The Society for Mathematical Biology

SMB NEWSLETTER

VOLUME 24 #1 - JANUARY 2011

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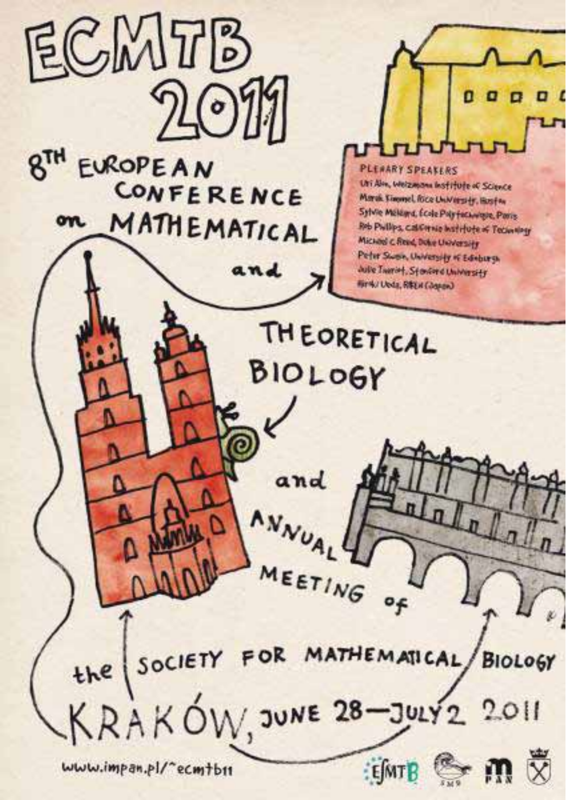


Mark your calendars!

European Conference on
Mathematical and Theoretical
Biology 2011
http://www.impan.pl/~ecmtb11/

The joint triennial meeting of
the European Society for
Mathematical and Theoretical
Biology
and annual meeting of the
Society for Mathematical Biology

will be held in

Kraków, Poland
June 28 - July 2, 2011

Dear SMB members,

2010 is rapidly drawing to a close, as are classes for the past semester. For some the semester will not end until in January, while for others the last lectures have been given and exams set and marked along with term papers in some cases. My own course, Mathematics 437 (Mathematical Modeling in Biology) ended the first week of December, and once again I was blessed with an absolutely outstanding group of 15 super keen and bright young minds that pushed and pulled my own mind with their learning and questioning. As I was grading the terms papers that reported on their individual or group research investigations, I came across three that could easily be turned into publishable work with some more effort. As always I am awed with the intelligence and keenness of our young students, and once again reminded why I enjoy teaching so much. It is just plain fun watching our students stretch their minds and their imaginations (and their teachers too!).

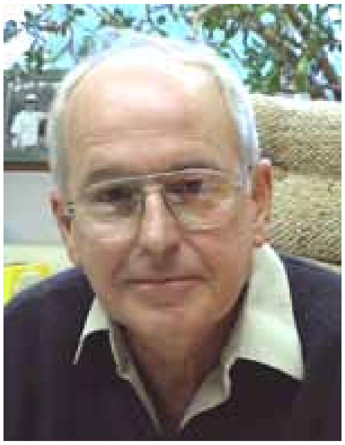
I have just come from two weeks in Mexico—the first week at the recent inaugural First North American Meeting on Industrial and Applied Mathematics held on the idyllic campus of the Universidad del Mar, Huatulco, Oaxaca México. The campus is literally a botanical garden and was a lovely setting for a rich variety of talks on many aspects of applied mathematics—including a lively day and a half of biomathematics. The meeting was jointly organized by the Sociedad Matematica Mexicana, the Society for Industrial and Applied Mathematics, and the Canadian Applied and Industrial Mathematical Society. It was great fun to meet up with colleagues who I had not seen for some time, and equally delightful to make new acquaintances with many Mexican colleagues who I knew only by name. The end of the week was capped by a lovely weekend in Tolcayuca, the village where one of my younger colleagues (Moisés Santillán Zeron) had grown up, savoring the sights and sounds and tastes of small-town Mexican life. My second week in Monterrey (at the Centro de Investigación y Estudios Avanzados del IPN Unidad Monterrey) was equally delightful. Having a chance to talk science for several uninterrupted days was a treat, and to see the vibrancy and youthful enthusiasm of biomathematics in Mexico again reinforced my conviction that the field is in the ascension.

