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IN THIS ISSUE

The Joint Annual Meeting of the
Japanese Society for Mathematical Biology
and the Society for Mathematical Biology
July 28 - August 1, 2014
Osaka, Japan
http://www.jsmb.jp

Letter from the President

Dear SMB Members,

When President Obama settles down to write his Saturday radio address, he has a swarm of advisors hovering around to make sure he doesn't say anything that inadvertently, or advertently for that matter, offends anyone. Although I need to compose the "Letter from the President" only 1/3 as often, and in the privacy of my own dining room, I definitely do not feel alone in this enterprise. Outgoing, and now Past, President Gerda de Vries is a remarkable leader who has made the transition smooth, and has been unfailingly helpful in showing me how to maintain the many improvements she initiated. Continuity, as we know from modeling, makes our lives much easier, and incidentally helps avoid hysteresis.

I have been equally impressed by the dedication and insight of those who keep the organization working, the Board of Directors, the Committee Chairs, the Editors of the SMB publications, and particularly Renee Fister and Heiko Enderling for heroic updating of the accounting system and the web site. Thanks to all for making sure that this exciting honor such a pleasure.

We are still cooling off from the brilliantly run SMB meeting in Tempe in June; thanks to Hal Smith, Fabio Milner and all the folks at ASU for an inspiring and busy time. I am already looking forward to the joint meeting with the Japanese Society for Mathematical Biology in Osaka. Do plan ahead for what is sure to be a cultural and intellectual adventure.

The leadership and involvement of our members and officers is the foundation for the next steps I envision for the Society. I want to establish us as the "go to modelers" across the full range of the life sciences, from environmental to biomedical science. A first step will be to cooperate with the core organizations throughout the life sciences, by sponsoring collaborative sessions at annual meetings, special journal issues, and joint educational initiatives. Our goal is not so much to foster the Society for Mathematical Biology itself, but to advance the science of mathematical biology and thus the whole life science enterprise. Every member of the Society contributes to the enterprise, but I think that we can do even more to capitalize on our collective expertise. Please get in touch directly with me or with any of the officers with ideas for joint enterprises.

With the fall semester upon many of us, we're busy, but often the activation energy for new ideas is less than it seems.

Sincerely,

Fred Adler

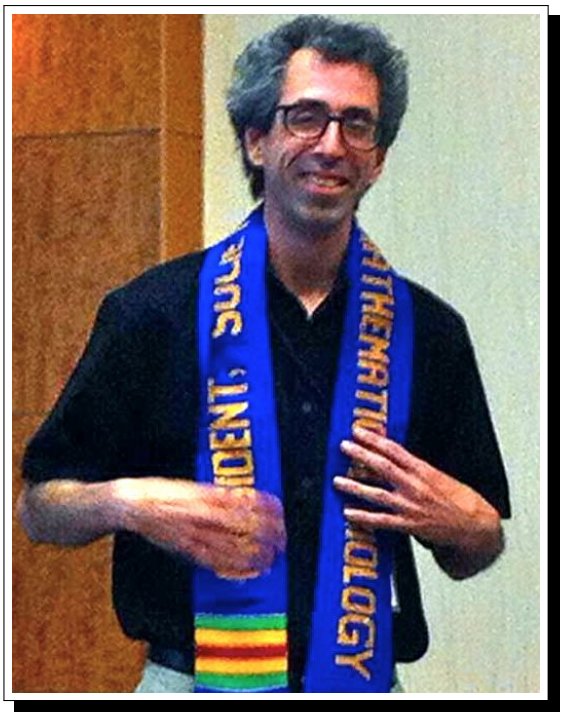
President's Report on the 2013 SMB Meeting

After getting back from the meeting in Tempe, my son was searching for "Worst Music Videos" of 2012, and stumbled on the priceless "Hot girls we have problems too. We're just like you, except we're hot." Well, we were hot in Arizona during the SMB meeting, but the science presented in the air-conditioned coolness of the Tempe Mission Palms was both cool and hot.

One of the great delights of the meeting was the diversity of topics. The plenary talks alone ranged from stroke, genetics, rabies to bacterial growth. Leon Glass presented the Winfree Prize talk on the role of mathematics in predicting the risk of sudden cardiac death, and coupled his elegant talk with memories of the creativity and personality of Art Winfree whose mathematical insight into biological oscillators continues to inspire. Rafael Pena-Miller gave the Segel prize talk, and showed an extraordinary and enviable link between mathematical models and the evolution of antibiotic resistance in microbes, and how quantitative thinking can challenge orthodoxies such as the need to take huge doses of antibiotics.

The contributed sessions and posters delved into these topics and more, and I amused myself during a rare free moment concocting a list of topics starting with every letter of the alphabet (I'll just mention quorum sensing and zoonoses here). One of the most effective elements was the "always-open" break session area, where I think the attendees nearly became a clique, in the best graph-theoretical sense of the term. I have one new collaboration, and am sure that many others do also. The line-up of restaurants on Mill Avenue and environs made meals easy, diverse and convivial.

Gerda de Vries handing the SMB scarf to Fred Adler



President Fred Adler wearing the SMB scarf with Pride

The SMB Business Meeting was brief, but to the point, with the passing of the stole of leadership from the remarkable Gerda de Vries to myself, and some great ideas on how to further increase the visibility and influence of the Society. Gerda, in addition to modernizing so many aspects of the SMB, showed her brilliant leadership by sitting far enough from the microphone at the banquet to avoid having any speeches, leaving people to instead focus on eating and chatting.

Math biologists, we have problems too, but our problems are the kind that everybody should envy. Such as how to use mathematics to make sense of the amazing biology around us, and how that amazing biology inspires new mathematics. That's what I call hot.

2013 Akira Okubo Prize Announcement

Dr. Nanako Shigesasda

The Society for Mathematical Biology and the Japanese Society for Mathematical Biology are pleased to announce that the 2013 Akira Okubo Prize will be awarded to Dr. Nanako Shigesasda, Professor Emeritus of Nara Women's University, Japan. In 2013, the Okubo Prize is awarded to a senior scientist whose lifetime achievements have been exemplary in developing innovative theory, in establishing superb conceptual ideas, in solving difficult theoretical problems, and/or in uniting theory and data to advance a biological subject. Professor Shigesada's outstanding accomplishments strongly fit the criteria and the spirit of the research of Professor Akira Okubo, in whose memory the Prize was established. In her long and successful career, Dr. Shigesada has made uniquely significant contributions to the fields of spatial ecology, and the ecology of invasion. In the 1970s she was an active member of a group organized by the late Professor Ei Teramoto who was a pioneer of mathematical ecology in Japan. The group published papers on structure, stability and efficiency of ecosystems under the name Mumay Tansky, which was an acronym of the names of the six members. In 1979, Dr. Shigesada turned her attention to the observational study of the spatial distribution of ant lions by a Japanese ecologist, Masaaki Morisita. She generalized the phenomenological concept of environmental density, which represents the degree of how unfavorable a habitat patch can be. She introduced a novel model that included population pressure due to mutual interference between individuals combined with environmental potential, regarding how favorable a habitat is. After explaining Morisita's observations using a spatially discrete model, she extended it through a continuous, nonlinear diffusion-advection model and was able to explain how coexistence of competing species can arise through spatial segregation. This pioneering work on density-dependent diffusion has continued to have a significant impact on studies of animal dispersal and spatial distributions.

Since Skellam's seminal work in 1951, the speed of traveling waves has been one of the central questions investigated for reaction diffusion models. Although most models predicted constant wave speeds of animal range expansion, data for the speed of invasion of non-native insects, plants and birds show considerably different patterns. This was a puzzle pointed out clearly by Prof. Akira Okubo himself in the 1980s. For the initial establishment of an invasive population in a small area and for range expansion with or without acceleration, Dr. Shigesada identified three patterns. She formulated a stratified diffusion model by combining the generation of new colonies by long-distance migrants with the short range expansion by neighborhood diffusion and explained the three expansion patterns by assuming three forms of the colonization rate. This very important research solved a long standing puzzle using an innovative approach. In the recent two decades, Dr. Shigesada began studying pine wilt disease which is caused by the pinewood nematode with a pine sawyer beetle as vector. Describing the population dynamics of pine sawyers and infected trees using a simple discrete-generation model, she estimated beetle densities and parameter values for the model and found that there is a threshold host density above which the disease can spread, and that the minimum density critically depends on the eradication rate. She also modeled the spatial spread of the disease by incorporating an empirically estimated distribution kernel and found that long-range dispersal is necessary to explain the rapid expansion of

the disease. These were novel approaches in analysis of pest control strategies.

A major feature of Dr. Shigesada's research has been the explicit introduction of spatial heterogeneity. To assess the effects of spatial heterogeneity on the speed of traveling waves, she considered an environment in which the growth and diffusion rates vary periodically. She defined a traveling periodic wave as a frontal wave that shifts by a characteristic distance with a lapse of a characteristic period of time and calculated the minimum velocity of the waves by concentrating on the leading edge of the waves. She extended her model to combine population growth and diffusion in a two-dimensional fragmented environment and clearly explained the range expansion pattern by introducing a frontal envelope for the two-dimensional spread. These efforts are illustrative of her prominent ability to solve a complicated problem using fresh new approaches.

Dr. Shigesada has long been recognized as one of the leading researchers in mathematical biology, and the textbook (1997) written with her principal collaborator, Kohkichi Kawasaki, on biological invasions has had a significant impact. Prof. Shigesada has also greatly contributed to the education of young researchers at Kyoto University, Nara Women's University and Doshisha University. Recently, she has served as the Research Supervisor for the Basic Research Program PRESTO in the research area "Innovative Models of Biological Processes and its Development", supported by the Japan Science and Technology Agency for 2007-2013 and has had a great impact on young mathematical biologists in Japan. She has contributed for many years to the Japanese Society for Mathematical Biology for which she has served as Secretary General and President. Based upon her contributions to developing original theory arising from observational studies and for advancing our understanding of spatial processes and patterns in natural systems, the Committee enthusiastically awarded the Akira Okubo Prize to Prof. Nanako Shigesada.

