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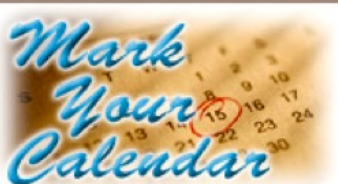
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THE 2015 ANNUAL MEETING OF THE SOCIETY FOR
MATHEMATICAL BIOLOGY
JUNE 30-JULY 3, 2015
ATLANTA, GA, USA

Letter from the President

Dear SMB members,



I am still remembering with wonder the time I got to spend in Japan both before, as a traveler with my family, and during the joint meeting with the Japanese Society for Mathematical Biology. There were so many highlights, scientific, cultural, and culinary, that I will leave it to others to attempt to summarize them: the quantitative data are impressively collated in Toshi Namba's report, and Kelsey's Gasior's letter gives a wonderful sense of the mood of the meeting. I will instead focus on some broader thoughts that I shared with the few people who could hear me over the roar of conversation at the banquet.

First, I want to thank Toshi Namba (conference organizer and incoming JSMB president) and Masayasu Mimura (outgoing JSMB president) for making the meeting such a success, and the Korean Society for Mathematical Biology and the Chinese Society for Mathematical Biology for their support. The SMB Board of Directors, Committee Chairs, and many volunteers helped keep the organization moving forward, with my special appreciation to outgoing Past President Gerda de Vries for her leadership, vision, and selfless assistance on matters ranging from crucial to trivial. Achi Dosanjh and Springer, the publisher of the Bulletin of Mathematical Biology, generously hosted the opening reception.

To this, I must add particular thanks to the chefs at the conveyor belt sushi restaurant we found near the train station. As the plates of himachi, toro, unagi and tamago and even sake streamed by, each on a special plate with its own price, I was reminded of the flow of ideas at this meeting, ecology, cancer biology, partial differential equations, surging past, complementing each other (and all for a single low price of registration), to be washed down by the sake, beer or roasted green tea of conversation with old and new friends. Instead of an "all you can eat" restaurant, this was an "all you can learn" meeting, with no risk of digestive upset at the end.

But Japan proved of course to be much more than food. It was almost overwhelming for the novice visitor; the language, the crowds, the constant motion. Yet nowhere else I have visited has such perfect havens of peace and order as its gardens, temples and shrines. Learning about, say, the biology of some previously unvisited part of the cell can feel the same; the overwhelming challenge of mastering the new language to describe crowds of molecules in constant motion. It is at this point that we mathematical biologists must serve as the architects and designers who find ways to create havens of order that, like bonsai in Japanese gardens, capture the essence of living things.

Sincerely,

Fred Adler

JSMB-SMB 2014



Report From The Local Organizers

by TOSHIYUKI NAMBA

The Joint Annual Meeting of the Japanese Society for Mathematical Biology and the Society for Mathematical Biology, Osaka 2014, was held in the Osaka International Convention Center, Osaka, Japan, from July 28 to August 1, 2014.

The joint meeting drew 538 participants including 104 students from 29 countries as follows: Australia 21, Austria 3, Canada, 5, China 7, Colombia 1, Croatia 1, Finland 1, France 14, Germany 12, Hong Kong 1, Hungary 1, India 1, Japan 296, Korea 18, Mexico 1, Netherlands 2, New Zealand 3, Philippines 2, Poland 5, Qatar 5, Russia 3, Saudi Arabia 1, Singapore 1, Spain 2, Switzerland 2, Taiwan 13, UAE 1, United Kingdom 34, and USA 81.

The scientific program included eleven plenary lectures, sixty-nine minisymposia, thirty-eight contributed sessions, and sixty-five poster presentations. A total of eleven plenary lectures were given as the following; Laura Miller, Departments of Mathematics and Biology, University of North Carolina, Chapel Hill, USA; Yanni Xiao, Xi'an Jiaotong University, P.R.China; Carson C. Chow, Mathematical Biology Section, National Institutes of Health, USA; Nanako Shigesada, Professor Emeritus, Nara Women's University, Japan (2013 Akira Okubo Prize); Iain D. Couzin, Department of Ecology and Evolutionary Biology, Princeton University, USA; Akiko Satake, Faculty of Environmental Earth Science, Hokkaido University, Japan; Ha-woong Jeong, Department of Physics, KAIST, Korea; Tatsuo Shibata, Laboratory for Physical Biology, RIKEN Center for Developmental Biology, Japan;

Steven A. Frank, Department of Ecology & Evolutionary Biology, University of California, Irvine, USA; Michael G. Watson, Institute of Petroleum Engineering, Heriot-Watt University, UK (2014 Lee Segel Prize for Best Research Paper); and Martin A. Bees, University of York, UK (2014 Lee Segel Prize for Best Student Paper).

Sixty-nine minisymposia contained topics in epidemiology, cancer, cell biology, developmental biology, pattern formation, virus, medicine, mathematics, ecology, evolution, biological movement, and networks. Thirty-eight contributed sessions covered most of the above topics and included sessions on dynamics, population biology, biophysics, and sociology. The joint meeting was co-sponsored by the Chinese Society for Mathematical Biology (CSMB) and the Korean Society for Mathematical Biology (KSMB). Financial support was provided by the Japan World Exposition 1970 Commemorative Fund and the Inoue Foundation for Science, and the Welcome Reception was sponsored by Springer.

