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**Renew Your Membership
or
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<http://www.smb.org/membership/application.shtml>

President's Message



Happy New Year! On behalf of the Society for Mathematical Biology, I extend my best wishes to you and your loved ones for a healthy and productive new year. The past few months have been a dynamic time for the Society. Through your contributions for mini-symposiums, the joint meeting of the European Society for Mathematical and Theoretical Biology and the Society for Mathematical Biology (ECMTB 2016, Nottingham, UK July 11-15) will be very exciting. The deadline to submit your abstract and contributed posters is February 14th, 2016. I strongly encourage the Society membership to submit their research and join us at the Annual Meeting.

We will continue providing travel and bridging funds to our members. In September 2015, we received another generous donation from Evelyn Landahl to support our Landahl Travel Award Program. This award was created in the memory of her husband, Herbert Landahl, who served as Editor-in-Chief of the Bulletin of Mathematical Biology

from 1972 to 1981, and as the second President of the Society between 1981 and 1983.

On January 1, 2016, Alan Hasting (University of California, Davis) and Reinhard C. Laubenbacher (University of Connecticut Health Center) assumed the role of Editors-in-Chief of the Bulletin. Philip K. Maini (University of Oxford) served for 14 years as Editor-in-Chief. We are very grateful for Philip Maini's leadership and service. In this issue the SMB Newsletter, you will find out how the Bulletin is expanding its scope in response to the new developments and changes that affect our interdisciplinary work at the interface between the mathematical and biological sciences, which are not always captured by the original research article. I look forward to reading your articles in the Bulletin!

The Society is also responding to the new methods of communication offered by social media and on the internet. We have an active Facebook page (<https://www.facebook.com/smb.org>), and Twitter account (@SMB_MathBiology). A few days ago, the Society inaugurated its YouTube Channel (<https://www.youtube.com/channel/UCI8n6gChUAULaOqMLau-xTw>). You will learn more about our channel in this issue of the Newsletter.

In the following weeks, the SMB Newsletter will be transitioning into a new online platform. The Newsletter content will be more dynamic, and easy to share through social media. The role of newsletter editor can be a challenging one. Our editor, Amina Eladdadi (The College of Saint Rose) has been working hard maintaining the continuous publication of the Society's Newsletter. I would like to ask for your help by joining the editorial board of the Newsletter. If you believe that you can help us expand the scope and diversify the content of the SMB Newsletter, please send me an email. I would like to hear your ideas, and suggestions pertaining to the SMB newsletter.

I would like to close this message by emphasizing how your continued support and commitment to mathematical and computational biology allows the Society to continue its mission of encouraging the development and dissemination of knowledge in mathematical and computational biology, your field of research. As you can appreciate through this message, the Society is going through very exciting times. I hope that you are enjoying your membership and if you haven't renewed it yet, I would like to ask that you renew your membership today.

Santiago Schnell (E-mail: schnells@umich.edu) is President of the Society for Mathematical Biology, and Professor of Molecular Integrative Physiology and Computational Medicine & Bioinformatics at the University of Michigan Medical School in Ann Arbor, Michigan, USA. You can follow him on Twitter @SantiagoSchnell.



Society for
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Updates

www.nottingham.ac.uk/cmmb

by MARKUS OWEN

Show your love for ECMTB/SMB 2016! Contributed talk and poster submissions are due by February 14, 2016

Preparations continue in earnest for the 2016 Annual Meeting of the Society for Mathematical Biology (SMB) at the University of Nottingham, UK, from July 11 to July 15, 2016. The conference will be held jointly with the 10th European Conference on Mathematical and Theoretical Biology (ECMTB), under the auspices of the European Society for Mathematical and Theoretical Biology (ESTMB, <http://esmtb.org>). The conference will feature eight plenary speakers: Ruth Baker (University of Oxford, UK), Sander van Doorn (University of Groningen, Netherlands), Julia Gog (University of Cambridge, UK), Leah Keshet (University of British Columbia, Canada), Johan van de Koppel (Royal Netherlands Institute for Sea Research), Hisashi Ohtsuki (Kanagawa, Japan), Johan Paulsson (Harvard University, USA) and Adélia Sequeira (University of Lisbon). John Rinzel (NYU, USA) will deliver the SMB Winfree Prize lecture. Minisymposia, contributed talks and posters will cover diverse themes in mathematical and theoretical biology and medicine.

The scientific committee is currently considering nearly 100 minisymposium proposals, a very large number which shows the strength and vitality of the mathematical biology community. Contributed talk and poster submissions will stay open until February 14, 2016 - please visit ecmtb2016.org for details. This date was picked simply to be two weeks before the end of the month, but someone on twitter have noticed its alternative significance: (<https://twitter.com/balazdan/status/658655981820334080>).

658655981820334080).

If you have any questions regarding the conference, please see ecmtb2016.org/FAQ or send an email to our dedicated address: ecmtb2016@nottingham.ac.uk. Please visit the website: <http://www.ecmtb2016.org> for more details. Questions regarding the conference can be directed to: ecmtb2016@nottingham.ac.uk.

Local Organizers: Markus Owen (Chair), Daniele Avitabile, Leah Band, Bindi Brook, Stephen Coombes, Etienne Farcot, John King, Reuben O'Dea, Rüdiger Thul, Jonathan Wattis.