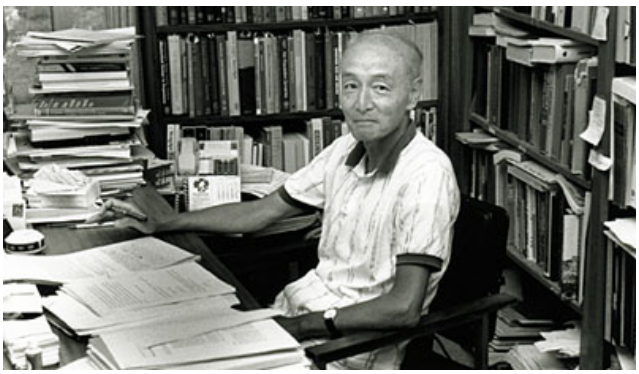
2013 Akira Okubo Prize Committee:
Toshiyuki Namba (Chair)
Louis Gross
Yoh Iwasa
Denise Kirschner
Toru Sasaki
Jonathan Sherratt

Response from Dr. Nanako Shigesada

I am very honored and grateful to receive the 2013 Akira Okubo Prize. I would like to express my sincere gratitude to the selection committee for awarding me this honorable prize. I am so pleased because it is the monumental book by Akira Okubo, *Diffusion and Ecological Problems*, that first spurred my interests in spatial ecology and has since provided continual inspirations for my research.

This honor would not have been possible without many people who helped me along the way. I am very grateful to my collaborators and colleagues with whom I had rich and fruitful discussions and many successful collaborative projects. Among them, my special gratitude goes to Dr. Kohkichi Kawasaki for his long-time and invaluable collaborations.

About The Akira Okubo Prize



The Akira Okubo Fund was established by the Society for Mathematical Biology and the Japanese Association for Mathematical Biology in memory of Akira Okubo. Okubo made major contributions to many fields, including mathematical ecology and oceanography, and was widely recognized for his scientific work, as well as for his exceptional humanity.

The objective of the Akira Okubo Prize is to honor a living scientist for outstanding and innovative theoretical work, for establishing superb conceptual ideas, for solving tough theoretical problems, and/or for uniting theory and data to advance a biological subject. Research areas include: mathematical biology, biomathematics, theoretical biology, and biological oceanography.

The 2013 SMB Annual Meeting Report from The Local Organizers

by HAL SMITH & FABIO MILNER

The Society for Mathematical Biology annual meeting and conference was held in the Tempe Mission Palms Hotel and Conference Center, Tempe, Arizona from June 10-13, 2013, and was hosted by Arizona State University, School of Mathematical and Statistical Sciences and the Mathematical, Computational & Modeling Sciences Center. The local organizing committee included Carlos Castillo-Chavez (SHESC), Erika Camacho (ASU West), Jim Cushing (UofA), Rebecca Everett (ASU Math Grad Student), Yun Kang (ASU-SLS), Fabio Milner (SoMSS), Brian Smith (SoLS), and Hal Smith (SoMSS). The conference secretary was Sherrie Conner.

The theme of this year's meeting was Physiology, Disease, Ecology, and Sustainability. The 2013 SMB meeting drew over 312 participants from 18 countries as follows: Australia 6, Brazil 1, Canada 21, Finland 1, France 3, Germany 1, India 1, Italy 1, Japan 11, Korea 2, Macedonia 1, New Zealand 1, Pakistan 2, Spain 5, Switzerland 1, Taiwan 1, United Kingdom 17, USA 236.

The scientific program included a combination of plenary talks by leading experts in Mathematical Biology, contributed talks by senior and junior scientists, a poster session, and a mentoring session. A total of six plenary lectures were given as the following: Carlos D. Bustamante, School of Medicine, Stanford University on "*Population Genetic Inference in the Personal Genome Era*"; Marie Doumic-Jauffret, INRIA, France, "*What governs the bacterial growth?*"; James Lechleiter, School of Medicine, University of Texas Health Science Center "*Targeting Astrocyte Mitochondrial ATP production as a Strategy to Treat Stroke*"; Rafael Pena-Miller, Department of Zoology, University of Oxford (Lee Segel Prize) "*Controlling the evolution of antimicrobial resistance*"; Shigui Ruan, Department Mathematics, University of Miami "*Modeling Transmission Dynamics of Rabies in China*"; Leon Glass, Centre for Nonlinear Dynamics, McGill University (2013 Arthur T. Winfree Prize) "*Predicting the Risk of Sudden Cardiac Death.*"

Thirty-two mini-symposia covered topics in ecology, epidemiology, cancer biology, neuronal networks, systems biology, physiology, immunology, and undergraduate research experiences (see http://math.asu.edu/SMB2013/minisymposia). Thirty-five contributed sessions covered some of the same topics as above and included a session on social networks and on microbiology (see `http://math.asu.edu/SMB2013/contributed-sessions`) A poster session featuring some 43 posters was held on Tuesday June 11, evening, attracting a big crowd.

A mentoring session focusing on successful preparation for job applications (Post-docs) and tenure (asst. profs.), led by Robert Smith?, was held at lunch time Wednesday, June 12, with 40 people attending. Lunch was provided courtesy of Colleen Burgess from MathEcology, LLC (see http://math.asu.edu/SMB2013/mentoring).

Financial support was provided by the School of Mathematical and Statistical Sciences, Arizona State University, Mathematical, Computational & Modeling Sciences Center, Arizona State University, Department of Mathematics, University of Arizona, Institute for Mathematics and its Applications, University of Minnesota, Mathematical Biosciences Institute, Ohio State University, and Pfizer, Inc. Number of travel/registration awards supported by local organizers was 65 participants.

Prizes awarded in this 2013 SMB meeting were: 2013 Arthur T. Winfree prize to Leon Glass, and 2012 Lee Segel Best Paper prize to Rafael Pena-Miller.

One the highlights of the 2013 SMB annual meeting and conference was the presidential transition from Gerda de Vries to Fred Adler.

Link to abstracts and photos:
`http://math.asu.edu/SMB2013/schedule`
`http://math.asu.edu/news-events/galleries/smb-welcome-reception`
`http://math.asu.edu/news-events/galleries/smb-poster-session`

Photos from the 2013 SMB Meeting

Fred Adler with participants at the reception

Members of the organizing committee at the reception

Participants enjoying the reception

Meghan Burke and Renee Fister at the SMB meeting

Chad Miller presenting his poster to a participant

Participants at the poster session

The 4th Conference on Computational and Mathematical Population Dynamics

North University of China, Taiyuan, May 29 - June 2, 2013

by SHIGUI RUAN

Late May was right in the middle of spring in Taiyuan, a northern city of China. The North University of China, located by the eastern bank of the Fen River and the Erlong (double dragon) mountain, was the site of the 4th Conference on Computational and Mathematical Population Dynamics (CMPD4), May 29 - June 2, 2013. More than 350 participants from 23 countries participated in this international conference; among them were more than 150 graduate students and post-doctoral fellows.

There were eight plenary lectures: Odo Diekmann (Utrecht U., The Netherlands), "*Infectious disease transmission on dynamic sexual networks*"; Hanna Kokko (The Australian National U., Australia) "*Is mother nature shortsighted? Evolutionary processes do not maximize population performance*"; Pierre Magal (U. of Bordeaux, France), "*Bifurcation in structured population dynamics*"; Sebastian Schreiber (UC at Davis, USA), "*Population persistence in the face of uncertainty*"; Zhilan Feng (Purdue U., USA), "*Bifurcation analysis of a model for plant-herbivore-predator interactions and its applications*"; Hisashi Inaba (U. of Tokyo, Japan), "*On recent developments in the theory of basic reproduction number*";

Frithjof Lutscher (U.of Ottawa, Canada), "*Population spread in patchy landscapes*"; Zhen Jin (North U. of China, China), "*Epidemic models on complex networks.*"

There were 200 talks in 20 different sessions. Sessions topics included gene regulation and molecular biology, Effects of Wolbachia on insect population dynamics, stochastic models of gene expression, population game dynamics, climate change and vector borne diseases, modeling of infectious diseases, influence of heterogeneity in disease dynamics and control, adaptive dynamics, spatial dynamics in population biology, immune modeling, modeling antibiotic-resistance bacteria, within-host models as building blocks for epidemic models, control problems in population biology, modeling of cancer growth and treatment, viral dynamics and drug treatment, bifurcation theory and applications in biology, structured population dynamics, and some other related subjects in population dynamics.

The local organizers did an excellent job in organizing this event. Conference participants were extremely impressed and appreciated the warmness and friendliness of the local people and volunteers. Taiyuan is well-known for noodles, foods, and Fen jiu (alcohol), which conference participants really enjoyed through the different daily menus.

On top of the tight talk schedule, there was a concert on local and Chinese folksongs and music performed by Faculty members and graduate students in the Department of Music at the North U. of China. In the last day, an excursion was scheduled to visit Pingyao city (a UNESCO World Heritage Site).

CMPD4 was generously supported by the National Science Foundation, the Fields Institute for Research in Mathematical Research, the European Mathematical and Theoretical Biology Society, the Society for Mathematical Biology, Yuncheng University, the China Animal Health and Epidemiology Center, the North University of China, and National Natural Science Foundation of China.

Group photo of the CMPD4.

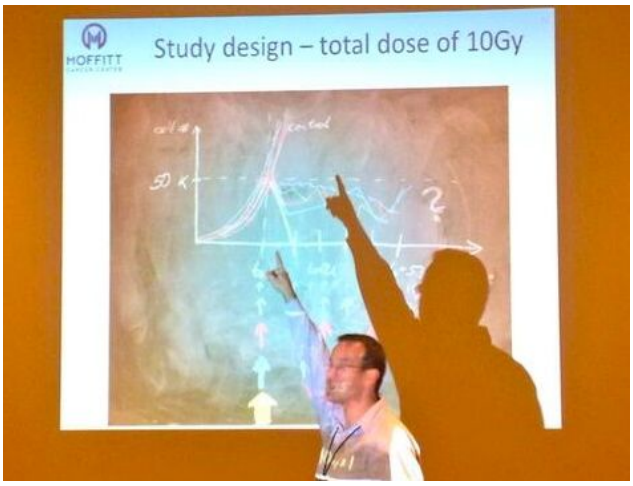
The 2013 SMB Annual Meeting
Report from a Landahl Award Recipient

by Russell C. Rockne

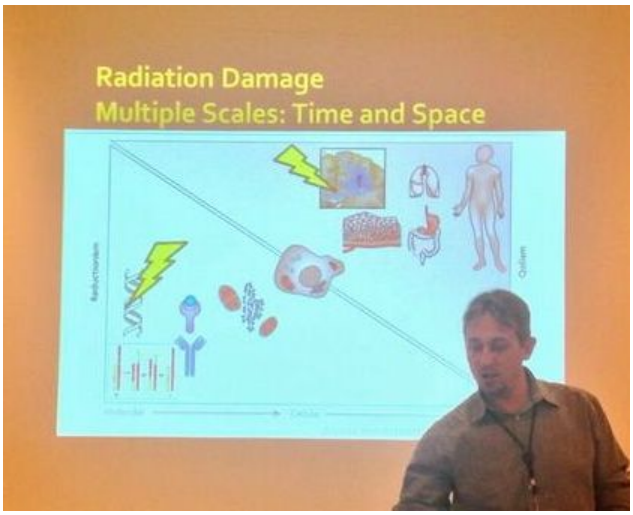
A Hot Time in Tempe

The SMB annual meeting, held in sweltering 110+ degree temperatures, ignited discussions, lectures, talks and posters that covered a wide range of topics in mathematical biology. SMB members beat the heat with complimentary snacks, cold beverages and frozen treats provided in the hotel courtyard, and ventured into the 90+ degree night air, where they were met with refreshing mist from restaurant patios. The meeting spanned 4 days, from the welcome reception Sunday evening to the last parallel session on Thursday morning. The meeting provided something for everyone, with over 60 oral presentation sessions, composed of equal parts minisymposia and contributed sessions.

