The Society for Mathematical Biology

SMB NEWSLETTER

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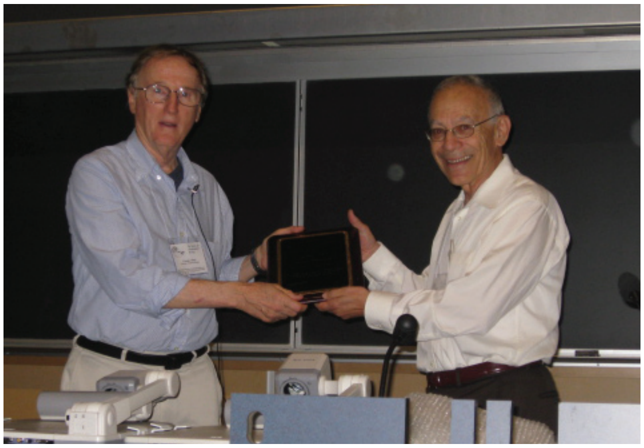


SMB Past-President Avner Friedman (right) presents the Art Winfree Prize to George Oster.

SMB 2009

Vishaal Rajani

The International Conference on Mathematical Biology and Annual Meeting of the Society for Mathematical Biology took place on July 27-30, during a tropical heat wave alongside the beautiful beaches of Vancouver, British Columbia.

The diversity of biological topics represented through posters and minisymposia throughout the conference was tied together seamlessly by eight plenary lectures that presented the unifying mathematical bridge between observation and discovery. Through these amazing plenaries on topics such as the analysis of stunning shapes and patterns of mollusks, the intercellular dance of chromosome movements and rotations, and the mechanics of snail locomotion, the SMB conference was able to establish its underlying theme of communicating through the common language of mathematics.

The success of the conference was not only set by the plenary talks, but by the 200 talks through 50 minisymposia, ranging from the study of ecosystems via the interaction and behavior of organisms, to the inner workings of the cell by linking mechanisms to biochemical pathways. Through these minisymposia, there was immense discussion on international concerns such as, threats against North American forests by destructive pests and the epidemiological modeling of disease dynamics—even a well-attended session on the modeling of an outbreak of zombie infection (featured on National Public Radio's All Things Considered). In addition to mathematicians, the minisymposia attracted a number of ecologists, cellular biologists, microbiologists and clinicians. This was a result of sessions that were dedicated to supplying a medium through which theorists and experimentalists could interact and debate, providing insight into the significant position of mathematics in scientific progress. This concert of interactions orchestrated the SMB conference into its very own unique and rewarding masterpiece.

The SMB conference was also enriched with many opportunities to discuss education in mathematical biology, and in particular to discuss opportunities in leadership for women in science. As a young researcher attending my first SMB conference, I found that my dreams of communicating ideas in an interdisciplinary community became a reality. I would like to thank the Society of Mathematical Biology and the organizers of this conference for setting up an unforgettable event in shaping the scientific community.

SMB Past-President Avner Friedman (right) presents the Akira Okubo prize to Hans Othmer.

Dear SMB Members,

This is the first time that I have had the pleasure of writing as President of the SMB. I am very much looking forward to the next two years.

Our July Annual Meeting in Vancouver was well attended, marvelously organized by Dan Coombs and Eric Cytrynbaum, and full of interesting talks and posters the whole week long. It was also notable in my experience because it was the hottest I have ever seen Vancouver in all the 45 years I have been going there!

We have an interesting slate of future annual meetings coming up: 2010 in Rio de Janiero (26-29 July), and 2011 in Krakow, Poland (28 June-2 July) jointly with the ESMTB. Our past president, Avner Friedman, is working closely with other mathematical biology societies world-wide to make a world congress of mathematical biologists happen in 2012. Exciting times ahead for our field.

This is being written at the bedside of my dying mother in Hutchinson, Kansas, and these days I have been ruminating about a lot of different things as people are wont to do in such circumstances. Life and death, of course. Somewhat surprisingly, in spite of the sadness that imminent death brings, I have mostly been thinking about life. When I go out to take a break, the heat takes my breath away today, but that minor discomfort is overshadowed by the beauty of the landscape. There are baby rabbits on the lawns around her care centre, and a swallow nest built outside the door on top of a fire alarm bell (I hope it doesn't go off!) has three little ones in it. It is quite fascinating to sit and watch the feeding pattern of the mother swallow, and how two of the three little ones are so much more aggressive than their third smaller sibling. Will the little mite get enough nourishment to survive? At sundown, after my mom has gone to bed, I go up to her third floor apartment where from the balcony you can see for miles to the North, West and South, and the sunsets are strikingly beautiful—like nothing ever to be seen in Montréal—with the Western sky blazing with colour. And the new moon the past two nights, low on the Western horizon, is tinged with redness from the sun that has disappeared. Jupiter is low in the sky and making the traverse chasing the Big Dipper. On some nights I am treated to a spectacular thunderstorm as only the Midwest can put on. In the morning, before the heat builds up, the hawks hunt over the fields (looking for baby rabbits no doubt), and I find their effortless soaring on the wind absolutely mesmerizing. No wonder Leonardo de Vinci was so struck by the possibility of man flying.

