful group of people, and one of the most stimulating environments I have ever worked in. The friends I made there - most notably Jim Murray himself - remain today as a global network of inspiration to me.

Back in the USA, at UCLA, it wasn't long before I discovered the field that has formed the majority of my subsequent career - calcium dynamics. It was all rather serendipitous, I suppose. As a young assistant professor, with no set research direction, I was given some good advice by Ken Lange, who was chair of UCLA Biomathematics at the time. "James", he said, "go to every single talk in the physiology department. Every talk, every seminar, boring or inter-

esting, go to them all." Well, probably not his exact words, but that was the gist of it.

So off I went, as instructed. It wasn't long before this guy called David Clapham came by to talk about his recent discovery in Xenopus oocytes of spiral waves of calcium. At that time there were very few examples of spiral waves in the math biology literature, but here was a new one. Brand new. When I saw those calcium spiral waves, all lonely and unmodeled, I knew I had hit the jackpot.

That was the start of my interest in calcium dynamics. About the same time I also met Mike Sanderson, who has become one of my closest colleagues and friends. Mind you, it didn't begin well. Mike gave a talk in the Physiology Department, on the topic of intercellular calcium waves. Very cool, I thought. I could do that. So I went up to Mike's lab, knocked on the door, and said to him, "I really enjoyed your talk. You want to work with a mathematician?". Mike looked at me, paused, and said "No. Not really." Mike denies this ever happened, but you can trust me. It did.

Anyway, I wasn't going to be put off. I wanted to work on calcium waves, and I wasn't going to let a bit of grumpiness deter me. So I went back, and back, and back, until finally Mike realized that (as the Borg say) resistance was futile. After a few years at UCLA I went home again, back to New Zealand. I was a bit concerned. Would I find stuff to do? Would I find collaborators in New Zealand? Would I get bored? I decided to make sure I didn't, and began making plans to write a book. I'd read Jim Murray's wonderful book, Mathematical Biology, many times and used it extensively, but (let's be honest here) it didn't have a whole lot of physiology, and I'd always thought that a shame. Students kept asking me "Well, what is Mathematical Physiology", and I'd answer "Er... um... well...".

The book I was thinking of was too big a job for one person. I needed a co-conspirator. As it happens, I'd always been a great fan of Jim Keener's work on excitable systems and cardiac models, so I asked him to help me write it. Fortunately he had a momentary failure of rational thought, and agreed. The result was five years of effort for the first edition of Mathematical Physiology, followed by another five years of effort for the second edition. Still, at the time we didn't know it was going to take up ten years of our lives, so we rushed in where sensible people fear to tread.

Since then I've basically just kept doing the same thing. Calcium dynamics, mostly. I've moved around a bit, to and fro across the world; University of Canterbury, University of Michigan (where I met David Yule), Massey University, University of Auckland. I've always worked closely with experimentalists; Mike Sanderson and David Yule have been doing experiments for me for years. They like to think I do models for them, and I encourage them to think so. It makes them feel better, I think. I've been very lucky. I came out of my PhD (in 1989) just as mathematical biology was taking off. I rode that wave to my first job, and I've ridden it ever since. Now mathematical biology is an enormous field, widely valued across Faculties of Science, Engineering and Medicine, and one of the most dynamic and fast-growing areas of applied mathematics. ItÕs rare nowadays to hear someone question the validity of mathematical modeling per se. (They might think your particular model is a pile of nonsense, but that is usually a rather different question.)

Although I was formally trained as a mathematician, I've never been one. Unapologetically. I don't care about mathematical rigor or proofs of theorems. I don'tt care what you can prove about your model, I care only about what your model can tell us about the physiology. I want to understand how cells work, how organs are put together, how they go wrong, and how you can fix them when they do. And mathematics is such a wonderful tool for doing just that.