With so much great mathematical biology to chose from, members and attendees were able to utilize social media to follow interesting talks in other sessions, as many SMB members tweeted the meeting. Some notable sessions were also posted to the SMB Facebook page. See what you might have missed on twitter with storify, a service which consolidates selected tweets with a common hashtag #SMB2013, (see: http://storify.com/ramblemuse/smb-2013).



Heiko Enderling from Moffit Center presenting his talk at the "*Mathematical Radiation Oncology*" minisymposium



Russ Rockne from the Univ. of Washington presenting his talk at the "*Mathematical Radiation Oncology*" minisymposium

To stay up to date on society information and related mathematical biology news, take a moment to "like" the society on Facebook if you haven't already done so.

Of particular interest to me, was the abundance of presentations and posters related to mathematical modeling of cancer. No fewer than 9 out of 33 minisymposia and several contributed sessions were focused on cancer modeling. I was pleased to see an increase in talks aimed at integration of both experimental and clinical data into comprehensive cancer research utilizing mathematical models. I personally organized a minisymposium titled "*Mathematical Radiation Oncology*", focused on radiation therapy, which is currently a hot topic in cancer treatment. Radiation damage and repair is known to take place on many spatial and temporal scales, which calls for a wide range of mathematical and computational modeling, demonstrated in talks by David Corwin, Heiko Enderling and Xuefeng Gao (Ryan), who presented modeling efforts ranging from biological optimization of radiation dose on the tissue scale to the effects of stem cells on radiation response at the cellular scale.

Landahl travel awardees Xuefeng Gao (Ryan) and Russ Rockne at the SMB2013 merchandise & donation desk serving Prof. Urszula Ledzewicz

The mathematics ranged from multi-objective optimization to partial differential equations, integro-differential equations and agent based models. To bring a clinical perspective, I invited Dr. Andrew D. Trister M.D., Ph.D. from the University of Washington to present clinical challenges in radiation oncology which I paralleled with modeling opportunities in a shared talk which emphasized clinically driven "mathematical oncology." Dr. Trister's attendance at the SMB meeting represents a growing interest in mathematical and computational modeling in the medical community, and also an interest in participating in the more biological side of SMB.

Notably, there appears to be a growing trend towards not only the integration of data into the mathematical models, but parameter estimation and uncertainty quantification as well, which are common challenges faced in any mathematical modeling effort. Of the many cancer related minisymposia and contributed sessions, common themes such as modeling of treatment, angiogenesis, tumor-stroma interactions, and cancer stem cells demonstrated a sustained and even growing interest in the many facets of cancer modeling and their translation to experimental and/or clinical situations to test model predictions. From melanoma to brain cancer, a wide variety of mathematical methods were presented that considered the often very different biological features of various cancers, from stochastic models, to cell based methods, to ODEs and PDEs, there is something of interest for every mathematician in the realm of cancer modeling.

Although there were no cancer-focused plenary talks this year, the topics ranged from bacterial growth to rabies transmission dynamics and included prominent mathematicians from around the world. This diverse and international lineup of plenary speakers provided society members with a veritable melting pot of contemporary mathematical biology research.

SMB merchandise including t-shirts, coffee mugs and water bottles sold like hotcakes, with the help of Heiko Enderling, who put Landahl travel award winners' and other SMB members' feet to the fire to volunteer and help staff the merchandise table. Despite the heat, I was delighted to see SMB stalwart Torcom Chorbajian from the University of Colorado at Boulder continue his Cal Ripken Jr. like streak of attendance at the SMB annual meetings, although I told him not to sweat it.

I would like to acknowledge the Landahl Travel Award for partly supporting my attendance at the meeting. I want to take this opportunity to personally thank my PhD advisor, Dr. Kristin Swanson, the local organizing committee at ASU for organizing this year's annual meeting, the new SMB president Fred Adler, the annual meeting coordinator Nick Britton, and the society treasurer Renee Fister.

Hot! Hot! Hot!

Biodiversity in a Changing World - CRM Workshop

Université de Montréal, July 22-26, 2013

by FRITHJOF LUTSCHER

This workshop on biodiversity and how it may be affected by global change took place at the Centre de Recherches Mathématiques (CRM) at Université de Montréal from July 22 - 26, 2013. It was one of ten workshops within the pan-Canadian thematic year on "Models and Methods in Ecology, Epidemilology and Public Health (http://www.crm.umontreal.ca/M2E2/). The workshop was organized by Frédéric Guichard (McGill) and Frithjof Lutscher (Ottawa) and was generously supported by CRM, NSF and SMB.

With the increasing impact humans continue to have on our planet, the ability to effectively understand and forecast biological, ecological, and environmental changes is more important than ever. This growing need for fundamental scientific research requires the interaction of many disciplines, and, arguably, one of the largest challenges of the field is translating results into adequate policy and guidelines for governments, agencies, and society to follow. The goal of this workshop was to bring together researchers from mathematical modeling and quantitative biology to exchange recent empirical results, novel ideas and modeling frameworks on the topic of biodiversity and its response to a changing world. A diverse range of mathematical aspects and theories are involved in solving such challenges; for example stability theory of deterministic and stochastic dynamical systems, multiscale modeling, transient dynamics, network theory, model-data fitting, and dealing with scarce and noisy data.

A recurring theme of the workshop was the question of how the stability of an ecosystem and its ability to deliver its services are affected by a decline or increase in biodiversity. In the opening talk, Michel Loreau (CNRS, France) stressed the importance of asynchrony of species response to environmental changes and explained how biodiversity is a "biological insurance" for stability. Using a model of two trophic levels, Shawn Leroux (Memorial) elucidated the importance of including nutrient cycling into ecological models to predict their response to a changing climate. Scaling up to entire food webs, Timothee Poisot (Rimouski) suggested that variation in productivity of an ecosystem can be predicted from its network structure. Sergio Vallina (ICM, Spain) demonstrated theoretically and empirically that a "kill-the-winner" predation strategy contributes to explaining a unimodal productivity-diversity relationship. The importance of scales continued as a theme throughout the afternoon of the first day. James O'Dwyer (Santa Fe Institute) identified a power law scaling of phylogenetic diversity of microbial communities, while Brian McGill (Maine) took the macroecology perspective and demonstrated the importance of traits (rather than species) functional diversity for the stability and response of ecosystems. Marie-Josée Fortin (Toronto) closed the first day of the workshop with a look at connectivity measures for heterogeneity at different spatial scales.

The second day began with Peter Chesson (University of Arizona) emphasizing that coexistence is a multiscale, multimechanism affair, and that coexistence studies would benefit from a general quantitative scale transition theory and classification of different coexistence mechanisms, as opposed to system-specific studies yielding coexistence bandwidths without tying it to some particular mechanism. Priyanga Amarasekare (UCLA) presented a framework for predicting the effects of climate change on biodiversity based on empirical temperature-function relationships included into multi-species interaction models. Annette Ostling and Rosalyn Rael (both University of Michigan) reported empirical and theoretical results on neutral and niche models and discussed their ability and limitations to explore mechanisms and make predictions.

We were particularly fortunate to have Simon Levin (Princeton) participate in the workshop. He also held a prestigious Aisenstadt Chair at CRM during that time and gave a total of three lectures in Montreal. He presented various models for the evolution of prosociality, inspired by game theory and economics and thereby posed the question of how to best turn insights on biodiversity and ecosystem function into policy and management practice. A

more detailed summary of all three lectures of Simon Levin will appear in the CRM Bulletin: http://www.crm.umontreal.ca/docs

In the final two presentations on the second day, Pedro Peres-Neto (UQAM) discussed the trends and pitfalls of spatial statistical modeling of biodiversity in response to climate change, and showed how this can be used judiciously to uncover hidden correlations between traits. Dominique Gravel (UQTR) contributed a spatial component to the stability-complexity debate, showing that complexity tends to enhance stability, and re-evaluated Robert May's famous works.

On Wednesday, Colleen Webb (Colorado State) presented a novel theoretical approach to predict community composition based on trait distributions and dynamic projections. Tadashi Fukami (Stanford) presented novel computationally intensive results on whether and to what degree community assembly is determined on its history, which raised the more general question to which extent it is predictable. Rafael D'Andrea (University of Michigan) studied methodologies that can help understand niche mechanisms for observed trait patterns. King-Yeung Lam (Ohio State) presented analytical results for the evolution of conditional dispersal in reaction-diffusion models with directed movement. In the afternoon, participants self-organized into discussion groups on various topics.

Thursday morning saw two more high quality invited lectured by Kevin McCann (Guelph) and Andrew Gonzales (McGill). McCann presented unifying results on food-web stability in terms of energy flux in the system. Gonzales first presented a theoretical and laboratory study on metapopulation adaptation, then switched gears and excited the audience with a large-scale study to identify ecologically relevant areas (reserves and corridors) in the Montreal metropolitan area that would allow species to migrate sufficiently in response to climate change to ensure their survival. Ian Hatton (McGill) demonstrated, on ecosystem scale, a 3/4 power law across thousands of communities of many taxa.

Gregor Fussmann (McGill) continued the topic evolutionary rescue effects with novel theoretical and empirical results. Mark Vellend (Sherbrooke) surprised the audience with empirical findings that local biodiversity is, on average, constant despite the global decline in biodiversity. A lively discussion followed about the consequences of these findings. Simon Levin closed the afternoon with his final Aisenstadt lecture, in which he took the audience on a breathtaking tour of how sustainability is threatened in this world and how mathematics could possibly help us manage our common resources better, and even sustainably.

