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THE 2016 JOINT MEETINGS OF THE SOCIETY FOR  
MATHEMATICAL BIOLOGY & THE EUROPEAN  
MATHEMATICAL & THEORETICAL BIOLOGY  
NOTTINGHAM, 11<sup>TH</sup>-15<sup>TH</sup> JULY 2016

## Letter from the President



I would like to first thank the membership of the Society for Mathematical Biology for the honor and privilege of serving as the 19th President of the Society. I would also like to thank all of the Society for Mathematical Biology Past-Presidents, as well as other members of the Society, whose leadership has influenced and shaped my career. The Society has played a central role in nurturing its members through its meetings, publications, mentoring and educational programs, and service opportunities.

Over the years, I have watched organizations struggle to move with time while maintaining the focus on their core mission. The Society for Mathematical Biology has always been a society that manages this difficult balancing act thanks to the valuable service of its members. For this reason, the Society has continued expanding with a healthy pace. Last year we observed an increase of 65% in student membership, thanks to the hard work of our Past-President, Fred Adler, the chair of the membership committee, Heiko Enderling, and the Board of Directors. In addition, the total funds of the Society have increased by 8.40%. The official journal of the Society, the *Bulletin of Mathematical Biology*, has become the mathematical and theoretical biology journal with the largest number of Highly Cited Papers indexed at the Essential Science Indicators published by the Institute for Scientific Information (Thomson Reuters). This is great news for the future of our Society and field.

The membership is fortunate that we have active, practicing mathematical biologists who are willing to generously share their time, talents and attention with the Society for Mathematical Biology. Dr. Renee Fister (Murray State University) our outgoing treasurer has modernized the society accounting system and consolidated our finances. Our outgoing Education Committee Chair, Dr. Elsa Schaefer (Marymount University), has increased the participation of mathematical biology educators at the annual meetings. The Educational Symposia and Workshops are now a staple of our annual meetings. I hope you take the time to thank them personally for their great work. You can also welcome our new leaders: Dr. Lisette de Pillis (Harvey Mudd College) is now our new Treasurer and Dr. William J Heuett (Marymount University) is the new chair of the Education Committee.

The Board of Directors and Society committee members care about many things, including education, the preservation of scientific rigor in our field and the importance of helping build and sustain an academic society and field that are driven by merit and totally committed to open science. During my Presidency, I will be working with the Board of Directors on new initiatives to advance and promote the careers of its members, and to represent and integrate more biological fields at our annual meetings. I will also provide updates to the mathematical biology community and our membership through the SMB Digest and our mailing list. If you are interested in volunteering to serve in the Society committees, please do not hesitate to contact me.

The Society cannot be effective without a large, active and engaged membership - ranging from undergraduate students to senior investigators in academia, government, and the private sector. All of us who are associated with our Society shoulder the vital responsibility of championing the fields of mathematical and computational biology so that successive generations may inherit the grit and substance given to us by our first presidents and Society members. I close by affirming my delight to serve as your president and work with you over the next two years.

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*Santiago Schnell (E-mail: [schnells@umich.edu](mailto: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.*



## 2016 SMB Outreach Fund Applications Open

The SMB Outreach Fund provides financial support to individuals and organizations in order to enable them to run a mathematical biology-based events and activities for public audiences at the 2016 USA Science Engineering Festival (<http://www.usasciencefestival.org/>).

Through the fund we can support our members to engage with different audiences and provide people with an entry point into mathematical biology. Through the Outreach Fund, we aim to encourage and support the development of projects that raise awareness of the place of mathematical biology in people's everyday lives, especially those not already interested in mathematics or biology, and/or develop the science communication skills of people who are already highly trained in mathematical biology.

We can only accept applications from individual members in good standing with the Society for Mathematical Biology. Applications from student members are strongly encouraged. Organizations can apply if the individuals directing the activity are Society members. Applicants must be 18 years of age or older at the time of submitting their application.

Applications should be submitted via email to [adler@math.utah.edu](mailto:adler@math.utah.edu). Please ensure that you have read our eligibility and criteria before completing your application form. If you have any queries about the application process, please get in touch with Fred Adler, SMB Past-President, E-mail: [adler@math.utah.edu](mailto:adler@math.utah.edu).

The deadline for application is **November 1st, 2015**. For more information, please visit SMB Outreach Fund: <http://www.smb.org/resources/education/outreachfund.shtml>.

SMB first participated in the USA Science & Engineering Festival in April 2014. SMB's booth showcased the fusion of mathematics, computer simulation, and social insect ecology. The goal was to show how mathematics can be used to understand complex biological processes. Participants were asked to think like an ant as they played three boardgames demonstrating how ant colonies think, search their environment, and fight. The most popular boardgame demonstrated how social insects, like proteins in a cell, collectively produce complex behavior despite relatively simple individual behaviors.

To read the full report on the 2014 SMB participation in the USA Science & Engineering Festival check out page 11 in the MAY2014 issue of SMB Newsletter: <http://www.smb.org/publications/newsletter/vol27no2.pdf>



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# The 2015 SMB Annual Meeting Report from the Local Organizers

by YI JIANG

The 2015 Annual Meeting for the Society for Mathematical Biology (SMB2015) was held on the campus of Georgia State University in downtown Atlanta, Georgia, from June 30 to July 3, 2015. The conference was hosted by the Georgia State University, its Department of Mathematics and Statistics, and the Neuroscience Institute. The local organizing committee included Yi Jiang (chair), Igor Belykh, and Andrey Shilnikov of Georgia State University, Eberhard Voit and Howie Weiss of the Georgia Institute of Technology, Ilya Nemenman and Alessandro Veneziani of Emory University, Meghan Burke of Kennesaw State University, Arni Rao of Georgia Regents University, and Ying Xu of the University of Georgia. Georgia State University, Georgia Tech, Emory, Georgia Regions University, as well as Springer and Elsevier, co-sponsored the event. The meeting drew 463 attendees from 26 countries around the world. The conference theme was "Disease, Medicine, Public Health, and Systems Biology." This theme was prominently featured in multiple plenary talks and many sessions devoted to topics such as modeling cancer, neurodynamics, cardiac dynamics and epidemiology. Seven plenary talks were delivered by: Andre Levchenko of Yale University on "Computation and Decision Making by Single Cells: Noise and Organization of Signaling Networks;" Eberhard Voit of Georgia Tech on "Weaving Biological Snapshots into Stories Through Mathematical Modeling;" Alissa Weaver of Vanderbilt University on "Extracellular Matrix-Tumor Interactions;" Eve Marder of Brandeis University on "Degeneracy in Neuronal Oscillators;" Michael Savageau of UC Davis on a "Mathematical Framework for Characterizing the Genotype-phenotype Map and its Evolution;" G. K. Ananthasuresh of the Indian Institute of Science on "Grasping Biological Cells;" Okubo Awardee Joshua Plotkin of the University of Pennsylvania "On the role of epistasis in molecular evolution;" and John R. Jungck of the University of Delaware on "Radical Equations: Engagement, Empowerment, and Esteem." Five special sessions were

designed to encourage biologists and public health workers to add a 'reality check' to the mathematical biology community. Sixty-five invited minisymposia, twenty-five contributed sessions, as well as a poster session with eighty-five posters, covered topics in ecology, epidemiology, cancer, neurodynamics, systems biology, immunology, modeling methodologies, and education. A particular highlight of the conference was a strong focus on interdisciplinary education in biomathematics with 7 invited sessions.