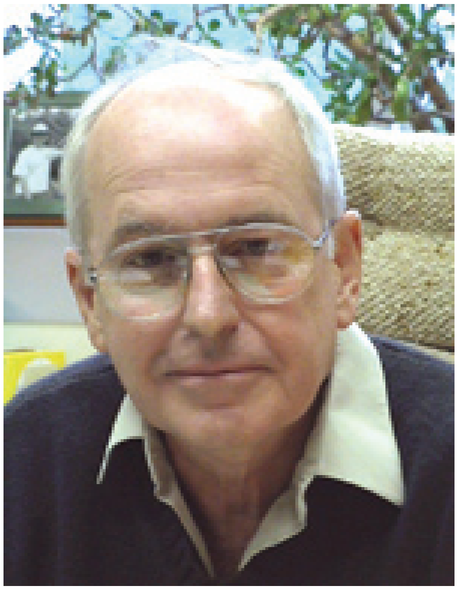
One of the things that has really struck me these days is the radical change in the field of mathematical biology in the relatively short time I have been involved in it. You could say that my first acquaintance with the area started when I was an undergraduate in 1961 (see my biographical sketch in this issue). Then the number of practitioners numbered, I would guess, less than a hundred, and the forerunner of the BMB was one of the few journals. By the time I was sufficiently trained to start going to meetings there was about one per year that I could/would attend. Now the number of journals is rapidly increasing along with the page count and the number of meetings are hard, if not impossible, to keep track of. Most importantly, mathematical biology has gained a broad acceptance from the biological community that was virtually absent then.

These are exciting times for all of us, and especially for the younger colleagues among us. And I am really excited about the possibilities! I hope you are too.

For many of us a new academic year is about to begin—either as a student or a faculty person, and I wish all of you a good start to a new academic year.

Sincerely,
Michael Mackey

SMB President



SIAM Conference
on Applications of
Dynamical Systems
May 17-21, 2009
Snowbird Ski and Summer Resort
Snowbird, Utah

SIAM Conference on Applications of Dynamical Systems

May 17-21, 2009
Snowbird Ski and Summer Resort, Snowbird, Utah

Dr. Somdatta Sinha

This meeting is held every two years at the same place. Once you reach Snowbird you would know why they do not want to change the venue. It is interesting - because long days spanning from 8:30AM to beyond 10PM some times, left no time for either skiing or trekking. Yet, all the six days, when I walked to the Cliff (conference center) from my place of stay, the silent mountains - on my right fully covered with snow, and the ones on the left all bare rock - cast a magic spell on me of serenity and quiet concentration.

The meeting started with a reception on Saturday (May 17) evening and almost all participants were in. There were 10 Invited presentations, 127 Minisymposia (about 30 concurrent each day), 42 Contributed Talks sessions, and about 60 posters scheduled. Only a handful got cancelled, and several presentations were shuffled between sessions. There were few special sessions, such as one where NSF representatives discussed about "Opportunities for Dynamical Systems Research", or, Panel Discussion on what kind of problems may be considered in future research on Dynamical Systems. The Activity Group on Dynamical Systems (SIAG/DS) business meeting was useful as their web portal DSWEB and journals were discussed.

The most significant feature of this meeting, to me, was the wide spread presence of biological problems. The two major themes of the meeting seemed to be Networks and Coupled Oscillators. The topics covered ranged from neuronal models, coupled neural cells, collective behaviour in spatially extended biological systems (heart, brain, ecological systems, etc), auditory systems, biochemical and gene regulatory networks, gene circuits, endocrine processes, central pattern generators, circadian rhythm, plankton flows and hydrodynamics, diseases such as cardiac arrhythmia, epilepsy, cancer, spread of infection (flu and HIV), and modeling DNA as elastic matter. All these being studied using dynamical systems methodologies – primary among them are nonlinear ordinary, partial, stochastic and delay differential equations, graph theory, with a lot of studies on ensemble of oscillators using Kuramoto model of phase oscillators. The large number of concurrent minisymposia that I could not attend covered the large variety of topics starting from applications of dynamical systems theory and methods to Astrodynamics, Engineering problems, Space mission, and new theoretical studies on fluid flow, mixed-mode oscillations, chaos, symbolic dynamics, etc.

The 10 invited presentations were on very well chosen topics by excellent speakers, who made it accessible to the audience. The Jurgen Moser prize lecture by Martin Golubitsky (USA) on "Catastrophes, Symmetry-Breaking, Synchrony-Breaking", Ute Ebert's (Netherlands) fascinating lecture on "The Multi-scale Dynamics of Lightning and a Moving Boundary Value Problem", "Stochasticity in Deterministic Systems" by Ian Melbourne (UK), Rachel Kuske's (Canada) impressive description of "Living on the Edge of Noise-Driven Order", and John Bush's beautiful experiments and theory on "The Fluid Trampoline: Droplets Bouncing on a Soap Film", were the treats of the week. There were few sessions on application of dynamical systems theory on modeling climate change, atmosphere-ocean interactions, civil violence, spread of religion, etc. Some of these topics and others, such as, use of dynamical systems theory to model financial systems, and other problems in Social Sciences, were considered to be future areas of study in the "Forward Looking Panel Discussion". More data analyses along with the use of statistical modeling, application of Game Theory, Complexity theory, were some of the other recommendations made.

