Mathematical Biology Newsletter

Volume 16 #3 – September 2003

The Society for Mathematical Biology
http://www.smb.org

Edited by: Elizabeth H. Scholl

Table of Contents

Whither Mathematical Biology?

Some Remarks upon becoming President of
The Society for Mathematical Biology, August 2003

The Dundee Conference and Annual Meeting of our Society was superb not just due to the phenomenal cuisine, camaraderie, illuminating mathematical discussions on topics from cancer to divorce, and the availability of a plethora of single malts, but also because it readily illustrates why the field of mathematical biology is so relevant today. The diversity of topics presented, the excitement of the younger researchers there, and the attention paid by the popular press to the presentation by Jim Murray are all testaments to the vibrancy of the field. We all owe a debt of gratitude to the outstanding efforts by our colleagues at Dundee, most particularly Mark Chaplain, who so ably managed this gathering. As I remarked at the Annual Meeting, the field of mathematical biology, and therefore the SMB, might best be viewed as a "big tent". It embraces all those who wish to provide a firm basis in mathematics for studies of biological systems, be they highly computationally-oriented or highly analytically-oriented, or anywhere in between. This firm basis in mathematics includes model formulation and analysis in addition to concern for working on problems that are of direct interest to biologists. As presentations at the Dundee Conference illustrated in profusion, this is not math for math's sake or math in the service of computation, but math contributing to biology.

Since biology inherently includes observation and experiment, this implies that connection to data is an inherent part of the practice of mathematical biology. Indeed, Jim Murray remarked to me at the Dundee gathering how wonderful it was that there was so much application work going on. This is a major change from many years ago when there were rare papers which dealt with data and its connection to model evaluation. Math biologists today care about providing results of interest to biologists, hence we must relate our work to the data upon which much of biology is built.

In addition to the trend towards application in our work, another hallmark is the acceptance of the great diversity of math and quantitative methods to address questions. It wasn't long ago when some math colleagues would say "I know x (PDEs, ODEs, etc.) and so I'm going to apply x to this particular problem". Now it is much more common for us to choose the methods appropriate to address a particular biological problem, learning new techniques or approaches as we go, or collaborating with experts as needed. This is true applied mathematics in that we let the underlying scientific questions drive the choices of mathematical approaches we use. I do not mean to imply by this that our efforts do not drive new and interesting mathematics. This may not be our scientific objective, but it arises because our work often pushes the limits of mathematical knowledge.

The splintering of biology that has occurred over the past century has begun to affect our Society as well. Several colleagues, when I asked if they were attending the Dundee meeting, informed me that they preferred to attend gatherings of theoreticians in their own particular sub-discipline of biology, and that they didn't see the need for overall mathematical biology conferences anymore. While I can't readily perform an experimental test of the hypothesis, I would guess that had they attended the Dundee Conference, two factors might have changed their opinion (leaving aside the single malts!).

First, biology, as all of science, is done by people. Unlike the popular notion that science is driven by unfeeling, creative automatons, it is in reality a very human enterprise, and very affected by the personalities of those who practice it. For biology to continue to expand, highly quantitative people are needed with sufficient skills to understand both the biology and the mathematics (as evidence, see the large number of ads in recent issues of Science and Nature for quantitatively-oriented biologists). However the pool of creative people with strong quantitative skills is quite limited. We need to do everything we can to attract these people to the life sciences and maintain their interest.

(continued on next page)

(continued from previous page)

Gatherings such as the one at Dundee therefore provide a unique guide for these young researchers, opening a window on the applications of quantitative approaches across a diversity of biological sub-disciplines, and the people who work in these areas. Mathematical biology is now so expansive that no institution of higher learning can offer its students access to the research-level expertise across biological applications that is available at gatherings such as Dundee. The success of the SMB Mentoring Program illustrates the importance of obtaining advice from outside a particular young researcher's cadre of interactions. These gatherings serve a unique role in preparing the researchers who will be the leaders of mathematical biology in the future.

Second, you never can tell when an application in another sub-discipline will lead to that “Aha” where you realize it applies to something you've been working on (or were stuck on) in a completely different context. This is part of the power of mathematics, but mathematical techniques and approaches have become so expansive that it would be difficult for any of us, no matter how broadly versed we attempt to be, to see all the potential connections. Keeping strictly to meetings in our own sub-disciplines could lead to inbreeding of ideas and approaches. A bit of a mutation from exposure to outside influences is likely good for all our science. The reverse is also true of course - something you have been working on may be ideally modified to apply in some other sub-discipline and then watch out - you might be coerced into an entirely different area of research. Some cross fertilization benefits all areas of the life sciences.

In sum, our field and our Society have tremendous opportunities available to us in the near and long-term. The advantages of mathematical approaches are now evident and accepted throughout biology. Our challenge is to not let this opportunity be dispersed among the numerous scientific societies, but rather gather together, as the Society has accomplished so ably in the past, so as to foster cross-fertilization of approaches, and a broad education for the math biologists of the future. This requires leadership, and it is appropriate for me to end this essay with a special thanks to Mark Lewis who so ably served as President of SMB over the past two years and whose research efforts epitomize my above points regarding the benefits of taking a broad perspective in science.

Lou Gross
Departments of Ecology and Evolutionary Biology and Mathematics
University of Tennessee – Knoxville

Dear SMB members,

Would you rather receive the SMB Newsletter as hard copy (the current way), or by email?

Please let us know by emailing Meredith Greer (mgreer@bates.edu) with your preference.