List of Books:

- J. Keener and J. Sneyd, Mathematical Physiology, Second Edition, Springer-Verlag, 2008. Two volumes. 1049 pp.
- J. Sneyd (Editor), Mathematical Modeling in Calcium Dynamics and Signal Transduction, Lecture Notes in Mathematics, Springer-Verlag, 2005.
- J. Sneyd (Editor), An Introduction to Mathematical Physiology, Cell Biology, and Immunology, Proceedings of Symposia in Applied Mathematics, American Mathematical Society, 2002
- S. Camazine, J.-L. Deneubourg, N. Franks, J. Sneyd, G. Theraulaz, E. Bonabeau, Self-Organization in Biological Systems, Princeton University Press, 2001.

For more books, check out: `http://www.math.auckland.ac.nz/~sneyd/books.html`

The Future of Mathematical Biology

Phuong T. T. Ngyuyen, University of Auckland
Former Student of Prof. James Sneyd

What attracted you to mathematical biology?
As a fourth year physics student at Faculty of Physics, Moscow State University, I decided to specialize in biophysics. I found biology attractive. Moreover, our professors always said that biophysics is one of the most "fruitful" areas of the physical sciences. At Moscow State University, I gained a very good background in investigating complex biological systems. Although there were many things that I could not digest at the time, I was very impressed by the Cell Biophysics course taught by Prof. Ataullakhanov Fazly Inoyatovich. At the time, I was pursuing research in the Biophysics of Photosynthesis group, led by Prof. Alexander K. Kukushkin. We were developing and analyzing mathematical models of biochemical reaction networks, when I realized that our biophysical models were on reality rather mathematical biology problems. So I applied to the PhD program in mathematical biology at the Department of Mathematics at the University of Auckland in New Zealand. I worked under the supervision of Profs. James Sneyd (New Zealand) and Paul Shorten (AgResearch in Hamilton, New Zealand).

What is your current research project?
I have recently completed my PhD in 2012. My PhD research focused on the regulation of steroid hormone synthesis by the activity and compartmentalization of steroidogenic enzymes and the availability of substrates. We used ordinary and partial differential equations to model the regulation of the hormone system.

What specific areas are you interested investigating?
I am interested in the mathematical modeling that addresses current clinical problems such as metabolic disease, cancer and disorders of the immune system. I am also interested in agriculture problems. I would like to build mathematical models to make predictions that could be used to propose diagnostic and therapeutic strategies or industrial application.

What do you hope to do now?
Presently I am applying for postdoctoral positions. I would like to get a position where I could study and solve problems in either clinical and/or agriculture applications. Ideally I would like to gain experience in modeling stochastic processes, and understanding when deterministic approaches are inadequate to model scientific problems.

What advice will you give to an undergraduate interested in a mathematical biology career?
Undergraduate students should join in a mathematical or biophysics research group as soon as they have an opportunity. I believe they will find the research experience more useful after taking courses in differential equations, statistics and probability, numerical methods, thermodynamics or engineering fundamentals.

What inspires you scientifically?
The complexity of living systems inspires me the most.

Why did you join the Society for Mathematical Biology?
I very much enjoyed attending the annual meeting of The Society for Mathematical Biology in Knoxville, July 2012. I was so impress with the quality of the talks, and enthusiasm of the participants that I decided to join the society.

James Sneyd, Phuong's former PhD supervisor, says:

Phuong is an excellent example of the next generation of mathematical biologists, in that her particular skill is the integration of biological information and data into a quantitative framework, and the interpretation of model results from an experimental perspective. I cannot emphasize strongly enough how important these skills are for the modern modeler. Communication with experimentalists is vital. Not just talking superficially once a month, or reading their papers on the bus into work, but detailed interaction. This, realistically, is most likely to come about if the modeler speaks the language of experiment - it is asking too much, I feel, to expect experimentalists to learn the language of differential equations and bifurcation theory - but this is a challenge not always mastered by those trained in solely theoretical approaches.

