2005 Annual Meeting of The Society for Mathematical Biology

We are glad to announce the forthcoming ECMTB05: European Conference for Mathematical and Theoretical Biology, Dresden, Germany, July 18-22, 2005, http://www.ecmtb05.org.

ECMTB brings together scientists from all over the world and will be THE event in 2005 to communicate the recent advances in mathematical and theoretical biology with a focus on ten selected key topics: Cellular biophysics, Regulatory networks, Development, Neural systems and the brain, Evolution and ecology, Immune system, Biomedical applications, Biotechnology, Innovative mathematical methods, and Inter-disciplinary education.

ECMB05 is the sixth tri-annual conference of ESMTB and the annual meeting of SMB.

Letter from the President

Dear SMB members,

As my term of office as President of our Society winds down, I wish to thank the many individuals who selflessly give their time (and financial support) to help the SMB maintain its activities. As a volunteer organization, we could not survive without the devotion of Board members, committee members and chairs, meeting organizers, and our officers. The current health of SMB arises in great part due to the volunteer spirit among our members, and I greatly appreciate all the wonderful people who have provided advice and assistance over my term. I know that incoming President Mark Chaplain will appreciate your continuing assistance and I encourage you to answer affirmatively if he requests your help.

As an educator, I have come to understand quite well the value of repetition in assisting the learning process. While SMB members are certainly adept at learning new fields in order to carry out research in our highly interdisciplinary area, it may still be beneficial for me to repeat some of the themes of my earlier letters. First, despite the fractioning of biology into numerous sub-disciplines, there is a great advantage to maintaining some contacts across these sub-fields. The unifying conceptual frameworks of mathematical modeling and analysis have so often found utility across quite different fields that it would be a shame if SMB members did not at least occasionally delve into areas they have had little experience with in order to learn about potential new conceptual approaches that might be beneficial for their own work. Some of the most fascinating scientific gatherings I've attended over the years have been ones in which I was invited as an "outsider" in order to bring a different perspective. I therefore encourage our members to not only attend meetings in their particular sub-field but to at least occasionally attend SMB and other gatherings that are more broad-ranging in scope.

Many of my comments over the past two years dealt with education matters, since I believe that SMB members can assist in many ways to develop appropriate methods for the interdisciplinary training required by modern biology. We are a very diverse group, culturally and politically, including as we do members from more than 50 countries. It is clear that uniqueness is not a property of the solution of interdisciplinary education - there are many different routes to success. While the recent explosion of specialized programs in mathematical and computational biology bodes well for our field, I hope that we also keep in mind the need for general understanding of science and seek ways to improve the public view of quantitative biology.

It has been a real pleasure to serve as your President. Thank you again for your support.

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Symposium on Computational Cell Biology

Athena Makroglou

The Symposium on Computational Cell Biology was held March 19-23, 2005, at the Cranwell Resort in Lenox, MA, USA. This meeting takes place every two years. This and the previous 2 meetings were organised by the National Resource for Cell Analysis and Modeling, University of Connecticut Health Center. The venue was the Cranwell resort, in the Berkshire Hills in western Massachusetts, which hosted the previous two symposia. It was sponsored by IBM Research, Zeiss and Teranode, and funded by the National Center for Research Resources and National Science Foundation.

It was attended by 125 scientists spanning a number of scientific areas in biomedical sciences, mathematical, physical, and information sciences, and engineering, giving thus the possibility of exchange of ideas between different disciplines and the opportunity to create or complement interest in the current advances of research in each other's field in the context of its relation to the modeling, the theory and applications and computer implementation of problems of cell biology.

The conference started with a plenary talk titled "Are bacteria individuals?" by Stan Leibler, Rockefeller University. Bacteria can have the same genes, same history, age, environment, so are they individuals? Prof. Leibler's talk described various aspects of bacteria individuality, e.g. nongenetic individuality (observed long ago), phenotypic variability, and bacterial resistance variability (antibiotic resistance).

The symposium consisted of talks at 5 sessions, poster presentations and software demonstrations and brief presentations during session slots. The sessions were on: Cell Signaling, Calcium Dynamics, Intracellular Networks, Cytoskeletal Dynamics and Cell Motility. The talks took place morning and evening. The afternoons were devoted to software demonstrations and to posters. All were of exceptional presentation quality, a joy to read.

The keynote presentation was given by Prof. Howard Berg, Dept. of Molecular and Cellular Biology and of Physics, Harvard University, "Watching E. coli compute". It was a very enjoyable presentation following a very enjoyable dinner at the conference banquet. Prof. Berg reviewed the history of the subject of the motion of flagellated bacteria and then gave details about the behavior of E. coli, "these remarkable living machines." A review article, "The rotary motor of bacterial flagella," H. Berg, Ann Rev Biochem 72: 19-54 July 2003, explains many of the points of Dr. Berg's talk.

Everything was organised to perfection, down to small details. The food was excellent, the stay very pleasant, the Conference organisation excellent too. The scenery was magnificent, with views to the not-so-distant mountains with their white tops from old and maybe recent snow too. These of us who arrived there from warmer climates were lucky to see snow falling during one of the days there (while attending the Monday's talks). It did not stay on the ground though. Tuesday was a sunny day making the beauty of the area even more noticed and appreciated.