The meeting was of very high standards, attended by more than 700 scholars from many countries. It was difficult to attend all the talks that one would have liked to hear. We are now at the age of understanding the workings of biological systems using mathematical models – a journey close to the heart of SMB. I thank the Society for Mathematical Biology for helping me to attend this meeting.

Joint SMB-CSMB Conference

Avner Friedman

The first international conference of the SMB and the Chinese Society of Mathematical Biology (CSMB) was held in Hangzhou, China during June 14-17, 2009; the meetings took place at Zhejiang University. The aim of the conference was to develop contacts among mathematical biologists: members of the SMB, and their counterparts in China. The conference included 150 participants; nearly half from outside China: the U.S., Canada, U.K., Denmark, the Czech Republic, New Zealand, Japan, Korea, Taiwan, India, Singapore, Israel, and Algeria. Many among the Chinese participants were young researchers, at the beginning or early stage of their career. The conference program included plenary talks, mini-symposia, and sessions of contributed talks.

"It is very important for young people who are beginning their career in mathematical biology to work on "good" problems," said Avner Friedman, the SMB president. With this in mind, the Scientific Committee invited ten SMB senior researchers and six CSMB senior researchers to review some of their current work and to suggest new directions for future research. Thus, for example, James Keener presented mathematical mechanistic models for the regulation of hook and filament length of flagella in Salmonella; Jonathan Sherratt talked about ecological invasions that are becoming increasingly frequent as a result of climate change and may transit from periodic oscillations to chaos; John Tyson reviewed his joint work with Bela Novak on cell cycle regulation in eukaryotes; James Sneyd described multi-scale modeling of the lung and discussed the effect of smooth muscles in undesired reduction of the airway function as in the case of asthma; Avner Friedman presented situations where the immune response to airborne diseases in the lung is "too slow"; models of cancer growth and metastasis were discussed by Mark Chaplain and Philip Maini; Shigui Ruan presented an age-structured epidemiological model of influenza A drift; Jun Zhu developed statistical approaches for analyzing complex traits in seed and plant models; and Wendi Wang described his work with Yasuhira Takunchi on adaptation of prey and predator between patches. There were many other equally interesting plenary talks by Michael Mackey, Lisa Fauci, Liu Shengqian, Sanyi Teng, and Meng Fan. The mini-symposia and the contributed talks dealt with impressively broad themes, including cell processes, diseases, biomedical applications, ecology and evolution, to name few. The mathematical methods to tackle these models drew upon many mathematical theories. Stochastic tools were introduced in a variety of talks; for example, in Chuan Xue's approach to bacteria pattern formation (joint work with Hans Othmer and Elena Budrene-Kac); PDE novel ideas on the interplay between diffusion and advection were presented in a series of talks by Chris Cosner, Stephen Cantrell and Yuan Lou which dealt with evolution dispersed in heterogeneous habitat; multiscale methods in tumor development were described in several talks, including Jiang Yi's presentations ("from molecule to tissue") and with Kejing He's work (with Yi Jiang) on a vascular tumor.

The conference ended with a boat ride on the famously beautiful West Lake and, for the international participants, in a visit to Seung Dynasty Park and its historic cultural theatre.

The conference was supported by the SMB, CSMB, and by Zhejiang University through its Vice President Dr. Jun Zhu. For more details on the conference, Google SMB-CSMB Hangzhou.

Above: Mark Chaplain and Avner Friedman work with Jun Liu and others in planning the conference.
Below: It was a well attended conference.

Poster prize winners at SMB 2009

Gerda de Vries

The SMB conference in Vancouver (July 27-30, 2009) had two poster sessions, held in parallel with receptions honoring prize lecture winners. Poster session A took place on Monday July 27, and Session B on Wednesday July 29, just before the closing banquet. In each session, two teams of judges (totalling approximately 40 members of the mathematical biology community) surveyed each poster, and selected those that were outstanding. In this way, each and every poster received attention, and many were viewed multiple times by judges (let alone other interested conferees). Competition was high, and judges had a hard time selecting the top two. However, after considerable review and discussion, the following consensus emerged.

For Session A: Gerda de Vries summed up the opinion of the judges as follows: 1st place went to Courtney Davis (University of Utah) who presented an exceptionally concise and clear research story in the field of immunology. Her statement of the problem was precise, the model investigations were well justified and to the point, and the conclusions were strong. 2nd place was awarded to Stephen Galsworthy (Oxford University) whose poster on the regional dynamics of plants was a beautiful example of research that seamlessly integrated experimental investigations with theoretical studies. The judges also awarded an Honorable mention to the poster by Ben Holder (Ryerson University).