What was memorable about the two weeks in Mexico aside from the science? First, the impressions of the Mexican people as a lovely, warm and outgoing group full of the zest of life. Secondly, the incredible array of wonderful flavors in Mexican cuisine to tempt the taste buds. The TexMex served up in Montreal is a sham offering of the culinary delights available in Mexico. The feeling of safety in walking the streets of Huatulcoa and Monterrey, a far different impression than one receives from news reports from North of the Mexican border. Yes, there are problems in Mexico, and they are severe but they are not paralyzing. As a North American neighbor, I realize that the USA and Canada are prime contributors to the problems that Mexico has in dealing with the drug trafficking problem. We are, after all, the major market for the drugs that define the problem, and our governments are, also, the origins of the obstacles that the Mexican government faces in trying to cope with the problem. The American (and hence Canadian) government's inability to face the reality of the drug usage problem has led to a schizophrenic and insoluble impasse in my opinion.

Enough serious stuff. As 2010 draws to a close, I wish all SMB members a good end to the first decade of the 21st century. Our next annual meeting will be held jointly with the ESMTB in Krakow, and Ryszard Rudnicki from Katowice and his team have been doing an exemplary job of organization (see http://www.impan.pl/~ecmtb11/index.php?file=main.html). I hope to be able to welcome many of you there as it promises to be a wonderful scientific meeting in one of Europe's loveliest historical settings.

Have a good end of the decade, rest and reflect, and return in 2011 renewed and refreshed.

Sincerely,
Michael Mackey



News from NIMBioS

Recent events at NIMBioS:

NIMBioS/ESA Ecology Education Webinar. An EcoEd Webinar: Math, Computing, Undergraduate Ecology Education and Large Datasets: An Example from a Citizen Science Program, sponsored by NIMBioS and the Ecological Society of America (ESA), was held Sept. 8, 2010. To view the archived webinar in its entirety, visit http://www.nimbios.org/press/ecoedwebinar_resources

NIMBioS Tutorial on High Performance Computing for Phylogenetics, Oct. 13-15. The HPC for Phylogenetics taught participants how to use TeraGrid, the CIPRES Portal, the iPlant Discovery environment, university clusters, and other typically free HPC resources for phylogenetic analysis. Besides NIMBioS, other co-sponsors were iPlant and the National Institute for Computational Sciences. http://nimbios.org/tutorials/TT_hpc2010

NIMBioS Investigative Workshop on Mathematical Modeling of Wildlife and Virus Zoonoses, Nov. 8-10. The goals of this workshop were to define, discuss, and develop approaches to collaboratively address critical gaps that remain in mathematical modeling of the ecology and natural history of zoonotic viruses. http://www.nimbios.org/workshops/WS_zoonoses.html

Undergraduate Research at the Interface of Mathematics and Biology, Nov. 19-20. More than 100 undergraduates from around the country attended the second annual Undergraduate Research Conference at the Interface of Biology and Mathematics. http://www.nimbios.org/education/undergrad_conf2010

Upcoming events and opportunities at NIMBioS:

Requests for Support. March 1 is the deadline for submitting proposals for new scientific and educational activities at NIMBioS. http://www.nimbios.org

NIMBioS Tutorial on Multi-cell, Multi-scale Modeling, May 18-21, 2011. To be realistic and predictive, biological models need to cover a broad range of scales from intracellular to multi-cell to whole organs and beyond. http://nimbios.org/tutorials/TT_multicell_modeling

NIMBioS REU/REV Summer Program, May 31 – July 22, 2011. Undergraduates in math, biology and related fields; veterinary students; and high school math and biology teachers are encouraged to apply. http://www.nimbios.org/education/reu2011 and http://www.nimbios.org/education/rev2011

See NIMBioS website for more information regarding:

NIMBioS Investigative Workshop on Malaria Modeling and Control, June 15-17, 2011.

NIMBioS Investigative Workshop on Modeling Johne's Disease, July 6-8, 2011.

NIMBioS Investigative Workshop on Mathematical Models of Metabolism and Body Weight Regulation, July 12-15, 2011.

Joint 2011 MBI-NIMBioS-CAMBAM Summer Graduate Program, July 25 – Aug. 5, 2011.

NIMBioS Investigative Workshop on Modeling Renal Hemodynamics, Aug. 1-3, 2011.

News from MBI

Workshop 3: Ecology and Control of Invasive Species, Including Insects (February 21-25, 2011) www.mbi.osu.edu/2010/ws3description.html

Workshop 4: Insect Self-organization and Swarming (March 14-18, 2011) www.mbi.osu.edu/2010/ws4description.html

Current Topic Workshop: New Developments in Dynamical Systems Arising from the Biosciences (March 22-26, 2011) www.mbi.osu.edu/2010/ddsdescription.html

Workshop 5: Coevolution and the Ecological Structure of Plant-insect Communities (April 4-7, 2011) www.mbi.osu.edu/2010/ws5description.html

Current Topic Workshop: Modeling and computation of biomolecular structure and dynamics (April 25-29, 2011) www.mbi.osu.edu/2010/mltdescription.html