Prizes awarded in the 2014 joint annual meeting were: the 2013 Akira Okubo Prize to Nanako Shigesada, the 2014 Lee Segel Prize for Best Research Paper to Steven McDougall, and the 2014 Lee Segel Prize for Best Student Paper to Stephen O'Malley.

We wholeheartedly thank the chair, the scientific advisory board, local organizing committee including the management and planning groups for their hard work, and commitment to organizing a very successful meeting.

For all materials related to the meeting, please check out the conference website:
<https://sites.google.com/site/jsmbsembjointmeeting2014osaka/home>

Photos from the 2014 Joint JSMB/SMB Meeting



Fred Adler and Masayasu Mimura presenting Nanako Shigesada with the Akira Okubo Prize



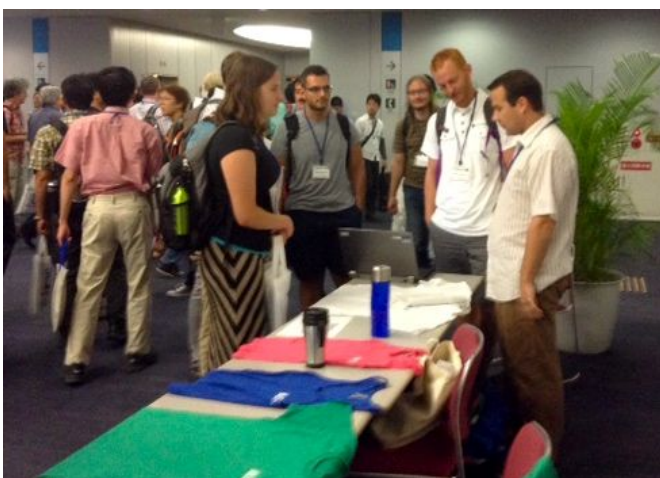
Fred Adler presenting Martin Bees with the Lee Segel Best Student Paper Award



Toshi Namba & Masayasu Mimura at the banquet



Participants at the banquet



Heiko Enderling selling SMB t-shirts and mugs



Philip Maini chatting with participants

The 2014 Lee Segel Prize for Best Research Paper

Osaka, Japan, August 1st, 2014

by MICHAEL WATSON

Thank You SMB and Springer!

On behalf of myself and my fellow awardees, I would like to express our great gratitude to all involved at the SMB and Springer for our receipt of the 2014 Lee Segel Prize for Best Research Paper. When first informed of this success back in December 2013 we were shocked and surprised, but nonetheless genuinely delighted to see our work receiving recognition from our peers in the field. The majority of the credit for this award should, of course, go to Dr. Steven McDougall and Prof. Mark Chaplain, for whom this prize recognizes many years of work developing the approaches applied in the manuscript.

A notable perk of winning the prize was an invite for one of the authors to present the work at the recent JSMB/SMB 2014 Meeting in Osaka. Steven, Mark and I were all lucky enough to be able to make the lengthy journey, but Steven kindly suggested that I be the one to deliver the presentation. At such an early stage in my academic career, this inevitably proved to be rather nerve-wracking, but it was a great experience and a real honor to have the opportunity to present our research at an excellent conference in a truly incredible city!



Michael Watson, Steven McDougall, and Mark Chaplain



by YI JIANG

The 2015 Annual Meeting of the Society for Mathematical Biology (SMB) will take place at Georgia State University in Atlanta, GA, USA, from June 29 to July 3, 2015. The conference will feature new foci on Mathematical Modeling in Medicine, Modeling in Public Health, and Molecular Systems Biology, that will complement the topics of traditional SMB symposia. In particular, we will have special sessions with experimental biologists, clinicians and public health researchers presenting problems that are challenges and opportunities for mathematical modeling and analysis. The conference will feature seven plenary speakers: G.K. Anatsuresh (Indian Institute of Science, India), John Jungck (University of Delaware, USA), Andre Levchenko (Yale University, USA), Bruce Levin (Emory University, USA), Eve Marder (Brandeis University), Michael Savageau (UC Davis, USA), and Alissa Weaver (Vanderbilt).

Atlanta is a diverse and vibrant metropolis. It is a power-house of research and education, and close to a number of academic institutions that are actively engaged in mathematical biology. Atlanta is easily accessible from most locations throughout North America and the World. Georgia State University campus is centrally located in the heart of downtown Atlanta, easily accessible by MARTA, Atlanta's subway system, which is directly connected to the airport. Downtown Atlanta offers a great variety of accommodation, dining and shopping options, as well as world-class attractions, such as the Georgia Aquarium, the largest aquarium in the world, the World of Coca Cola Museum, Centennial Olympic Park, and the CNN Center, all within a few minutes' walking distance from conference hotels and lecture

halls. The High Museum of Art and the Atlanta Symphony Hall are a few subway stops away and easily accessible. The new Atlanta Streetcars will also be running, connecting all main attraction sites.