A career development workshop organized by Robert Smith? and Meghan Burke took place on June 29th, right before the conference. In addition to presentations on topics such as writing a dissertation, getting a job, and the tenure process, the workshop also included a panel discussion on non-academic careers, grant writing, and time-management. Panelists included Mary Ann Horn from NSF, Paul-André Genest from Elsevier, Craig Giroux from NIH, and Abba Gumel from Arizona State University. The panel session was moderated by Robert Smith?. The workshop drew a big crowd of over 80 people, most of whom were students and early career bio-mathematicians. Complementing this workshop was a mentoring program with one-on-one matching between senior mentors and young faculty. A special presentation by Craig Giroux on funding opportunities and grant review procedures also attracted a large audience.

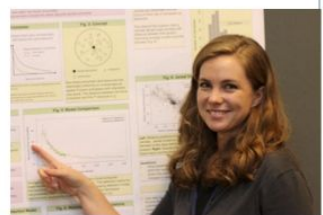
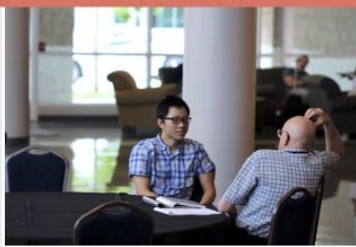
Several prizes were awarded at SMB2015: the 2015 Akira Okubo Award was awarded to Joshua Plotkin, and the 2015 Arthur T. Winfree Award went to John Rinzel. Moreover, two Best Paper prizes were awarded. The 15th Bellman Prize was awarded to Piero Poletti, Marco Ajelli and Stefano Merler for their paper titled "Risk perception and effectiveness of uncoordinated behavioral responses in an emerging epidemic", published in *Mathematical Biosciences* in August 2012. A new IMA Best Paper prize from *Mathematical Medicine and Biology* was given to Angela Jarrett, Nick Cogan, and Mark Shirtliff, for their paper entitled "Modeling the interaction be-

tween the host immune response, bacterial dynamics and inflammatory damage in comparison with immunomodulation and vaccination experiments", published in May 2014.

Finally, the presidential transition of the society took place at SMB2015. The outgoing president,

the scientific committee and the many local student volunteers for their hard work making the conference possible, and all of the attendees for making the conference a great success. Links to the complete conference program, attendee list, abstracts, and photos are available at <http://math.gsu.edu/~smb>.

# PHOTOS FROM THE 2015 SMB MEETING





## Announcing the 2016 Annual Joint Meetings of SMB & ECMTB

<http://www.ecmtb2016.org>

by MARKUS OWEN

The 2016 Annual Meeting of the Society for Mathematical Biology (SMB) will be hosted by the Centre for Mathematical Medicine and Biology 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 (ESMTB, <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) and Johan Paulsson (Harvard University, USA). John Rinzel (NYU, USA) will deliver the SMB Winfree Prize lecture. Minisymposia, contributed talks and posters will be invited to cover diverse themes in mathematical and theoretical biology and medicine.

Nottingham is a vibrant city centrally located in the United Kingdom, and easily accessible by road, rail and air travel. Most conference activities will be held on the beautiful University Park Campus, located two miles from the city centre, and accommodation will be available on campus in halls of residence. A new tram line and frequent buses link the campus and city centre, with its Castle (at the heart of the Robin Hood legend and starting point for the English Civil War), the "Oldest Inn in England" (with

its own caves), galleries, theaters, shopping, restaurants, hotels and nightlife. The conference dinner will be held at Kelham Hall, a magnificent Victorian country house, built in 1863 and set within a large expanse of gardens and parklands.

Proposals for minisymposia with topics of significant current interest and importance at the interface of mathematics and biology, including all areas of the life and medical sciences, are welcome. Minisymposium submissions are due by **December 18<sup>th</sup>, 2015** and Contributed talk and poster submissions are due by **February 14<sup>th</sup>, 2016**.

Please visit the website: <http://www.ecmtb2016.org> for more details. Questions regarding the conference can be directed to: [ecmtb2016@nottingham.ac.uk](mailto: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 Eglen, 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](mailto:Markus.Owen@nottingham.ac.uk)  
[www.nottingham.ac.uk/cmmb](http://www.nottingham.ac.uk/cmmb)

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## Highlights From BMB

The Bulletin of Mathematical Biology (BMB) is the official journal of SMB. It promotes the dissemination of research at the interface between the mathematical and biological sciences. Articles published in BMB offer a combination of theory and experiment, documenting theoretical advances with clear exposition of how they further biological understanding.

The Bulletin is with the largest number of 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. The Bulletin has published 1.5 times more highly cited papers than the Journal of Theoretical Biology, 12 times more than Theoretical Biology and Medical Modeling and 23 times more highly cited papers than the Journal of Mathematical Biology or BMC Systems Biology.

The Society is building a collection of Highly Cited Papers published in the Bulletin. Here we present a highlight from one of those articles:

Matthew J. Simpson, Benjamin J. Binder, Parvathi Haridas, Benjamin K. Wood, Katrina K. Treloar, D.L. Sean McElwain and Ruth E. Baker (2013). Experimental and modeling investigation of monolayer development with clustering. *Bulletin of Mathematical Biology* 75 (5), 871-889.