Workshop 6: Ocean Ecologies and their Physical Habitats in a Changing Climate (June 20 - July 1, 2011) www.mbi.osu.edu/2010/ws6description.html

2011 Summer Graduate Program (July 25-August 5, 2011) www.mbi.osu.edu/eduprograms/graduate2011.html

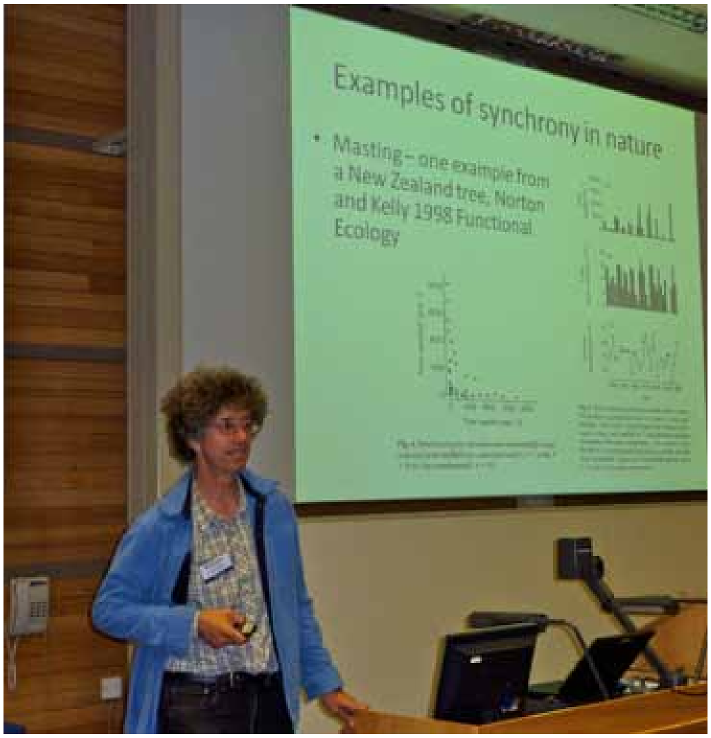
Report on Animal Movement, Dispersal and Spatial Ecology Modeling Meeting

Christina Cobbold

September 1-3, 2010, the University of Leicester in the UK hosted the conference: Models in Population Dynamics and Ecology 2010: Animal Movement, Dispersal and Spatial Ecology. This was my first time attending this conference series, which has now entered its fourth year. This year there were 63 participants from 16 countries; the diversity of participants really fostered some great discussions.

The organizers, Sergei Petrovskii and Andrey Morozov put together a great programme of talks which included an exciting mixture of plenary talks by Nick Briton, Helen Byrne, Alan Hastings, Richard Law, Horst Malchow, Nanako Shigesada and Igor Sokolov.

The main theme of the meeting was spatial population dynamics, and the modelling approaches presented were diverse, from classical PDE modelling to Markov chain models and evolutionary game theory. The problems that were addressed were equally diverse, spanning insect foraging and spread of infections across networks to predator-prey dynamics and their relevance to vascular tumor growth. In his inspiring talk on spatial synchrony Alan Hastings also revealed that UK's old London buses had found a new home in Davis. Horst Malchow revealed the true location of Osnabrück before giving a great talk on competitive invasion.



Alan Hastings gives a talk on synchrony

You will be able to read more about the research presented at the meeting in a special issue of Theoretical Ecology which will appear sometime in 2011. There are already plans afoot for future meetings in this series, with the meeting becoming international in 2012, heading to Santa Maria in Brazil and then on to Osnabrück in Germany in 2013.

In the conference closing remarks, Sergei Petrovskii observed that 'the interdisciplinary nature of the talks could almost be described as a cooking recipe: 'take 1/3 biology 1/3 math 1/3 physics and add some stats and cook on a slow fire'. In reply Karl Hadeler charmed the audience with his summing up of the conference: 'There has been a good mix of real biology, data mining, statistics and real mathematics and a nice crowd. It was nice to see all the young people interact, even with the old people like me!'

Participants at the meeting enjoy tea breaks socializing and discussing research presented

BEER 2010

Olcay Akman

The Symposium on Biomathematics and Ecology: Education and Research (BEER-2010) took place in Normal, IL on September 4-5, 2010. The third meeting of its series attracted about 100 participants with nearly 60 presentations in biomathematics and ecology.

The presentations featured problems from various disciplines, such as mathematics, biology, ecology, statistics, physics and actuarial science. Curriculum development and biomathematics education issues were also discussed in several parallel sessions as well as in half-day long workshops.