The final day saw three more presentations and a concluding plenary discussion. Gulnaz Jalilova (Hilfswerk Austrian International) reported on-the-ground work for poverty alleviation in central Asia's high mountain regions in the face of global change. Gyorgy Barabas (University of Michigan) presented a framework for sensitivity analysis in community ecology. Stephen Rush (Guelph) proposed generalized Hill numbers for species richness in conjunction with the colon microbiome and infection treatment.

The workshop was a great success: excellent talks inspired lively discussions, ample time for breaks fostered cross-disciplinary connections. The welcoming atmosphere at the CRM and the excellent organization behind the scenes by its experienced and extremely helpful staff bas the base for success. All participants enjoyed the location of the CRM on Mount Royal and the vistas from the roof terrasse, combined with the great variety of excellent local restaurants.

Pfizer and the 2013 SMB Annual Meeting

by RICHARD ALLEN

This year, for the first time, we (Pfizer) were delighted to sponsor several awards to support travel for investigators to the SMB annual meeting in Tempe, AZ. These awards were arranged with the help of Dr. Fabio Milner (ASU), who organized the travel awards for this year's meeting, and several colleagues at Pfizer.

Why did Pfizer want to support and contribute to the 2013 SMB Annual meeting?

Those who attended the 2012 meeting in Knoxville may recall that I participated in the career panel to provide an industry perspective. The prevailing feedback I received was general surprise that Pfizer sees value in mathematical modeling. This is in strong contrast to the reality: Pfizer is heavily invested in "*Quantitative Systems Pharmacology (QSP)*"(1). This is a paradigm where decision making in the drug discovery and development process is strongly informed by quantitative approaches (such as mathematical modeling). Due to this dichotomy between perception and reality, I realized there was significant value (to both Pfizer and the Society) in increasing our exposure in the field by participating in the 2013 SMB annual meeting both by sponsorship and organizing a mini-symposium.

The title of the mini-symposium I organized was "*Academic and Industry Approaches to Modeling Disease and Therapy*". There is growing recognition that industry collaborations with academia are highly fruitful, and have huge potential to deliver real benefits to patients going forward. It is therefore imperative that these valuable industry-academic collaborations are formed and maintained in the mathematical biology community. A necessary precursor to facilitate such collaboration is a shared dialogue and understanding of where approaches and goals are complementary (or not). A strong motivating factor for this session was to facilitate this dialogue.

I am delighted that the mini-symposium was extremely well attended and received. It sparked many interesting interactions with interest in our approaches, working in industry, as well as several participants very enthusiastic about getting feedback on their own work from our perspective. I found our involvement in the entire meeting highly positive, and this reaffirmed the value to Pfizer of engaging with the wider field in this manner.

Figure 1: Clinical Drug Development is challenging, expensive and time consuming. The failure rate is highest in Phase 2.

Why is Pfizer engaged in Mathematical Modeling?

The answer to this question lies in the cost and efficiency of developing new drugs. Of all the drugs tested in humans, only about 16% ever become a drug approved to treat disease (2). Unfortunately, this high failure rate translates into unmet medical needs. Prior to registration and approval new drugs are first tested for safety (phase I), followed by efficacy (phase II) and then safety and efficacy in larger, more relevant, populations (phase III), figure 1. The failure rate is at its highest in phase II - where nearly 60% of drugs tested fail (2).

If we can predict efficacy (and hence phase II success) earlier time and resources can be devoted to developing drugs for the most promising targets (3). This is where a quantitative, predictive technique such as mathematical modeling can have a huge impact, for relatively little cost.

Models of physiological systems represent a quantitative assimilation of current biological knowledge. For complex systems the integration of this knowledge is imperative for making predictions. The predictions are particularly valuable prior to new therapies entering the clinic for testing, but can impact decision-making throughout the entire process of drug discovery, figure 2. We use physiology and disease models to test mechanistic hypotheses such as "will modulating this pathway lead to a clinically meaningful improvement in the disease". When addressing mechanistic questions our group usually applies ODE models, but across Pfizer there is a broad array of techniques applied (for example, PDEs, statistical models, network analysis, etc.)

Often the most satisfying outcome of our work is suggesting novel experiments to clarify critical uncertainties, and to see the impact of those experiments on decision making. It is extremely exciting to be working in an environment where there is significant enthusiasm for such experimental and computational collaboration!

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Richard Allen is a member Pfizer's Systems Biology group, under the direction of CJ Musante, within the "Cardiovascular and Metabolic" Research Unit. Richard has a Ph.D. in Mathematical Biology, and was previously a Postdoctoral researcher at the University of North Carolina under the supervision of Tim Elston and Klaus Hahn.

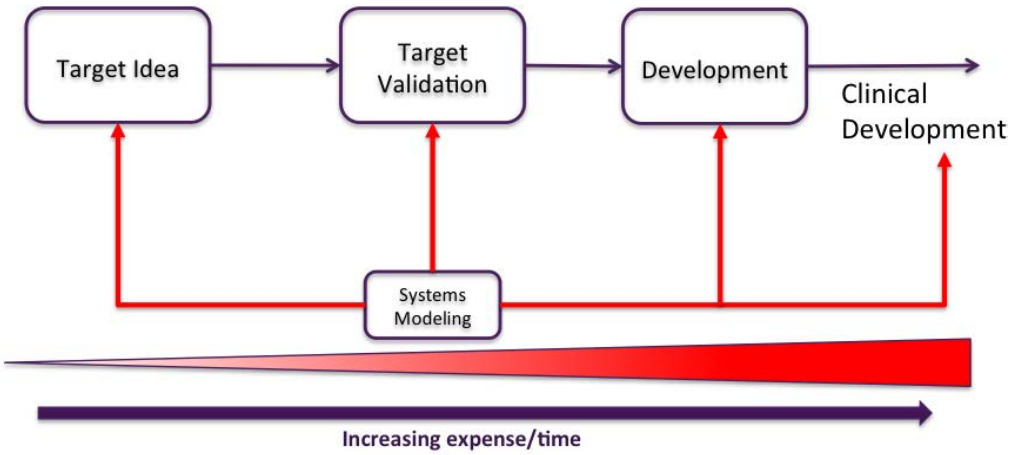


Figure 2: By applying predicative quantitative techniques, such as mathematical modeling, earlier in the development process critical uncertainties can be resolved or minimized prior to clinical testing.

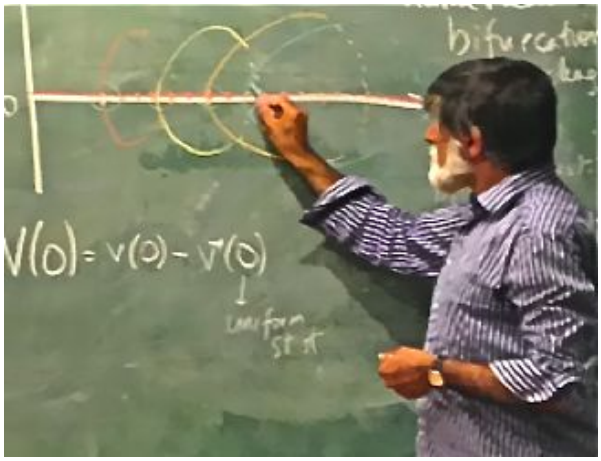
AARMS-Summer School on Dynamical Systems and Mathematical Biology

Memorial University of Newfoundland , July 15 - August 9, 2013

by KELSEY GASIOR

The Atlantic Association for Research in the Mathematical Sciences (AARMS) Summer School took place at Memorial University of Newfoundland (MUN) in historic and scenic St. John's, Newfoundland, Canada between July 15 and August 9, 2013. Dr. Xiaoqiang Zhao from the Department of Mathematics and Statistics at MUN organized the program, which gave participants from around the world the opportunity to study under several respected mathematical biologists.

During these four weeks, 44 students and two postdoctoral fellows were able to participate in four different classes, each of which exposed them to a variety of advanced mathematical techniques. Two of the more technical subjects were Stochastic Modeling with Applications in Biology, co-taught by Drs. Linda and Edward Allen, and Reaction-Diffusion Equations and Applications, taught by Dr. Steve Cantrell. In one of the most popular courses, Mathematical Modeling in Developmental Biology and Medicine, Dr. Philip Maini integrated the introduction of bifurcation analysis and Michaelis-Menten kinetics with a discussion on substrate activity and cellular dynamics. Similarly, in Mathematical Methods to Gain Biological Insights, Dr. Odo Diekmann used discussions on enzyme kinetics, population modeling, and diffusion models as catalysts for his mathematically based lectures.



Prof. Maini lecturing on Mathematical Modeling in Developmental Biology and Medicine

In addition to the courses, what made the summer school unique was the atmosphere. The courses pushed students to extend the concepts via-out-of class projects, which encouraged a collaborative environment. Students were able to seek each other out in order to discuss possible ideas and perspectives and, due to the vast array of backgrounds present, they were able to see that working with biologists, ecologists, and other biomathematicians can lead to a better understanding of the topics at hand. Ultimately, this experience gave the students a taste of what it is truly like to work in the collaborative field that is mathematical biology.

The summer school also fostered an informal environment that allowed attendees to take advantage of all the knowledge the professors had to offer. The professors were always very welcoming to those who stopped by their offices, whether it was to discuss the class material or shared research interests. As a young scientist who is just entering the field of mathematical biology, the opportunity to extend my learning outside of the classroom was actually an excellent way to deepen my understanding of my current research. I found it quite interesting to learn more about the derivation of Michaelis-Menten and mass action kinetics, which I have been recently studying. Also, as someone who is interested in cancer and cell biology, I thoroughly enjoyed the opportunity to speak with Dr. Maini about the recent advances and changes occurring in the field.

Even though the coursework was their first priority, students made sure to take advantage of their free time and all that St John's had to offer. Summertime was in full swing in July, which allowed for a lot of outdoor activities. During the first weekend, some students went on a whale watching boat tour. The following day, a few brave souls hiked 15 miles along the East Coast Trail in order to visit Cape Spear, the most easterly point in North America. The hike was by far a highlight of the trip, allowing classmates to bond and enjoy breath-taking views of the Atlantic Ocean and Newfoundland coastline. Students also took part in a lot of activities that were

located in downtown St John's. One spot that was very popular with students was Signal Hill, which was only a few miles from campus. Many students woke up early in the morning on several different occasions to see the sun rise over the Atlantic Ocean. Additionally, a small group embraced the tourism industry and went on a "haunted ghost tour" with Drs. Maini and Cantrell. The tour was very charming and an excellent way to learn more about the history and folklore surrounding the town.