Scientific Committee: Linda Allen, Ellen Baake, Jim Cushing, Andreas Deutsch, Odo Diekmann, Susanne Ditlevsen, Stephen Eglén, Amina Eladdadi, Yoh Iwasa, Eva Kisdi, Santiago Schnell, Artie Sherman, Jonathan Sherratt

Markus Owen,
on Behalf of the Organizing Committee
email: Markus.Owen@nottingham.ac.uk
www.nottingham.ac.uk/cmmb



Markus Owen is a Professor of Mathematics in the School of Mathematical Sciences at the University of Nottingham, Director of the Centre for Mathematical Medicine & Biology and Head of the Mathematical Medicine and Biology Research Group. (<https://www.maths.nottingham.ac.uk/personal/mro/>)

ECMTB/SMB 2016 Joint Annual Meetings Poster

ECMTB / www.ecmtb2016.org

Nottingham

11-15 July 2016



**10th European Conference on Mathematical and Theoretical Biology
and Annual Meeting of the Society for Mathematical Biology**



**Society for
Mathematical
Biology**



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The Society for Mathematical Biology YouTube Channel

Scientific discoveries and education are at the heart of modern life. The internet and social media are offering new venues of communication. The Society for Mathematical Biology has created a YouTube Channel (<https://www.youtube.com/channel/UCI8n6gChUAULaOqmLau-xTw>) to offer online seminars, courses, and educational resources for our community. At the same time, our YouTube channel is an excellent opportunity to communicate with the general public. Often, the general public does not understand the connection between our members' current research and the resulting products or findings many years down the road.

The Society has inaugurated its channel by uploading video seminars of the talks presented at the 2015 Annual Meeting of the Society for Mathematical Biology, which was held at the Georgia State University campus in Atlanta, Georgia, USA from June 30 to July 3rd, 2015. We are very grateful to the annual meeting organizers for providing us with the video recordings of the talks. Now, we are asking you to help us grow the Society for Mathematical Biology video collection. We welcome submissions of seminars, workshops, and courses from members of the mathematical biology community. If you have created a video about your research findings that could help the general public to better understand what you do and why it is critically important to society, we will also consider it for the Society for Mathematical Biology YouTube Channel.

Let's work together in disseminating research and knowledge at the interface between the mathematical and biological sciences.

The Bulletin of Mathematical Biology Update

by SANTIAGO SCHNELL, ALAN HASTINGS & REINHARD LAUBENBACHER

The Bulletin of Mathematical Biology (BMB), the official journal of the Society for Mathematical Biology, has long been a premier venue for the dissemination of research findings at the interface of mathematics and biology. Since its founding, it has been a driver of the dramatic evolution that has transformed and expanded the field of mathematical biology, as more phenomena in the life sciences have become amenable to mathematical analysis and more areas of mathematics have found applications in biology. Philip Maini, FRS (University of Oxford), the past Editor-in-Chief of the Bulletin of Mathematical Biology, deserves much of the credit for assuring that the Bulletin is recognized as a scientific journal of the highest quality with high impact on the field.

Beginning on January 1, 2016, Alan Hastings (University of California-Davis) and Reinhard C. Laubenthaler (University of Connecticut Health Center) assumed the role of Editors-in-Chief, when Philip Maini, concluded his 14th year tenure at the helm of the Bulletin. We are very grateful for Philip Maini's leadership and service. His shoes will be difficult to fill.

As times change, the nature of scientific publishing changes, and so does the role that scientific journals play in the research enterprise. This is particularly true in the field of mathematical biology, which is advancing at breakneck speed, driven by technological innovations that provide data, ever increasing in quantity and quality, which makes mathematics a key enabling tool for much research in the life sciences. And so the Bulletin must also continually adapt to these changes in order to remain a vibrant leading outlet for publications in mathematical biology. Articles reporting original research of scientific significance to the mathematical biology community will remain its core focus. There are no restrictions on length and format, and can range from biologically motivated investigations in the mathematical sciences, broadly defined, to

results that combine concepts and tools from the mathematical sciences with experiment or observation. All contributions, however, must be focused on a substantial advance in biological understanding. The aim of the journal is to be of major interest to all researchers working at the interface of biology and the mathematical sciences, and articles should take care to address this broad audience.

Mathematical biology has become a multi-faceted and fast-moving field, and researchers need to be cognizant of a plethora of new developments and changes that affect their work, which are not always captured by the original research article format. Therefore, the Bulletin will serve its readers through several new kinds of articles.

Reviews: These offer an in-depth treatment of an important topic, emerging research area within mathematical biology, or significant recent development, and provide an excellent guide for researchers new to a subject or researchers established in the field who are looking for a new view of their area. A review should not be a mere summary of a field; it should be a critique with new points of view, synthesizing the existing literature from a variety of authors.

Methods: Mathematics is a key enabling technology for the life sciences. The Bulletin will publish peer-reviewed articles that describe new mathematical, statistical, or computational methods relevant to a range of biological problems or processes, or new experimental methods that are substantially based on tools or concepts from the mathematical sciences.

Editors' Choice: Select articles, chosen by the Editors-in-Chief, will be the subject of a shorter "Insight" article published in the same issue. Insights are provided by experts in the field of the research article: they explain why the reported results are significant and outline some of the relevant challenges remaining in the field. These articles will be commissioned by the Editors-in-Chief. Articles are peer-reviewed at the discretion of the editors and will typically be one to four pages in length.

Perspectives: This type of article will focus on a broad range of subjects relevant to the field and its practitioners: science policy and research funding, careers in mathematical biology, research conduct, public engagement, and a variety of other related topics, including opinion pieces. These articles will be peer-reviewed at the discretion of the editors or the editorial board.

Unsolved problems: These peer-reviewed articles will discuss a research topic of importance to the mathematical biology community that is poorly understood and is in need of attention. They can include unexplored or challenging questions, emerging opportunities, or unexplained phenomena. These articles are intended to stimulate researchers, including students, to think about future research directions inside or outside their area of expertise. They should be aimed at a broad audience, and should include a discussion of why the problem is important, relevant background information, and what work has been done toward solving the problem. Furthermore, this discussion should also cover any competing hypotheses and major challenges that exist, and if applicable, should also include commentary regarding the advances that will be necessary to solve the problem.