Call for mini-symposium proposals will open soon. Please visit the website:

<http://www.mathstat.gsu.edu/conference/smb/> for details. Questions regarding the conference can be directed to: smb15@gsu.edu.

Topics for Mini-Symposia and Contributed Sessions include but not limit to: Biomechanics of Soft Biological Tissues. Biological Networks and Systems. Bioinformatics. Bio-Imaging and Pattern Quantification. Evolution and Ecology. Infection and Immune Response. Infectious Diseases / Public Health Management. Mathematical and Quantitative Oncology. Mathematical Modeling in Medicine. Mathematical and Computational Modeling of Cardiodynamics. Molecular Systems Biology. Multiscale Modeling Techniques in Biology. Computational and Mathematical Neuroscience. Population Dynamics. Stochasticity in Biology. Special session on Education in Theoretical, Mathematical, and Systems Biology. Special Forum on Career Development: how to communicate with biologists, how to publish in high impact journals, how to land a tenure track position, how to obtain funding, how to manage a research lab...

Local Organizers: Yi Jiang (Chair), Andrey Shilnikov, Igor Belykh, Georgia State University; Eberhard Voit, Howie Weiss, Georgia Tech; Ilya Nemanman, Alessandro Veneziani, Emory University; Ying Xu, University of Georgia; Meghan Burke, Kennesaw State University; and Arni Rao, Georgia Regents University.

The SMB Prizes

Call For Nominations for 2015

The Akira Okubo Prize

Nominations are being invited for the Akira Okubo Prize, which, for 2015, will be awarded to a living junior scientist under the age of 40 (this condition may be relaxed to account for career breaks at the discretion of the selection committee).

The prize will be awarded for outstanding and innovative theoretical work, for establishing superb conceptual ideas, for solving tough theoretical problems, and/or for uniting theory and data to advance biological science. The areas of research are mathematical biology, biomathematics, theoretical biology, and biological oceanography.

The Akira Okubo Prize is jointly awarded by the Society for Mathematical Biology (SMB) and the Japanese Society for Mathematical Biology (JSMB). For the 2015 award, the SMB and JSMB invite the prize winner to deliver two lectures, one at the SMB Annual Conference to be held in Atlanta, GA, USA on June 30-July 3, 2015 and the other one at the JSMB Annual Meeting to be held on August 25-29, 2015 at Doshiha University in Kyoto City, Japan.

Rules for the prize can be found at: <http://www.smb.org/prizes/index.html>. The Akira Okubo prize was initiated in 1999 and the previous winners in the junior scientist category are Martin Nowak, Jonathan Sherratt, Fugo Takasu and Michio Kondoh.

To nominate a person for the Okubo prize, the following information should be submitted to Amina Eladdadi: eladdadi@gmail.com

1. Name, address, phone number, affiliation and email address of the nominator
2. Name, address, phone number, affiliation and email address of the nominee
3. A detailed statement describing why the originality of the nominee's research and its impact on mathematical biology merits consideration for the prize.

Closing date for the nominations is October 31, 2014.

The 2015 prize selection committee is:
Professor Yoh Iwasa: yohiwasa@kyudai.jp
Professor Michio Kondoh: mkondoh@rins.ryukoku.ac.jp

Professor Michael Neubert: mneubert@whoi.edu
Professor Hans Othmer: othmer@math.umn.edu
Professor Jonathan Sherratt: j.a.sherratt@hw.ac.uk
Professor Yasuhiro Takeuchi: takeuchi@gem.aoyama.ac.jp



The Arthur T. Winfree Prize

The Arthur T. Winfree Prize was established in memory of the contributions to mathematical biology by Arthur T. Winfree. Winfree was one of the legendary figures in the field, one of the very few who combined brilliant theory with imaginative and masterful experiments. Many careers were built on his pioneering work in biological periodicity and pattern formation. Winfree's genius was frequently hidden by his modest, even self effacing manner. Beyond his scientific contributions, he was an exemplary scientist and human being. The objective of the Arthur T. Winfree Prize is to honor a theoretician whose research has inspired significant new biology. Nominations of individuals to be considered for the prize may focus on a single paper or series of papers which illustrate the close connection between theory and experiment, or may be based upon a larger body of theoretical work produced by the individual which has led to significant new biological understanding affecting observation/experiments. Rules for the prize can be found at: <http://www.smb.org/prizes/winfree/winfree.shtml>.

Closing date for the nominations is November 1, 2014.

The 2015 prize selection committee is:
Prof. Michael Mackey, chair
Prof. Charlie Peskin
Prof. Jim Keener

Application of Ecological and Mathematical Theory to Cancer: New Challenges

Daejeon, South Korea, May 12-15, 2014

by YANGJIN KIM

Report By an SMB WOC - Grant Recipient

The goal of this conference was to bring together applied mathematicians and experimentalists working in various fields of mathematical ecology and theoretical oncology in order to exchange ideas and initiate collaborations among researchers from South Korea and other countries. The workshop was held May 12-15, 2014 at NIMS in Daejeon, South Korea, an institute similar to the Division of Mathematical Sciences at NSF in the USA.