While participating in the summer school, students also had the opportunity to attend the 2013 AARMS Mathematical Biology Workshop that took place at MUN from July 27- 29, 2013. The workshop was organized by Drs. Amy Hurford and Xiaoqiang Zhao and featured several parallel sessions and seven plenary lectures. Including the summer school students, there were 84 attendees from Europe, Canada, the United States, and Asia.

The first day of the conference focused on the discussion of ecology and epidemiology. After several parallel sessions in the morning, Dr. Linda Allen gave a plenary lecture on "*Relations Between Deterministic and Stochastic Thresholds for Disease Extinction*". Dr. Allen's talk was further complemented by the plenary lecture given in the afternoon by Dr. Odo Diekmann entitled "*Infectious Disease Transmission on Dynamic Sexual Networks*". Additionally, following the parallel sessions, Dr. Mark Lewis spoke about "*Mathematics Behind Stream Population Dynamics*". In between the lectures and parallel sessions, junior and senior scientists had the chance to interact with one another and extensively discuss the research topics presented at the conference.

The second day of the conference was geared towards cellular processes, pattern formation, and population dynamics and the discussion of these topics was enhanced by the plenary lectures given. Dr. Edward Allen spoke on "*Application, Derivation, and Computation of Continuous and Discrete Delay SDE Models in Mathematical Biology,*" while Dr. Philip Maini later spoke on "*Modeling Collective Cell Movement*". Following the lectures of the second day, attendees were treated to a public lecture by Dr. Simon Levin, as well as a banquet at the Suncor Energy Fluvarium. Dr. Levin's lecture on "*Challenges in Mathematical Ecology: Scaling and Collective Phenomena*" was an excellent discussion on how the concepts observed in ecology help humans question their own financial and global resource sustainability.

The third and final day of the conference focused on population dispersal and evolution. A series of parallel presentations were followed by the final plenary lecture: Dr. Steve Cantrell concluded the conference with his discussion of "*Nonlinear Diffusion and Resource Matching in Population Dynamics*".

Being a part of the AARMS Summer School and Workshop was a once in a lifetime experience and we would like to thank all of those that made it possible. Substantial financial support for both events was provided by AARMS. In addition, the National Science Foundation provided funding for the US participants to travel to the AARMS Summer School, as well as for US scientists to attend the AARMS Workshop. Additional support for the AARMS Mathematical Biology Workshop was provided by The Conference Fund, the Dean of Science, and the Mathematics and Statistics Department at Memorial University, and by the Centre of Recherches Mathématiques that provided travel support for Dr. Simon Levin. Thank you to Easton White of the University of California Davis and Amanda Swan of the University of Alberta for sharing their notes, as well as Dr. Urszula Ledzewicz of Southern Illinois University Edwardsville, Sonia Pozzi of the University of Insubria and Xiaodong Tai of the University of Science and Technology Beijing for sharing their photos. Finally, thank you to Drs. Zhao and Hurford for organizing such amazing events. Further information about the meetings can be found here: http://www.aarms.math.ca/summer/2013/index.html and `http://www.math.mun.ca//~ahurford/aarms/`

Group Photo of AARMS Mathematical Biology Workshop attendees

The 2013 World Conference on Natural Resource Modeling

Cornell University, June 18th - 21st, 2013

by CATHERINE A. ROBERTS

In June 2013, the Resource Modeling Association (RMA) held its annual conference, the 2013 World Conference on Natural Resource Modeling at Cornell University in Ithaca, New York. Our meetings are characterized by being small (typically under one hundred delegates) and audaciously interdisciplinary. One photo shows one of our keynote speakers, John Livernois (Univeristy of Guelph, Canada) starting his address "Empirical tests of Nonrenewable Resource Modeling: What Have We Learned?" During his address, he mentioned that this was the most interdisciplinary conference he had attended. The other photo shows our conference organizer, Jon Conrad (Cornell University, USA) entertaining us with his band during our conference banquet, a BBQ held at Taughannock Falls State Park. Please visit our website at http://www.resourcemodeling.org and consider joining us in the future. Next year, we will be in Vilnius, Lithuania.

Talks that may have been of particular interest to members of SMB include: Evan Cooch (Cornell University) "*Inferences about Coupling from Ecological Surveillance Modeling: Application of Information Theory to Nonlinear Systems*";

John Livernois giving the opening talk

Jon Conrad entertaining with his band during the conference banquet

Mike Neubert (Woods Hole Oceanographic Institute) "*Strategic Spatial Models for Fisheries Management*; John Hearne (RMIT Australia) "*Spatial-temporal Optimization Models to Reduce Risk from Wildfire*"; Steven Phillips (AT&T Research Labs) "*Multiclass Modeling of Arctic Vegetation Distribution Shifts and Associated Feedbacks under Climate Change*"; Mary Lou Zeeman (Bowdoin College) "*Resilience in Natural Resource Models*", plus many other interesting talks. Check out the schedule of speakers on our website.

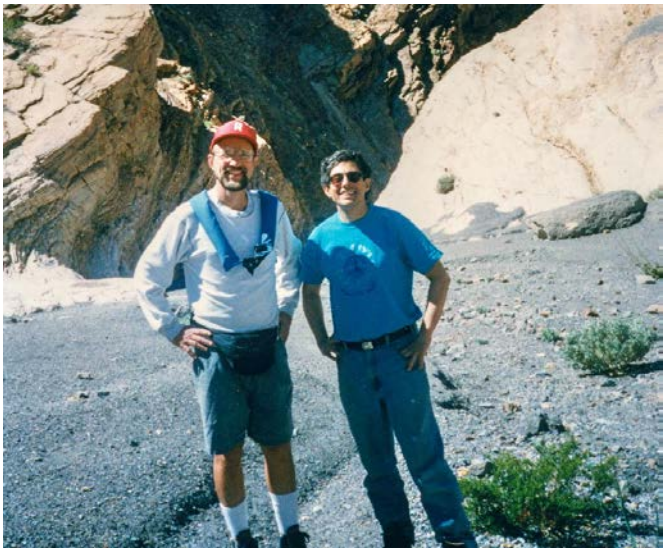
The three winners of our student competition (cash prizes from $100 - $300) were: Adam Walker "*Optimal Control of a Stochastically Spreading Invasive Speacies in Linear Space*"; Adrian Lopes "*Poaching and Protection of an Endangered Species: A Game-Theoretic Approach*"; Jacob Hochard "*Grey Wolf Population Projection with Intraspecific Competition*"

Please consider joining our society, which includes access to our journal Natural Resource Modeling.

Discussion with Leon Glass: Winner of the Arthur T. Winfree Prize

by Thomas Quail & Lennart Hilbert

Leon Glass, Isadore Rosenfeld Chair in Cardiology and Professor of Physiology at McGill University and CAMBAM member, has recently been awarded the Arthur Winfree prize by the Society for Mathematical Biology. The Arthur T. Winfree Prize honors a theoretician whose research has inspired significant new biology. On this happy occasion we have posed a few questions to Leon Glass. Again, a reminder that Leon is not only a brilliant theorist, but is hardly found short of experiences, insights, and worthwhile pastimes to talk about.



Arthur Winfree and Leon Glass in Death Valley

You were friends with Arthur Winfree for many years. How did Winfree's ideas influence your scientific trajectory?

Art Winfree had an incredible geometric intuition into biological dynamics. One of his early papers described phase resetting of a simple model of a nonlinear oscillator in which the limit cycle had a circular path. Although others, including Poincaré had looked at similar models for oscillations, Art predicted that biological oscillations described by nonlinear equations should display topological differences in the phase resetting curves depending on the amplitude of the stimulus. This was a fascinating approach-going from a simple mathematical idea to generic predictions for experimental findings. The specific model also was a stimulus for thinking about the effects of periodic stimulation of biological oscillators and was one of the important factors that led to the experimental and theoretical work with Michael Guevara and Alvin Shrier on the entrainment of cardiac oscillations. A geometric approach to studying nonlinear dynamics has always seemed the natural way to proceed - Art's pioneering work has been crucial to my thinking.

How do you choose your topics/problems to work on?

I like to choose problems that seem interesting to me and where there seems to be something basic that I do not understand. There should be the possibility of some mathematical analysis using tools that I understand or feel that I could understand with a bit of work. I also strongly favor problems where there is some local expertise in the biological aspects that would facilitate collaborative work involving both theory and experiments. Since lots of work now is done in a collaborative fashion with students, finding problems that are suitable for a particular student also plays a big role. I once heard Richard Feynman say that he chose problems to work on by optimizing the product: (importance of the problem) X (ability to solve the problem). That might be a bit too calculating for me, but it sounds like good advice to pass on.

When do you know to invest the time to see it through or to cut off a project?

Although I have sometimes, particularly when I was younger, not published work that would have been worth publishing, I rarely cut off projects. I have worked and continue to work in diverse areas - cardiac arrhythmias, genetic networks, visual perception. I am tenacious. I recently went back and worked on a problem related to the wagon wheel illusion-following up on work that had lain dormant for over 35 years but which was still interesting to me and worth pursuing.

You have worked closely with experimentalists

throughout your career. What are the key ingredients of a successful collaboration?
Most important is having great respect for the knowledge and abilities of your experimental collaborators and finding someone who shares common interests. It also helps to realize that experimental findings will generally trump the theory in terms of the importance and interest. When carrying out research, I like to go into the laboratory when data is being collected and look at data carefully. This helps to focus on dynamics that may be the most interesting mathematically. Finally, experimentalists usually have way overcommitted the funds, so it helps to be willing to cover the costs of students and if possible to share in the costs of the experiments.

How do you ensure depth in research while working with very diverse topics and using various methods?
I do not worry about whether the problems I am studying are "deep". However, I try to focus on questions in which there are interesting mathematical and physical problems that go beyond a descriptive model of some phenomenon. I prefer analyses where there appear surprising emergent properties of the mathematics that were not anticipated at the initial formulation of the theoretical model. It helps if we find experimental evidence also for the unexpected dynamics. In some cases the unexpected experimental findings help set the agenda for the mathematical analyses.

We know you are very interested in music, playing an instrument yourself. Any parallels or connections with science or mathematics that you would like to mention?
I just enjoy the sound of the French horn and the challenge of trying to play it better. Although it would be nice if the study of complicated rhythms of the body improved my ability to play the French horn (or even to count in music), as far as I can tell these are occurring in separate regions of my brain and there is no carryover from one to the other. Both science and music are fun - and I have been privileged to have the opportunity to enjoy them both.