Education: Interdisciplinary training and education is particularly challenging and of crucial importance for the future of mathematical biology. The Bulletin will contribute to this effort by publishing articles that discuss ideas, methods, tools, and activities to enhance research and education, both inside and outside of the classroom. They can take several forms, ranging from historical reviews to practical tutorials. Articles can also provide practical knowledge and background information on important mathematical or computational methods and approaches used to investigate interesting biological problems. These articles will be peer-reviewed.

By broadening the scope of the journal and providing flexible contribution formats, we expect the Bulletin to remain an important resource for its authors and readers, helping them move mathematical and quantitative biology forward, as they meet ever more complex and exciting challenges in the life sciences. The new Editors-in-Chief will strive to provide a publication process that is author-friendly, and as speedy as possible, while maintaining the highest scientific standards. The Bulletin of Mathematical Biology will continue to evolve with the times, and the incoming editors, Alan Hastings and Reinhard Laubenbacher, welcome input to ensure that the journal serves the needs of the mathematical biology community. We look forward to reading your papers published in the Bulletin in a near future!

Summer High school Internship Program in Integrated Mathematical Oncology

Tampa, Florida , USA, Summer of 2015

by HEIKO ENDERLING & SANDY ANDERSON

The main goal of the Department of Integrated Mathematical Oncology (IMO) at the H. Lee Moffitt Cancer and Research Institute in Tampa, Florida is the integration of theoretical and computational modeling tools into clinical and experimental cancer research to aid in both the core understanding of cancer processes and the mechanisms that drive them. By using a range of mathematical modeling approaches targeted at specific types of cancer the IMO aids in the development and testing of treatment strategies. This multi-model, multi-scale approach allows for a diverse and rich interdisciplinary environment that has created many novel approaches for the treatment and understanding cancer. To educate a new generation of scientists at the interface of tumor biology and quantitative modeling, we have developed an internship program for rising junior and senior high school students. The inaugural eight-week (summer of 2015) High school Internship Program in Integrated Mathematical Oncology (HIP IMO) attracted 7 students (see picture below) to participate in hands on research projects that apply mathematical techniques to a specific problem in cancer biology or clinical oncology.

During the first week the students received introductory lessons in Cancer Biology, Mathematical Modeling, and Ecology and Evolution, as well as hands on programming modules in Java, Matlab, and Python. The second and third week included Journal clubs, paper presentations and reproduction of results from recent Moffitt IMO publications. The students then spent the remainder of the internship on individual projects mentored by IMO's Sandy Anderson, Bob Gatenby, David Basanta, Jacob Scott, and Heiko Enderling. Projects included simulation of optimal radiotherapy protocols, prediction of patient-specific treatment response, game-theoretical models of prostate cancer, radiotherapy of glioma, predicting the evolution of prostate can-

cer during hormone therapy, and evolution of intratumoral heterogeneity in different environmental conditions. Some of the projects have continued after the internship and are currently being written up for publication in peer-reviewed journals. The students attended and actively engaged in departmental and institutional seminars, and participated in social and networking events with other internship programs at Moffitt Cancer Center (Summer Program for the Advancement of Research Knowledge, SPARK; Leaders In New Knowledge, LINK).

Our first experience to teach mathematical biology, and mathematical oncology in particular to high-school students was overwhelmingly positive. The students were exceptionally motivated and grateful for the opportunity to learn how mathematics can be applied to real life problems, and the different careers that are possible with a fundamental understanding of mathematics and physics. We will monitor the future of our HIP IMO students with periodic questionnaires to evaluate the impact this internship had on their choice of college education and future career. With the help of our recently awarded Physical Sciences in Oncology Network Center program, we will continue to further develop the HIP IMO program this year (and the coming years).

Applications are now open for the 2016 HIP IMO summer program. Details and application forms can be found online at <http://labpages.moffitt.org/imo/hip-imo/>. The application deadline is March 1, and notifications of acceptance will be sent by end of March.

Heiko Enderling is an Assistant Member, Director for Education and Outreach, Integrated Mathematical Oncology at Moffitt Cancer. Sandy Anderson is the Chair of the Integrated Mathematical Oncology (IMO) department and Senior member at Moffitt Cancer Center. (<http://labpages.moffitt.org/imo/>)



Pictured above is the HIP IMO class of 2015, left to right: Rebecca Titus, Pranav Sharat, Sid Ramesh, Raj Warman, Sameer Puri, David Gamero, Abhi Bukkapatnam



Group Photo with Students and Mentors

Mathematics and The Quest for The Fundamental Principles of Biology

Salt Lake City, Utah, USA, December 13-14, 2015

by FRED ADLER

A group of theoretical and mathematical biologists gathered in Salt Lake City on Dec 13-14 to take on what is perhaps the greatest challenge in our field: avoiding humiliation at a workshop without any name tags. While that fundamental issue was being addressed, participants moved on to one nearly as great: presenting their life's work in a π minute talk. After the name tags and short talks were delivered, the path was clear to take on our official charge of establishing the fundamental principles of mathematical biology and set the course for the field for the remainder of this century.

Remarkably, a grand theme did emerge; that of stochasticity, whether rightly called noise, variability, or unpredictability, and its effects on the availability and storage of information. This variability is rarely just unstructured noise imposed by the external environment. Some is generated by organisms or cells themselves, for example when plants modulate the rates and magnitudes of system-resetting fires, or when cells use stochasticity in production of RNA transcripts or protein molecules to generate phenotypic diversity in their genetically identical descendants. Furthermore, variability has structure in the form of predictable ranges of temporal frequencies and spatial scales, as with ocean waves, pulses of odor in a turbulent plume, and daily or seasonal cycles. The sizes of organisms and cells and the temporal scales at which they function determine how the stochastic and predictable variation in their world affects them, and which they in turn can affect.

The challenges and opportunities of noise and variability influence all living beings, including the mathematical biologists who think about them. Clear thinking about how life persists and flourishes in a noisy world demands that we develop new methods to capture these mechanisms without being overwhelmed by real or apparent complexity.