The corresponding author of this paper is Matthew Simpson, who is Professor of Applied Mathematics, and Australian Research Council Future Fellow at the School of Mathematical Sciences in Queensland University of Technology. Professor Simpson provides us a brief Summary of the paper:

Standard mathematical models used throughout mathematical biology, including ordinary differential equations and partial differential equations, rely on invoking a mean field assumption. This amounts to assuming that individuals within the population interact with each other in direct proportion to the average population density. The formation of patterns and structure in population dynamics, such as clustering and patchiness, directly challenges this fundamental assumption that underpins all mean

field models used throughout mathematical biology. Theoretical developments have introduced a new class of models, known as moment dynamics models, which account for the dynamics of individuals, pairs of individuals, triplets of individuals, and so on. Moment dynamics models provide a way of approximately accounting for the formation of spatial structure, such as clustering and patchiness. Although moment dynamics models are established in the ecology and disease transmission literature, they have not been applied to modeling collective cell behavior, such as wound healing and malignant spreading processes. In this article we present a first attempt at calibrating a moment dynamics model and a traditional mean-field model to new experimental observations describing the formation of a monolayer of cells from an initially disperse population of cells. We deal with two different cell types: fibroblasts, and a breast cancer cell line. The fibroblast cells grow to form a confluent monolayer, and our visual interpretation of the experiments indicates that the monolayer forms without clustering. In contrast, the breast cancer cells exhibit a high degree of clustering as the monolayer forms. Calibrating both a mean field and a moment dynamics model to the data confirms that both models give similar parameter values for the non-clustering fibroblast cells. This indicates that the more complicated moment dynamics model is unnecessary when spatial structure is absent. In contrast, a similar calibration procedure for the breast cancer cell line leads to very different parameter values for the mean field model and the moment dynamics model. This implies that the mean field model is inappropriate for the observations involving clustering. In summary, our study suggests that mean field models ought to be applied with care because the underlying assumptions inherent in these models are not always satisfied. This is an important topic for the mathematical biology community because mean field models are widely used to study collective cell spreading processes without checking whether the mean field assumption is valid. Professor Matthew Simpson's website is: <http://www.mj-simpson.com/>

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# Recent Conference Reports

SMB is very pleased to share summaries of some of the mathematical biology meetings that took place over this summer. In this issue there are five reports from SMB members :

## **The International Conference on Micro and Macro Systems in Life Sciences Bedlewo, Poland June 8 - 13, 2015**

### **Urszula Ledzewicz & Avner Friedman - Recipients of The SMB-WOC Funds**

It is our pleasure to write the report of another interesting scientific event made possible by the co-sponsorship of the Society for Mathematical Biology. The International conference "Micro and Macro Systems in the Life Sciences" took place June 8-13, 2015 at the Stefan Banach International Mathematical Center of the Institute of Mathematics of the Polish Academy of Sciences, ... read more here : [http://www.smb.org/SMB2015/Bedlewo\\_Report.pdf](http://www.smb.org/SMB2015/Bedlewo_Report.pdf)

## **My Experience at The 2015 SMB Annual Meeting**

### **Georgia State University, Atlanta, June 30 - July 3, 2015**

#### **Katy Gaythorpe - Recipient of Landahl-Busenbergl Travel Award**

This year the annual conference for the Society for Mathematical Biology was held in Atlanta, Georgia on June 30 - July 3. We had a beautiful, sunny week for it, bar the occasional thunderstorm, and I definitely enjoyed the morning walks from the suburbs to GSU where the conference took place ... read more here: [http://www.smb.org/SMB2015/Katy\\_Report.pdf](http://www.smb.org/SMB2015/Katy_Report.pdf)

## **IX Congresso Latino-Americano de Biomatemática SOLABIMA 2015**

### **Botucatu, Brazil, July 13 - 17, 2015**

#### **Paulo F. A. Mancera - Recipient of The SMB - WOC Funds**

The IX Congresso Latino-Americano de Biomatemática (IX Latin American Conference on Biomathematics) - SOLABIMA 2015 was held at the Institute of the Biosciences, UNESP, Botucatu, Brazil. SOLABIMA included thirteen plenary talks and four short courses. ... more on this workshop can be found here: [http://www.smb.org/SMB2015/Paulo\\_Report.pdf](http://www.smb.org/SMB2015/Paulo_Report.pdf)

## **CompuCell3D and SBW 11th User Training Workshop**

### **Indiana University, Bloomington, IN, USA, August 9 - 15, 2015**

#### **Khaphetsi Joseph Mahasa**

The workshop on developing multi-scale and virtual tissue simulations with CompuCell3D and Systems Biology Workbench (SBW) was held at the Indiana University, Bloomington, USA, on August 9-15, 2015. The event, organized by Dr. Maciej Swat from Indiana University (IU), brought together more than twenty participants representing wide range of biomedical expertise .... more on this workshop: [http://www.smb.org/SMB2015/Mahasa\\_Report.pdf](http://www.smb.org/SMB2015/Mahasa_Report.pdf)

## **Beg Rohu Summer School 2015 - Statistical Physics, Biology, Inference and Networks**

### **Beg Rohu, France, 24 August - 5 September 2015**

#### **Linus Schumacher - Recipient of The SMB Travel Fund**

The Beg Rogu Summer School, also known as "Wind and Physics" describes itself as an atypical summer school, combining physics lectures and sailing lessons on the French peninsula of Quiberon ... more here: [http://www.smb.org/SMB2015/Schumacher\\_Report.pdf](http://www.smb.org/SMB2015/Schumacher_Report.pdf)



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# Mathematical Biology: A Personal Journey

Ami Radunskaya



I've always loved watching the patterns of change: how a fern unfolds, how the sky changes as the sun sets, how a fugue evolves. I've always loved the patterns in numbers: how they pile up in a particular way as they are added together, how simple geometric shapes can be scaled and glued together to make organic fractals, how simple rules applied repeatedly can result in fabulously intricate constructions. I can point to some early milestones and guides along my current journey: my father brought home conic sections for us to play with, instead of the usual rectangular blocks; I found a slide-rule gift-wrapped under the tree one Christmas; my uncle Jack told me about Scriabin's fascination with color, number and musical tones. I asked myself: can numbers describe everything? Are music, mathematics, growth and evolution articulations of the same laws? These questions led me first to a serious love affair with music, a ten-year career as a profes-

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<sup>1</sup>Math major, Pomona College, Ph.D. in mathematics from UC Berkeley, followed by a long and distinguished career at NASA's Jet Propulsion Laboratory.

sional 'cellist, then an undergraduate math degree at Berkeley, followed by a Ph.D. from Stanford in ergodic theory. Eventually I found myself as an Assistant Professor at Pomona College where I tried to fill the shoes of my mentor, Ken Cooke, a pioneer in mathematical biology.

One of the classes I taught that first year was "Mathematical Modeling". I asked Ken Cooke, my mentor and the wonderful mathematician whose shoes I would try to fill, "What am supposed to do in this class?" He gave me plenty of concrete advice, but warned me that "you'll see: mathematics can be used to solve just about everything". I learned along with the students, who modeled swimming fish, the collapse of civilizations and segregation in churches.