Many internationally renown researchers from institutes and universities/colleges in South Korea, the US, UK, Japan, Australia, and other countries participated in the workshop and delivered talks presenting the main trends and directions in the field. Modeling aspects of cancer were addressed in general by P. Maini and H. Othmer on cell motility as well as in the context of more specific cancers by Y. Kuang on prostate cancer, E. Kashdan on bladder carcinoma, H. Kang on lung cancer, Y. Park and W. Lee on glioma. While constructing models for any cancer, an important aspect that needs to be taken into account are tumor-immune interactions. Such aspects were well addressed by A. Friedman on interleukins, S. Nakaoka on immune therapies, and by Y. Kim and P. Kim on oncolytic viruses. But immunotherapy is only one of many possible cancer treatments and other treatment strategies were presented such as targeted gene therapies by C. Yun,

anti-angiogenic therapy by T. Jackson and metronomic chemotherapy by U. Ledzewicz. Before treatment can commence, detection is required and in this direction an interesting approach using oncogenes by B. Aguda was complemented by a more theoretical, algebraic approach presented by P. Hinow. The workshop also hosted a poster session for undergraduate/graduate students and young scientists, mostly from Korea, which gave them a chance to present their research and interact with more senior researchers in a field that is still considered somewhat new in this country. Numerous scientific discussions took place after the talks, during the breaks and led to an open panel discussing both challenges in the field and the educational aspects at the end of the workshop.

The workshop had a rich social program starting from traditional Korean meals which were served both in Daejeon and Seoul to the cultural tour of royal palaces, gardens of Seoul and the legendary Seoul tower. The organizers hope that the scientific benefits of the workshop will result in possible collaborations and dissemination of the results presented should help in achieving this goal. The proceedings of the workshop will be published as a special issue of the Mathematical Biosciences and Engineering with A. Friedman, U. Ledzewicz, Y. Kim and E. Kashdan as editors.



The 9th European Conference on Mathematical and Theoretical Biology

Gothenburg, Sweden, June 15-19, 2014

by RICHARD SCHUGART

The 9th European Conference on Mathematical and Theoretical Biology was held in Gothenburg, Sweden from June 15-19, 2014. "There was an impressive number of high quality talks and posters presented," said Torbjörn Lundh, Chair of the Conference Local Organizing Committee. There were "more than 600 registered participants," according to Andrea Pugliese, President of ESMTB and Chair of the Conference Scientific Committee. There were 42 mini-symposia that showed "how diverse and constantly innovative mathematical biology is," said Torbjörn.

Mathisca de Gunst, VU Univ. Amsterdam, officially started the conference describing the use of statistics in neuroscience network modeling. Sebastian Schreiber, U. of California, Davis, presented on species coexistence, while David Rand, U. of Warwick, showed experimental and theoretical results involving the cell cycle, circadian clocks and signaling systems. Matthias Birkner, Johannes Gutenberg U., Mainz, presented on population genetics, while Mikael Fortelius, U. of Helsinki, talked about combining fossil records with mathematical and computational approaches to obtain information about the behavior of the Earth System. Tom Britton, Stockholm U., described the role of key epidemiological parameters on emerging infectious diseases, while Marie Doumic, INRIA Paris-Rocquencourt, talked about amyloid diseases. The last plenary talk was given by Trevor Graham, Queen Mary U. of London, who discussed how within-tumor diversity can be used to describe future prognosis in cancers and premalignant lesions.

Following the last plenary talk were presentations from previous Reinhart Heinrich Doctoral Thesis Award winners. The first presenter was Stefan Höhme, who was the 2011 award winner. He received his PhD from the U. of Leipzig for his work on liver growth and regeneration. The second presenter was Christoforos C. Hadjichrysanthou, who was the 2012 award winner. Hadjichrysanthou received his PhD from City U., London for using evolutionary game and graph theory to study structured populations. The 2013 winners, Andreas Raue from

the U. of Freiburg and Abraham Leendert Willem Kuijper from U. College London, are expected to present at the 10th ESMTB Conference. The meetings closed with prizes for the best conference talks and posters. There were four winners for best conference talks. They were Majid Abedi, Technical U. Dresden, Florence Debarre, U. of Exeter, Weini Huang, Max Planck Institute for Evolutionary Biology, and Jan Teichmann, City U., London. First prize for best poster was awarded to Birgit Bruggemeier, U. of Oxford. There was a tie for second prize. They were David Breuer, Max Planck Institute of Molecular Plant Physiology, and Michael Kücken, Technical U. Dresden.

The conference also included a social program. There was a reception in the meeting hall of the City Council, an afternoon excursion before the conference banquet, and a day trip to a traditional countryside Midsummer Eve Celebration after the conference ended. Overall, both Andrea and Torbjörn believe that it was a successful conference. "I think it was successful because of the number of participants and especially the quality and variety of the presentations," said Andrea. Torbjörn added that "mathematical biology is an active, expanding and constantly improving field." This trend should serve the organizing committee well for the 10th ESMTB Conference, to be held jointly with the Society for Mathematical Biology in Nottingham, UK, July 11-15, 2016.