For Session B: 1st place went to Laleh Samii (Simon Fraser University) for a well-thought out and constructed mechanistic model of processive motion. 2nd Place was awarded to Atsushi Yokoyama (Ritsumeikan University, Japan) whose poster had counter-intuitive results on an interesting question, good application, and well presented. An Honorable mention went to Michel Tchuenche (Guelph University) whose poster discussed an important question, and used real data from Zimbabwe, which is hard to come by. Another honorable mention went to Theodore Roman (Case Western) for the core signalling pathway for WNT, with a well-presented, interesting approach and thoughtful discussion.

The meeting organizers were grateful to the judges who spent time, effort, and energy on this hard selection process, and to all the fine poster presenter who brought their fascinating posters to the meeting.

Multiply Structured Populations in Biology, Bath 2009

Christina Cobbold

The BICS Conference Multiply Structured Populations in Biology held at the University of Bath on July 1-3, 2009 brought together over 40 scientists from a range of disciplines. From graduate students to professors, participants came together from across Europe and further afield, including Japan, China, and North America, to the gloriously sunny town of Bath in the UK. The organisers, Ben Adams, Nick Britton, Dick James and Jane White had carefully timed the meeting to coincide with some lovely sunny summer days which set the scene for many outside discussions during the coffee breaks. The theme of the meeting was to discuss the state of the art in the development, analysis and application of models for biological populations with multiple layers of structure. The exciting mixture of plenary talks by Hans Metz, Akira Sasaki, Jonathan Sherratt, Katia Koelle, Troy Day and Yoh Iwasa covered subjects from evolution, epidemiology and ecology.

Epidemiology was a strong theme in the meeting with the talks often drawing on aspects of evolution and ecology. The wide range of epidemiology talks spanned the innovative modelling of the influenza phylogenetic tree and strain evolution, comparing models of Chlamydia screening used for public health decision making, to exploring the effects of spatial scale on virulence evolution. The diversity of modelling approaches was also broad and was one of the highlights for me. Approaches ranged from novel variations on classic ODE and PDE models to stochastic genetic models of within-host strain dynamics and energy budget models of tree masting.

The meeting also provided an opportunity for young researchers to present their work and the conference show cased some excellent talks and posters by graduate students. The meeting was the perfect size to stimulate lots of questions after each talk which really highlighted for me the interesting science that was being presented.

Lively discussions at the poster session.

My Career in Mathematical Biology
A Personal Journey

Michael C. Mackey

In 1959, at the age of 16, I went to the University of Kansas to study mathematics, and looking back I realize I had no clue what I was going to do with it. Nevertheless, KU was a great place to be an undergraduate as the faculty were very student oriented and I had a whale of a good time learning all sorts of mathematics. Then math majors were expected to also take a number of physics courses which I quite enjoyed, along with the philosophy courses that I took, and both have surely shaped my long lasting interest in foundational questions in statistical mechanics and quantum mechanics.

Like many things in life, my interest in mathematical biology was awakened by a totally serendipitous event. I was in the KU book store one day late in my sophomore year, perusing the Dover book section, and found a two volume book entitled Mathematical Biophysics by Nicolas Rashevsky (founder of the Bulletin of Mathematical Biophysics, now the Bulletin of Mathematical Biology). I bought both volumes ($5 for the set!) and started to read through different chapters. I was quite amazed that you could really make mathematical models of biological processes just as physicists made models of the physical world. My advisor (Lee Sonneborn) had an interest in biology and agreed that I could do a reading course under his direction in my junior year using the Rashevsky volumes, and Lokta's book Elements of Mathematical Biology. So that is how I got started.

I finished my degree at KU in January 1963, and really didn't know what I wanted to do. Finally, I landed a job in the research department of Hallmark Cards, and quickly discovered that corporate life (at least the type they had) was not the way I wanted to spend the rest of my career. Eventually I ended up as a graduate student in the Department of Physiology at the University of Washington. The department then, as now, was very quantitatively oriented and my thesis advisor, J. Walter Woodbury, was a physicist turned physiologist. Walt was a wonderful mentor, because he gave me enough slack to do pretty much what I wanted and I learned a lot of physiology in addition to taking much more math and physics to feed my love for those areas. And, most importantly, I learned through his example how to nurture my students.

My Ph.D. was completed at the height of the Vietnam War in early 1968, and after fulfilling my military obligations I went to take an Assistant Professorship in Physiology at McGill University in 1971. Physiology at McGill has a long and rich history of employing quantitatively oriented physiologists which is curious but also very pleasant for someone like me. One of the perks is that I have been able to supervise graduates students in Physiology, Mathematics, and Physics and I have been blessed with many incredibly bright students and postdocs over the years (15 hold academic positions, four are in business, one is a physician, and one is a potter). Though I intended to stay in Canada for only a couple of years, a combination of events has kept me happily in Montréal for almost 40 years. Currently I am the Joseph Morley Drake Professor of Physiology at McGill as well as holding appointments in the Departments of Physics and Mathematics.