The meeting was sponsored by the Illinois State University (ISU) Department of Mathematics, School of Biological Sciences and College of Arts and Sciences as well as the Department of Mathematics and the Colleges of Science of Benedictine University (BU). Participation of several junior researchers was supported by travel grants from the Society for Mathematical Biology.

The local organizing committee members were Olcay Akman and Steve Juliano from ISU and Tim Comar from BU. Among many parallel sessions, Hannah Callender of University of Portland organized two sessions and moderated a panel discussion on biomathematics education, while Saziye Bayram of Buffalo State College organized a session on biomathematics modeling.

Survey: “Who is a Mathematical Biologist?”

Maya M. Shmailov, a graduate student at the “Science, Technology and Society” program at Bar Ilan University, Israel, is researching the history of mathematical biology, with a particular interest in the development of the expertise of mathematical biology. As part of her research, Maya is conducting an online survey to find out who is the modern-day Mathematical Biologist, to gain a better understanding of their field of practice.

Everyone in the field of mathematical biology - from students to veterans - is invited to fill in this online survey. The survey will be online until March 15th. We would be very grateful for your participation.

The results of Maya’s research will then be published in the Bulletin of Mathematical Biology.

Link: https://www.kwiksurveys.com?s=HCJIGL_62ad154

Submitted by: Ramit Mehr, The Mina & Everard Goodman Faculty of Life Sciences, Bar-Ilan University

Participants in the Symposium on Biomathematics and Ecology: Education and Research 2010

My Career in Mathematical Biology
A Personal Journey

Albert Goldbeter

Many paths lead to Mathematical Biology. I started my journey by studying Chemistry at the Université Libre de Bruxelles (ULB). During my studies, I was much influenced by a series of remarkable teachers in the life sciences. A key bifurcation occurred after I presented my examination in Quantum Mechanics to the satisfaction of my teacher, who was a coworker of Ilya Prigogine. He asked me what my plans for the next year were, and when I told him that I intended to do my Master thesis in the field of enzymology and cellular regulation, he suggested me to talk to Prigogine, who had a long-standing interest in self-organization phenomena, and was turning, he said, to the study of biological systems. Thus, I went to see Ilya Prigogine, who was later to receive the Nobel Prize in Chemistry (in 1977). He was a formidable charismatic figure, enthusiastic, and generous with students. After listening to him for half an hour, I was so enthralled that I decided to do my Master thesis in his group, on the mathematical modeling of spatiotemporal organization in an enzymatic system. This I did under the guidance of René Lefever, who was only a few years older than me. I was hooked: instead of moving afterwards to biochemistry, I went on to do my PhD in Prigogine's group, on the analysis of an allosteric model for glycolytic oscillations, under the guidance of René Lefever and Grégoire Nicolis. My first article published on this work appeared in 1972. I remember that one referee wrote "the scientific value of this paper is nil", while the other two reviewers thought that the paper warranted immediate publication! I never forgot this initial experience, which taught me that referees should be constructive rather than destructive, and that one should not get too discouraged by negative comments!

At the end of my PhD I spent two years of post-doctoral work at the Weizmann Institute of Science, in Rehovot (Israel). Much of my time was devoted to the preparation of a review article with Roy Caplan on oscillatory enzymes. I was also fortunate to meet there Lee Segel, who had recently arrived as the new head of the department of Applied Mathematics. I was close to Lee for many years, and miss him dearly. With him I worked on the mechanism of oscillations and relay of cyclic AMP during the aggregation of Dictyostelium amoebae. Even if the period was initially not well suited to scientific research —I arrived one month before the Yom Kippur war—, the situation gradually changed and I fully benefited from this truly unique environment. I vividly remember the smell of orange trees when emerging around midnight from an evening of work at the computer center. During this period I also traveled to Germany where I briefly worked on glycolytic oscillations in yeast, both experimentally and theoretically, with Benno Hess at the Max-Planck Institute in Dortmund. From him I learned the importance of comparing theoretical predictions with available experimental data.

I returned to Brussels where I first had a non-tenured appointment at ULB. After a few years, at the end of the seventies, I decided to move again, this time to California, where I spent two memorable years in Berkeley, working with Dan Koshland. For the next decade I returned every summer to Berkeley, where I often worked in cafés around the campus. Initially I focused on models for adaptation in bacterial chemotaxis. In the course of this work we observed that sharp thresholds may occur in systems regulated through reversible phosphorylation. The paper describing this phenomenon, which we called "zeroorder ultrasensitivity", is one of my best research achievements: although it was barely noticed for some 20 years, with the rapid rise of Systems Biology it was cited hundreds of times in the last decade.