Participants in countryside manor with folk music & maypole

Report on the JSMB/SMB Annual Meeting

Osaka, Japan, July 28th-August 1st, 2014

by KELSEY GASIOR

Report By a Landahl-BusenberG Grant Recipient

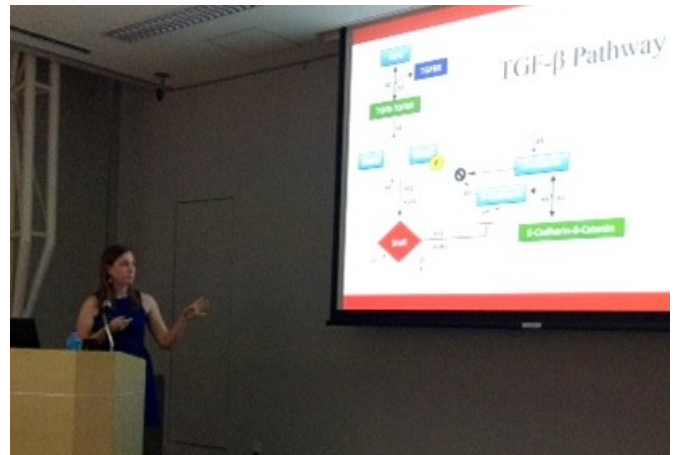
The 2014 Joint Annual Meeting of the Japanese Society for Mathematical Biology and the Society for Mathematical Biology took place in the beautiful and historic city of Osaka, Japan from July 28th-August 1st. Even though the weather was sweltering, with temperatures reaching over 95 degrees and 90+% humidity during the day, this did not stop members from engaging in academic pursuits or enjoying all that Osaka had to offer.

On the first day of the meeting, after welcoming participants, President Fred Adler made a request that set the tone for the upcoming week. Although everyone came to the meeting in hopes of seeing presentations given on their particular specialties, Dr. Adler asked that everyone take time to attend a session whose focus was not in line with their immediate interests. He requested that everyone travel outside of their comfort zones and enjoy the material presented on other subjects. With 40 contributed sessions, 71 mini symposia, and 65 posters, it was not really a question of "*is there a session on a topic I am unfamiliar with?*" but, rather, a question of "*where do I start?*" Personally, I was interested in attending the sessions focused on cancer and was happy that I was able to attend several, such as "Mathematical Models of Tissue Regulation and Cancer Development" which was led by Ignacio Rodriguez-Brenes. I also found the work shown by my fellow presenters during our symposium, Mathematical Modeling of Tumor Growth and Therapy led by Amina Eladdadi and Heiko Enderling, extremely fascinating.

However, I also made it a point to heed Dr. Adler's advice and attended several non-cancer related sessions. What great advice this turned out to be! Even though the sessions I attended weren't related directly to my biological interests, I learned a lot about different techniques that I could apply to my own research. In particular, I found Angela Jarrett's presentation on Modeling the Immune Response to MRSA and Insights from Global Sensitivity Analysis fascinating and extremely helpful. I think her techniques regarding sensitivity analysis will be quite useful for my project in the upcoming months.

I was also pleasantly surprised to see a number of presentations focused solely on biological work that has been carried out. As a student who is new to performing her own experiments, it was inspiring to hear about their own trials and ultimate success with their own work.

I would personally like to thank Drs. Amina Eladdadi and Heiko Enderling for inviting me to present at the meeting. I would also like to thank the Society for Mathematical Biology for providing funding via the Landahl-BusenberG award and the Research Training Program at North Carolina State University for helping fund my trip to Osaka. Finally, I would like to thank my advisors, Dr. Marlene Hauck and Dr. Sudin Bhattacharya, for their unwavering support during the project whose results I presented.



Kelsey Gasior giving her presentation



View of the Beautiful Osaka!

SMB Education Highlights

A Sampling of Mathematical Biology Graduate Programs

by WILL HEUETT & ELSA SCHAEFER

As the number of programs in mathematical biology has grown over the past five to ten years, we thought some information about the available programs would be useful for those of us who are helping students to find pathways to their future careers. In particular, we sought information for a mathematics student who is interested in a PhD program that includes biomathematics. We asked three questions to about twenty-five PhD programs in mathematical or computational biology, and received ten responses.

Academic careers available to PhDs in mathematical biology are still predominantly in single-discipline departments. Therefore, PhD programs in mathematical biology are typically offered either under an umbrella of mathematics or biology, or through a much more pointedly multidisciplinary approach. We hope that the answers from this diverse set of institutions to our simple questions can inspire future PhD students with the broad range of programs and careers that are now available.

Please see the SMB webpage (<http://www.smb.org/resources/education/degree.shtml>) **for the full responses from the ten programs.** The programs' full responses are illuminating in understanding the breadth of programs available and in helping a prospective student to determine which type of program is best suited for that individual. Readers may also enjoy a recent article in The Scientist Magazine (<http://www.the-scientist.com/?articles.view/articleNo/38979/title/New-School/>) about interdisciplinary biomathematics programs.

Here are the questions we asked:

1. What careers are your program's graduates entering?

The responses to this question were encouraging. The more recently-initiated programs cite strong post-doctoral placements and a wide array of industrial placements, while the older programs list good tenure-track placements. We noted that the programs with multidisciplinary structure tended to place a larger proportion of graduates in industrial careers.