How do you feel about receiving the 2013 Arthur T. Winfree Prize?
I am deeply honored to receive this award. Art Winfree was not only an extraordinary scientist, but he was also a colleague and close friend. His intense scientific curiosity and high personal integrity have been beacons in my own career. Since completing my PhD in Chemistry, I have identified with the Mathematical and Theoretical Biology communities, going back to early Gordon Conferences in the 1970s. I have also had the privilege of having been the President of the Society for Mathematical Biology. Mathematical Biology is still a young field, with only a few prizes - I am truly delighted to have been selected for this award.

The original interview appeared on June 10, 2013 on the "Inside CAMBAM" blog (`http://blogs.mcgill.ca/cambam/2013/06/10/interview-leon-glass/`) with questions by Thomas Quail and Lennart Hilbert, graduate students in Physiology at McGill University. Additional editing and question by Amina Eladdadi.

About The Arthur Winfree Prize

The Arthur T. Winfree Prize was established in memory of the contributions to mathematical biology by Arthur T. Winfree. Winfree was one of the legendary figures in the field, one of the very few who combined brilliant theory with imaginative and masterful experiments. Many careers were built on his pioneering work in biological periodicity and pattern formation. Winfree's genius was frequently hidden by his modest, even self effacing manner. Beyond his scientific contributions, he was an exemplary scientist and human being. Winfree passed away from an aggressive brain tumor in the fall of 2002. His generosity and kindness to his colleagues and students is sorely missed. The objective of the Arthur T. Winfree Prize is to honor a theoretician whose research has inspired significant new biology.

Perspective on "*Get Thee Behind Me, Data*"?

by CHRIS WIGGINS

As biology has transitioned over the past decades into a data-driven field, we must decide: are we to embrace or to shun the new questions (and the appropriate tools for biological modeling) in the next century? Rather than living by "get thee behind me, data", now is a great time to develop and adapt the right tools for the right job.

The ability of simple mathematical models to generate rich, complex patterns drew me to research and to a career in applied mathematics. In fact, my first research project was in numerical simulation of chaotic dynamical systems arising in physics. This fascination stayed with me as I began graduate research in biological pattern formation, working carefully through the excellent review article of Cross and Hohenberg (3), focusing on the Turing instability as one striking and general example of how the visual complexity of biology could be reproduced and interpreted via simple models.

This fascination was tempered in 1995 after reading John Horgan's article (5) critiquing modelers for what the mathematical biologist Jack Cowan termed "reminiscence syndrome" – the phenomenon of finding patterns in our simulations reminiscent of those in nature and declaring the former an explanation of the latter. I looked for opportunities to apply data to constrain and guide mathematical models, though the gulf seemed large between the experiments in the adjacent molecular biology building and the models and simulations.

This gulf closed rapidly with the first sequencing of free-living organisms. Sequence data produced a flood of information – astronomical by biological standards, though biological by astronomical standards. Initial collaborations in learning from sequence data focused on inferring sequences, e.g., by solving the problem of assembling short contiguous sequences into whole genomes. This led almost immediately, however, to functional genomics and statistical systems biology. Both in the field of microarray analysis and biological network analysis, I found that the questions being asked by biological theory were diverging: either those focused on complex behavior from simple models, or those focused on complex data – which were really statistical or machine learning tasks in disguise.

The questions most of interest in understanding biological complexity had suddenly become data-driven or, as we would now say, "data science" or "big data" questions. [1]

Here, biological pattern formation shares in common with biological data science the question of how best to model natural complexity. Within machine learning this question is termed 'model selection'. Here, rather than asking which of, for example, two nonlinear PDEs, or two low-dimensional nonlinear dynamical systems is the better for a model, typically one allows a large-dimensional (or even infinite-dimensional) class of possible best models, and turns to the data for quantitative criteria which allow the data to reveal the best model.

To do this we face competing definitions of the 'best model'. Scientists model to predict or to explain – in many biological modeling tasks the emphasis is on the latter; in machine learning it is squarely on the former. In fact, many machine learning methods are quite opaque, and difficult to interpret, as the statistician Breiman emphasized (1). Scientists entering the field should remember that prediction and interpretation do not have to compete with each other; generative models (2; 8), for example, permit inference from copious data constrained by mechanistic understanding of the biological systems from which these data were produced. Similarly, one can build sparse models from individually-interpretable features, even in the context of machine learning methods (see for example (7; 6)). We must also remember not to conflate prediction, post-diction (reproducing quantitative or qualitative observations), and explanation. The focus of machine learning on prediction provides a clear quantitative

[1] While the terms are often used interchangeably outside of the fields, big data practitioners focus on software engineering challenges necessary for large datasets, whereas data science focuses on applications of statistical inference and machine learning to answer research questions, often drawn from the natural sciences.

The question for the next century is how complex systems can also be understood by the complex data they produce and the models we can learn from these data.

method for model selection. Specifically, when data are abundant, one can test the predictive power of models empirically, by setting aside some of the data and evaluating the error of a model trained on the remaining set. This process, termed 'cross validation' in machine learning, provides a quantitative procedure to let the data decide the natural complexity of a model, without the quantitative assumptions underlying criteria such as AIC, BIC, etc. (4).

As biology has transitioned over the past decades into a data-driven field, we must decide: are we to embrace or to shun the new questions (and the appropriate tools for biological modeling) in the next century? Rather than living by "get thee behind me, data", now is a great time to develop and adapt the right tools for the right job. Embracing data in biological modeling is not always easy, I recognize. In one case a lecture I gave to an audience of biological modelers erupted in a near riot, where statistical methods were denounced as 'numerology'. Turing, Lorenz, Feigenbaum, and others in a great tradition of scientists have shown us that complex behavior can be produced my simple models; this is now literally undergraduate understanding. The question for the next century is how complex systems can also be understood by the complex data they produce and the models we can learn from these data.

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About The Author:

Dr. Chris Wiggins is an Associate Professor in the Department of Applied Physics and Applied Mathematics at Columbia Engineering, a founding member of Columbia's Center for Computational Biology and Bioinformatics, and cofounder of hackNY.org, a nonprofit organization that connects students with career options in New York City–based start-ups. Dr. Wiggins is an applied mathematician with a Ph.D. in theoretical physics working on computational biology. Focus areas include applications of machine learning, statistical inference, and information theory for the inference, analysis, and organization of biological networks. For more information check out his website: http://www.columbia.edu/~chw2

Research Interview

What Happens When We Interact Together in Societies?

David Sumpter talks with Santiago Schnell about his work in collective behavior in biological and social systems

Your research is focused on collective behavior. What attracted you to that field?
I am fascinated by patterns created by large numbers of interacting individuals. Many of the most spectacular examples are seen in animal groups. Ant trails, fish schools and bird flocks all involve thousands or millions of individuals, all apparently unaware of the fantastic, dynamic structures they have created. Other examples are found at all levels of biology: from cell interactions in developmental biology up to human society. What makes animals good case studies for mathematical biologists is that they are open to observation. We can film them, watch how they interact and try understand how these interactions produce the collective.

What do you classify as your most important contribution to the collective behavior field?
Linking models to data. An incomplete list of some of the systems I have worked on includes: fish swimming between coral in the Great Barrier Reef; pigeons flying in pairs over Oxford; clapping undergraduate students in the north of England; Swedish wood ant trails; rock ants choosing a new nest; swarms of locusts traveling across the Sahara; disease spread in remote Ugandan villages; the traffic of Cuban leaf-cutter ants; the gaze following of city commuters; dancing honey bees from Sydney; and the tubular structures built by Japanese slime mould. Each of these is a small contribution in a particular area, but in each case I have written articles together with biologists that combine experiment, data analysis and models. My contribution is having developed an approach to collective animal behavior based on this modeling cycle.

Is there a particular question you are trying to answer in your group at the moment?
We have been focusing on what we call the "rules of motion" of animal groups. When I first started working in this area there were lots of models of bird flocks and fish schools, but none of them were solidly grounded in biology. The models could be simulated to produce patterns that looked life-like, but did not necessarily reflect what real animals do. Now that we can track fish movements in detail we can build biologically motivated models. We are tracking the movement of fish, pigeons, ants and other species, and trying to model their interactions. Given that there are billions of plausible models for these interactions, it is a big challenge. Some people in our research group work more on biological intuition and others on formal model fitting. Finding a good balance between these approaches is central to finding out what is really going on in these systems.

What do you imagine will be the next big breakthrough in your field?
I get asked this question a lot and have to admit I am not very good at answering it. I come in to work in the morning, I get an email or someone tells me what they are working on, maybe an experiment they have done or a model or that they have just read an exciting paper, and I start researching and thinking about that problem. I try to interest my PhD students in the problem, or work on it myself. Maybe this isn't what I write when I apply for a research grant, where predicted breakthroughs are central! But if I am honest, it reflects my way of working.

What is your favorite animal model?
Here again I don't really want to answer the question. I work with so many different animals and with different researchers, that I find it hard to pick one.

One highlight is house hunting rock ants, on which I have worked on three or four different models. There are several research groups around the world, all working on this particular species, making them something of a model system for group decision-making.

Have you got a favorite mathematical or computational technique that you prefer to work with?
My ambition is to model a wide range of systems with the most appropriate method for that particular system. This means that I can't be choosy about what mathematics I use. I have modeled using agent-based models, Markov chains, stochastic differential equations, ODEs, Bayesian models, random walks and a whole lot of other techniques. I choose whatever works best. On the other hand, the problems that I might sit with a little bit longer and work with just for fun are always those in probability. I love things like the central limit theorem, power law distributions and random walks.

Who or what inspired you to become a scientist in the first place?
When I was young I had very little interest in science in the broad sense. I was a computer geek. I loved programming and problem solving. I thought science and, in particular, biology was about learning pointless facts. When I finished my degree in computer science and statistics, I started to wonder how I could use the skills I'd learnt. I wanted to model and simulate something. I didn't care so much what that something was, so I started a PhD in applied mathematics. It was then my PhD supervisor, Dave Broomhead, who showed me that science was just as much about careful thinking as it was about how many facts you could digest. He would always start thinking about problems from the basics, gaining knowledge as he went along. I knew then that I had something to contribute as a scientist.