After my return from Berkeley I eventually secured a tenured position at ULB, where I built a unit of theoretical chronobiology within the department of Physical Chemistry headed by Ilya Prigogine. I was lucky to pursue my work on modeling biological oscillatory behavior with brilliant students over the years, thus focusing, with Olivier Decroly on chaos and multiple oscillatory regimes (birhythmicity), with Jean-Louis Martiel on the role of receptor desensitization in cyclic AMP signaling in Dictyostelium, and with Yue-Xian Li (now in UBC, Vancouver) on frequency coding in pulsatile intercellular communication.

A new chapter of activity opened when Michael Berridge came to Brussels for a series of lectures in 1988. We initiated a collaboration, which led to the publication of a minimal model for calcium oscillations based on the role of IP3 and calcium-induced calcium release. During this most fruitful collaboration, Geneviève Dupont joined us and did her PhD in my group, within which she pursues her work on modeling calcium oscillations and waves. Yet another great experience was the development of a minimal cascade model for the mitotic oscillator driving the early cell cycles in amphibian embryos. I soon left this topic (but later returned) to study models for circadian oscillations in Drosophila and to publish a book in 1996 on biochemical oscillations and cellular rhythms, of which a new edition is underway.

The next step was to extend with Jean-Christophe Leloup the Drosophila model to the mammalian circadian clock, while with Didier Gonze we investigated the robustness of circadian rhythms with respect to molecular noise. Using the mammalian model allows us to obtain insights into human syndromes associated with dysfunctions of the circadian clock.

I later worked with Olivier Pourquié, who discovered the segmentation clock, on modeling the role of bistability and oscillations in somitogenesis. More recently, I returned to modeling the dynamics of the cell cycle, this time in mammals. With Claude Gérard we analyzed a 39-variable model for the cell cycle, while with another PhD student, Atilla Altinok, and with a French oncologist, Francis Lévi, we used an automaton model for the cell cycle to probe the effect of circadian delivery of anticancer drugs.

My fascinating journey in Mathematical Biology thus brought me from one rhythm to another, and from surprise to surprise. What I like most in research are the encounters with colleagues and friends, and the interactions with experimentalists and students. Working in academia is a unique privilege: I cherish the freedom in selecting research topics and the creative aspects of the work. What I appreciate less is the pressure to submit more and more research proposals, too many of which eventually fail...

I never regretted my choice of focusing on the mathematical modeling of regulatory networks that underlie cellular rhythms. This topic exemplifies many aspects of the field now known as Systems Biology and possesses a strong aesthetic component. The mathematical approach gives a broad perspective and allows one to move easily from one topic to another, while retaining a global perspective. In selecting a research topic, the best is certainly to follow one's own deep interests, rather than obeying to transient, fashionable trends. As the French designer Coco Chanel said: fashion is what comes out of fashion!

Selected publications

A. G., R. Lefever. Dissipative structures for an allosteric model. Application to glycolytic oscillations, Biophys J (1972), 12, 1302-1315.

A. G., L.A. Segel. Unified mechanism for relay and oscillations of cyclic AMP in Dictyostelium discoideum, Proc Natl Acad Sci USA (1977), 74, 1543-1547.

A. G., D.E. Koshland, Jr. An amplified sensitivity arising from covalent modification in biological systems, Proc Natl Acad Sci USA (1981), 78, 6840-6844.

O. Decroly, A. G. Birhythmicity, chaos, and other patterns of temporal self-organization in a multiply regulated biochemical system, Proc Natl Acad Sci USA(1982), 79, 6917-6921.

A. G., G. Dupont, M.J. Berridge. Minimal model for signal-induced Ca++ oscillations and for their frequency-encoding through protein phosphorylation, Proc Natl Acad Sci USA (1990), 87, 1461-1465.

A. G. A model for circadian oscillations of the Drosophila period protein (PER), Proc R Soc Lond B (1995), 261, 319-324.

A. G. Biochemical Oscillations and Cellular Rhythms: The molecular bases of periodic and chaotic behaviour. Cambridge University Press, Cambridge, UK, 1996.

D. Gonze, J. Halloy, A. G. Robustness of circadian rhythms with respect to molecular noise, Proc Natl Acad Sci USA (2002), 99, 673-678.

C. Gérard, A. G. Temporal self-organization of the cyclin/Cdk network driving the mammalian cell cycle, Proc Natl Acad Sci USA (2009), 106, 21643-21648.