2. What coursework and summer experiences best prepare undergraduates for admission to your program?

The responses to this question were helpful in differentiating the available programs. The desire for students with some experience with research was universal, while the balance between mathematics and science was not. Some programs are looking for students with a strong mathematics background; others want to see demonstrated interest and coursework in biology; finally, there are some that are intended primarily for biology undergraduates with strong quantitative skills.

3. When should a student enter a mathematical biology MS or PhD program versus an Applied Mathematics program in which the student specializes in biomathematics?

Some programs are designed with a priority in preparing students to be able to find an academic home within an institution that may not house interdisciplinary positions, while other programs have chosen to be fully interdisciplinary in name and structure. There are advantages to each choice, and the descriptions provided by the institutions are compelling.



Mathematical Biology: A Personal Journey

Nanako Shigesada



My favorite subjects in high school were mathematics and physics. In 1960, I entered Kyoto University and majored in physics. I gave up another option, pure mathematics, since I was rather interested in real natural phenomena. I took a graduate course in statistical mechanics under the supervision of Prof. Ei Teramoto, who was well known for his innovative work in high-polymer physics. Under his influence, I studied diffusion-controlled reactions in liquid for my PhD thesis.

In 1969, when Teramoto moved to the newly founded Department of Biophysics at Kyoto University, I was luckily hired as an assistant professor in his new lab. In the same year, student protests broke out throughout Japan. With no exception, the campus of Kyoto University was filled with the clamor of demonstrations almost every day. After the student strife finally subsided in the early 1970s, the campus was left with an air of apathy all over. However, there also arose among students strong anticipations for exploring new fields beyond the

boundaries of traditional academic disciplines. Leading such trends, Teramoto launched a laboratory for mathematical biology, the first of its kind in Japan. Since then it has served as an important center for those aspiring to his high aim for the subsequent two decades.

Many ambitious students gathered there: Norio Yamamura, Hisao Nakajima, Kohkichi Kawasaki, Yoh Iwasa, Toshiyuki Namba, Masahiko Higashi, and even John Milton, who joined from Canada under the JSPS invitation fellowship. They engaged in enthusiastic discussions and seminars, literally day and night. The Teramoto lab eventually grew into a lively salon for interdisciplinary exchanges with additional participants, such as Prof. Masaya Yamaguti and his student Masayasu Mimura from the Applied Mathematics Department in Faculty of Engineering, and researchers from the fields of ecology and agriculture. Participants introduced hot topics such as bifurcation theory, chaos or singular perturbation theory from the mathematical field, and the ESS game theory, adaptive strategy and evolutionary biology from the ecological field. Every day I was excited to learn new things, either about mathematics that I had used to yearn for or about the marvelous behaviors and evolution of organisms that I had been largely ignorant of.

On one of those days, I received another strong impact by reading a book *Diffusion and Ecological Problems* as written in Japanese by Akira Okubo (1975). (Its English edition was published first in 1980 and then in 2001 as the expanded second edition coauthored with S. Levin.) In this book, Okubo introduced studies of biological diffusion done by a number of Japanese entomologists. I was particularly impressed by the environmental density theory proposed by Masaaki Morisita. He quantitatively evaluated the population pressure due to interference between individual animals by ingenious experiments using antlions. On the basis of his data, I demonstrated in collaboration with Kawasaki and Teramoto in 1979 that the population pressure can be formulated by nonlinear diffusion equations. Encouraged by this outcome, I wanted to learn directly from Okubo and made a sabbatical visit with him at SUNY, Stony Brook, in 1979.

Okubo kindly arranged opportunities for me to meet his friends working on mathematical biology. First, he introduced me to Simon Levin by taking me to Cornell University at Ithaca. I can still remem-

ber Akira and Simon exchanging joyous conversations over happenings in mathematical biology in the US. Judging from what I heard from them, the field of mathematical biology in those days seems to have been still in the rising phase. Simon then introduced me to his student, Peter Kareiva, who had been measuring flight paths of butterfly at that time. Peter took me to his cabbage field and enthusiastically told how his experiment was going. Our discussions started there culminated in a joint article on the "correlated random walk" as published in 1983.

When I returned to Kyoto, Teramoto had been thinking about providing young Japanese scientists with an arena for international exchanges. In cooperation with M. Yamaguti and S. Levin, he organized the International Symposium on Mathematical Biology in Kyoto in 1985. He invited many world-class experts, including V. Capasso, C. Clark, D. Cohen, O. Diekmann, J. Gillespie, L. Ginsberg, A. Goldbeter, S. Kauffman, S. Levin, R. May, H. Meinhardt, R. Miura, A. Okubo, G. Oster, H. Othmer, L. Ricciardi, J. Rinzel, R. Rosen, L. Segel, and G. Sugihara. The symposium indeed gave immeasurable impacts to all participants, young and old alike.