Thank you,

The Publications Committee

SMB03: The View from Dundee

The Organisers' Final Report

As the summer draws to a close here in Dundee, like most other universities we are now preparing for the new semester which begins on 22nd September. Before the memories of SMB03 tend to zero (i.e. $\mathrm{Mem}_{\mathrm{SMB03}} \rightarrow 0$), we provide a report of the SMB03 Meeting from a local Dundee perspective. Like all good stories, we start at the beginning…

From a local perspective the conference began in earnest in late June with the production of all the conference material such as the book of abstracts, the programme and timetable and the delegates' welcome packs (conference bag, mouse mat and mug – more about the mug later). All material was designed by the Dundee University Design Studio following the basic ideas and images given by the Local Organising Committee, reflecting the research carried out by the Mathematical Biology Research Group at Dundee. The underlying theme of the meeting was "social aggregation" as witnessed by the images of *Dictyostelium* amoebae streaming and endothelial cell migration to sources of attracting chemicals (cAMP, TAF and VEGF). Over the course of the conference (6 - 9 August) replace amoebae and cells by conference participants and cAMP, TAF and VEGF by Côtes-du-Rhone, Shiraz and Chardonnay and a picture of how the meeting ran begins to emerge…

From our local perspective the meeting began in real earnest on Tuesday, 5th August, with registration from 2 - 5pm in the foyer of the West Park Conference Centre. After a hard afternoon handing out 225 delegate packs, badges, bags and mugs (more about the mugs later) everyone was ready for something a little more formal – cue the Civic Reception hosted by Dundee City Council on board the RSS Discovery, the sailing ship built in Dundee in the 1890s that took Captain Robert Scott on his voyage to the South Pole. Thankfully the weather was more Barbados than Baltic and the Deputy Lord Provost of Dundee, Councillor Charles Farquhar, welcomed the conference participants with the traditional Gaelic mantra "*Cead Mile Failte!"* - one hundred thousand welcomes. Further social aggregation took place before the return to West Park Centre.

The following morning, Wednesday, 6th August, after a short welcome to all delegates by Professor David Boxer, Vice-Principal of Dundee University, the conference began in scientific earnest at 9 am with an opening lecture by Professor Leah Edelstein-Keshet. The high quality of the opening presentation in style and content was subsequently maintained throughout the week as delegates were treated to a mathematical biology feast of five further Plenary Talks, the 2003 Okubo Prize lecture (Prof. J.A. Sherratt), nine Minisymposia (three talks per Minisymposium), 101 contributed talks in the parallel sessions and 50 posters (displayed throughout the meeting and with a dedicated poster session during the afternoon of Thursday 7th August). Throughout the week the four local organisers (MacAnderson, MacChaplain, MacDavidson and MacVasiev), easily visible in conference T-shirt and kilt, were on hand to field questions on a wide range of topics from bio-resource management ("what's on the menu this evening?"), through bio-fluid dynamics ("where's the nearest pub?"), pattern formation ("what tartan is your kilt?"), bio-informatics ("do you have e-mail facilities?"), computational biology ("how much is a T-shirt?") to complex interacting particle systems ("where's the SMB Board Meeting being held?").

Now that the scientific programme was in full swing, care had to be taken not to forget to maintain the social aggregation theme of the meeting. With a wine reception provided by Springer Verlag on the Wednesday evening, the afternoon of Friday devoted to organised excursions (or a free afternoon) and a sherry reception prior to the conference dinner on Friday evening, all was well.

The social highlight of the week was very definitely the Conference Dinner on Friday evening. After another splendid meal laid on by the West Park staff, out-going President Mark Lewis handed over the Presidential Stole to in-coming President Lou Gross. After a few words from President Gross, we were into the final phase of the evening - the award of the prizes. Having made the Springer poster prize awards to P. Namy, R. Salinas and A. Matzavinos, it was time for the final event of the evening, "The D'Arcy Thompson Look-a-Like Competition". With such a high quality field of entrants, the panel of judges had a very difficult task in choosing the winners. However, in a closely fought contest and after much debate the top three places went to:

3rd place: Prof. P. Maini
2nd place: Dr. Nick Britton
1st place: Prof. J.D. Murray

(continued on next page)

(continued from previous page)

After the presentations of the prizes there was time for one last round of social aggregation…

In summing up we would like to thank everyone for their participation and helping make the conference a success – even the weather was good!! Finally, special thanks go to the main sponsors of the meeting: the Engineering and Physical Sciences Research Council of the UK (EPSRC), Scottish Enterprise and GlaxoSmithKline (particularly Frank Tobin).

See you all next year in Michigan,

Haste Ye Back!

The Conference Organisers
SMB03

P.S. For those participants who have not already done so – please fill your conference mug with HOT liquid and all will be revealed (literally!).

SMB Dundee Report

by Brynja Kohler

The conference kicked off with *Discovery*! It certainly was an "ice-breaker" to tour around the Royal Research Ship (*RRS Discovery*) built for Antarctic exploration. Before wine and appetizers, SMB participants had plenty of time to get to know one another as we played around with the various hands-on exhibits at the museum and toured the ship. We all got checked in at the conference site by our warm and friendly hosts, who were easy to spot in their black SMB T-shirts and tartan kilts. Then, after lost baggage managed to roll in Wednesday morning, Leah Edelstein-Keshet started the scientific content of our meeting with her plenary talk on the immunology of autoimmune diabetes.

The meeting could be quickly summarized by: terrific talks, stimulating questions, discussions, reunions and introductions. I particularly enjoyed an Ecology session of contributed talks which included a great talk by Jerome Percus (Courant Institute) on small population effects in dynamical models. Frank Lynch (University of Utah) reports a "very interesting talk" by Steven Webb (Loughborough University) about models of ligand-receptor interactions in the Developmental Biology Minisymposium. Frank says, "He talked about uniting models by Collier et al. (1996) and Wearing et al. (2000). The pattern formation was driven by the combination of positive and negative feedback (locally). At the end of the talk, he alluded to the biological existence of long range connections. I'd be interested to know how this distant feedback influences the system." More topics included cancer models, cell motility, stochastic PDE, virus strains, reaction-diffusion equations, simulations, integral equations, epidemics, forests and bears, pattern formation and molecular motors. Our Okubo Prize Lecture by Jonathan Sherratt began with some illustrative demonstrations of Mexican Waves, and then stressed the significance of boundary conditions to yield periodic travelling waves in his model of field voles. This meeting's talks certainly had something for everyone -- even Scotland's tabloid newspapers found something to write about when James Murray gave his plenary talk on how to predict marital misery or marital bliss.