Often fellow academics complain about a variety of things in their jobs, but my personal opinion is that being an academic is one of the most privileged of jobs in our society—and being at McGill has been an absolutely marvelous experience for me. I have been left to decide what I will teach, to develop my own administrative initiatives and programmes, to travel as I wish for collaboration, and I have valued colleagues at McGill and other universities around the world. Early in my career Leon Glass was fortunately hired in our department and we have had a significant influence on each others research. Our work on dynamical diseases and our book From Clocks to Chaos has had a major impact in some areas, and I rank the insights from mathematical modeling in hematology and cardiology as two of these. Additionally we have had colleagues like Michael Guevara, Peter Swain, Maurice Chacron and Danny Kaplan who were trained in other than physiology and who have enriched the academic life at McGill beyond all expectations, forming the McGill core of the Centre for Nonlinear Dynamics in Physiology and Medicine (CND) that has been in existence since 1989. The CND and mathematical biology have matured to the point that we are now in the process of launching the Centre for Applied Mathematics in Bioscience and Medicine (CAMBAM), supported federally by MITACS (a Canadian National Centre of Excellence for applied mathematics).

There are all sorts of mathematical biologists. Some of us even work in areas that are seemingly unrelated to biology, and I would rank myself as one of them. However, no matter how strange some of my research appears to someone interested in biology the problems are almost always motivated by biological questions in some fashion or another. One of the most influential encounters of my professional life was meeting the Polish mathematician Andrzej Lasota, for his teaching and our common research has very much cemented together concepts from ergodic theory and dynamical systems theory to enable one to examine the statistical properties of truly chaotic systems.

Mathematical biology has changed dramatically since I first started. In the early 70's going to the Gordon Conference and the Oberwolfach meeting, and talking with all of the key players, was sufficient to bring you up to speed on what the new and exciting stuff was. No more! And, too, as it has evolved and matured, the field has had its share of bandwagons, some of which have died a natural and well-deserved death and some of which have borne fruit and persisted. Such is the case in all areas of science, and it always will be. The important thing for young investigators, in my opinion, is to follow their nose and indulge their curiosity rather than blindly following the crowd in their current stampede whatever it may be.

Selected Publications:
M.C. Mackey & L. Glass. "Oscillation and chaos in physiological control systems", Science (1977) 197, 287- 289.

A. Lasota & M.C. Mackey. Chaos, Fractals and Noise: Stochastic Aspects of Dynamics. Springer-Verlag, 1994.

L. Glass & M.C. Mackey. From Clocks to Chaos: The Rhythms of Life, Princeton University Press, 1988.

M.C. Mackey. Time's Arrow: The Origins of Thermodynamic Behaviour. Springer-Verlag, 1992. Reprinted by Dover Publications, 2003.

M. Santillán & M.C. Mackey. "Why the lysogenic state of phage λ is so stable: A mathematical modelling approach", Biophy. J. (2004) 86, 75-84.

C. Beck & M.C. Mackey. "Could dark energy be measured in the lab?", Phys. Lett. B (2005) 605, 295-300.

M.C. Mackey & M. Tyran-Kamińska. "Deterministic Brownian Motion: The effects of perturbing a dynamical system by a chaotic semi-dynamical system", Phys. Reports (2006) 422, 167-222.

M. Santillán & M. C. Mackey. "Quantitative approaches to the study of bistability in the lac operon of Escherichia coli", J. Roy. Soc. Interface (2008), 5, S29-40.

M. Santillán & M. C. Mackey. "A proposed mechanism for the interaction of the segmentation clock and the determination front in somitogenesis", PLoS ONE (2008), 3(2): e1561. doi:10.1371/journal.pone.0001561.

C. Foley & M.C. Mackey. "Dynamic hematological disease: A review", J. Math. Biol. (2008), 58, 285-322.

C. Foley & M.C. Mackey. "Mathematical model for G-CSF administration after chemotherapy", J. Theor. Biol. (2009), 257, 27–44.

Participants in the Leadership Workshop. Front Row (left to right): Zhilan Feng, Gerda deVries, Mary Ann Horn, Renee Fister. Back Row (left to right): Rebecca Segal, Ellen Daniell, Holly Gaff

Opportunities for Leadership Workshop at SMB Annual Meeting

K. Renee Fister, Holly Gaff, and Rebecca Segal

This workshop sponsored by SMB and SIAM was geared to the development of women in bio-mathematics, by fostering both tangible and "intangible" qualities that are the makeup of leaders. There were approximately 40 participants with a healthy mix of men and women. Participants had the opportunity to hear about perspectives and lessons learned from professional women at different career stages pertaining to tenure and/or industrial jobs. The workshop was organized by Holly Gaff from Old Dominion University, Renee Fister from Murray State University, and Rebecca Segal from Virginia Commonwealth University. The workshop involved a lunch sponsored by SIAM, a presentation by Ellen Daniell, a break out session to simulate the aspects of a group session, and a panel discussion oriented toward issues about career and family balance, the art of saying no, and making choices about one's goals.

For over 30 years, Ellen Daniell, author of Every Other Thursday: Stories and Strategies from Successful Women Scientists has been part of a professional problem-solving group of women (and some men) who have attained extraordinary distinction in various scientific fields. The group meets every other week to help one another with the professional and personal challenges of managing highly competitive careers and fulfilling lives. In her talk, Dr. Daniell described how the group works and some specific experiences of its members during the course of their careers. The talk highlighted the importance of cooperation and of not going it alone in a competitive world.