My department chair walked into my office one day: "We just got a call from an alum, Tom Starbird <sup>1</sup>. His oncologist needs an explanation of chaos theory." New at the job and eager to please, I hiked it over to St. Vincent's Hospital in downtown L.A. where a dozen doctors in white lab coats were gathered in the basement cafeteria grappling with a paper describing a mathematical model of cancer growth. They were stumped by descriptions of growth dynamics that deviated from the simple exponential growth models they had learned in medical school. Eager learners, they quickly picked up the ideas of self-limiting growth and competition models. Won over by the group's enthusiasm, I joined M.O.M. (Mathematics Of Medicine), a study group led by Dr. Charles Wiseman, and fairly soon we came up with our own mathematical models of tumor growth. We met monthly for over eight years; along the way we explored scaling laws (using data from Chuck Wiseman's nephew's pet lizards), model selection, Bayesian analysis, agent-based models, network analysis and experiments on binding kinetics. In 1999 I asked my colleague from Harvey Mudd College, Lisette de Pillis, to join us. I believed that Lisette's numerical expertise would be valuable in implementing and analyzing mathematical models of cancer dynamics. I was right: we have been close collaborators ever since.

From the outset, the focus of M.O.M. was the relatively new field of immunotherapy: harnessing the immune system to fight a tumor. I knew that

our models would be meaningless unless we could communicate with medical practitioners outside of M.O.M. We decided to present our latest model at the Society for Biotherapy's annual meeting. At this conference I met James Mulé, now a Vice President of Applied Science at Moffitt Cancer Center. Through his encouragement, I began to believe that we mathematicians *can* make a real contribution to the development of clinically relevant treatments. Moffitt now has an Integrated Mathematical Oncology Center, populated by math biologists. Way to go, Jim! Around this time (2005), we were also able to publish one of our models of tumor-immune interactions in *Cancer Research*, "the most frequently cited cancer journal in the world"<sup>2</sup>. In this paper, we present a model that Chuck Wiseman has dubbed the "DePillis-Radunskaya Law". I am proud of this paper because, despite the differences in communication styles between the mathematics world and the medical world, we persisted in our attempts to adapt, and were ultimately successful in appeasing the referees. Since 2009 *Cancer Research* makes an intentional effort to publish articles in *Mathematical Oncology*. Way to go, *Cancer Research*!

A few years earlier, personal reasons led me to New Zealand. I immediately fell in love with Aotearoa, the "Island of the Long White Cloud", and decided to spend my next sabbatical there. And so began a fruitful collaboration with Professor Sarah Hook, an Immunologist at the University of Otago. Sarah has taught me about the deep mysteries of the immune system, and the difficulty in finding a quantitative description of the complex immune cascade. We have worked together for the past 10 years on models of immune kinetics, and on the design of effective cancer vaccines. In 2007, Sarah and I organized a workshop at Otago focusing on articulating and solving mathematical problems in biomedicine. This workshop has led to many new collaborations, most recently studying the delivery of drugs through the blood-brain barrier. My new collaborators include pharmacologists, neurologists, biochemists and hematologists. I have spent two sabbaticals at Otago, and during each visit I discover new questions in biology and medicine that can be attacked with a mathematical toolbox.

I am attracted to mathematical biology because it is collaborative and interdisciplinary by necessity. I am constantly learning new things and meeting people in fields I know very little about. While I started out in dynamical systems, I have had to learn programming, statistics, and machine learning. I use stochastic, deterministic, continuous and discrete models. I use ODEs, PDEs and DDEs - whatever it takes. I love brainstorming with colleagues about approaches to a problem, and then implementing some of those approaches. I want to share this excitement with everyone, so I spend a significant amount of time working with younger mathematicians. I am fortunate to work each year with talented undergraduate researchers: many of them are motivated by the biological problems to learn new mathematics. One of the most rewarding experiences I have had was organizing WhAM!, a workshop for Women in Applied Mathematics (the "h" is silent). This five-day workshop was supported by the Institute for Mathematics and its Applications (IMA) in 2013. My co-organizer, Trachette Jackson, and I brought together 47 women mathematicians to work on 9 problems in biology and medicine. A monograph containing results from the workshop has just been released by Springer<sup>3</sup>. The feedback from the group was: "fun and fruitful". Since then, two more WhAM! workshops have been held, and I hope that there will be many more.

Most problems in mathematical biology are hard. There is too much data, but not enough of the right kind. The questions are too big, and the tools too clumsy. There is a huge gap between the vocabulary of the biologist or the clinician, and that of the mathematician. There are unavoidable uncertainties and as many variants as there are individuals. But these challenges make our lives more exciting: there are so many problems, so many things to try! I encourage you to sit down with a biologist or a doctor, particularly someone who insists that they "forgot all the maths they ever knew". Take your time: you will both come out the wiser. I am grateful to those who had patience with me.

For more information see  
<http://pages.pomona.edu/~aer04747>

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<sup>2</sup><http://cancerres.aacrjournals.org/site/misc/about.xhtml>, August, 2015

<sup>3</sup>*Applications of Dynamical Systems in Biology and Medicine*, Springer (2015) ISBN: 9781493927821

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# The Future of Mathematical Biology

*Tae Jin Lee*

*Augusta University, Augusta  
PhD Student of Prof. Arni S.R.  
Srinivasa Rao*



## **What attracted you to mathematical biology?**

The most attractive feature of mathematical biology for me is its approach in handling biological information. The biological centered problem solving method inspires me and model building a joyful process. I first learned about mathematical biology at second year of my biostatistics PhD program as I was taking mathematical epidemiology class taught by Dr. Arni Rao. I fell in love with the subject instantly. It is really beautiful and powerful. I was astounded to find out the ability of such simpler mathematical formulas to explain complex phenomena. Also I really like the diversity: I believe that mathematical biology is a melting pot of many mathematical and

biological disciplines.

## **What is your current research project?**

I am investigating effect of eCD4-Ig, a new molecule, on HIV therapy for possible cure. The therapeutic vaccine methods for HIV is in renaissance now, and it is important to study the most potent HIV neutralizing compound, eCD4-Ig.

## **What specific areas are you interested in investigating?**

I am interested in immune system, and how to apply the knowledge to translate into clinical practices. Starting from studying their dynamics and possible new mechanism, it is very fascinating to study the effects of vaccination, effect of gene therapy, effect of immunotherapy, etc. Another interest is the one health approach on neglected tropical diseases (NTD) and zoonosis. Traditionally, our focus centered on human health only; however, emergence of zoonosis such as SARS, Ebola, and MERS has broadened our attention to incorporate the animals and environmental health. This is the one health approach, and I am interested in to apply this approach to study zoonosis and NTD.