Between talks, popular hangouts included various local pubs, walks past the parks along the Firth of Tay, and the line for the four internet computers we all shared. (Can someone please tell those kids to get off those chat sites so we can do some science?) Aside from the over-salted aubergine, the conference fare was delicious and certainly plentiful. In particular, participants raved about the breakfasts, all the desserts, the curry, salmon and of course the £1 lager in the conference pub (which was especially enjoyable to sip while out on the front lawn in the evenings). On Friday, many of us enjoyed a distillery tour and the taste of a single-malt in Pitlochry, while others toured the castle Blair Atoll. That evening, the banquet dinner was full of laughs. James Keener, Wolfgang Alt, Aaron Fogelson, Nick Britton, and Philip Maini were all awarded recognition (even parrots!?) for their resemblance to D'Arcy Thompson (1860 - 1948) , with special recognition made to James Murray. Mark Lewis began a new tradition of passing along a presidential stole from Ghana to Lou Gross as he takes on his new responsibilities as SMB president. On Saturday after some final excellent talks, plenty of heat-activating mugs were left over as rewards for those of us who booked our flights out late enough. Some of us went on to explore the rest of Scotland or catch some Festival shows in Edinburgh, while the poor Brits immediately went home and back to work. :)

The University of Michigan's Preliminary Report for SMB 2004

We have determined the best possible dates for the meeting to be July 25th - July 28th. The co-chairs of the conference are Patrick Nelson, Trachette Jackson, and Carl Simon from Mathematics and David States, Director of program in Bioinformatics. We have numerous people from UM who have agreed to serve on the local organizing committee. An updated web site with this information can be found at:

http://www.math.lsa.umich.edu/~pwn/SMBindex.html

Conference attendees will be housed in hotels located on campus where we have already reserved blocks of rooms at the university rate. There is also more affordable student housing available for our student attendees. We have contracted UM's conference planning to handle all aspects of on-sight and online registration and for all exchanges of funds. We have also contracted a conference planner to handle the logistics of meeting space, audio-visual, catering and lodging. We are negotiating a reduced fair with Northwest Airlines for participants. We have lined up a wonderful class of plenary speakers including:

Dr. Michael Waterman, University of Southern California
Dr. James Sneyd, Massey University
Dr. Alan S. Perelson, Los Alamos National Lab
Dr. Charlie Peskin, Courant Institute
Dr. Simon Levin, Princeton University
Dr. Tamar Schlick, NYU
Dr. Rakesh Jain, Harvard
Dr. Bard Ermentrout, University of Pittsburg

Conference themes include:

1. Computational Biology (bioinformatics, genetics and biofluid dynamics)
2. Medical Applications (infectious diseases, cancer, neurobiology and physiology)
3. Developmental Biology (cell signaling, receptor-ligand binding and pattern formation)
4. Ecology (animal movement and population dynamics)
5. Complex Systems Modeling (delay differential equations in biology, stochastic differential equations in biology and non-linear dynamics)

We have a web site set up for the conference which will allow for easy registration, abstract submission, local information and schedules. We plan on soliciting more mini-symposia topics in November and abstracts for contributed sessions in March.

* * *

Reminder: Sources of Good Information

Below is just a small selection of upcoming meetings that may be of interest to SMB members. For a more comprehensive list, as well as links to the meetings' websites, please visit the SMB website's meeting page at: http://www.smb.org/meetings. Other important information and announcements, including job openings, new publications and important upcoming deadlines relevant to the SMB, can be found be reading the digest.

Workshop on Discrete Models for Genetic Regulatory Networks
November 5-6, 2003, Hilton Conference Center College Station, Texas, USA

Digital Biology: The Emerging Paradigm
November 6-7, 2003, Bethesda, Maryland, USA

Red Raider Minisymposium on "Mathematical and Computational Modeling of Biological Systems"
November 6-8, 2003, Texas Tech University

Third Brazilian Symposium on Mathematical an Computational Biology
November 24-26, 2003, Rio de Janeiro, Brazil

Neural Information Processing conference
Dec 8-10 2003, Vancouver, Canada

Carla Wofsy 1944-2003

Carla Wofsy passed away on August 4. She and her husband Byron Goldstein were dear friends for many years, so it is natural for me to write of her personally. A comprehensive professional assessment seems out of place when the pain of her loss is still fresh.

Carla was diagnosed with breast cancer 26 years ago. Treatment submerged the symptoms for 20 years, but the disease then reappeared and required numerous methods to keep it at bay. Throughout all this Carla remained active and forward-looking; her wonderful warm sensitive and intelligent soul shone as always.

Trained in probability (Berkeley and Wisconsin), Carla years ago decided to become interested in mathematical biology. She was directed to a Gordon Conference as a way to get introduced into the field. Good advice, for there she met Byron.

When her disease became more threatening, Carla took early retirement from the Mathematics Department at the University of New Mexico, where she won awards for her dedicated teaching. She joined Byron at the Los Alamos National Laboratory to continue, even more intensively, their years of remarkable collaborative research. Their work centered on modeling the molecular-level complexities of signal transduction. They were leaders in the field because of their wisdom in working very closely with leading experimentalists, coupled with their wide-ranging combined abilities in mathematics, physics, and biology.

I was privileged to be at Carla's funeral in Santa Fe. Scores of friends and colleagues gathered to hear beautiful, detailed, appreciations of Carla by her brother David and her friend and UNM colleague Ruth Kovnat. Notable amidst the sad recounting of what we all lost were gleams of humor, recalling high moments from the past. Carla would have liked that.

Lee Segel

Surf the Next Wave to Boost Your Career

Kirstie Urquhart, European Editor, Science's Next Wave

Science's Next Wave (www.nextwave.org) is a weekly, online, career development magazine aimed at postgraduates, post-docs and junior group leaders. Ideally, every early career scientist would get the mentoring they need, from their PI, or through schemes such as the SMB's own meeting mentoring program. But not everyone is fortunate enough to find a mentor who can give them the advice they need at the right time.