Following Dr. Daniell's talk, the participants formed small groups in order to replicate a group problem solving session. It provided an opportunity for participants to present a problem and to have peers give opinions and food for thought. The interaction was extremely fruitful in that it illustrated the powerful dynamics of a group. It also allowed participants to meet other bio-mathematicians and to expand their professional network.

The session concluded with a lively panel discussion. The panel involved Zhilan Feng from Purdue University, Gerda deVries from the University of Alberta, Mary Ann Horn from the National Science Foundation, Renee Fister from Murray State University, Holly Gaff from Old Dominion University, Ellen Daniell, author. Rebecca Segal from Virginia Commonwealth University moderated the session and initiated thought provoking questions for the panelists to address.

New Expectations for Medical Students: An Undergraduate Preparation Perspective

Meredith L. Greer

On June 4, 2009, a new report called for extensive changes in the mathematics and natural sciences training of medical students. In its most sweeping feature, the report identifies several competencies - skills, knowledge, or attitudes – for students to master at both the undergraduate and medical student levels. For undergraduates planning to apply to medical school, this approach contrasts sharply with taking a collection of prescribed courses. For professors at undergraduate institutions, this approach allows far greater freedom for curricular innovation than has existed previously. For mathematicians, like myself, this approach deserves special note for its quantitative/mathematical component.

The Recommenders

A committee of 22 scientists, physicians, and educators, convened by the Association of American Medical Colleges (AAMC) and the Howard Hughes Medical Institute (HHMI), created the report. Both AAMC and HHMI had concerns generated by the quickly increasing pace of biological and medical research. They believe that physicians must not only have strong science backgrounds, but also possess the inquisitiveness and skill set to integrate new scientific discoveries into their work for their entire careers. The committee further felt that medical school course requirements and admissions testing, notably the MCAT (Medical College Admission Test), did not reflect the most appropriate knowledge and thought processes. In fact, many undergraduate faculty had reported that current medical school requirements and testing actually restrict opportunities for innovation in undergraduate science curricula. Such concerns had been stated in BIO 2010, published by the National Academies in 2003, and had become a topic of continued conversation since.

The Recommendations

The committee describes two sets of expected competencies: one for students, frequently undergraduates, seeking to enter medical school, and one for students completing medical school. Accompanying each competency are several learning objectives, each with examples to illustrate specific goals.

This article focuses on the undergraduate requirements because so many of us, through our teaching and in many cases our research partnerships, have an impact at that level. For these students, some of the competencies focus on a general area of knowledge – chemistry, basic physical principles, biomolecules, evolution – and how to apply that area to the study of living systems, cells, or the diversity of life on earth. One competency focuses on the process of scientific inquiry, and expects students to be able to explain how scientific knowledge is discovered and validated. Another competency asks students to apply their understanding of the principles of how molecular and cell assemblies, organs, and organisms develop structure and carry out function. Yet another competency states, "Explain how organisms sense and control their internal environment and how they respond to external change."

The remaining competency requires students to "[a]pply quantitative reasoning and appropriate mathematics to describe or explain phenomena in the natural world." The subsequent list of learning objectives provides important details. Students must demonstrate quantitative numeracy and speak the language of mathematics. Working with data sets is extremely important: students need to be able to communicate data visually and otherwise, make statistical inferences, and extract information from large data sets. Mathematical modeling, algorithmic approaches, and principles of logic should all be familiar to an applicant to medical school. The detailed examples make clear that medicine is ever-changing. Long after medical school, physicians need to seek out new studies, sometimes reading multiple data-filled sources on a topic, then sort out conflicting information and ultimately draw their own conclusions.

The Future

"A fundamental component of any curricular change is to ensure that the faculty ultimately responsible for the education of students and physicians assume responsibility for determining the knowledge, attitudes, and skills required to achieve the competencies." With this, as with several other statements, the committee from AAMC and HHMI makes clear that its report is not a mandate. Many other institutions will play their own parts in updating the expectations for medical students. Most immediately, while the committee has identified competencies, individual colleges, universities, and medical schools will determine the level of performance required within each of the competencies. Indeed, the report encourages curricular innovation, so that students can achieve excellence at the competencies via a wide variety of academic offerings.

Assessment is a longer-term project. This includes assessment of the competencies in students. The MCAT, which AAMC administers, is currently undergoing a comprehensive review. The suggestions from this report are part of those discussions. Ultimately, AAMC and HHMI plan to assess the system of competencies, its relationship to curriculum, and the assessment of students, altogether.

In time, the competencies themselves are subject to change. This is an expected and important part of the new system. For now, undergraduate programs wishing to offer a liberal arts and/or integrated science approach have a report showing the enthusiastic support of the AAMC and HHMI.

For more information, the full report: http://www.hhmi.org/grants/pdf/08-209_AAMC-HHMI_report.pdf, Report summary and other information: http://www.hhmi.org/grants/sffp.html, AAMC's home page: http://www.aamc.org/, HHMI's home page: http://www.hhmi.org/, BIO 2010. National Academies Press, 2003.