A. Altinok, D. Gonze, F. Levi, A.G., An automaton model for the cell cycle, Interface Focus (2011), 1, 36-47

OCCAM
OXFORD CENTRE FOR COLLABORATIVE APPLIED MATHEMATICS

Profs. John Archer, Philip Maini and Jim Murray

OCCAM Conference on Modeling at Different Scales in Biology: 2010

Amina Eladdadi

The Oxford Centre for Collaborative Applied Mathematics (OCCAM) at the University of Oxford organized a conference on Modeling at Different Scales in Biology during a gorgeous early-summer week of June 21-23, 2010. The conference was hosted at St. Anne's College in the charming city of Oxford, famously known for its medieval university and its rich and controversial history. The organizers were professors Paul Bressloff, Jonathan Chapman, David Gavaghan and Philip Maini from the OCCAM. The conference was sponsored by King Abdullah University of Science and Technology (KAUST). The aim of this three-day meeting was to bring together leading scholars from a number of disciplines faced with multi-scale challenges and from mathematical disciplines able to address these challenges. The conference included presentations from twelve international endowed mathematicians and senior scientists actively involved in the research of mathematical models of biological phenomena. The conference program included twelve plenary talks and a poster session.

The president of OCCAM, John Ockendon, kicked-off the conference by welcoming all of the attendees to Oxford. The plenary talks were given by Jim Murray (Oxford, UW, Princeton), "Vignettes from a mathematician's odyssey in biology and medicine"; Alain Goriely (OCCAM), "Continuous modeling and mechanics of proteins"; Benoit Perthame (Université Pierre et Marie Curie, France), "Adaptive evolution: a population view"; Mark Alber (Notre Dame, US), "Multiscale Modeling of Bacterial Swarming"; Michael Mackey (McGill, Canada), "Intrinsic and extrinsic noise effects on molecular distributions in bacteria: A modeling study"; Wolfgang Alt (University of Bonn, Germany), "Elementary mechano-chemical models for analyzing and understanding cell motility"; John Tyson (Virginia Tech, US), "Modeling Mammalian Signal Transduction Networks That Control Cell Growth, Division and Death"; Juan Soler (Granada, Spain), "Do morphogen gradients arise by diffusion?"; Leah Edelstein-Keshet, (UBC, Canada), "How do ducks line up in rows: Inferring individual rules from collective behaviour"; Helen Byrne (Nottingham, UK), "Applications of multiscale modelling to solid tumour growth"; Lisa Fauci (Tulane, US), "Multiscale models: Biological fluid dynamics of swimming and pumping"; Hans Othmer (Minnesota, US), "Multi-Scale Deterministic and Stochastic Analysis of Reaction Dynamics"; John Archer (Cambridge, UK), "Bio research at KAUST".

A total of 43 posters (eleven from the OCCAM) were presented by young researchers. The poster session centered on multiscale modeling of a wide range of biological problems such as cancer,

Prof. Helen Byrne and postdocs working during coffee break

Group discussion during the coffee break

population dynamics, wound healing, epidemics, ecology, to name a few. The modeling approaches were diverse and ranged from novel variations on classic ODE and PDE models, to stochastic and other hybrid models. This poster session provided an opportunity for young researchers to present their work and to interact directly with expert researchers in the field of biomathematics, which will eventually lead to developing long term collaborations. The conference was the perfect size and was perfectly timed to fit with some beautiful sunny summer days which set the scene for many outside discussions during the coffee/tea breaks. The conference schedule allowed for many informal and meaningful discussions and interactions between senior and junior scientists over coffee breaks, lunch, dinner and the reception. The organizers got very positive feedback from the participants who expressed interest in similar meetings in the near future. The program structure of this OCCAM conference was clearly beneficial for stimulating interdisciplinary dialog and providing participants with an understanding of the theory and modeling at different scales in biology.

On behalf of all participants, I would like to thank all of the speakers for their outstanding talks. I would also like to thank the organizers, particularly Prof. Philip Maini and the staff at OCCAM, for their guidance, assistance, and hospitality. Finally, I would like to acknowledge the financial support of the Society for Mathematical Biology and the School of Math and Sciences at the College of Saint Rose.

A detailed description of the conference can be found here: http://www.maths.ox.ac.uk/groups/occam/forthcoming-events/occam-conference-modelling-different-scales-biology

Participants at the poster session

Positions Available

Postdoc, Mathematical Biology

Applications for a one-year (renewable up to three years) post-doc fellowship at the Mathematical-Biology group at the Institute for Theoretical Physics, São Paulo State University, Brazil, are welcomed. The applicant should hold a PhD either in Physics, Applied Mathematics or Theoretical Ecology, obtained after 2006. The group focus is in application of population biology to ecological problems. We foster collaboration with biologists/ecologists and the successful applicant should be motivated to work in an interdisciplinary setting. The group is presently formed by Roberto Kraenkel and five PhD students. Please see http://www.ift.unesp.br/users/kraenkel. Funding is provided through the São Paulo State Science Funding Agency (FAPESP, http://www.fapesp.br/en/). The present value of the fellowship is R$ 5000/month, approx. 2200 euros per month, or US$ 2900 per month. Application process is twofold, a first selection taking place at the group, and the final decision taken by FAPESP. Candidates should send an e-mail to Roberto Kraenkel kraenkel@ift.unesp.br with a CV and a statement of interests. Further details may be asked later. The position remains open until a suitable candidate is found and confirms interest.