Which is why Next Wave was founded, back in 1995, to provide a platform for peer-to-peer mentoring. Our original strap line, "for young scientists, by young scientists," reflected that ethos. We changed it, because we didn't want to exclude anyone who could use Next Wave's help, be they mature students, or early career scientists who were no longer "young" because of career breaks and the like. But our spirit remains the same. Next Wave is a place where early career scientists can benefit from the experience of others.

We cover the sorts of issues that can still, unfortunately, seem taboo: work-life balance, juggling the needs of bringing up a family or a partner who is also a scientist with those of your own career development, what it's like to be a scientist from an ethnic minority background or with a disability. Our columnists offer advice on job hunting, writing up your thesis or research papers, and setting up your lab. Our news articles keep you informed of the latest funding opportunities and science policy developments which affect the job market for scientists. And if you decide that the academic career track is not for you, you can read about how other scientists have used their scientific training as a door-opener to a vast range of other careers, from patent law, to grants administration, to science writing and editing.

Access to all this is free to readers in Europe and Canada, and to readers at subscribing institutions in the United States - if you're based elsewhere and would like to have a look at what Next Wave has to offer, please get in touch. Whatever your career question, we hope that you can find some guidance somewhere on Next Wave. After all, our archive stretches back 8 years! But if you can't find the answers, or have a story to tell that you think would help other early career scientists, we'd love to hear from you! Please email me at kurquhart@science-int.co.uk

Reasons to Be Involved in the Activities of SMB (& Other Professional Societies).

Ramit Mehr, publications committee chair

In almost every SMB meeting I find myself trying to recruit volunteers for some SMB activity, such as the publications committee. To convince people to volunteer I often have to explain why it is good for the individual, especially the junior faculty or student, to participate in organizing activities or join the various committees; so I decided to share this insight with all SMB members, in the hope of having an easier time recruiting volunteers or soliciting Newsletter submissions in the future.

We all know the reasons why NOT to volunteer our free time for “public service” activities. Students are busy with course duties and research; post-docs want to focus on research, in order to be able to compete for an independent position; and once we have finally secured our first independent position, our life revolves around the tenure issue – how long will it take to get there, how much do we have to achieve to get there, and how does one survive the overwhelming amount of teaching, grant writing and service work and still manage to do any research – and I haven’t even mentioned the career-family balance issue yet… Once a person reaches the tenured stage, they are burdened with even more obligations and duties, or so I am told.

I’ve had more than my fair share of the above difficulties in all stages of my career so far, and it’s not over yet. However, in spite of that, I have been involved in SMB activities – mainly the publications committee, but quite a few other projects as well – in the last decade or so. Moreover, this involvement has so far been immensely rewarding, not just in terms of the satisfaction of initiating various projects and seeing them grow, but also in its contribution to the advancement of my career. The best example to make this point is the story of how I got involved with the publications committee. When I was still a grad student, in the days before the World Wide Web (www) took over, I offered to create, with Ray Mejia, an ftp database of all the information that might be useful to SMB members: job openings, funding opportunities, meetings, etc. Need I spell out the use of such an endeavor? All the available information was passing my desk on its way to being archived – which made sure I don’t miss anything that was good for me! This is how I learned, for example, about the Association of Women in Science, and the Association of Women in Mathematics (see the Women’s Resources page I put on the SMB website for details): I was told about them by colleagues who wanted to spread the word. I took membership in these two associations, got many useful materials from AWIS, and had my travel to no less than three meetings funded by the AWM!

I probably need not elaborate on the importance of going to meetings and interacting with colleagues. About 9 out of 10 of my current collaborations, including the ones with whom I have two significant research grants, are with experimentalists I met in various meetings; so knowing about meetings was also very helpful. Furthermore, my last three positions (two post-docs and my tenure-track position at BIU) were obtained through contacts I originally met in SMB meetings. My involvement with publications, which has grown into chairing the publications committee, has led me to participate in quite a few SMB board meetings in the last few years. From these, I have learned a great deal about the management of scientific activities – and this knowledge is directly applicable to other areas of my work. My efforts of soliciting Newsletter articles covering the activities of regional societies a few years ago have raised the awareness to the needs of biomathematicians in developing countries, and eventually led to the creation of the SMB world outreach committee. I expect that, in the long run, encouraging research and education activities throughout the world will increase the selection of interesting locations for future SMB meetings! My “instigation” of the mentoring program, and various other actions aimed at preventing discrimination and helping junior scientists, may not directly help my career at this stage, but will certainly help my students, and this will hopefully return to me as “revenue” in terms of these students’ success.

The most important benefit, however, is the fact that through the SMB I have acquired a number of lifelong friends, who are much more than colleagues, who have supported me in times of need, and are still supporting me in all stages of life. I hope that the above stories have convinced all readers to rush and volunteer to help in various SMB activities – just contact me, the “to-do” list is still quite long!

Bulletin of Mathematical Biology – Some Facts and Figures

Santiago Schnell and Philip K. Maini,
Editors of the *Bulletin of Mathematical Biology*

The Society for Mathematical Biology owns the *Bulletin of Mathematical Biology* (BMB). This is a world class journal devoted to the interface of mathematics and biology. In this report, we present a brief history of the journal and report on how the journal impact factor has grown substantially in the last few years.

History of the Bulletin

The BMB was first published in March 1939 with the title *Bulletin of Mathematical Biophysics* as a supplement to the journal *Phychometrika*. The Bulletin was published in March, June, September and December and was devoted to publications of research in mathematical biophysics, as contributing to the physico-mathematical foundations of biology. The papers covered physico-mathematical theories as well as any other mathematical treatments of biological phenomena, with the exception of purely statistical studies. The Bulletin was sent free to all members of the Psychometric Society.

The *Bulletin of Mathematical Biophysics* was founded by Dr Nicolas Rashevsky, who is generally recognised as the founder of the first organised group in Mathematical Biology in the world. This group had been formed at the University of Chicago in 1947 as the interdisciplinary Committee on Mathematical Biology from the previous one on Mathematical Biophysics. The latter had been founded by Rashevsky in 1934 after obtaining a Rockefeller Fellowship on the basis of his many investigations of the mathematics of biological phenomena, in particular the effects of surface tension and diffusion drag forces during cell division and nerve excitation.