Meanwhile, I gradually focused my interests on the spatial ecology of biological invasions. As a representative classical work in this field, Fisher (1936) and Skellam (1951) had used a reaction-diffusion equation to demonstrate that the range front of invasive species advances at a constant speed. This clear-cut result vividly exemplifies the beauty and power of mathematical modeling. However, there remained two essential problems, as Akira taught me in New York. First, the environment was assumed as homogeneous in the Fisher model. How would the spreading speed be affected if the environment were heterogeneous as is often the case in nature? Thus, I studied with Kawasaki and Teramoto the range expansion of invasive species into periodic patchy environments by using an RDE of the Fisher type. We discovered that a species succeeding in invasion expands its range in a spatio-temporal pattern termed "traveling periodic wave", and we obtained a mathematical formula for the spreading speed. Second, various field observations have shown that the rate of the spread of invasive species is not necessarily constant, but often tends to accelerate with time. To explain this phenomenon, I constructed together with Kawasaki and Takeda a stratified diffusion model, which assumes that a small proportion of individuals sporadically makes

a long-range dispersal, while the remaining majority undergo ordinary random diffusion. Compiling these results with a series of my preceding studies, I published a monograph on invasion in Japanese in 1992.

In 1992, I moved to Nara Women's University. Soon after that, a letter arrived from Robert May, to my great surprise, inviting me to publish an updated English version of my Japanese book as part of the Oxford series in Ecology and Evolution. This turned out to have been mediated by a kind recommendation of my book to May by Joel Cohen, who once visited me and saw a draft of that book in 1990 when I was in Kyoto. Although the original Japanese book was authored by me, the English version was coauthored by Kohkichi Kawasaki, since most of its content had been worked out by indispensable collaborations with him.

In February 1996, both Ei Teramoto and Akira Okubo passed away. In the same year, I happened to be organizing an international symposium on mathematical biology in Kyoto. Thus I switched it to a memorial conference dedicated to them. We deeply missed their warm and selfless humanity on top of their love for and foresight in science. In Nara, I continued to develop theories of biological invasion by cooperating with my students - Noriko Kinezaki, among others - and many colleagues such as Fugo Takasu, K. Kawasaki, Kazuro Iwata, and so on. We also investigated the epidemic spread of the pine wilt disease in Japan with field researchers Katsumi Togashi, Yoich Kishi and Kazuyoshi Futai. Moreover, I hosted several foreign visitors, including Hal Caswell, Horst Malchow, and Sergei Petrovskii, and enjoyed fruitful discussions and collaborations with them.

In 2005, I retired from Nara Women's University and moved to Doshisha University, where I worked until 2012. Fortunately, there I was able to converse daily with Kawasaki, who had been working at the same university. Consequently, we succeeded in solving some of our pending problems.

In 2013, I was awarded the Okubo Prize. I feel so honored and humbled to be selected for the prize crowned with the name of Okubo. As a whole, my personal journey has been blessed with countless lucky encounters with great mentors, colleagues and students. I would like to express my heartfelt thanks to all of them. My new email address is: nshiges@oak.dti.ne.jp

Research Interview

Finding a Home in Academics



Ruth Baker talks with Mark Whidden about her life and work at the University of Oxford

Who or what inspired you to become a mathematical biologist?

Although I enjoyed studying mathematics as an undergraduate and wanted to continue in the field, I felt that I needed to do something useful with it. In my third year, I took a course “Mathematical Biology and Ecology” lectured by Professor Philip Maini, and immediately I knew that was the field in which I wanted to work. Philip was my doctoral advisor and has been a fantastic mentor ever since.

Tell us about your academic background and research training.

I have pretty much always been in Oxford! I did my undergraduate and graduate degrees in Oxford, and just as I graduated I was awarded a 5-year fellowship here. During my fellowship I spent periods of time in Germany, Australia and the USA, and upon completion, I gained a permanent position in Oxford.

What are you currently researching?

The main focus of my work is developing and applying mathematical and computational tools to study aspects of embryo development. I try to work on a

range of projects, ranging from the solely theoretical to the completely experiment-driven.

What’s the next big thing in mathematical biology?

I think we need to develop new tools to extract quantitative summary statistics from biological data, and understand how to use these statistics to estimate model parameters, do model inference and feedback our discoveries into directing experimental design. This is the only way we will really be able to help drive forward the frontiers of our understanding.

Is it difficult to be a female scientist?

When I was a student, I didn’t really think there were any issues associated with being a female scientist, but as I progress that view is changing all the time! Although I don’t think I have been particularly affected to-date, I do think there are multiple ways in which the playing field is not level at the moment. These begin at the undergraduate level and continue all the way to the top.

How have you maintained an active academic lifestyle with a newborn child?

I have a fantastic group here in Oxford, and great collaborators in both the US and Australia. I have also had to become better at only saying yes to the really important things, and actively prioritizing research above all the other demands on my time at work!

What advice would you give to a young and aspiring mathematical biologist?

I think my main advice would be to think about what kind of environment they want to work in long-term. For example, would they like to have their own lab and do experiments, or would they prefer to be based in a mathematics department and interact with experimental collaborators in other departments and/or institutions.

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

There is not a lot these days, but I spend most of my time hanging out with my family, and if there is time, cycling and snowboarding.