KEYSTONE SYMPOSIA™
on Molecular and Cellular Biology
Accelerating Life Science Discovery

Systems Biology of Dendritic Cells
April 2009
Keystone Symposia

Uri Hershberg

Mathematical Biology straddles two fields that traditionally have few interactions. Despite enormous recent progress, few biology conferences include sessions featuring the work of mathematical and computational biologists. We tried to address this issue by organizing a workshop on “Systems biology of Dendritic Cells” as part of the April 2009 Keystone meeting on Dendritc Cells.

Our goal was to showcase to a mostly experimental audience how computational and mathematical tools, often in direct combination with experiments, could be a key factor in the ability to pursue research in the biology of Dendritic Cells. With the help of the Society of Mathematical Biology (SMB) and the Program for Research in Immune Modeling and Experimentation (PRIME), we invited six speakers who presented cutting edge findings on dendritic cell biology where computational and mathematical methodologies played a central role. Through their specific research examples, the speakers were able to demonstrate how computational modeling can provide a framework to integrate observational data, collected from multiple modes of experimentation, and can provide insight into immune cell function in health and disease.

Judging by the turnout for our session, interest in systems biology is on the rise. The session (though one of three parallel sessions) was filled to capacity with 100+ attendees. This is in fact the second computationally-oriented workshop we have organized at a Keystone meeting with the help of SMB. The first was part of the 2006 Keystone meeting on B cells in health and disease. That session was successful enough that a similar session was also included as part at the next Keystone meeting on B cells. We hope to repeat that record with the Dendritic cell meeting.

An overarching theme of our session was the multi-scale nature of immune interactions. Presentations ranged from the level of cellular signaling, through the level of pathogen / cell interaction and up to the level of cell populations. The specific topics covered, moving from the molecular to the systemic, were:

Sonja I. Buschow (Nijmegen Center for Molecular Life Sciences) presented a novel method to use modular description to generalize the various signaling pathways of the dendritic cell.

Laszlo Nagy (University of Debrecen) presented a gene array analysis of receptor signaling in the dendritic cell and its direct relationship to lipid interactions.

Uri Hershberg (Yale School of Medicine) presented a novel method of time dependant promoter analysis that indicated that a tightly controlled transcriptional cascade controlled the first 18 hours of the dendritic cell anti viral response.

Simeone Marino (University of Michigan) described several stochastic and differential equations models of the dendritic cell’s rolls in anti-viral and anti pathogen responses.

Burkhard Ludewig (Kantonsspital, St.Gallen) presented a combination of experimental results and linked dynamic models that together described plasmacytoid dendritic cell function in cytopathic virus infection

Elodie Segura (The Walter and Eliza Hall Institute of Medical Research, Melbourne) presented a plasma membrane comparative proteomic analysis that was used to reveal the functional specialization of dendritic cell subsets.

More information can be found at: https://www.keystonesymposia.org/Meetings/ViewPastMeetings.cfm?MeetingID=986)

Keystone Symposia is a 501(c)(3) non-profit organization directed and supported by the scientific community. Keystone Symposia will serve as a catalyst for the advancement of biomedical and life sciences by connecting scientists within and across disciplines at conferences and workshops held at venues that create an environment conducive to information exchange, generation of new ideas, and acceleration of applications that benefit society.

Positions Available

Postdoc: Plant Community Ecology.

Helene Muller-Landau (Smithsonian Tropical Research Institute) is seeking a postdoc to join in investigating plant species coexistence in tropical forests. The successful candidate will work with the PI and collaborators on theory development and tests of theoretical predictions using large, species-specific, spatially-explicit data sets from tropical forests. The position is based at the Smithsonian Tropical Research Institute in Panama. Applicants should possess a background in theoretical ecology, expertise in coding mathematical and statistical models, and strong writing skills. Appointment is initially for one year, with the possibility of renewal. The starting date is flexible; earlier start dates are preferred. To apply: Send CV, one relevant publication or manuscript, and names and e-mail addresses of 3 references to Helene Muller-Landau, mullerh@si.edu. Applicants who will be attending the 2009 ESA meetings in Albuquerque should plan to meet with Helene during the meeting. Review of applications will begin immediately and continue until the position is filled.

Postdoc: Cross-scale Theory for Viral Emergence

We invite applications for a postdoctoral research fellowship to develop novel evolutionary theory for the emergence of viral pathogens across species boundaries. The post is linked to an NSF-funded project addressing the joint dynamics of viral invasion and adaptation subject to multiple scales of selection (i.e. replication within hosts and transmission between hosts). The project will build a theoretical framework based on population genetics, population dynamics, metapopulation ecology, and epidemiology, and will work with leading empirical groups to link the theory to field and experimental data. The position will be based in the lab of Jamie Lloyd-Smith (UCLA) and will collaborate closely with John Novembre (UCLA) and Sebastian Schreiber (UC Davis). We are looking for an enthusiastic and motivated individual to join our research team. The ideal candidate will have a PhD in a quantitative field, with previous experience in stochastic modeling of population genetics or population dynamics. Strong quantitative skills are essential, and good written and oral communication skills are highly desirable. The position is available as early as September 2009, and can last up to three years. Inquiries and formal applications (CV, 1-2 page statement of research interests, 2 publications, and names of 3 references) can be submitted to James Lloyd-Smith <jlloydsmith@ucla.edu>. Review of applications will begin on August 24 and will continue until the position is filled.