The *Bulletin of Mathematical Biophysics* quickly became the classical journal in general mathematical biology and served as the principal natural publication outlet for the majority of mathematical biologists. Many classical papers have appeared in the Bulletin and several of these are familiar to biologists. It has become an important avenue for the exchange and transmission of new ideas and approaches to biological problems and incorporates both the quantitative and qualitative aspects of mathematical models and characterisations of biological processes and systems.

Dr Rashevsky remained the editor of the *Bulletin of Mathematical Biophysics* until his death on January 16th, 1972. During the last year of his life he founded *Mathematical Biology, Inc.* which became the publisher of the Bulletin. In June 1972, Volume 34, Number 2, he was succeeded by Herbert D. Landahl from University of California at San Francisco (Chief Editor), and George Karreman from University of Pennsylvania and Anthony F. Bartholomay from the Medical College of Ohio at Toledo working as editors.

In February-April 1973, Volume 35, Numbers 1-2, the *Bulletin of Mathematical Biophysics* was re-titled the *Bulletin of Mathematical Biology* and became the official journal of the recently incorporated Society for Mathematical Biology. The BMB continued to be published bi-monthly and the editorial policy remained the same as that of its predecessor, the *Bulletin of Mathematical Biophysics*. The annual dues for membership in the Society for Mathematical Biology were $25, which included a subscription to the Bulletin. Herbert D. Landahl continued as Chief Editor with Hugo M. Martinez as Assistant Editor until Volume 43, Number 6, 1981. Hugo Martinez took over as Chief Editor in Volume 44, Number 1, 1982 with Julie S. Ransom (The University of California, San Francisco) as Editorial Assistant. They retired in 1986, Volume 48, No. 3/4. Lee A. Segel from the Weizmann Institute of Science, Israel, became the first non-American editor of the Bulletin in Volume 48, No. 5/6, 1986. Lee Segel in his Editorial Announcement of Volume 49, No. 1, pp. i-iv, 1987, changed the scope of the journal to offer the publication of research at or near the interface of theoretical and experimental biology. An ideal article for the Bulletin would be a symbiotic combination of theory and experiment. Lee Segel also welcomed papers providing documentation of a purely theoretical advance together with a clear exposition of how this advance furthers biological understanding. Philip K. Maini became the present editor in 2002, Volume 64, Number 1. As he mentioned in his Editorial (Volume 64, No. 1, p. 1), he took over as editor of the Bulletin at a very exciting time for mathematical biology. The advances made in molecular biology over the past three decades have resulted in the generation of a vast amount of experimental data. The need to understand this data requires the development and analysis of mathematical and computational models; this is increasingly recognised as a number of interdisciplinary centres have recently been set up for modelling in life sciences and more faculty positions are being advertised.

(continued on next page)

(continued from previous page)

This also confirms the great insight shown by those who set up and worked as editors for this particular journal, and it is reflected in the present position of the BMB in the Journal Citation Reports.

Bulletin in the Journal Citation Report

The Journal Citation Reports (JCR) is a comprehensive and unique resource for journal evaluation from the Institute of Scientific Information (ISI)[1]. It is employed by scientists, universities, research institutes, publishers and government to evaluate the impact of journals in the scientific community, and also to select preferred journals in which to publish. The JCR can show you the highest impact journals, most frequently used journals, "hottest" journals and largest journals. It uses citation data drawn from over 8,400 scholarly and technical journals worldwide, collected from 1981. Coverage is both multidisciplinary and international, and incorporates journals from over 3,000 publishers in 60 nations.

The most widely used index from JCR is the journal impact factor, which is a measure of the frequency with which the "average article" in a journal has been cited in a particular year. The impact factor is calculated by dividing the number of current citations to articles published in the two previous years by the total number of articles published in the two previous years. This index helps to evaluate a journal's relative importance, especially when compared to others in the same field. In the table below we show the JRC results for the BMB in the year 2002.The trends in the impact factor show that the BMB has increased its impact from 0.980 in the year 1997 to 1.408 in 2002. In fact, the impact has been increasing from 2000 when it was 1.002 and 1.316 in 2001. The JCR gathers journals into subject categories for comparison with journals in the same field. The Bulletin is in two subject categories: "Mathematics (Interdisciplinary Applications)" and "Biology (General)".

In the subject category "Mathematics (Interdisciplinary Applications)", the BMB is ranked 7th in a list containing 30 journals, if the list is sorted by the impact factor. The top journal is *Econometrica* (2.737), *Journal of Computational Neurosciences* (1.855), *Educational & Psychological Measurement* (1.661), *Journal of Mathematical Psychology* (1.641), *Archive for Rational Mechanics and Analysis* (1.585). However, these journals are not strictly mathematical biology journals. The BMB is the top mathematical journal with interdisciplinary applications to biology and medicine. We show this in the following table:

Rank	Abbreviated Journal Title	2002 Total Cites	Impact Factor	Immediacy Index	2002 Articles	Cited Half-life
1	Bull. Math. Biol.	974	1.408	0.178	45	8.3
2	Math. Biosci.	1609	1.080	0.141	71	>10.0
3	Biometrics	7469	1.077	0.115	96	>10.0
4	J. Math. Biol.	1219	0.980	0.283	53	>10.0
5	Biometrika	6742	0.970	0.117	77	>10.0
6	IMA J Math. Appl. Med. & Biol.	215	0.658	0.333	3	7.5
7	Biometrical J	287	0.250	0.071	70	8.0

In the subject category "Biology (General)", the BMB is ranked by impact factor in 21st position out of 62 general biology journals. The top journal on this category is *Bioessays* (7.888), followed by *FASEB Journal* (7.252), *Biological Reviews* (5.730), *Quarterly Review of Biology* (5.200), *Philosophical Transactions of the Royal Society of*

---

[1] ISI Journal Citation Report® is a product of the Thomson Corporation (http://www.isinet.com). It is delivered via Journal Citation Reports® on the Web (http://jcrweb.com) or via CD-ROM. The web service for UK Education is http://wok.mimas.ac.uk.