About Ruth E. Baker

Dr. Ruth Baker is an Assistant Professor in mathematical biology at Oxford. For more info: <http://www.maths.ox.ac.uk/~baker>

The Future of Mathematical Biology

Angela Jarrett

Florida State University

*PhD Student of Profs. Nick Cogan &
M. Y. Hussaini*



What attracted you to mathematical biology?

I was originally a biology major as an undergraduate with every intention of going to medical school. As I continued to take math courses, I was eventually recruited to join the Bachelor's/Master's program in Mathematics. At FSU, I was exposed to the applications of mathematics to biology through several courses which meld biology, math modeling, and programming together. These classes opened my eyes to wonderful relationships between biology and mathematics. Next thing I knew I was talking to professors, starting projects, and applying for graduate school.

What is your current research project?

Currently I am working on the phenomenon of *S. aureus* nasal carriage. Mysteriously, *S. aureus* is able to persistently or intermittently colonize individuals nostrils while escaping the hosts innate immune response. Antibodies are formed, but the immune sys-

tem does not actively try to eliminate the nasal infection. In fact, these carriers are considered healthy individuals, but carriage is a major risk for subsequent infections in other parts of the body. Previously, we worked on a general compartmentalized ODE model for the immune response to a osteomyelitis MRSA infection in mice - looking at the affects of immunomodulation therapies and vaccination. Using global sensitivity analysis (both PRCC and Sobol' Indices), we were able to identify the dominant parameters for each of the biological experiments we simulated. Now we have created a PDE system to model the behavior of the infection and immune response in the nasal mucus. We are curious about changes in the mucus viscosity and persistence of the bacterial population, and we are looking at different non-constant diffusion scenarios including a possible therapy control. We hope this model will help shed light on some of the biological hypotheses about nasal carriage, and we are applying the global sensitivity analysis techniques to further investigate the problem.

What specific areas are you interested investigating?

I am very interested in different types of bacterial and viral diseases, especially those with antibiotic resistance and no vaccination therapies. I am interested in both the clinical and epidemiological viewpoints. I want to learn more about their spread through populations and the response of the host immune system to these pathogens. I want to look at the uses of sensitivity analysis in other infectious disease models to help identify targets for therapy and to reduce uncertainty in models. I am also looking into data assimilation via optimal control theory to incorporate data collected directly into the model both for parameter estimation and to improve models themselves.

What do you hope to do after graduation?

I hope to get a post-doc furthering my research in infectious diseases for clinical or epidemiological problems. If I could continue modeling and working on *S. aureus* infection, I would like to look at the evasion mechanisms of MRSA and possible non-antibiotic therapies.

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

If your focus is math in biology, take as many biology classes as you can. The only way to be relevant is to understand the experiments and needs of biologists. It is important to look at the biological problem and determine which mathematical system or tools would be best suited for the problem, and only a good understanding of the biology will allow you to do this well.

What inspires you scientifically?

Anything disgusting, really, that is just who I am. If it is "gross," I'm interested. I think it is fascinating how life can be so messy but can still be explained using the logical framework of mathematics.

Why did you join the Society for Mathematical Biology?

I think it is extremely important to encourage relationships between biologists and mathematicians. What are we doing if we aren't working together? What is the point? This is why I joined SMB, to contribute to the conversation between mathematicians and biologists. Also, I would like to thank SMB for contributing to my trip through Landahl-Busenberglund to participate in the 2014 Osaka Annual Meeting.

Prof. Nick Cogan, Angela's current PhD advisor, says:

Angela is an example of how mathematical biology continues to mature into a distinct field of mathematics. While she is driven by the biology and that motivates most of her research, she understands that this requires more mathematics than otherwise. In some ways this is one of the underlying challenges of mathematical biology, since small changes in the experimental approaches, or biological details require substantial changes in the mathematical approaches. Often our models change in ways that are far removed from the classical extensions from spatially homogeneous to one dimensional on to three dimensional. In order to stay within the biological constraints, she has had to continue to add to her mathematical toolbox so that she can address the biological questions at the heart of her dissertation. This means that she knows a lot of classical mathematics (ODEs, PDEs, Dynamical Systems, etc.) but

she also uses cutting edge techniques for quantifying the uncertainty and sensitivity of her models. She has shown herself to be highly skilled at learning, understanding, and implementing an extremely wide variety of mathematics and using this to address very important biological questions focusing on *S. aureus* infections.

She is also a tremendous mentor to the younger students in my group and leads them to look deeper and think more clearly about their own projects. We are looking at the final stages of her Ph.D right now and discussing her future plans - this is both a bit sad and very exciting. I expect that she has a very bright future and will continue demonstrating her eagerness to blend current mathematics with current biology to address important problems.

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)



Editor's Notes

We invite submissions including summaries of previous mathematical biology meetings, invitations to upcoming conferences, commentaries, book reviews, or suggestions for other future columns. The deadline is the 15th of the month prior to publication.

The SMB Newsletter is published in January, May, and September by the Society for Mathematical Biology for its members. The Society for Mathematical Biology is an international society that exists to promote and foster interactions between the mathematical and biological sciences communities through membership, journal publications, travel support and conferences. Please visit our website: <http://www.smb.org> for more information.

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