We discussed many ways that living beings cope with or capitalize on noise, each of which raises new challenges for modelers. Networks can be com-

partmentalized to contain error propagation, tasks can be outsourced to other organisms, such as our gut bacteria, to let them suffer the consequences of errors, and dynamics can be tuned, through such newly understood mechanisms like miRNA, to produce novel forms of robustness. Responding appropriately depends on gathering information from a recalcitrant world, with many mechanisms falling under an umbrella related to the Brownian ratchet, searching physical or information space through a random walk, but with periodic evaluation to effectively control randomness, and organismal control over the timing and magnitude of steps. For example, small organisms can capitalize on micro-scale information in fluids and biochemistry, and cells can use diffusion as a source of information when patterns are sharpened through filters and positive feedbacks.

As scientists, we must formulate principles and models that capture stochasticity as part of the process, rather than as extrinsic noise. In some sense, like all organisms, we must continually solve inverse problems, extracting information even when we know that details and specific mechanisms are non-identifiable or lost in the haze of the past. The ease of collecting huge biological datasets at all scales raises an acute problem: what mechanistic parameters can, even in principle, be determined and from what types of data? We cannot simply assume that sufficient data can resolve any biological problem, because there are already examples of massive data collection efforts that are provably unable to distinguish between alternative underlying processes. Mathematically, we can approach these challenges with methods to predict the dynamics of distributions, not just individuals, and ideally understanding informative underlying patterns such as the relationship of sample means to sample variances. Alternatively, we can seek simplicity amidst the complexity through finding how networks are built from relatively simple network motifs to create robust dy-

namics.

These issues have implications beyond basic scientific understanding. If ensembles, ranging from groups of cells to collections of individuals, provide one way to cope with noise and integrate information, they create problems of their own regarding maintenance of cooperation, including avoiding the tragedy of the commons and breakdown of collective regulation, such as in cancer. The hidden potential of those individuals can backfire, such as when cancer cells recall the tricks they used as single-celled organisms to survive the challenges of an unpredictable environment to evade the controls of the whole organism.

Addressing these challenges demands not just new techniques or even new ways of thinking, but also new structures to support progress and new ways to frame the goals of our enterprise. We tend to think of scientific success in terms of identifying a novel mathematical approach that makes sense of stochasticity and making predictions that could not be made before, ideally while simultaneously elucidating new mechanisms and proposing new experiments. But in some cases should scientists begin to think more like engineers, handling things on an ad hoc basis with a goal of intervention and forget about building general theories? Should we be working with experts in machine learning to develop a "high-throughput" mathematical biology even at the cost of traditional mechanistic understanding?

Nature provided an opportunity to put some of these concepts to work in the form of an epic snowstorm that fell over the night during the middle of the workshop. The distraction of worrying about getting to the airport had surprisingly little impact on our ability to focus, except perhaps for forgetting to take a group photo amidst the piles of snow. We left thinking about how to support the genuinely high risk research needed to build the new tech-

niques and ways of thinking that will push the field forward.

We thank the Army Research Office and the University of Utah College of Science for funding this workshop.

- Fred Adler (University of Utah)
- Reka Albert (Penn State University)
- Elizabeth Allman (University of Alaska)
- Marissa Basket (University of California, Davis)
- Ben Bolker (McMaster University)
- Joel Cohen (Rockefeller University)
- Daniel Coombs (University of British Columbia)
- Lisa Fauci (Tulane University)
- Jim Keener (University of Utah)
- Mimi Koehl (University of California, Berkeley)
- Katia Koelle (Duke University, in spirit, turned back by weather)
- Reinhard Laubenbacher (University of Connecticut)
- Simon Levin (Princeton University)
- Mark Lewis (University of Alberta)
- Marc Mangel (University of California, Santa Cruz)
- Alex Mogilner (New York University)
- Virginia Pasour (Army Research Office)
- Joshua Plotkin (University of Pennsylvania, in spirit, stopped by sick child)
- Mike Reed (Duke University)
- Sean Rice (Texas Tech University)
- Jon Seger (University of Utah)
- Adam Siepel (Cold Spring Harbor Laboratory)
- Jim Tabery (University of Utah)



Fred Adler is the Immediate-Past-President of the Society for Mathematical Biology, and Professor of Mathematics at the University of Utah, Salt Lake City, Utah, USA. (<http://www.math.utah.edu/~adler>).



Mathematical Biology: a Multidisciplinary Endeavor

UNAM-Juriquilla, Querétaro, México, January 11-14, 2016

by JORGE X. VELASCO-HERNÁNDEZ

The morning of Monday January 11th the first dedicated mathematical biology meeting since 2002 in Mexico, started. There had passed 14 years since the Congreso Latinoamericano de Biología Matemática took place at CIMAT, Guanajuato. In that occasion, also with the support of the Society for Mathematical Biology, the meeting brought together biomathematicians working in Latin America. This time, in Juriquilla, Querétaro, the scope was broader and more inclusive.

With the support of the Society for Mathematical Biology, the Instituto de Matemáticas UNAM, the Center for Mathematical Sciences, CINNMA A.C. and the National Council for Science and Technology (CONACyT) and the Sociedad Matemática Mexicana as the main sponsors, researchers from France, Germany, United States, Chile and Mexico got together with several objectives. The first one was to formally reinsert biomathematics into the organized research activities of the country, with the aim of fostering activities in the area and opening its national perspectives to broader international arenas. In Mexico, biomathematics has flourished since the early 80s but no recognized groups yet exist, only personalities with influence and impact but essentially isolated in terms of international recognition. Mexico needs the conformation of groups to impact the important problems and challenges in epidemiology, neurobiology, genomics, medicine, cancer research, genetics, and so many other areas of biological R&D with the quantitative tools that the interaction between the mathematical and biological sciences can bring.