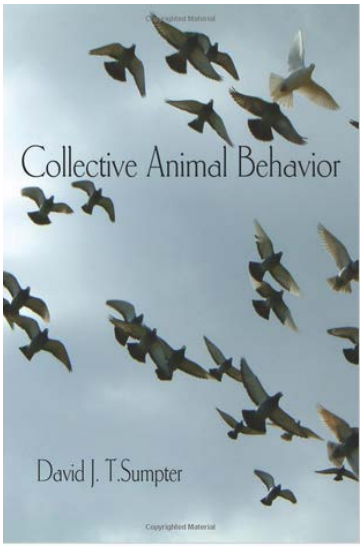
What would your message to a young and aspiring mathematical biologist be?
Enjoy yourself. You have a lot of freedom as a PhD student or Postdoc and you should use it. Don't focus too early on career goals or think about impact factors and stuff like that. Think instead about what interests you. Don't spend a lot of time reading until you have actually done some work in an area. And don't be scared to do something because you think someone might have done it before. You learn from everything you do. I have a whole load of platitudes to pass on, and I think my own PhD students get bored of listening to them. But they all come down to developing independent thinking, not being intimidated by the apparent confidence of your peers and professors, and making sure you are doing something which interests you.

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

If you have any spare time, what do you do when you are not working?
I have lots of spare time! In Sweden we have very generous holidays and I take them. I don't think it is good to just work all the time. You lose perspective. I spend a lot of time with my family. My kids are at an age where we can go camping, swimming in lakes and skiing in the winter. I also run quite a lot. I am almost equally proud of running the Stockholm Marathon this year as I am of my scientific output. Almost.

About David Sumpter

David Sumpter is professor of applied mathematics in Uppsala, Sweden. In 2010, he published the book "*Collective Animal Behavior*", about using a combination of mathematical models and experiment to understand group behavior of animals.
For more info: `http://www2.math.uu.se/~david/David_Sumpter/Home.html`



My Journey into Mathematical Biology and Beyond

Ramit Mehr

I started my career as a physicist, and was fascinated by the analysis of complex systems and emergent phenomena. I already had a couple of papers published, but then had to quit my PhD program due to a problematic pregnancy. After my son was born and all was well, I started looking for a new research topic. Because I was interested in complex systems and algorithms, I broadened my search to also include the chemistry and mathematics departments. In the math department of the Weizmann Institute of Science, I met two mathematical biologists who have influenced my career since: Zvia Agur, who offered me a part-time job so I can try doing math biology and see whether I like it, and the late Lee Segel, who ended up being one of my PhD supervisors.

Moving from physics into biology was not just a matter of overcoming a language barrier - it was a culture shock. Biology in the 1980s was not an exact science, and nobody in biology believes in math - some did not even believe in statistics! I could forget about measuring anything to the seventh decimal point. What was challenging and intriguing, however, was the staggering complexity I discovered. I decided that biology is fractal: no matter what scale you looked at, and you found just as much complexity as in the higher scale. Besides, my field of research was immunology, and the immune system is one of the most complex systems in our body.

My work in the field started with modeling lymphocyte development. Prior to my PhD work, only the pathways of T cell development were known, but there was no quantitative framework within which one could evaluate changes to the dynamics of these pathways in aging or disease. I was the first to create, simulate and tune mathematical and computational models of the population dynamics of T cell development in the thymus. These studies led to the discovery of feedbacks in T cell development, that is, the positive and negative effects exerted by mature T cells on developing thymocytes. Further studies led to the discovery of blind homeostasis in peripheral T cell populations - that is, the fact that the system only "senses" decreases in the total number of T cells, but does not distinguish between decreases in CD4+ and CD8+ T cell numbers. When I presented these studies in conferences in the early 1990's, it became clear that they have serious implications for the dynamics of human immunodeficiency virus (HIV) infection. They explained why pediatric infections, occurring while the thymus is still developing and growing, develop so much faster and are so much more severe than adult infections, and why the CD4:CD8 ratio does not properly recover under antiviral therapies. These conclusions have revolutionized the way the within-host dynamics of HIV infection are treated by modelers - who could no longer ignore the role of the thymus, the feedback from mature T cells (or lack thereof during HIV infection), and the blind homeostasis, in exacerbating the reduction in the CD4:CD8 ratio during the infection.

Further work from my group over the years created the first models for B and NK cell development and maturation, with interesting discoveries. The models were later applied to understand the reasons for reduced lymphocyte production in aging, or the role of key molecules that affect lymphocyte production. Already in the mid 1990's, however, I realized that the unique genetic and cellular processes that create and shape lymphocyte repertoires are even more interesting. I became interested in the process of antigen receptor gene rearrangement, which creates the immensely diverse T and B cell repertoires: I asked how gene segments are chosen for rearrange-

ment and how the structure of the V(D)J segment locus affects the resulting repertoire. The studies of these questions led to the discoveries of DNA order biases in gene segment selection for rearrangement, the delineation of the parameters governing this process, and the formation of a quantitative theory of repertoire selection. All this work - done over several years in Los Alamos, NM and Princeton, NJ - has earned me a tenure-track position in Bar-Ilan University, where I established my research group in 1999. As the systems I studied became more complex and the work had to integrate genetic, molecular, cellular and repertoire-level features, I found myself doing what has later become known as multiscale modeling. Among such models, my group and I developed models for the humoral immune system and isotype class switch recombination. During an immune response, B cell repertoires undergo complex genetic modifications - somatic hypermutation (SHM) of their antigen receptor (immunoglobulin, Ig) variable region gene, accompanied by antigen-driven selection, and isotype class switch recombination (CSR). While the dynamics of the humoral immune response have been extensively modeled prior to my work, I was the first to provide an explanation of the phenomenon of repertoire shift, that is, why secondary (memory) B cell responses are dominated by different clones from those dominating primary responses.

The latter modeling work has sparked my interest in Ig gene lineage-tree based analysis of B lymphocyte clonal dynamics during the response. The idea was suggested by Martin Weigert, my supervisor in Princeton, and my group was the first to develop and test quite a few of the current methods for analysis of the information thus gained. We have applied these methods in studies of the alterations in B cell clonal dynamics in several situations, including aging, chronic inflammation, autoimmune diseases and B cell malignancies. My group also created the first models for the development of natural killer (NK) cell repertoires, from receptor gene expression to selection of functional, non-harmful cells. Going down to the molecular level, we developed the first computer simulations of the dynamics of NK cell immunological synapses.

Thus, over the years, I have carved my "niche" of research - the analysis and modeling of lymphocyte repertoires. The recent development of high-throughput methods for repertoire data collection - from multicolor flow cytometry through single-cell imaging to deep sequencing - presents us now, for the first time, with the ability to analyze and compare large samples of lymphocyte repertoires in health, aging and disease. This has a huge potential for identification of subtle defects or changes in immune function, and developing between vaccines, better interventions in autoimmune diseases and malignancies, and better ways to rejuvenate the immune systems of elderly people. The exponential growth of these datasets, however, challenges the theoretical immunology community to develop methods for data organization and analysis. This task is orders of magnitude more difficult than standard sequencing and genomic analysis. First, there is the repertoire complexity itself, which means that one cannot use "reference genes" in the analysis, and the available computational tools are of no use for theoretical immunologists; research groups must struggle to create the correct experimental controls and computational tools, as in the software tools we developed for Ig gene sequence data analysis. Only a few research groups worldwide currently address these challenges. Thus, a central theme in my research plans is to keep developing these methods, and collaborating with leading groups, in order to remain in the cutting edge of Ig gene research.

When I started working in this area in the beginning of 1991, molecular markers and methods for investigating lymphocyte development and behavior were just being developed, and the human genome project was in its infancy - it has just presented as a possible plan to the US congress. During the years of my work in the field of theoretical immunology, I have seen it grow from a small group of interested individuals to a rich, active and challenging research field, whose members are becoming better integrated within the general immunology community. Theoretical immunology is still growing and has not yet fulfilled its potential, however. Thus, one of my career goals - aside from research - is to continue helping integrate theoretical work within all subfields of immunology. My choices of activities in professional society boards, conference and workshop organization, review and consulting boards reflect this career goal.

Related Links:

- My home page: http://immsilico2.lnx.biu.ac.il
- My personal journey - in the Science Careers Life and Career column: http://sciencecareers.sciencemag.org

Co-authoring a Book with Lee Segel

by Leah Edelstein-Keshet

A Patchwork Quilt in Mathematical Biology

My job was to make this into a "quilt", using what I knew of Lee, and adding some material to stitch it together...

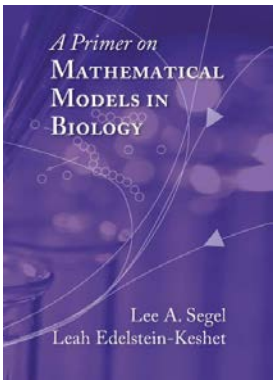
It was about twelve years ago, one summer in June, in New England. Lee Segel and I were both at a Gordon Conference in Theoretical Biology and Biomathematics. Those conferences had run out of Tilton, NH since before I was a graduate student. One of the local traditions was to take the conferees out on canoe trips, and spend some afternoons outdoors. I remember that John Jungk was my regular canoe partner over many years, those pleasant afternoons are great memories.

At any rate, in the van en route to the river, Lee and I sat together and chatted. He told me about a new book he was writing, then in early stages. To my surprise, he asked me if I would be willing to ensure that this book saw light of day in the unlikely case that he could not complete it. The reason that this was surprising is that Lee was then in peak health, and more physically fit than I was! So it was easy to say yes, and be quite sure that such an agreement would be a mere formality.

It goes without saying that when I heard that Lee Segel was unwell a few years later, it came as a complete shock. This was true for all of us who knew him, and who knew the kind and supportive mentor and friend that he was to many young scientists (me included). Losing him so rapidly, and at a relatively young and fit stage was terribly sad, and left a void in the community of applied and mathematical biology.

The files I eventually received from Joel Segel (his son) with help from the rest of the family were an initial patchwork of topics that Lee had taught over several years. My job was to make this into a "*quilt*", using what I knew of Lee, and adding some material to stitch it together. Time will tell whether the resulting patchwork quilt will be one that proves useful to students. These days, mathematical biology has been changing at an ever accelerating rate, and some of the classical material may be more or less relevant to newcomers.

I can say that working on the book was fun, puzzling at times, and not the mere formality I had envisioned back on that placid New England afternoon. It was great luck that SIAM agreed to publish this book, and their help, together with suggestions from a number of reviewers certainly made it all possible.



This textbook introduces differential equations, biological applications, and simulations and emphasizes molecular events (biochemistry and enzyme kinetics), excitable systems (neural signals), and small protein and genetic circuits. SIAM 2013.

Lee A. Segel (1932-2005) was a Professor at the Weizmann Institute of Science, Rehovot, Israel, where he served as Chairman of Applied Mathematics, Dean of Mathematical Sciences, and Chairman of the Scientific Council. Lee Segel was an Ulam Scholar at the Los Alamos National Laboratory, a Fellow of the American Association for the Advancement of Science, and a member of the Santa Fe Institute, where he continued his work on complex adaptive systems.