(continued from previous page)

London Series B – Biological Sciences (3.410). There only two journals above the BMB which accept mathematical biology papers, these are the *Proceedings of the Royal Society of London Series B – Biological Sciences* (3.396), now known as *Proceedings: Biological Sciences*, and the *Journal of Theoretical Biology* (1.552).

Rank	**Abbreviated Journal Title**	**2002 Total Cites**	**Impact Factor**	**Immediacy Index**	**2002 Articles**	**Cited Half-life**
1	Proc. Roy. Soc. Lond. B Biol.	12798	3.396	0.478	347	6.0
2	J. Theor. Biol.	7501	1.552	0.273	238	>10.0
3	Bull. Math. Biol.	974	1.408	0.178	45	8.3
4	Math. Biosci.	1609	1.080	0.141	71	>10.0
5	Biometrics	7469	1.077	0.115	96	>10.0
6	J. Math. Biol.	1219	0.980	0.283	53	>10.0
7	Biometrika	6742	0.970	0.117	77	>10.0
8	Biosystems	806	0.846	0.112	80	6.5
9	Comput. Biol. Med.	430	0.814	0.125	40	7.7
10	Theor. Biosci.	78	0.705	0.167	12	
11	IMA J Math. Appl. Med. Biol.	215	0.658	0.333	3	7.5
12	C. R. Acad. Sci. III – Vie. *	1842	0.528		0	9.4
13	Acta Biotheor.	264	0.522	0.000	13	>10.0
14	J. Biol. Syst.	98	0.282	0.000	26	
15	Riv. Biol.- Biol. Forum	72	0.220	0.083	12	

* Re-titled *Comptes Rendus Biologies* in 2002.

Note that in these tables we show other indices. Citation and article counts are important indicators of how frequently current researchers are using individual journals. By tabulating and aggregating citation and article counts, the JCR offers another perspective for journal evaluation and comparison. Citation counts are an acknowledgment to previously-published research, publicly recorded in the references listed by contemporary authors. This is measured by the **2002 Total Cites** column in the raking tables. It indicates the total number of times that each journal has been cited by all journals included in the *ISI* database during the period 1981-2002.

The **2002 Articles** column shows the number of articles published in each journal in 2002. Editorials, letters, news items, and meeting abstracts are not included in article counts because they are not generally cited. The journal **Immediacy Index** is a measure of how quickly the “average article” in a journal is cited. The immediacy index indicates how often articles published in a journal are cited within the same year. It is calculated by dividing the number of citations to articles published in a given year by the number of articles published in that year. The immediacy index is useful for comparing how quickly journals are cited. Because it is a per-article average, the Immediacy Index tends to discount the advantage of large journals over small ones. However, frequently issued

(continued on next page)

(continued from previous page)

journals may have an advantage here, because an article published early in the year has a better chance of being cited than one published later in the year. For comparing journals specializing in cutting-edge research, the Immediacy Index can provide a useful perspective.

The **Cited half-life** is the number of publication years from the current year which accounts for 50% of current citations received. This index evaluates the age of the majority of cited articles published in a journal. Only those journals cited 100 or more times have a cited half-life. A higher or lower cited half-life does not imply any particular value for a journal. For instance, a primary research journal might have a longer cited half-life than a journal that provides rapid communication of current information.

Journals citing articles published in BMB

The *JCR* also identifies those publications that most frequently cited a particular journal. These citation links can reveal a journal's subject orientation, point to its closest peer or competitor publications, and describe specialty-specific networks of journals. The BMB has received 974 citations since 1981. The journal citing most articles in the BMB is the *Journal of Theoretical Biology* with 41 references to the Bulletin. It is followed by *Physical Review E* citing articles 32 times in the BMB. These two journals are followed by *Bulletin of Mathematical Biology* (24 citations), *Mathematical & Computer Models* (24 citations), *Journal of Mathematical Biology* (22 citations), *Biosystems* (18 citations), *Proceedings of the Natural Academy of Sciences of USA* (16 citations), *Bioinformatics* (15 citations), *IMA V Math* (15), *Ecological Modelling* (14), *Journal of Computational Biology* (12), *Biophysical Journal* (11), *International Journal of Bifurcation and Chaos*, *Network-Computation in Neural Systems*, *SIAM Review* and *Zeitschhrift fur Physikalische Chemie – International Journal of Research in Physical Chemistry & Chemical Physics* have cited articles 10 times in the BMB, *American Naturalist*, *Indian Journal of Pure & Applied Mathematics*, *Lecture Notes on Computer Science*, *Physica A* all have 9 references to BMB, *Ecology* has 8 references to BMB; *Applied Mathematics & Computation*, *Chaos, Solitons & Fractals*, *Mathematical Biosciences*, *Mathematical Model & Methods in Applied Sciences*, *Nature*, *Neurocomputing*, *Proceedings of the Royal Society of London Series B – Biological Sciences*, *Physica D*, *Theoretical Computer Science* all have 7 citation to the BMB; *BioEssays*, *International Journal of Engineering Science*, *Journal Computer & System Sciences* and *Theoretical Population Biology* have 6 references to the BMB. The rest of the citations are in journals citing the BMB five or less times, among these journals we can find *Trends in Ecology & Evolution*, *Nucleic Acid Research*, *Physical Review Letters*, *Annual Review of Genomics & Human Genetics*, *Behavioural & Brain Science*, *Journal of Biological Chemistry*, *Journal of Molecular Biology*, *AIDS*, *Diabetes*, *Genome Research*, *Journal of Neuroscience*, *Journal of Virology*, *Neuroimage* and *Systematic Biology*.

This shows that the BMB is making an impact in the experimental community as well as in the theoretical community. However, it is vital that we do not become complacent. We must continue to increase the awareness among our experimental colleagues of articles in the BMB.

An expanded version of this report detailing the different areas of research in which articles have recently appeared in the BMB will be published in the journal.