## **What do you hope to do after graduation?**

I would like to get into postdoctoral position after graduation, and continue research.

## **What advice will you give to an undergraduate interested in a mathematical biology career?**

Mathematics is bread and butter here, thus I would like students, especially those whom studying biology, to take as many mathematics classes as possible so that they can have many tools under their belts. For mathematics students, I would like them to take several biology classes since I find out the amount of knowledge of biology we handle is not trivial.

## **What inspires you scientifically?**

Homeostasis is inspiring to me. Even the smallest level of biological system, such as biochemical systems are extremely complex and it is awe-inspiring that proliferation of a living organism requires tons of those systems to be finely tuned and works together in harmony. Maintenance of such an overwhelmingly complex system amaze me. If we turn

eyes on population and ecological level data, then similar phenomena are happening, and the power and ability of biological system on maintaining itself is very impressive for me.

### **Why did you join the Society for Mathematical Biology?**

The reason I joined the society is that I think networking with people with same interest is important. Other than preventing me to become a frog in a well, it is enjoyable to know what other people with similar interest are doing. I had participated in the 2015 SMB annual meetings held in Atlanta, GA, USA, which was first conference experience for me, and had great time. Also, I am very thankful for SMB for awarding me the Landahl-Busenbergl Travel award (\$500) to attend this meeting.

### **Prof. Arni S.R. Srinivasa Rao, Tae Jin's current PhD advisor, says:**

Tae Jin Lee has shown exceptional maturity in the classroom as well as a comprehensive understanding of the courses that I taught, namely, Stochastic Process and Mathematical Epidemiology. He has the right blend of biology, statistics and mathematics backgrounds. He started his PhD dissertation work with me during his third year (in Fall 2014) after completing two years of required course work. Tae Jin has impressive technical abilities in mathematical model building as well as an understanding of the biological underpinnings of the content. What impresses me most is that Tae Jin can comprehend the biological information that is needed before he begins to think about the mathematical techniques to address key research questions. He is also excellent at statistical data analysis and using computing software. All together this makes him a candidate for a productive career in mathematical biology.

For his PhD dissertation, Tae Jin has chosen a

topic that is cutting-edge in the field of HIV immunology. He has begun to study the HIV virus dynamics with respect to the latest experimental results on HIV binding to the eCD4-Ig molecules and CCR5 proteins that were published by clinicians in early 2015 and 2014 in leading journals such as Nature. He will collaborate with me in developing models to understand the impact of the new strategies to arrest the virus spread in the host through incubating eCD4-Ig in the human body. These models will assist in HIV management and HIV vaccine strategies. He is focusing on both ODE and PDE type of models with a blend of Markov process in addressing questions in his dissertation

In addition to this, he has previously studied the role of human and animal interactions in spreading certain diseases, for example, the spread of Schistosoma within snails and in humans. He built and analyzed the model by considering a case study for the Tanzanian data. He will take this project to the next level by incorporating the impacts of therapy in controlling the spread of Schistosoma. I am very excited to look forward for Tae Jin Lee's research career in general and PhD dissertation productivity in particular.



**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:

Russ Rockne (russrockne@gmail.com)



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# Clean-Room Writing

by MARC ROUSSEL

## *How to commit plagiarism*

Over the last few years, I have noticed more and more problems with student plagiarism. I have spent a lot of time thinking about where these problems come from. I do not generally think that they are due to deliberate attempts to cheat. Rather, I think that modern tools create situations where plagiarism becomes almost inevitable unless you are both conscious of the issue and careful. It is very important to be aware that plagiarism is considered a serious issue in academia. The U.S. National Institutes of Health classifies plagiarism a form of scientific misconduct, which can have serious consequences for the individual, their institution, and science. The NIH defines plagiarism as "the appropriation of another person's ideas, processes, results, or words without giving appropriate credit."<sup>4</sup> For this reason, I think it is important to address it. In this article, I suggest a method for avoiding plagiarism that I think most of us should adopt. It is not a panacea, but it is better practice than what many students are doing right now.

Plagiarism has both gross and subtle forms, so we should start by examining in more detail what plagiarism is. My thinking has been strongly influenced by a great document produced by the Office of Research Integrity of the U.S. Department of Health and Human Services<sup>5</sup>

The first and most obvious form of plagiarism involves simply cutting and pasting from a source. Most people would agree that is wrong, although a remarkable number of students appear not to entirely get that. When we think of plagiarism as cheating, this is generally what we are thinking about.

The second form, which often has a very similar appearance, is using someone else's words in your text. While this sounds like cutting and pasting, it often happens in a different way, often when we write something while we are looking at a source, perhaps, we think, so that we get the details right. Peo-

ple who commit this form of plagiarism are often not even aware they are doing it. The net effect though is text that generally looks an awful lot like the original source, with only a few words changed here and there. If you do not believe that you are prone to this problem, try reading the Wikipedia's historical summary of the third law of thermodynamics.<sup>6</sup> (I picked this topic because few people know much about it. Plagiarism becomes all the more likely when writing about topics with which one is not intimately familiar.) Having read the article, immediately try to write your own text on this topic. While you are writing, keep the Wikipedia article open and look back at it for details from time to time. Most people find it very difficult to write sentences and paragraphs that differ significantly from the original text under these conditions. This is plagiarism.

If you somehow avoid writing sentences that look like those in the original text, you are likely to at least mimic the structure of the original text, with the same facts presented in the same order. This is the third and most insidious form of plagiarism. It is hard to detect, and people who commit this form of plagiarism will often deny vehemently that they have done anything wrong. However, when you do this, you have not told us what you think about a subject. You have just told us what the writer of, in this case, the Wikipedia article thinks. You may have done it in different words, but you did not organize the facts yourself, which is the key difference between original writing and plagiarism. There are occasions when it's appropriate to write something that is organized like someone else's coverage of a topic. I will come back to this in a later blog post.

Thinking about the exercise I proposed above, I would suggest that there are at least three distinct issues leading to unwitting plagiarism:

1. Writing while looking at a source, or immediately after reading a source. It is extremely difficult to come up with your own words and

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<sup>4</sup>[http://grants.nih.gov/grants/research\\_integrity/research\\_misconduct.htm](http://grants.nih.gov/grants/research_integrity/research_misconduct.htm)

<sup>5</sup><http://ori.hhs.gov/plagiarism-3>

<sup>6</sup>[http://en.wikipedia.org/wiki/Third\\_law\\_of\\_thermodynamics#History](http://en.wikipedia.org/wiki/Third_law_of_thermodynamics#History)

an original way to organize the facts when you are doing this. The perfectly good words and organization chosen by the original writer become "the obvious way" to write about a topic, and it's virtually impossible to break out of that.