The second objective was the introduction of the Multidisciplinary Node of Applied Mathematics and Biomathematics, a recent initiative of the Instituto de Matemáticas of UNAM to develop applied mathematics through multidisciplinary collab-

orations. This group is integrated by a majority of young researchers recently hired with the support of the Young Research Fellows Program of CONACyT, centered at the multidisciplinary campus of the National Autonomous University of Mexico (UNAM) at Juriquilla, Queretaro. Mathematical Biology: a Multidisciplinary Endeavor, included talks on bioinformatics, genomics, epidemiology, ecology, evolution, neurobiology, cell biology, pattern formation, systems biology and also mathematical methods as partial differential equations, optimal control, stochastic processes, numerical methods and dynamical systems. The organizers with were able to offer 50 full fellowships for graduate students and also senior undergraduates from State and Federal Universities all over the country. Mathematical Biology: a Multidisciplinary Endeavor was indeed an international event with nation-wide impact. We expect to have new meeting in two years to continue the promotion and to help to further the development of mathematical biology and applied mathematics in Mexico. The role that the World Outreach Committee of the Society for Mathematical Biology has played in the success of the meeting is fully acknowledge. Without its generous and open support this meeting would not have had the national impact it had particularly among students and young researchers. More information about the meeting can be found here: <http://matmor.unam.mx/mathbio/>



Jorge X. Velasco-Hernández (jx.velasco@im.unam.mx) is a Professor of Mathematics at Universidad Nacional Autónoma de México Mexico City, Mexico.

(<http://www.matem.unam.mx/fsd/velasco>)

Mathematical Biology: A Personal Journey

Saber Elaydi



I was born in Beersheba, Palestine from Bedouin parents. In 1948, my parents moved to a refugee camp, called Al Maghazi, in central Gaza Strip where I went to schools ran by the United Nations. As early as middle school, I discovered my love to mathematics. My parents wanted me to go to medical school and become a medical doctor, which would bring prestige and wealth to the family. As a rebel teenager, I rejected my parents' plan and went to college in Cairo, Egypt, where I majored in mathematics and physics. The only two other subjects that I studied were chemistry and biology. In those years, I never thought that later in my life I will be excited about biology. My mind was set on mathematics and mathematics alone. My other interests were in languages, literature, history and philosophy. I augmented my formal education by doing intensive reading of western and eastern literature, history, and philosophy. After few years of teaching in high school, I attended few courses on modern mathematics at the University of Kuwait. As a stateless person, I thought I had no chance in getting a visa to Western European or North American countries. So I started applying to graduate schools in

the Soviet block. To my chagrin, I found out they are only accepting applications via friendly governments, something I did not have. In desperation, I applied to a student visa at the American Embassy in Kuwait. To my greatest surprise, I got the visa. This was the most dramatic change in my life, a bedouin stateless boy is going to pursue a PhD in the US. I studied mathematics at the University of Missouri-Columbia under the supervision of Ping-Fun Lam, David Carlson, and Roy Utz. My PhD thesis was on topological dynamics which is the study of the action of a topological group or semi-group on a topological or metric space. This is a very abstract subject and far from any applications to natural sciences. I spent the first ten years of my academic life at the University of Kuwait and the University of Colorado teaching and doing research in pure mathematics with a focus on topological dynamics.

In 1989, I had the first experience working on difference equations where I supervised a Master's thesis on difference equations at the University of Colorado. A year later, I moved to Trinity University where I made my crucial move to do research exclusively on difference equations and discrete dynamical systems. In 1994, I founded the *Journal of Difference Equations and Applications*, now in its twenty second volume. My first book on the subject "*An Introduction to Difference Equations and Applications*, Springer, 1996" was the first book in this field to include substantial examples from ecology and epidemiology. In 2000, I wrote my second book titled "*Discrete Chaos*, Chapman Hall/CRC" focusing on discrete dynamical systems with a sizable number of examples from biological models.

My serious switch to mathematical biology, however, came in 2003 when I met Bob Sacker of the University of Southern California. Bob made a name for himself studying ordinary differential equations. I met him at the right time when he was searching for a new direction. So I convinced him to work jointly on a problem, now known as the "*Cushing-Henson Conjecture*", concerning the global stability, attenuation and resonance of a periodically fluctuating Beverton-Holt model. From that moment on, I have worked exclusively on problems in mathematical biology that are modeled by difference equations. To my pleasant surprise, I found out that my background in topological dynamics has given all

the necessary mathematical tools to delve deeply into the mathematical analysis of multi-species models. In particular, the investigation of stability and bifurcation of discrete-time models have become my research trademark.

In 2006, Jim Cushing and I founded the Journal of Biological Dynamics in an effort to promote the fields of ecology and epidemiology. To consolidate our efforts, a year later, in 2007, we initiated a biannual series of international conferences titled "*International Conference on Modeling and Analysis of Populations in Biological Systems (ICMA)*." ICMA was held in Tucson, Arizona (2007), Huntsville, Alabama (2009), San Antonio, Texas (2011), Lubbock, Texas (2013), and London, Ontario (2015). ICMA VI will be held in Tucson, Arizona in October 2017.

With all these activities, I felt that there was something missing. Though I was involved in the highest level of research in mathematical biology, to my chagrin I was not able to filter this down to my undergraduate students at Trinity University. The prevailing culture in mathematics at the time was that you cannot do research with undergraduates. I was determined to bring my excitement in mathematical biology to my students, I applied and got a 5-year NSF institutional undergraduate Biomathematics grant, which was extended to seven years. For the last six years, I worked with four research teams, where each team consists of a biologist, two to three undergraduate students and one or

two mathematicians. The research projects include grass invasion, infection of a bacteria by a virus in a chemostat, mammal distribution in North America, and Alzheimer disease. My main task in these teams is to develop a mathematical model in the form of a difference equation that better represents the biological phenomena under study. The other main task is to train students in the art of creating discrete-time models and how to improve them to fit

the collected data. My intensive joint work with the biologists in the last six years has given me the best possible insight and experience and made me a much better modeler. My interaction with biologists has been the impetus for creating and teaching a course on mathematical models in the life sciences from my lecture notes. These lecture notes will be published in a book titled "Discrete-Time Mathematical Models in Life Sciences" with Springer. To my knowledge, this will be the first on mathematical biology that uses exclusively difference equations in modeling biological phenomena.