It is in this manner that Phuong shines particularly. Much of her PhD training was in a research institute in close proximity to experimentalists, and she has learned the pitfalls and advantages, the difficulties and rewards, of experimental work. To this knowledge she brings skills in mathematics and computer modeling, and thus produces output of biological insight, useful and comprehensible to experimentalists, but based on quantitatively rigorous methods. It is an impressive combination that will stand Phuong in excellent stead as she searches for a modeling job in mathematical biology.

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

From The Bulletin of Mathematical Biology

Mathematical Biology Reviews

Good review articles are important. They are good for the field, and they're good for your career. A review article is an opportunity to present your research area, in a digestible way, to potential graduate students, present or future colleagues, even to people who might be sitting on grant review boards. Since they are accessible outside your own narrow group of specialists, reviews can spur interest in your research, can help establish your name as a leader in the field, and can help to establish your research as significant. If you're already rich and famous, a review article can be an excellent way to lead the field, and to guide the research of others. I do love a good review, and there aren't enough of them.

The Bulletin of Mathematical Biology has asked me to act as a review collector. Rather like a tax collector, I suppose, but less remunerative. I invite submissions of review articles, which offer an in-depth treatment of an emerging research area, or a significant recent development, in the general area of computational, theoretical and mathematical biology. Reviews can be submitted at any time, and will be reviewed in the normal manner. Reviews can be submitted directly to me (James Sneyd, sneyd@math.auckland.ac.nz), or through the regular submission website (http://www.editorialmanager.com/bmab/). All submissions will be peer reviewed in the normal manner.

I know it takes work to write a good review. It takes a lot of thought and a lot of time. But the benefits are significant, and it's well worth the effort.

Prof. James Sneyd
Department of Mathematics
University of Auckland, NZ

Positions Available

PhD in Mathematical Biology, Dept. of Mathematics, U. of Auckland, NZ: Closing date: 1st July, 2013. A good background in mathematical modeling and scientific programming is desirable. Previous knowledge of biological systems is not required but may be an advantage. The project will be supervised by Dr Claire Postlethwaite (Mathematics) and Prof Michael Walker (Biology). Stipend is NZ$25,000 pa (tax free) for three years plus tuition fees. Start date is flexible but would preferably be between October 2013 and March 2014. Interested candidates should send an email expressing their interest, along with a CV and academic record, to Dr Claire Postlethwaite at c.postlethwaite@auckland.ac.nz

PhD in Fast and Furious: The nature of anticipation, U. of Reading, UK: The project will develop and apply tools from nonlinear dynamical modeling and signal analysis in order to investigate the mechanisms of anticipation using motion tracking experimental paradigm where two subjects learn via interaction to perform coherently their motion. To apply for this studentship please submit an application for a PhD in Cybernetics to the University at: www.reading.ac.uk/graduateschool/ Please quote the reference GS13-14 in the "Scholarships applied for" box which appears within the Funding Section of your online application.

Postdoc in Math/Algorithms for Biology, INRIA at U. of Lyon 1, Lyon, France: Seeking highly qualified and motivated applicants in mathematics (statistics, probability, combinatorics, graph theory) and/or algorithmic. A strong interest for biological problems would be important. The postdoc fellow will develop formal models and algorithms to analyze both publicly available and newly produced data. For more information on the group and on the SISYPHE project, please write to us at: Marie-France.Sagot@inria.fr. You may also consult the web page of the team: https://team.inria.fr/bamboo/en/job-offers/

Postdoc: Immunological Modeling, Louvain-la-Neuve, Belgium: This position is partly funded by GSK Vaccines, the vaccine division of the GSK Group. The modeling work will be done in close collaboration with another postdoc researcher working in the group of Prof. Jean-Christophe Renauld. The position should ideally start on September 1st and is offered for 2 years. Applicants should send a cover letter, a detailed CV, a brief statement of research interests, and names and contact information for three references. For further information, contact Emmanuel Hanert emmanuel.hanert@uclouvain.be. More info: http://www.bru.licr.org/