2. Excessive reliance on a single source. If you use multiple sources to inform your thinking, the particular way any one author organized his or her writing is much less likely to have a dominant effect on how you write about something.
3. Not having clearly distinguished research, outline, writing and revision phases in the writing process. This is perhaps the greatest failing of modern students in their approach to writing. If you start by doing some research, taking brief notes as you go, then write an outline as a way of organizing your thoughts, then write text based on your outline, and finally go through several rounds of revisions, it becomes much less likely that you will commit plagiarism because you will really be writing about a topic from your perspective, and not from that of another writer.

### ***How not to commit plagiarism***

Having talked about these issues with many students, and given the pervasive nature of information technology, which puts sources at our fingertips almost anywhere, anytime, I have concluded that the best way to fight plagiarism is to adopt what I call clean room writing techniques. Much of what I am going to describe is essentially the research, outline, writing, revision cycle described above. However, I think that we need to go a little farther given how easy it is to unconsciously plagiarize material now.

There is a similar problem in the software industry. Let's say you want to write a piece of software that does the same thing as another existing piece of software. Because software is protected by copyright, you're not allowed to copy someone else's software. You may want to peek, but in the end you have to write your own, original implementation. The way this is done is to have people write the software (even if they previously peeked at the other company's software) in a "clean room", which is a room where you have everything you need to do your work except the other company's software.

Depending on how paranoid you are, such a room might not have a direct connection to the Internet. Sometimes, the people who peek are different from the people who write the new software. Sometimes, peeking is just not allowed.

To avoid plagiarism, you need to write in something like a clean-room environment. What I mean by this is that looking at your sources and writing should not occur at the same time. Your research for whatever you are writing (term paper, thesis introduction, article manuscript, ...) should happen at a different time than the actual composition of text. Text should be written from notes which were not generated by simple cutting-and-pasting from a source. Yes, I know, cutting-and-pasting is quick and efficient. The problem, as explained above, is that you are almost certain to use someone else's words if you do that. When you take notes, write in your own words what you thought was important or interesting in some particular text you are reading.

Once you have composed a draft of a text, you can of course fact-check against the original sources. Having given the ideas your own form by writing a draft without direct access to the sources, you are much less likely to unintentionally borrow someone's words during revision. Note that clean-room writing does not lift the responsibility of citing your sources. Your notes should clearly link content to references, so you should be able to cite your sources as you write. Occasionally, you will need to make a note to yourself to chase down a reference later. You can still add references during the revision stage if you at least note the places in your text that will need to cite sources.

This may seem a bit radical, but I have seen too many students get in trouble for plagiarism over the last few years, and I know that many of them did not intend to plagiarize. It just happened, for the reasons I explained in the first part of this column. Eventually, you can relax this strict approach a little, but if you are an inexperienced writer, it is best to go into the metaphorical clean room anytime you are writing new text.

Prof. Marc Roussel is Professor and Chair of the Department of Chemistry and Biochemistry, University of Lethbridge. His research lies at the intersection of chemistry, biology and mathematics, and he has been an SMB member for some years. This article was adapted from his blog: <http://blogs.ulethbridge.ca/roussel>.

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# NIMBioS: Assessing Core Quantitative Concepts in a Biological Context

by PAM BISHOP & LOU GROSS

Many SMB members involved in undergraduate education have devoted a lot of effort to illustrating mathematical concepts using biological examples. Indeed, one of us (LG) along with Erin Bodine and Suzanne Lenhart wrote an entire textbook (Mathematics for the Life Sciences, Princeton University Press, 2014) that uses life science data and examples to motivate the key quantitative concepts in statistics, probability, linear algebra and calculus. Many major reports on mathematics education suggest that students are more likely to understand and be able to apply quantitative concepts when taught these in a real-world context. Much of the quantitative life science education community has followed this route.

Somewhat surprisingly though, evidence for the effectiveness of learning quantitative concepts through concrete examples over abstract methods is mostly anecdotal. There have been very few studies investigating learning gains in mathematics arising from the use of scientific examples, and some studies provide evidence that the use of examples actually reduces a student's comprehension of general mathematical concepts. We suspect that many SMB members have personal experiences informally indicating that students "get it" when the mathematics is related to something about which they have some intuition, so the mathematics then more readily relates to the students' mental models for the world. However, there is essentially no educational research affirming this.

A first step toward evaluating the potential impact of biological examples on mathematics comprehension is to develop a robust assessment tool designed for college-level math concepts. The National Institute for Mathematical and Biological Synthesis (NIMBioS) has been awarded a two-year, \$299,990 grant from the National Science Foundation to develop such an instrument, a Quantitative Biology Concept Inventory (QBCI). Once developed and evaluated, the QBCI could serve as a model for

measuring the effect of using real-world interdisciplinary examples from other areas of science on enhancing mathematical comprehension in undergraduates.

The first phase of the project involves developing a comprehensive inventory of core quantitative competencies in mathematics for life science majors. Leading experts in both biology and mathematics education, many of whom we expect will be SMB members, as well as undergraduate students in the life sciences will evaluate potential inventory items for inclusion in the final QBCI. The Draft QBCI will then be piloted using two groups of students: those who have been exposed to the mathematical topics in a biological context and those who have taken a more typical mathematics course not driven by real-world examples. Our hope is that the project will provide a unique tool to enhance student learning of mathematical concepts and also provide a novel means to assess different pedagogical approaches to learning mathematics.

Once finalized, the QBCI could be disseminated for nationwide usage in mathematics education, particularly in courses geared toward students interested in the STEM (science, technology, engineering or mathematics) fields. Pam Bishop, NIMBioS Evaluation Manager, will lead the project and other team members are Lou Gross, NIMBioS Associate Director for Education and Outreach Suzanne Lenhart, NIMBioS Education and Outreach Coordinator Kelly Sturner, as well as an outside evaluator. We hope that SMB members who are asked to assist with evaluating potential inventory items will help us with this. NIMBioS is also seeking a Postdoctoral Fellow to help in this effort. The grant has helped fund the new NIMBioS Postdoctoral Fellowship in Science Education Research and Evaluation. More information about the fellowship and NIMBioS Evaluation Services is available at: <http://www.nimbios.org/about/evaluation>.

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# The Future for MBI

by MARTY GOLUBITSKY

The news from MBI (Mathematical Biology Institute) is bad and good. Many of you know about the bad news – I want to tell you the good news and a little about the future.