I promised NSF and Trinity University to create a new type of scientists that are bilingual in both biology and mathematics and we have succeeded. I hope I have become as bilingual as my students.

Saber Elaydi is a Professor and Chair Department of Mathematics at Trinity University, San Antonio, Texas, USA. (<http://ramanujan.math.trinity.edu/selaydi/index.shtml>)

Editor's Notes

We invite submissions from SMB members 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 promotes and fosters 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.

Editor: Amina Eladdadi, The College of Saint Rose, Albany, NY, USA.
email: editor@smb.org

Research Interview

Modeling Anticancer Therapies



J. Héctor Morales-Bárceñas talks with Mark Whidden about his research on drug delivery in tumors

What are you currently researching?

I am doing mathematical and computational modeling on diffusion and transport of drug carriers in solid tumors. In this research, we study different factors of why the efficiency of transport and distribution of drugs inside tumors is limited. This research is conducted in collaboration with the National Cancer Institute of Mexico (INCan).

What attracted you to the field of cancer research?

Mainly the multidisciplinary nature of this research as well as the multi-scale dynamics of the disease. The research on the field has many challenges that requires collaborations with colleagues with different backgrounds, like physicians, medical physicists, cancer biologists, etc. Not only do we need to learn different terminologies but also understand the phenomena involved on the problem.

How can mathematical modeling be used to make contributions in this populated area of research?

The degree of cancer complexity is high enough to make room for everyone's approach to solve different aspects of cancer. Mathematical models are very convenient to evaluate therapy efficiency, because we can "play" with the model to our will, on the computer, without any risk for patients or lab animals. It does mean that we can make "experiments" with our models on the computer in order to get conclusions that support the medical or biological therapies, before putting them in practice.

Do you ever find the complexity of cancer biology daunting?

Yes. Most of the time we are faced with big challenges in understanding the puzzling pieces of cancer biology. For instance, in our models we cannot incorporate all the knowledge that cancer biology offers. Instead, we have to neglect many influences of the outside environment of tumors using a reductionist approach. Otherwise, the model would not be useful at all. The main point of modeling this disease is to decide, together with the experimentalists, what would be the traits that we must incorporate to the models. Actually, we have to restrict our models to some level of description of the problem: molecular, cellular, tissue or the whole organism.

What aspect of your research do you find most intriguing?

Cancer is an evading disease and its response is dynamic. There is, indeed, no mathematics for cancer. We have to make use of all kind of models to our disposal to face it.

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

No matter how much you master mathematics, you still need to understand other scientific disciplines such as physics and biology.

Who or what inspired you to become a mathematical biologist?

"The Feynman Lectures on Physics." In them, there is an old but splendid point of view on a master of science to biology. Feynman continues to be an inspiration for everyone.

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

A detective.

For more info, please visit: <http://sgpwe.izt.uam.mx/Profesor/509-J-Hector-Morales.html>

The Future of Mathematical Biology

Ahmadreza (Farzin) Ghaffarizadeh
The University of Southern
California,
Postdoctoral Fellow of Dr. Paul
Macklin



What attracted you to mathematical biology?

The mysteries of our body from the molecular level to the whole organism, and the way it self-organizes, have always amazed me. Back home (Sirjan, Iran), I needed to choose my field between mathematical/physical sciences or biological sciences when I was in high school. Due to my innate interest in computer science, I chose to pursue mathematics/physics field, however, I always wanted to do something in biology. My first bioinformatics project

during my M.S studies was the beginning of my journey in mathematical biology– the journey that I continued during my PhD and postdoctoral research.

What is your current research project?

I am currently working on three projects: 1) **Digital livers**: 3-D computer models of bioengineered human liver tissues constructed from several data sources. Digital livers are combined with dynamical models of colon cancer cells (see #2 below) to conduct simulation studies of colon cancer metastases in the liver. The models are integrated with high-throughput imaging data from bioengineered liver tissues and in vitro experiments. 2) **PhysiCell** (PhysiCell.MathCancer.org), a physics-based cell model and simulator, and **BioFVM** (BioFVM.MathCancer.org), a biological transport solver: two cutting-edge open source computational platforms for use in patient-calibrated cancer simulations. 3) **MultiCellDS** (Multicellular data standard), a data standard for sharing multicellular experimental, simulation, and clinical data. I hope that these three projects will bring us closer to a future where physicians can create patient-specific models of tissues, seed them with personalized digital tumors, and simulate many possible treatment choices to select the best one.

What specific areas are you investigating?

As it can be seen from the projects that I am working on, my research studies are all centered around cancer. I am working as part of a multi-institutional team to build computational models that can be tailored to individual patients, and used to predict how their cancers will grow and respond to many treatment choices. I hope my work can address a pressing clinical need: treatments designed specifically for each patient, rather than for the average population.

What do you hope to do after graduation?

I hope to be able to continue my research studies as a scientist at a research institute. A lab of my own at some point? That would be a dream!

What advice would you give to an undergraduate interested in a mathematical biology career?

Read, read, read! Try to read as many state-of-the-art papers from different aspects of mathematical biology as you can. However, don't let the literature bias your thoughts! At this point, mathematical biology needs people who can think out of the box and grasp concepts that are different from the norm.

What inspires you scientifically?

The war on cancer and the patients that we lose every day in this battle.

Why did you join the Society for Mathematical Biology?