Studentships in Ecological Modeling, University of Guelph

Opportunities are available for Ph.D. studentships in ecological modeling at the University of Guelph, Canada. Students are to be co-supervised by Professor Madhur Anand (Canada Research Chair in Biology, Laurentian University, Sudbury) and Professor Chris Bauch (Mathematics and Statistics, University of Guelph). Possible topics include, but are not limited to: models for forest growth, self-organized criticality and facilitation. Techniques to be used include cellular automata, matrix simulation models, individual-based models, and other spatial models.

For further details, please email manand@nickel.laurentian.ca or cbauch@uoguelph.ca and enclose a curriculum vitae with a covering letter. Due to the volume of inquiries, it may unfortunately not be possible to reply to all emails.

Trends in Biomathematical Research: A Series of Mini-Reviews.

Ramit Mehr

Note: the publications committee intends to solicit a series of brief (2-3 pages) reviews of current research in the various sub-fields of mathematical biology, such as: Developmental Biology, Ecology, Epidemiology, Immunology, Molecular Biology, Morphology and Pattern Formation, Neurobiology, Pharmacology, Physiology, Population Biology, Computational Biology and Bioinformatics. These reviews are intended for the benefit of all readers, and may also later serve as a basis for promotional materials for the SMB.

To start this series, I wrote the mini-review below on the contributions and challenges of theoretical immunology. This is a very general mini-review, focusing on the reasons why modeling is necessary in immunology, rather than on past work. The latter is reviewed only briefly, mentioning a few sample review or research articles; there was no intention to give a full review of this rich and diverse field.

We (the publications committee) would very much appreciate receiving additional such articles; please contact me if you are willing to volunteer to write one.

Mathematical and Computational Modeling in Immunology: Contributions and Challenges.

Ramit Mehr

Biological systems, from the genetic and molecular to the ecological, are the most complex systems studied by contemporary science. Understanding biological systems on the level of detail necessary for generating predictions is a formidable challenge, which can only be met by using mathematical and computational tools of simulation and analysis. One such challenge is the detailed study of cellular systems, in which processes occur simultaneously on multiple levels: genetic and molecular processes form the biochemical programming and inputs determining each single cell's behavior, while the observable behavior of the system as a whole is the sum total of the behaviors of all participating cells and the complex interactions between them.

A good example for the complexity of biological systems is the vertebrate immune system. The adaptive immune system of vertebrates is one of the only two biological systems capable of continuously learning and memorizing its experiences. This is a distributed system, in which recognition of pathogens (harmful agents), decision-making and action are performed by an interacting network of specialized cells – primarily lymphocytes, with each lymphocyte expressing a receptor specific for a particular antigen (foreign or self molecule or parts thereof). Unlike the nervous system, where information is encoded in the system's structure (synaptic connections between neurons), immune system cells are in constant motion, surveying the organism for signs of damage. Hence all the information is encoded in the numbers and locations of cells of each type, and their activation status.

The main cell types of the immune system's cells [1] are: antigen presenting cells, B and T lymphocytes, and Natural Killer (NK) cells. B lymphocytes produce pathogen-binding antibodies, while T lymphocytes specialize in either killing of virus-infected or malignant cells (killer T cells), or helping with and coordinating the communication between all immune cells (helper and regulatory T cells). Antigen presenting cells are those who first encounter the antigen, engulf and digest it, and present parts of it to helper T cells, thus activating the adaptive, antigen-specific response. Each B or T lymphocyte expresses a receptor which is specific for one molecular structure (antigenic epitope), such that the organism contains rich repertoires of B and T lymphocytes expressing very different receptors. Immune learning and memory are embedded in the dynamical states of the complete lymphocyte repertoire, and cannot be understood by studying the behavior of single cell types. This complexity, further increased by the non-linear behavior of each component, can only be elucidated by using theoretical tools to complement experimental and clinical studies.

Classical theoretical immunological research uses mathematical modeling of whole cell and pathogen populations. Mathematical models have been used to elucidate the complex interactions between the immune system and bacteria

(continued on next page)

(continued from previous page)

[2] or viruses [3,4], including the human immunodeficiency virus which attacks the immune system itself. Such models have led to improvements in anti-viral therapy [5]. Similarly, models for cancer chemotherapy have led to optimization of the treatment, such that the damage to the tumor is maximized while minimizing the damage to the immune system and other drug-sensitive body cells [6]. Mathematical models have also been used to understand the development of immune system cells [7] and the regulation of the immune response [8], and how these processes change in pathological situations, such as immunodeficiency [9], or during natural ageing [10].

In spite of the tremendous benefits of classical models, they usually neglected – for reasons of mathematical tractability, or due to lack of sufficient experimental data – the inherent diversity in the rich, co-evolving repertoires of both lymphocytes and pathogens. More complex models are needed to study the forces shaping lymphocyte repertoires, including the generation of antigen receptor repertoire diversity through interacting processes of antigen receptor gene rearrangement, the selection of useful and weeding of potentially harmful lymphocytes, the subsequent fine-tuning of the repertoires by clonal selection and (in B lymphocytes) somatic hypermutation as a result of encounters with antigens, and the changes to these dynamics under various immune-deficient conditions. Similarly, pathogen repertoires utilize rapid mutation, antigenic variation, or other ways of evading the immune system; such that the two types of repertoires – of pathogens and lymphocytes – are continuously co-evolving.

The difficulty in modeling lymphocyte repertoires does not result from the astronomic numbers of lymphocyte clones in the human patient or the experimental animal, because studies on a smaller number of clones can often give sufficient insight into the behavior of the whole system. The main difficulty stems from the need to formulate a description of the system on several levels: genetic, molecular, cellular and systemic [9]. For example, when studying T cell development, the rearrangement of T cell receptor genes, and the selection based receptor interaction with its ligand (major histocompatibility (MHC)-peptide complexes), must be taken into account if one is to understand the rare events that lead, e.g., to the escape of auto-reactive T cell clones (which may lead to autoimmune disease) or to lack of responding cells for specific pathogens. Similarly, multi-level descriptions are required in order to understand the dynamics of pathogen repertoires, and the co-evolution of pathogen and lymphocyte repertoires. Hence it is not only the population dynamics within each clone (i.e., cell division, differentiation and death processes) that must be modeled, but also the *meta-dynamics*: creation, selection and elimination of whole clones in the population, and the discrete genetic changes or complex molecular interactions that form the basis for these meta-dynamics. Modeling these complex processes is the challenge that theoretical immunologists currently face.