The Future of Mathematical Biology

Vivi Andasari, PhD, Research Fellow
Wake Forest University of Health Sciences
Winston-Salem, North Carolina
Former PhD Student & Post-doc of Prof. Mark Chaplain

What attracted you to mathematical biology?
Since school times in my home country, Indonesia, I had been fascinated with mathematics for reasoning and logics. I also liked biology because we could use it to understand nature, particularly our body and the complicated processes that occur in it. When I was doing my master's studies in Engineering Mathematics at Chalmers University of Technology in Sweden, I was so enthralled knowing that mathematics and biology could be combined into a very interesting field. I immediately knew this is something I want to do for my career.

What is your current research project?
Currently, I am working on multiple myeloma cancer growth at the Wake Forest Medical Center in Winston-Salem, North Carolina.

What specific areas are you interested investigating?
I am interested in all biological and medical problems where I can utilize my skills and expertise in multiscale modeling and simulation. My current research project is building multiscale models of myeloma cancer in bone marrow. In the past, for my PhD and previous postdoc post which both were supervised by Prof. Mark Chaplain of the University of Dundee, our research was focused on cancer cell invasion from continuum and multiscale modeling approaches. I also worked on chick embryo gastrulation in collaboration with Prof C.J. Weijer from the Life Sciences, University of Dundee. For my work in multiscale modeling, I use CompuCell3D - developed by the Biocomplexity Institute at Indiana University.

What do you hope to do after your postdoctoral work?
I want to do a job where I can have a life that reflects my values and satisfies my interests in research, particularly in using mathematics to understand the complexity of natural phenomena everywhere around us and inside us. The humble aim is to make my work beneficial for others.

What advice will you give to an undergraduate interested in a mathematical biology career?
I would strongly encourage them to consider a minor in biology for math majors and a minor in mathematics for biological sciences majors, to take advanced applied mathematics and biology courses, and to read from many sources. I would definitely urge them to attend workshops and conferences in mathematical biology whenever possible. Also, I would advise them to join related societies like the SMB for networking and getting updated information in the field. Another important attitude is to have honesty, at all times.

What inspires you scientifically?
Everything in the universe was created in proportion and exact measure. This is the fact that always motivates and inspires me in my work.

Why did you join the Society for Mathematical Biology?
At the beginning, when I was looking for a PhD position, I subscribed to the SMB weekly digest just to get information on advertised positions. Then I saw more advantages of becoming a member, such as the possibility to attend the SMB annual meetings and related conferences/workshops in order to meet with people who share the same research interests,

and more importantly the opportunity to get funded to attend these meetings, etc. As a matter of fact, I would like to take this opportunity to thank SMB for partly funding me to attend the US-Casablanca Workshop in Mathematical Biology held in June 2011 in Morocco, and for the Landahl Travel Grant to attend the 2009 SMB Annual Meeting at the University of British Columbia, Canada. It pays to be an SMB member! So I strongly urge the juniors to join SMB.

Mark Chaplain, Vivi's former PhD and postdoctoral advisor, says:

Vivi was a first-rate PhD student whose thesis was concerned with modeling cancer invasion. Vivi worked closely with colleagues in Ninewells Hospital (clinical oncologists) to gather data which she used to parameterize her models. The models themselves were systems of nonlinear PDEs with nonlocal terms accounting for adhesion between cancer cells and the cancer cells and ECM. Vivi developed a 2D continuum model which she compared with experimental data from organotypic invasion assays. After her PhD, Vivi spent one year as a post-doc with me developing individual-based models for gastrulation and again initiated contacts with experimental colleagues in the Division of Developmental Biology. Vivi has an excellent skill set for a mathematical biology researcher (numerics, analysis, modeling) which will equip her well for her future research career. She is conscientious and very hard-working and has a bright future ahead of her.

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

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

by TOSHIYUKI NAMBA

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

This is the third joint meeting of the JSMB & SMB, and the first to be held in Japan-previous meetings were held in Hilo, Hawaii in 2001 and in San Jose in 2007. The meeting is 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. 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).

Call for mini-symposium proposals for the conference will open soon. Please visit the website, http://www.jsmb.jp, for details. Proposal of mini-symposia with topics of significant current interest and importance at the interface of mathematics and its application to biology, including all areas of the life and medical sciences are welcome.

Osaka is the central city of the second-largest economic zone, Kansai, located in western part of Japan. Osaka is famous for merchant culture and comedies. However, it is surrounded by two historic capital cities, Kyoto and Nara, and a beautiful port town Kobe. The participants will be able to enjoy lots of different atmosphere at different cities. Questions regarding the conference can be directed to Toshiyuki Namba at: tnamba@b.s.osakafu-u.ac.jp.

Positions Available

PhD Position: Plant Cell Biomechanics, U Dundee: Plant cell biomechanics: Mathematical modeling and analysis of the interactions between plant cell microtubules and cell wall microfibrils. If you are interested in this PhD position please contact Mariya Ptashnyk, Division of Mathematics, University of Dundee, mptashnyk@maths.dundee.ac.uk. Please include a cover letter, a full CV detailing the taken undergraduate courses and corresponding grades, as well as contact information of two referees.

PhD Position: Math Bio., Epidem., & Networks, RMIT U, Melbourne: We invite applications for a PhD studentship in the School of Mathematical and Geospatial Sciences, RMIT University, Melbourne. The applicant will work on subjects that cross the interface of mathematical biology, epidemiology and network theory. The Department has a vibrant group of active researchers in these areas. Please contact Prof. Lewi Stone (RMIT University and Tel Aviv Uni) in the first instance by emailing: lewistone2@gmail.com

Post-doc: Personalized Medicine, Harvard Medical School: The Center for Biomedical Informatics (CBMI), Harvard Medical School has one research fellowship available for immediate appointment. The position is part of the Laboratory for Personalized Medicine (LPM, lpm.hms.harvard.edu) program. Email applications including curriculum vitae, summary statement of personal objective and research interests, PDFs of no more than three papers, and the names and email addresses of three references to: Peter J. Tonellato, Ph.D., peter_tonellato@hms.harvard.edu, 617-432-7185

Post-doc: Stochastic Biochemical Kinetics, U Edinburgh: Applications are invited for a postdoctoral research assistant to work on an interdisciplinary project aiming to develop a stochastic theory of chemical kinetics in non-dilute & macromolecular crowded environments. The start date for the project is 1st November 2013 or as soon as possible after this date. For more information on how to apply: http://grimagroup.bio.ed.ac.uk/vacancies.html

Post-doc: Mechanical Models of Membranes, Grabe Lab, U Pittsburgh: A postdoctoral position is currently available in the Grabe lab at the University of Pittsburgh, Department of Biological Sciences to develop mechanical models of membranes. This work is currently supported by an NSF CAREER award, and it is aimed at using continuum elasticity theory to describe membrane deformations around embedded membrane proteins. For more information on the Grabe Lab please visit our website http://mgrabe1.bio.pitt.edu/. Interested individuals should send their applications to Michael Grabe: mdgrabe@pitt.edu

Tenure-Tracks: Applied Mathematics, U Colorado-Boulder: The Department of Applied Mathematics at the University of Colorado Boulder seeks to hire two tenure-track Assistant Professors to begin August 2014. Authority to fill this position is pending budgetary approval. Review of applications will begin October 1, 2013 and continue until finalists are identified. Applications are accepted electronically at https://www.jobsatcu.com, postings #F00596 and #F00595.

Tenure-Track: Biomath/Biostat, College of William & Mary: The Department of Mathematics at the College of William and Mary seeks applications for a tenure-track position at the Assistant Professor level in Mathematics. More details: http://www.wm.edu/as/mathematics/positions Applicants should submit application letter, CV, and research statement to https://jobs.wm.edu. Review of applications begins October 15, 2013 and will continue until an appointment is made.

Tenure-Track: Mathematical Biology, U. Idaho: The Department of Mathematics at the University of Idaho invites applications for a tenure-track faculty position in Mathematical Biology. This is an academic year (9-month) position at the rank of Assistant Professor beginning August 17, 2014. Review of applications will begin November 1, 2013, and continue until a suitable applicant pool is identified. Please direct any questions regarding this position to math@uidaho.edu. For a complete description of the announcement, how to apply, and information about the department, visit http://apptrkr.com/378796

Announcements

Upcoming Events & Opportunities at NIMBioS

NIMBioS Wins NSF Renewal Award: NIMBioS was pleased to learn in July that the National Science Foundation awarded $18.6 million to the University of Tennessee, Knoxville. For more details, visit http://www.nimbios.org/press/pressreleases

Undergraduate Research Conf. at the Interface of Math & Biology, Nov. 16-17, 2013: The fifth annual conference, to be held at the Univ. of Tennessee Conference Center, in Knoxville, TN. Application deadline to request funding for the conference is September 27, 2013. For more information about the conference and details about the funding request, visit http://www.nimbios.org/education/undergrad_conf2013

Postdoctoral Fellowships: December 11, 2013, is the next deadline for submitting applications for postdoctoral fellowships at NIMBioS. Fellowships are for two years. Apply at http://www.nimbios.org/postdocs/

NIMBioS Investigative Workshop: Vectored Plant Viruses, March 17-19, 2014. Applications are now being accepted for this workshop, which will bring together experts in plant pathogens, agronomy, and vector and plant virology, physiology, and ecology with mathematical and statistical modelers to discuss problems in prevention and control of vector transmission of plant pathogens. Application deadline: Oct. 28, 2013. For more information about the workshop and how to apply, visit http://www.nimbios.org/workshops

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. http://www.nimbios.org/education

About Mathematics of Planet Earth 2013-Plus (MPE2013+): The Center for Discrete Mathematics and Theoretical Computer Science (DIMACS) is sponsoring new program, MPE2013+, grew out of the current program, Mathematics of Planet Earth 2013, For more information on MPE2013+, visit the MPE2013+ website at http://dimacs.rutgers.edu/Workshops/index-mpe.html

How to Apply: Information on the Mathematics of Planet Earth: Challenges and Opportunities workshop can be found at: http://dimacs.rutgers.edu/Workshops/MPE2013PreWorkshop/

For more information: contact Dr. Eugene Fiorini at mpe2013plus (at) dimacs.rutgers.edu.

Financial support to attend a workshop "Mathematics of Planet Earth: Challenges and Opportunities": A workshop "Mathematics of Planet Earth: Challenges and Opportunities" will be held at Arizona State University January 7-10, 2014. Financial support is available to support participants to attend this workshop and to participate in follow-up activities.

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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