Postdoc in Infectious Disease Dynamics, U. of Notre Dame: An exciting opportunity exists to join the highly innovative, inter-disciplinary Global Epidemiology and Biostatistics Group led by Prof. Edwin Michael at the U. of Notre Dame in the Dept. of Biological Sciences and the Eck Institute for Global Health. The position has funding available for 2 years in the first instance. Salary is based on NIH guidelines for postdoctoral fellow salaries. Qualified individuals should send in PDF format a cover letter, CV, statement of research interest, and three letters of reference to the search committee chair, Dr. Edwin Michael at eigh@nd.edu. For info: http://hr.nd.edu/employment

Postdoc & Programmer Positions in Computational Systems Biology, OIST, Okinawa: Seeking programmer/postdoc to work in interdisciplinary projects aimed at developing novel (1) stochastic/multiscaled simulation algorithms and (2) parameter estimation techniques. The ideal candidates should have a strong background in Computer Science and/or Applied Mathematics (numerical analysis and probability) as well as a strong interest to collaborate with experimental biologists and theoreticians. More info: http://www.oist.jp/careers/

Life and Health Risk Modeler/Programmer, Boston: This position is in the infectious disease modeling team within the Research and Modeling department. The team has developed techniques for modeling risk from catastrophic pandemics using a global metapopulation SEIR model that explicitly accounts for population movement and epidemiologic disease spread. This position will allow for expansion of the team's existing capabilities and provide support for the increasing set of responsibilities. Requirements: MPH/MSPH/MS in public health, natural science, or engineering or BS with related experience, and a background in epidemiology, biology, or biostatistics a plus. More info: https://aircareers-isofamily.icims.com/jobs/25455/job

Announcements

Upcoming Events & Opportunities at NIMBioS

Requests for Support: September 1, 2013 is the deadline for submitting proposals for new scientific and educational activities at NIMBioS. Potential organizers of activities in areas of molecular biology, cell biology, network biology, immunology and systems biology are particularly encouraged to submit requests for support of Working Groups or Investigative Workshops. Application information is also available on our website for Postdoctoral Fellows, Sabbaticals and Short-term Visitors for activities beginning spring/summer 2014. Visit: http://www.nimbios.org/research/

NIMBioS Visiting Graduate Student Fellowship: NIMBioS is now offering 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. For more information about the fellowship and how to apply, visit: http://www.nimbios.org/education/

Mathematical Biosciences Institute

MBI: The Keyfitz Centennial Symposium on Mathematical Demography, June 24-28, 2013: Cosponsored by MBI and the OSU Institute for Population Research (IPR). Nathan Keyfitz (1913–2010) made fundamental and highly influential contributions to demography over a long and productive career. His work was characterized by an elegance of approach and a depth of insight that came from a deep recognition of the interplay among models, data, and interpretation. This symposium, marking the 100th anniversary of his birth, will bring together a diverse set of scientists studying, to use Keyfitz's term, the mathematics of population. For more information and to apply, please visit: http://mbi.osu.edu/2012/keydescription.html

MBI Undergraduate Research Program- Capstone Conference: This conference offers undergraduate students doing research projects in the mathematical biosciences an opportunity to present their work on the national stage. This student centered conference features: recruitment fair for graduate studies, panels on jobs and graduate opportunities, keynotes from prominent Math Biologist, and social event at the Columbus Zoo/Aquarium. Deadline for application: July 12,2013. For more information and to apply, please visit www.mbi.osu.edu/eduprograms/upcapstone2013.html

The 2013 Resource Modeling Association (RMA) Meetings June 18th-21st, Cornel University

The RMA meeting will be held at the Cornel University starting the evening of Tuesday, June 18th and ending at noon on Friday, June 21st. For all the details on the 2013 RMA Meetings, how to submit an abstract, registration, and lodging, and social events go to: http://www.rmameeting2013.org/

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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