Suggested reading (references given are only samples and do not intend to reflect the whole body of research in this field).

1. Textbooks in immunology: most recommended: Janeway, Travers, Walport and Capra, Immunobiology: the Immune System in Health and Disease, Garland Publishing, New York.
2. Theoretical and experimental approaches for studying factors defining the Helicobacter pylori-host relationship. Falk PG, Syder AJ, Guruge JL, Kirschner D, Blaser MJ, Gordon JI. *Trends Microbiol*. 2000; 8(7):321-9.
3. Mathematical models of HIV pathogenesis and treatment. Wodarz D, Nowak MA. *Bioessays*. 2002; 24(12):1178-87.
4. Modelling viral and immune system dynamics. Perelson AS. *Nat. Rev. Immunol.* 2002; 2(1):28-36.
5. Hepatitis C virus kinetics. Herrmann E, Neumann AU, Schmidt JM, Zeuzem S. *Antivir. Ther.* 2000; 5(2):85-90.
6. A computer algorithm describing the process of vessel formation and maturation, and its use for predicting the effects of anti-angiogenic and anti-maturation therapy on vascular tumor growth. Arakelyan L, Vainstein V, Agur Z. *Angiogenesis.* 2002; 5(3):203-14.
7. Regulatory feedback pathways in the thymus. Mehr R., Perelson A. and Globerson A. *Immunol. Today*, 1997; 18:581-585.
8. How instruction and feedback can select the appropriate T helper response. Bergmann C, van Hemmen JL, Segel LA. *Bull. Math. Biol*. 2002; 64(3):425-46.
9. T cell dynamics in HIV-1 infection. Clark DR, de Boer RJ, Wolthers KC, Miedema F. *Adv. Immunol*. 1999; 73:301-27.
10. Effects of age on antibody affinity maturation. Dunn-Walters DK, Banerjee M, Mehr R. *Biochem. Soc. Trans*. 2003; 31(2):447-8.
11. Modeling the Meta-Dynamics of Lymphocyte Repertoires. Mehr R. Arch Immunol Ther Exp 49:111-120 (2001).

ICIAM 2003

Raymond Mejia

The 5th International Congress on Industrial and Applied Mathematics was held in Sydney, Australia during July 7 - 11, 2003.Registration exceeded 1700 with approximately 1700 presentations. Among the many invited talks, minisymposia, and contributed and poster sessions were several on biomathematics topics.

Invited speakers included Nancy Kopell and Peter Deuflhard. Nancy, in a talk titled "Rhythms of the Nervous System: Biophysics and Dynamical Systems", described rhythmic electrical activity and cognitive behavior, while pointing to several levels of study: animal, functional networks, larger but local networks, small networks and single cells. Using examples, Nancy showed how different biophysics corresponds to different dynamical structure in the rhythms, with implications for function. Peter Deuflhard, in his talk titled "New Math for New Drugs against New Diseases", described Perron cluster analysis techniques applied to identify meta-stable molecular conformations for use in drug design. See http://www.iciam.org/iciamHome/iciamHome_tf.html for abstracts of invited talks.

Areas of presentations in minisymposia and contributed and poster sessions included bioinformatics, ecology, evolutionary biology, epidemiology, immunology, genomics, modeling diseases, modeling fluids, neuroscience, physiology and structural biology. Session topics included:

Blood Flow and Waves
Cardiac Modeling
Cell Signaling and Chemical Dynamics
Developmental Biology: the Role of Domain Growth
Developmental Biology: the Role of Signaling Systems
Epidemiology
Genes/Organ Modeling/Ecology
Mathematics in Medical Imaging
Mathematics in Medicine
Mathematics in Medicine; Today's Challenges
Pattern Formation in Neuronal Systems
Recent Developments in Nonlinear Techniques for Neural systems
Reef fish - Dispersion, Connectivity and Marine Reserve Design
Tumor Dynamics
Tumor Modeling

Search for abstracts at http://www.iciam.org/alt_abstracts/cgi-bin/talks.cgi

---

First Announcement:

The 9th International Conference on Difference Equations and Applications

ICDEA-9

ICDEA-9 (Main theme: Mathematical Biology) will take place on August 2 - 6, 2004 at the University of Southern California located in Los Angeles under the auspices of the International Society of Difference Equations.

Organizers: Robert J. Sacker, chairman (rsacker@math.usc.edu), Saber Elaydi (selaydi@trinity.edu), Don Lutz (lutz@math.sdsu.edu) and George Sell (sell@math.umn.edu).

Further details, including names of the plenary speakers, will be posted on the WWW as they become available. See http://math.usc.edu/~rsacker or the web site of the International Society of Difference Equations, http://mywebpages.comcast.net/dedds/isde.html for links soon to be added.

The Faces of SMB

Pictures from the 2003 Annual Meeting

Each year, after the annual meeting, we like to publish some pictures taken at the meeting so that those who were able to attend could look back fondly, and those unable to attend might be able to see some of their fellow SMB members. This year we decided to have a photo contest.

The winners are…..

FIRST PLACE

Fishing? Philip Maini examining the prize he got in the D'Arcy Thompson look-alike contest

SECOND PLACE (tie)

The ideal formula for divorce: Mark Chaplain presenting a newspaper article reporting on Jim Murray's recent research.

SECOND PLACE (tie)

Fashion Tips - the men in kilts are SMB 2003 conference staff.

Mark Lewis presenting Lou Gross with the Presidential Stole

Andreas Deutsch experiences some Scottish culture

Gerda de *Vries, Leah Edelstein-Keshet, Nalini Joshi, Meghan Burke and Mary Myerscough enjoy the unusually sunny weather in Scotland*