It is the community that enables the communication of mathematicians and biologists— the most fundamental need in mathematical biology field. The SMB annual meetings, in addition to other SMB-sponsored workshops and conferences, provide a unique opportunity for people with similar research interests to meet and share their findings. I would like to thank SMB for a Landahl travel grant for attending 2013 annual meeting in Arizona.

Dr. Paul Macklin, says: I first met Ahmadreza at the 2012 SMB Annual Meeting in Knoxville Tennessee, when he was a graduate student of professor Nick Flann (Utah State University). His technical skill set was very impressive, but I was really struck by his inner "scientist's conscience": a deep-seated drive to do science right, to ask the right questions, to verify his work, and to contribute work that makes the world better. It is no accident that he is emerging as a leader in computational oncology: his curiosity, drive, and interest in helping people made it almost inevitable!

When Farzin joined my lab in August 2014, he brought with him considerable expertise in com-

puter science and agent-based simulations. He became our point person for an NIH-funded project to simulate colon cancer metastases in bioengineered livers. He worked one-on-one with our biologists to understand their microscopy data, import and stitch together high-resolution images, segment tissues and cells, and extract simulation parameters. He developed 3-D liver architectures and 3-D simulation tools to use them. The first fruits of this work (BioFVM: a 3-D diffusion solver for biology) was recently published in *Bioinformatics* (DOI: 10.1093/bioinformatics/btv730). The 3-D agent-based model should be submitted very soon. In the next year, I anticipate exciting results on image processing, analysis, and simulation of colon cancer metastases. Through all this hard work, Farzin has shown a positive, "can do" attitude that makes him an absolute joy to work with. When he's ready, he'll make a fantastic lab leader. His skills and experiences will lead him to solve problems that push the boundaries in computational medicine and make lives better. And I'll be proud to say I worked with him.



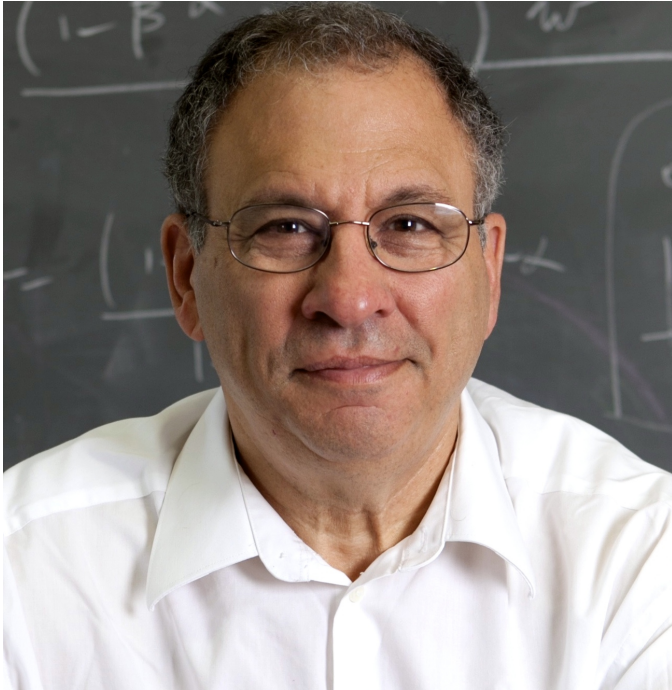
The Future of Math Biology is a column intended to highlight graduate students and postdocs in Mathematical Biology. Do you want to nominate a student or a postdoc from your research group? Please send your nomination to:

Russell Rockne (russrockne@gmail.com).



Former SMB President Simon Levin Awarded The National Medal of Science

by FRED ADLER



Prof. Simon Levin

Photo Credit: Princeton University

Simon Levin, who served as President of SMB from 1987-1989, has been awarded the National Medal of Science. To quote from the official announcement on whitehouse.gov "The National Medal of Science was created by statute in 1959 and is administered for the White House by the National Science Foundation. Awarded annually, the Medal recognizes individuals who have made outstanding contributions to science and engineering."

Levin received his bachelor's degree in mathematics from Johns Hopkins University in 1961, and his doctorate in mathematics from the University of Maryland-College Park in 1964, and began his work in mathematical biology not long thereafter. Among his many remarkable accomplishments, his highly influential work on disturbance and spatial patterning with Bob Paine initiated the thread of understanding how behaviors of individuals lead to large-scale patterns. In addition to addressing this question widely within ecology and evolutionary biology,

Levin took the risk of bringing his work into the broader sphere of policy through modeling of public goods, synthesized in his book "Fragile Dominion". He has led the way in finding scientifically grounded ways to guide the behaviors of individuals and financial markets for the wider good, and indeed for the protection of the whole planet.

One could build an extraordinarily well-rounded overview of theoretical biology simply by studying his publication list (highly recommended for those with some spare time). As testimony to his influence in our field, he served as advisor for three subsequent SMB Presidents (Alan Hastings, Lou Gross, and Fred Adler). On a personal level, Simon is one of those rare people who brings out the best in those around him, which should make him and President Obama fast friends if time arises at the official White House ceremony.

Read more about it here: http://www.nsf.gov/news/news_summ.jsp?cntn_id=137247&WT.mc_id=USNSF_51&WT.mc_ev=click



The National Medal of Science is the nation's highest scientific honor. In 1962, President John F. Kennedy awarded the first Medal of Science to the late Theodore Von Karman, professor emeritus, California Institute of Technology. Credit: NSF

Highlights

from the Bulletin of Mathematical Biology

The Bulletin of Mathematical Biology is the official journal of the Society for Mathematical Biology. The Bulletin is devoted to research at the junction of computational, theoretical and experimental biology. Articles offer a combination of theory and experiment, documenting theoretical advances with clear exposition of how they further biological understanding. Its aim is to be of major interest to theorists and experimental biologists alike.