Research Assistant/Postdoc, Viral Pathogenesis

This job is to provide high-level scientific support to facilitate several projects using high-throughput technology (deep sequencing) to study the pathogenesis of HIV and hepatitis C (HCV) infections. This position is funded by an NHMRC Program Grant investigating the immunopathogenesis of HIV and HCV infections with a view to vaccine development. The appointed person will be involved in several scientific projects within the Program, which share a common theme of deep sequencing datasets. This is a full time position, fixed term for one (1) year, with the possibility of a further extension being offered, contingent upon ongoing funding. The position is based at the University of New South Wales, but the collaborative projects in the Program are partly based at the University of Melbourne and the University of Adelaide. The successful applicant will have the opportunity to contribute to a range of projects. The selection criteria are: high-level quantitative skills, and the ability to pick up statistical and bioinformatics techniques to analyse deep sequencing data. Masters (required) or PhD (desirable) in bioinformatics, Statistics, Physics, Mathematics, or related fields. Demonstrated research activities in biostatistics or bioinformatics. Demonstrated experience working in a research environment. Highly experienced computing skills. Knowledge of statistical package, such as R, and programming script languages (Python, Perl). Knowledge of OHS responsibilities and a commitment to attending relevant OHS training. Any queries regarding the application process may be addressed to Fabio Luciani, email: luciani@unsw.edu.au

Postdoc, Modelling of Viral Evolution

A post-doctoral position funded by the Australian Research Council is available at the University of New South Wales (UNSW), Sydney, Australia. The successful applicant will be part of a collaborative team involved in modelling the evolution and epidemiology of viruses. The investigators of the team are Mark Tanaka and Peter White (UNSW), Katia Koelle (Duke University) and Roland Regoes (ETH Zurich). The post-doctoral researcher will develop mathematical models, implement computer simulations, and design statistical methods to analyse genomic data. The successful applicant will have the opportunity to contribute to a range of projects. The selection criteria are: a PhD in a quantitative discipline such as theoretical biology, bioinformatics, mathematics, statistics, physics or computer science; a strong research track record in mathematical modelling or biostatistics; an interest in viral evolution; proficiency with Linux or Unix and computer programming languages, preferably C and R; excellent oral and written communication skills; the ability to work effectively as part of a team as well as independently; knowledge of OHS responsibilities and a commitment to attending relevant OHS training; knowledge of equal opportunity principles. For the full information package see http://www.hr.unsw.edu.au/services/recruitment/jobs/26111020.html. Informal enquiries to Mark Tanaka, email: m.tanaka@unsw.edu.au

Postdoc, Mathematical Medicine

The Centre for Mathematical Medicine (CMM), hosted at the Fields Institute, invites applications from candidates for two Fields-CMM postdoctoral fellowships of a duration of one year to commence July 1, 2011 (or on a negotiable date thereafter). Candidates should have strong interest in current interdisciplinary activity at the Centre. While positions are open to all areas of mathematical medicine and biology, preference will be given to those individuals whose research is concerned with the current principal areas of CMM focus: mathematical oncology, computational neuroscience, bioinformatics, or biomechanics of soft tissues. In particular, we are looking for individuals interested in collaborative interaction with clinicians and experimentalists. The fellowships provide for a period of engagement in research and participation in the Centre's activities. They award a stipend of $20,000 and are offered in conjunction with a Fields Affiliate or Principal Sponsoring University. The partner institution matches Fields' support, and fellows may also teach (at most) one university course per semester for an additional stipend. On the cover sheet of your application, please list any faculty members at these partner institutions who may be appropriate supervisors. You are encouraged to apply directly to these universities as well. Applicants seeking postdoctoral fellowships funded by other agencies (such as NSERC or international fellowships) are encouraged to request the Fields Institute as their proposed location of tenure, and should apply to the Institute for a letter of invitation. Eligibility: Candidates who will have a recent PhD (awarded normally not more than five years before tenure of the Fellowship) in any of the above fields, or a related area of the mathematical sciences, are encouraged to apply. The Fields Institute is committed to diversity and welcomes applications from women, members of First Nations or visible minorities, persons with disabilities, members of sexual minority groups, and others who may contribute to the diversity of ideas. To guarantee consideration, applications should be received by April 1, 2011 (late applications will be accepted until the positions are filled). Applicants must apply through https://www.mathjobs.org/jobs/jobs/2677

Graduate program, Cell Analysis and Modeling

The Graduate Program, part of Ph.D. in Biomedical Sciences, specifically targets students with backgrounds in mathematical or physical sciences and provides students with interdisciplinary training at the interface of cell biology, biophysics, chemistry and computation. Combined Ph.D./M.D. and Ph.D./D.M.D. programs are available. Information about CAM is available at http://www.ccam.uchc.edu/cam/cam_predoc.html and http://grad.uchc.edu/prospective/programs/phd_biosci/concentration/cellanalysis_mod/index.html websites. Information about graduate studies at UCHC is available at http://grad.uchc.edu/prospective/index.html. Please contact the Program Director Charles Wolgemuth at cwolgemuth@uchc.edu with any questions.