First, the bad. MBI received a three-year continuation grant from the NSF Division of Mathematical Sciences with no opportunity for additional DMS funding when this grant expires. This news is particularly disappointing for the SMB community, since NSF funding for NIMBioS ends at approximately the same time.

You may ask: Why did the DMS Institute Management Team and the DMS Division Director reach its decision about MBI (and about IMA), especially since the MBI external review committee was enthusiastic about MBI? One reason given by DMS was in the form of a principle. Interdisciplinary institutes (Math + X as they were termed) should be half-funded by X. However, whatever the reason, MBI must live with the DMS decision and plan accordingly.

Second, the good. The funding that MBI did receive will enable the institute to operate at more or less full tilt for the next three years. MBI will continue its emphasis programs, its postdoctoral fellows program, and its education programs. We are in the process of organizing and running four excellent semester emphasis programs: Mathematical Molecular Biosciences (Fall 2015); Dynamics of Biologically Inspired Networks (Spring 2016); Analysis of Complex Data in Biological Systems (Fall 2016); and Growth and Morphogenesis (Spring 2017). We encourage members of the SMB community to take full advantage of these programs.

The MBI postdoctoral fellows program remains active: four post-docs are starting this Fall and MBI will be hiring two-year post-docs for terms start-

ing in Fall 2016. Please tell your students that this opportunity continues and that applications are due in early December. (FYI: So far, MBI has trained more than 80 postdoctoral fellows.) MBI's distributed summer undergraduate REU and Capstone Conference have also been funded (by a separate NSF grant) for the next two years (and applications will be due in late winter). MBI will also be hosting a multi-institutional graduate summer school on the Mathematical Modeling of Infectious Disease Spread.

Finally, the future. We all know that math biology is a large, vibrant, and growing branch of the mathematical sciences and that this growth will continue. The math sciences benefits greatly from contact with the life sciences. Indeed, as noted in the Math 2025 report, interdisciplinary research, coupled with vibrancy in the core, is the key to the success of the mathematical sciences and MBI has been part of this Ohio State has been a strong supporter of MBI and its interdisciplinary research program. Together with the University administration, MBI will explore ways in which MBI's stimulation of research at the interface of the math and life sciences can continue. A variety of funding models are possible, but these models will likely require that MBI becomes more of a directed research center (taking even greater advantage of Ohio State's substantial research strengths) and less of a visitor institute (which is the DMS Institute mold). However, for at least the next three years, MBI will continue to promote visitor institute research (spurred by contacts formed at institute programs and relying on serendipity and curiosity-driven research), and it is quite likely that MBI's track record will help it to promulgate this approach into the future.



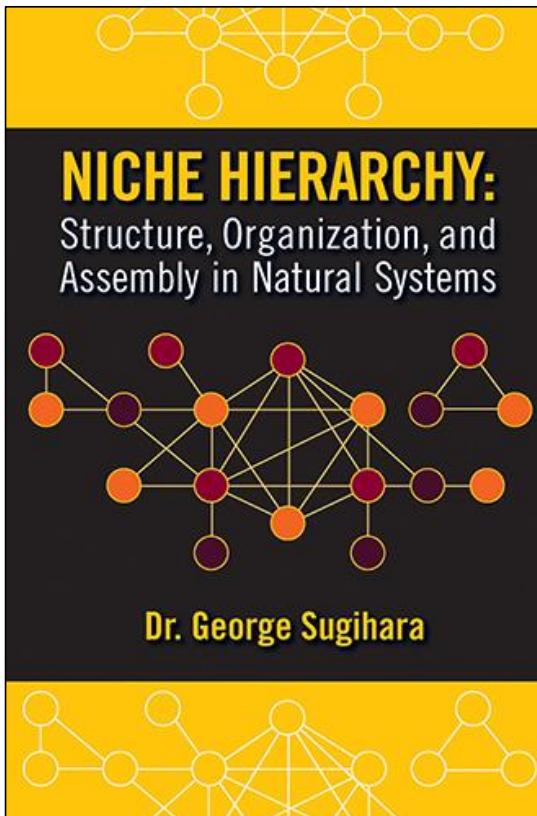
## Announcement - New Book

**COMING OCTOBER 2015**



### **NICHE HIERARCHY: Structure, Organization, and Assembly in Natural Systems**

**This often-cited, historic and pioneering work by Dr. George Sugihara is finally available in print!**



ISBN: 978-1-60427-128-7, Hardcover, 8.5 x 11, Oct. 2015

**PRE-ORDERS NOW BEING ACCEPTED**

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- Shows how the specific topological features uncovered in food webs resonate with the niche hierarchy model of species abundance – a model with no free parameters that reproduces two universal empirical regularities in ecological species-relative-abundance data (the ubiquitous canonical lognormal species abundance distribution and the species area constant  $z=1/4$ )
- Shows the development of several novel data-transformation models (transformations of empirical food web matrices) based on graph theory and algebraic topology
- Includes Sugihara's "Resource Graph", the "Consumer Overlap Graph", and the "Simplicial Complex" model of the niche
- Contributions from Robert, Lord May of Oxford; Jordi Bascompte; and Louis Bersier

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# New Job Postings

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## Research Scientist in Computational Bioinformatics/Systems Biology (209457) The Henry M. Jackson Foundation for the Advancement of Military Medicine (HJF)

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The Henry M. Jackson Foundation (HJF) is looking for junior and senior scientists to join the U.S. Army Medical Research and Materiel Command's Biotechnology High Performance Computing Software Applications Institute (BHSAI) [[www.BHSAI.org](http://www.BHSAI.org)]. HJF provides scientific, technical, and programmatic support services to the BHSAI. This opening is for dynamic scientists interested in working in an interdisciplinary environment.

### Responsibilities:

1. Develop and apply computational solutions to biomedical problems involving computational bioinformatics and systems biology approaches.
2. Analyze and model protein networks relevant to infectious diseases and human disorders, cell signaling, and gene regulatory networks using, among others, ordinary/partial differential equations and stochastic simulation algorithms.
3. Work simultaneously on multiple projects, involving a diverse and interdisciplinary team of scientists across multiple laboratories.

The candidate should have a Ph.D. in a related discipline, extensive computational experience, and a strong publication record. PLEASE ONLY APPLY IF YOU HAVE PROVEN COMPUTATIONAL BIOLOGY EXPERIENCE.

Foreign nationals are welcome to apply. U.S. citizenship or permanent resident status is not required. This position is located in Frederick, Maryland.

Please apply on-line at [careers.hjf.org](http://careers.hjf.org) click "Advanced Search" and enter job number 209457 in the Job Opening ID box. The Henry M. Jackson Foundation for the Advancement of Military Medicine (HJF) is an equal opportunity and affirmative action employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability, protected veteran status or other status protected by law.