Postdoc: Modeling & Phylogenetics

Applications are invited for two postdoctoral research fellowships in epidemiological and ecological modeling and phylogenetics of Avian Influenza Viruses. These posts are part of a long-term collaborative project between Dr. Pej Rohani (University of Michigan) and Drs.. Drake and Stallknecht (University of Georgia). One postdoctoral position is NSF-funded and will focus on the development of mathematical and computational models relating to the persistence, transmission dynamics and evolution of Avian Influenza Viruses within North American wild bird populations. This position will be primarily supervised by Dr. Pej Rohani and the candidate will be based at the University of Michigan. The second position, funded by the James S. McDonnell Foundation will focus on the phylodynamics of avian influenza viruses. This position will be primarily supervised by Dr. John Drake at the University of Georgia. The ideal candidates would have a PhD in a highly quantitative field, with previous experience in the analysis of ecological or epidemiological systems. For further information about the University of Michigan project, contact Pej Rohani (rohani@umich.edu). For further information about the University of Georgia project, contact John Drake (jdrake@uga.edu). Applicants should send a detailed CV, together with a brief statement of research interests and three references. Review of applications will start on October 1 and will continue until the posts have been filled.

Postdoc: Modelling of Photorespiration

A postdoctoral position is available in the Systems Biology Research Group at the University of Rostock, Germany (Olaf Wolkenhauer, www.sbi.uni-rostock.de). Photorespiration represents one of the major elements in plant primary metabolism, constituting the second-most important process in the land-based biosphere. Applicants should have a strong background in mathematical and computational modeling and motivation to carry out an interdisciplinary project with experimental groups. The project is funded for an initial period of three years, with a possible extension for three more years. The salary is according to the German University payment scheme (E14) for an experienced postdoc (equivalent to a research group leader). Interested candidates should send their CV and documents in pdf format to: olaf.wolkenhauer@uni-rostock.de

Postdoc: Infectious Disease

We invite applications for two 3-year postdoctoral positions to join Professor Blower's research group in the Semel Institute at the David Geffen School of Medicine at UCLA. The positions are in Infectious Disease Modeling with particular emphasis on modeling the computational, mathematical and statistical aspects of the evolution and transmission of drug-resistant HIV in resource-rich and resource-constrained countries. Support is through two recently funded NIH grants. Applicants must have a doctorate in Applied Mathematics, Biostatistics, Biomathematics, Theoretical Biology or a closely related field. Please visit http://www.semel.ucla.edu/biomedicalmodeling/ for more information. If you are interested in either of these positions please contact Professor Sally Blower at sally.blower@gmail.com

Postdoc: Biophysical Modeling

The Wolgemuth lab at the Center for Cell Analysis and Modeling (CCAM) at the University of Connecticut Health Center is looking to fill one or two postdoctoral positions in biophysical modeling of cellular motility. These positions will use analytic and computational methods to explore the biophysics of single cell motility and the collective migration of cells in tissues, both of which are relevant and/or directly applicable to processes such as wound healing, cancer metastasis, and development. In addition, there are experimental projects in the Wolgemuth lab that will complement these theoretical investigations. CCAM is a unique interdisciplinary group that brings together cell biologists, biophysicists, biochemists, optical physicists, mathematicians, and computer scientists. These postdocs will interact with the modeling laboratory in CCAM, a small group of mathematicians and physicists immersed in an experimental biology setting, which fosters collaborative efforts integrating cell biology and physical modeling. The positions are available pending final approval of NSF funding and involve physics-based modeling which emphasizes the solid mechanics, fluid mechanics, and statistical mechanics of eukaryotic cell motility. Candidates should have a strong background in one or more of the following areas: theoretical physics/chemistry, computational physics, and applied mathematics. For more information or to apply, contact: Dr. Charles Wolgemuth, Department of Cell Biology, Center for Cell Analysis and Modeling, University of Connecticut Health Center, 263 Farmington Avenue, Farmington, CT 06030-3505, cwolgemuth@uchc.edu.

Postdoc: Eco-epidemiological System Dynamics (Cod. 038_AMB_PDESD)

We are looking a highly motivated researcher that will carry out data analysis and modelling of eco-epidemiological system dynamics within the Ace-Sap research project (http://acesap.fem-environment.eu). Tasks of the post doc are the data management and analysis, the application of statistical methods to the solutions of eco-epidemiological problems and the use of advance statistical software packages and development of specific procedure in compatible programming languages. It is required a two-year post-doc experience in fields related to statistical and mathematical eco-epidemiology. Knowledge of analysis of variance and covariance, regression techniques, non-linear model fitting and analysis of differential equations including stability analysis and matrix theory are preferred. Deadline for application: 15th of September 2009. More info at http://snipurl.com/o7apu.

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 of Mathematical Biology for its members. The Society for Mathematical Biology is an international society which 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.

Holly Gaff, Editor, editor@smb.org