Postdoc/PhD: Epidemiology/Delay DEs

Applications are welcome to the newly established EPIDELAY research group at the Bolyai Institute, University of Szeged, Hungary. Bolyai Institute is one of the major mathematical research centers in Central Europe. A strong group, led by Tibor Krisztin, already works on nonlinear functional differential equations. Applications in epidemiology will add a new research direction. The EPIDELAY team is funded by ERC and led by Gergely Rost. The main goal of this research group is to build and strengthen bridges between functional differential equations and practical epidemiology, thus applicants are welcome from both directions. Salaries are set to Hungarian scale, starting date is negotiable. CV and the contact information of two reference persons are to be submitted to epidelay@math.u-szeged.hu

Postdoc, Control of Brain Dynamics in Epilepsy

A postdoctoral position is available in collaborative group of Drs Talathi and Khargonekar and Carney (Dept of Pediatrics and Electrical and Computer Engineering) at the University of Florida, Gainesville, US. Our ongoing research is in the general area of applications of computational neuroscience and control systems for epilepsy. The work initially will focus on the development of computational models and control strategies using optogenetic actuation signals to control pathological brain activity implicated in epilepsy. There will also be ample opportunity to test the resulting controllers in an experimental set up involving animal models of epilepsy. The postdoctoral associate will be expected to interact with faculty, postdoctoral associates, and graduate students within the group, make presentations regarding his/her research, to publish high quality papers in peer-reviewed journals, and to assist in grant proposal preparation. Candidate should have a PhD degree in a relevant discipline (electrical engineering, applied mathematics, computational neuroscience, and related fields). A deep interest in interdisciplinary collaboration, strong quantitative skills and good oral and writing skills are expected. While prior knowledge of dynamical modeling in neuroscience and control theory is not required, individuals with strong background in these fields are particularly encouraged to apply. The salary will be commensurate with the qualifications and experience of the individual. The initial appointment will be for one year, with renewal for two or more years subject to satisfactory progress and mutual agreement. Interested candidates should submit their curriculum vitae, a statement of interest and the names and contact information of three references to Sachin Talathi (talathi@ufl.edu) or Pramod Khargonekar (ppk@ece.ufl.edu). Review of applications will begin December 15th 2010 and will continue until a suitable candidate is identified.

Editor's Notes:

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

The SMB Newsletter is published in January, May and September by the Society for Mathematical Biology for its members. The Society for Mathematical Biology is an international society 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 web site: http://www.smb.org for more information.

Holly Gaff, Editor, editor@smb.org

Don't Forget to Renew for 2011!!

If you haven't already renewed, we would like to invite you to renew your Society for Mathematical Biology membership for 2011. If you have already renewed, thanks!

There is one important change to the membership process this year. Springer has increased the number of issue of the Bulletin of Mathematical Biology to 12 issues per year! While this is wonderful news, it comes at a price with regards to mailing hard copies. To keep our membership prices down, we have kept membership prices the same as last year for those who only need electronic access to BMB issues. For those who would still like to receive paper copies in addition to the on-line version, the fee will be an additional US$25.

As a reminder, here is how it works.
Please go to:
http://www.smb.org/membership/index.shtml
or directly to:
https://payments.botany.org/joinsmb/index.php
If you provided SMB with your email address or renewed on-line in the past, you are in the database and can use the "Renew your membership with the Society" option. Your username is generally your e-mail address unless you changed it to something else. If you have forgotten your password, simply fill in your email in the "Forgot your login details" section and push "Send reset details". This will send you an automatically generated email with a link to login. If your email address isn't recognized, please email hgaff@odu.edu to request your login information.

You can use this renewal process to pay on-line using a credit card, or you can opt to send a check by mail. We encourage you to use the on-line process either way, as it will allow you to fill in your address accurately. There is also a pdf version of the membership application form on the first link given above. This form can be filled out and mailed or faxed as instructed on the form.

Please let us know if you have any troubles. One quick troubleshooting trick to try is to clear your Internet browser cache if you get an error and then try again.