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**Research Scientist - Metabolic Network Modeling (209456)**  
**The Henry M. Jackson Foundation for the Advancement of Military Medicine**  
**(HJF)**

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This opening is for a dynamic scientist with interest in working in an interdisciplinary environment with a focus on the development and application of computational solutions to biomedical problems, including toxicology, drug resistance, and infectious disease.

**Responsibilities:**

1. Use computational modeling to integrate transcriptomic and metabolomic data with metabolic networks to understand malaria host/pathogen responses to different physiological stressors, including drug treatment.
2. Perform both basic and applied research in close collaboration with experimental laboratories.
3. Simultaneously work on multiple projects, involving a diverse and interdisciplinary team of scientists across multiple laboratories.

The candidate should have a Ph.D. in a related discipline and a strong publication record. Experience in high-performance computing, biostatistics or population genomics, mathematical modeling, and biological network analysis is a plus. Expertise in at least one of C, C++, Java, Python or Perl is a must. **PLEASE ONLY APPLY IF YOU HAVE PROVEN COMPUTATIONAL BIOLOGY EXPERIENCE.**

Foreign nationals are welcome to apply. U.S. citizenship or permanent resident status is not required. This position is located in Frederick, Maryland.

Please apply on-line at [careers.hjf.org](http://careers.hjf.org) click "Advanced Search" and enter job number 209456 in the Job Opening ID box.

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## Metabolic Network Modeling Research Scientist (210727) The Henry M. Jackson Foundation for the Advancement of Military Medicine (HJF)

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The Henry M. Jackson Foundation (HJF) is looking for junior and senior scientists to join the U.S. Army Medical Research and Materiel Command's Biotechnology High Performance Computing Software Applications Institute (BHS AI) [[www.BHS AI.org](http://www.BHS AI.org)]. HJF provides scientific, technical, and programmatic support services to the BHS AI.

This opening is for a dynamic scientist with interest in working in an interdisciplinary environment with a focus on the development and application of computational solutions to biomedical problems, including toxicology, drug resistance, and infectious disease.

### Responsibilities:

1. Use computational modeling to integrate transcriptomic and metabolomic data with metabolic networks to understand malaria host/pathogen responses to different physiological stressors, including drug treatment.
2. Perform both basic and applied research in close collaboration with experimental laboratories.
3. Simultaneously work on multiple projects, involving a diverse and interdisciplinary team of scientists across multiple laboratories.

The candidate should have a Ph.D. in a related discipline and a strong publication record. Experience in high-performance computing, biostatistics or population genomics, mathematical modeling, and biological network analysis is a plus. Expertise in at least one of C, C++, Java, Python or Perl is a must. PLEASE ONLY APPLY IF YOU HAVE PROVEN COMPUTATIONAL BIOLOGY EXPERIENCE.

Foreign nationals are welcome to apply. U.S. citizenship or permanent resident status is not required. This position is located in Frederick, Maryland.

Please apply online at [careers.hjf.org](http://careers.hjf.org) click "Advanced Search" and enter job number 210727 in the Job Opening ID box.

The Henry M. Jackson Foundation for the Advancement of Military Medicine, Inc. (HJF) is an equal opportunity and affirmative action employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability, protected veteran status or other status protected by law.

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Chair and Professor  
Texas Tech University  
Department of Mathematics and Statistics

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The Department of Mathematics and Statistics at Texas Tech University invites applications for the position of Department Chair and Professor beginning fall 2016. The salary will be competitive and commensurate with qualifications and experience.

Candidates must have demonstrated outstanding vision, leadership, and scholarship, possess strong commitments to interdisciplinary research and educational activities, and be a collegial motivator and advocate for faculty. A Ph.D. in mathematics or statistics is required. The successful candidate is expected to work with the faculty to develop the department under a strategic vision, foster excellence in research and teaching, and provide appropriate service to the college, university, and profession.

The department currently has 45 full-time faculty members with active research groups in pure and applied mathematics and statistics. Six degrees are offered: B.A., B.S., M.A., M.S., and Ph.D. in Mathematics and M.S. in Statistics, as well as several interdisciplinary and combined undergraduate and graduate degrees. For further information regarding the Department of Mathematics and Statistics, please refer to the department's website: <http://www.math.ttu.edu>.

Texas Tech University, located in west Texas in the city of Lubbock, was founded in 1923. The student population is 35,000 and is anticipated to grow to 40,000. Texas Tech is a state-designated national research university. Its strategic plan charts a course for becoming a great public research university by 2020. The university has the characteristics of a Carnegie-classified doctoral granting university with very high research productivity.

Applicants should apply at <http://www.texastech.edu/careers/> using Requisition 4369BR. Applicants should submit a detailed letter of application along with a current résumé including externally-funded research, teaching, administrative experience, publications, and four letters of professional reference. Questions about the position and/or the application process can be directed to [mathchairsearch@ttu.edu](mailto:mathchairsearch@ttu.edu)

Review of applications will begin immediately. Applications will be accepted until the position is filled, with those received prior to **October 1, 2015**, assured full consideration.

As an Equal Employment Opportunity/Affirmative Action employer, Texas Tech University is dedicated to the goal of building a culturally diverse faculty committed to teaching and working in a multicultural environment. We actively encourage applications from all those who can contribute, through their research, teaching, and/or service, to the diversity and excellence of the academic community at Texas Tech University. The university welcomes applications from minorities, women, veterans, persons with disabilities, and dual-career couples.

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## Two Tenure-Track Assistant Professors Mathematics, Amherst College

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Amherst College has two tenure-track Assistant Professor Mathematics positions, one with a preference for applied mathematics. We seek applicants who can teach and encourage students of diverse backgrounds, including first-generation students, international students, and students with varying mathematical preparation. Amherst College is an equal opportunity employer and encourages women, persons of color, and persons with disabilities to apply. The college is committed to enriching its educational experience and culture through the diversity of its faculty, administration, and staff. Responsibilities include teaching two courses per semester and supervising undergraduate theses. Requirements: Ph.D. in mathematics or a related field, strong commitment to research, passion for teaching. Submit cover letter, curriculum vitae, list of publications, research statement, teaching statement, and at least three letters of recommendation, at least one specifically addressing teaching, to MathJobs.Org. Applications accepted until the positions are filled; those received by **December 1, 2015**, will be guaranteed consideration.



### 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 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.

Editor: Amina Eladdadi - email: [editor\(at\)smb\(dot\)org](mailto:editor(at)smb(dot)org)