The Bulletin has numerous Highly Cited Papers indexed at the Essential Science Indicators of Institute for Scientific Information (Thomson Reuters). The Institute for Scientific Information defines highly cited papers as those which received enough citations to place them in the top 1% of its academic field based on a highly cited threshold for the field and publication year. Here we present a highlight from one articles currently listed in the Highly Cited Papers indexed at the Essential Science Indicators: Chad M. Topaz, Andrea L. Bertozzi, Mark A. Lewis (2006). *A nonlocal continuum model for biological aggregation*. *Bulletin of Mathematical Biology* 68 (7), 1601-1623.

The corresponding author of this paper is Chad M. Topaz provides us a brief summary of the paper: From bird flocks to insect swarms to fish schools, groups of social organisms may capture one's interest both for their ecological consequences and for their ability to arrange into striking patterns. Benefitting from the legacy of population continuum models established in seminal work of Okubo,

Keller, Segel, Edelstein-Keshet, Mogilner, and others, this paper proposes a nonlocal partial integro-differential equation model for biological aggregation. The primary model inputs are short-range social repulsion described with nonlinear diffusion and long-range social attraction described with a convolution-type term whose kernel decays with distance. These inputs are minimal, but retain essential features of organisms? sensing and behavior. The model produces compactly supported clumps of population with steep edges. In the limit of large population sizes, solutions approach a constant internal density whose value is independent of population size, reflecting the tendency of many organisms to maintain a preferred spacing over large variations number. The model and its generalizations have been the subject of intensive subsequent applied analytical work investigating existence, uniqueness, regularity, global attractors, and properties of steady states, as well as further biological modeling.



Chad M. Topaz is a Professor of Mathematics in Department of Mathematics, Statistics, and Computer Science at Macalester College, St. Paul, MN, USA. You can learn more about him by visiting his website: <http://www.chadtopaz.com/>



The 7 Habits of Highly Effective Writers

by DAPHNE GRAY-GRANT

Have you ever wondered why some people write easily and fluently, while others struggle and strain as if trying to squeeze a 185-lb body into a size six pair of jeans? In 30 years at this trade, I've noticed that effective writers tend to share seven traits. So, with apologies to Stephen Covey, here is my own list of 7 habits worth adopting.

Effective writers...

1) Separate the writing and the editing processes. When they write, they write, without worrying about the quality of their work. Writer/director Cecil Castellucci says: "The best flowers are fertilized by crap." Remember this and give yourself permission to write a really crummy first draft. Editing is a job for later. That's when you'll have plenty of time to rearrange big chunks of text, monkey around with sentence structure, obsess over word choice and fix punctuation.

2) Focus on the interesting. Effective writers (and speakers) always tell lots of stories. If they have to communicate something "theoretical," they illustrate it with real life examples and anecdotes. They know that human beings don't just crave food – they are also starved for stories.

3) Tap into the power of metaphor. As metaphor expert Anne Miller likes to say, "metaphors lead to instant understanding." There are at least three metaphors in this short newsletter (can you find them all?)

4) Do adequate research. There is nothing more painful than trying to write when you have nothing to say. Effective writers understand that good research is all about asking interesting questions – of themselves, of the books, websites and reports they read and of anyone they interview. And this needs to be completed before any writing can begin.

5) Learn from the writing of others. Effective writers understand that they are lifelong apprentices. They learn by reading – constantly. Note: this is not just passive, "flip-through-a-thriller-while-sitting-on-the-pool-deck" kind of reading. This is active sit-up-and-pay-attention-to-technique dissection – similar to what a scientist would do in a lab. You won't want to read this closely all the time, of course (it's work – although fun work, to my mind). But effective writers do some of this every week.

6) Write in small bursts. Creative work doesn't require oodles of time. That first draft you need to write? It's best done in dribs and drabs, a little bit at a time. Instead of procrastinating, effective writers persuade themselves to write a little each day, no matter how frazzled and frantic they feel. (Editing, on the other hand, usually needs space, time and quiet.)

7) Read their work out loud. Language isn't just meaning – it's also music. The most effective writers can often be found sitting by the computer keyboards, madly whispering to the screen, repeating their words back to themselves. Yes, it looks kooky and coworkers may become alarmed. But effective writers don't care. They do it because it works.

Follow these 7 habits and watch your writing improve dramatically.



Daphne Gray-Grant is a Publication Coach. Her website is: <http://www.publicationcoach.com/>. She provides a free weekly newsletter with writing tips and advice. Her email is: daphne@publicationcoach.com.

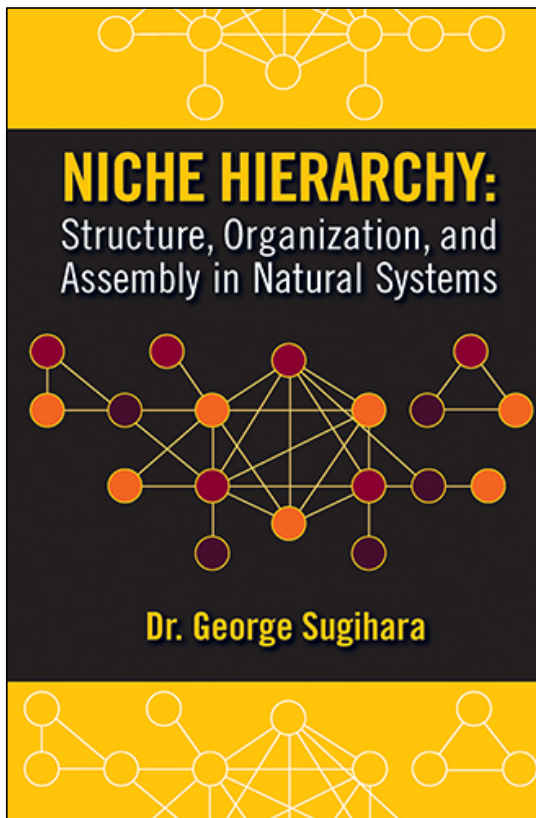
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New Job Postings

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