The next meeting on Computational Cell Biology will be organised by Professor John Tyson of the Computational Cell Biology Lab, Virginia Polytechnic Institute. It will take place in two years time, maybe in the Cranwell resort again, maybe at Virginia Tech. I am sure every participant will be looking forward to the next meeting.

The meeting's web page is http://www.ccbsymposium.org and has links to the speakers, talks, and software. The author of this report participated with partial support from SMB, which is gratefully acknowledged. An extended version of this report can be found at http://www.tech.port.ac.uk/staffweb/makrogla/athena/confrep/report_comp_cell_biology_2005.pdf.

Professor Lee Segel, 1932-2005
Simon Levin, James M. Hyman
and Alan S. Perelson

Lee Segel passed away on January 31, 2005. With his death, the applied mathematics community lost one of its finest practitioners, and the theoretical biology community lost a true pioneer who was still a leader at the cutting edge of so many subjects. And most importantly, the world community lost a true mensch, a compassionate and loving individual who inspired so many with his brilliance, his enthusiasm, his sense of humor, and his concern for others. Our hearts go out to his beloved Ruthie, his partner of half a century; to his children, Joel, Susie, Daniel, Michael, and their spouses; and to all of his grandchildren and other family members. Lee was a very special human being.

Theoretical and mathematical biology went through a critical transition in the 1970s, and Lee was one of the leaders in forging a marriage between mathematical theory and empirical fact; it was efforts such as his that all but obliged experimentalists to take notice of mathematical theory, and of the insights that were possible. His exceptional taste in choosing problems and his standards for good work will have an enduring influence, even beyond his numerous and brilliant specific contributions. The criteria for good theoretical biology that young scientists take for granted today were not always in evidence in the field. The early work could easily have left a legacy of irrelevance but for the efforts of a few scientists like Lee Segel, who recognized the primacy of the biology in determining what was worth doing.

Lee Segel was well established as an applied mathematician before he turned his attention to biology. He received a PhD from MIT in 1959, working with C.C. Lin. In 1960, he joined the outstanding faculty at Rensselaer Polytechnic Institute and began to publish fundamental work in continuum mechanics and related subjects. His first two beautiful books, Mathematics Applied to Deterministic Problems in the Natural Sciences (with C.C. Lin, 1974) and Mathematics Applied to Continuum Mechanics, remain cornerstones of applied mathematics courses throughout the world. Because of its preeminent position in the literature, the 1974 Lin and Segel book has become a classic; indeed, in 1988 SIAM distinguished it by making it the first volume in its Classics in Applied Mathematics series.

By the late 1960s, realizing how rich a treasure trove biology represented for mathematicians, Lee had begun to work seriously on problems in the field. He spent an important sabbatical at Cornell Medical School and the Sloan-Kettering Institute, where Sol Rubinow had created a superb unit in biomathematics, and where such mathematicians as Joe Keller and Hirsh Cohen were frequent visitors. Lee's two great early contributions, both with Evelyn Fox Keller, created frameworks for modeling bacterial chemotaxis, and for understanding related problems in the development of the cellular slime mold, a model system for studying development, multicellularity, and social biology. Lee quickly

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earned the respect of the leading experimentalists and theoreticians in these subjects, in particular John Bonner and Ted Cox at Princeton, and Howard Berg, then at Colorado. More than thirty years later, the Keller–Segel models remain the gold standards in these fields.

Lee's interests in biology knew no limits, but he was no dilettante; his later contributions to development, to ecology, to evolutionary biology, to immunology, and to neurosciences established him as one of the broadest yet deepest theoretical biologists of his generation.

Lee moved in 1973 from RPI to the Weizmann Institute, where he became dean of the Faculty of Mathematical Sciences and, later, chair of the Scientific Council. At both RPI and Weizmann, he mentored a diverse assemblage of outstanding young scientists who went on to join the ranks of the leaders of their fields. At Weizmann, an institution known for its excellence in experimental biology, he instituted a course on mathematical modeling, not for mathematicians but for biologists who had a year of calculus. The course, which he taught for about twenty years, led to his inspiring and insightful text Modeling Dynamic Phenomena in Molecular and Cellular Biology (1984). He was working on a sequel when his untimely death occurred.

His collaborators were legion, and anyone who ever worked with him will remember mainly how much fun it was. Lee laced every interaction with humor, and no pun was beneath him; many were subtle enough to make their way past editors into his published papers. Lee had a tremendous sense of responsibility to family, students, and community. As editor of the Bulletin of Mathematical Biology, he transformed it from a marginal journal into one of the leading vehicles for new results. He was a central figure in the Gordon Research Conference in Theoretical Biology for decades, and played a key role in the development of the field. At Los Alamos National Laboratory, he was a summer consultant to the theoretical biology group from 1984 to 1999, and he was named Ulam Visiting Scholar for 1992–93; he also became a fixture at the Santa Fe Institute.

No single individual is more clearly identified with the face of theoretical and mathematical biology today. He was a dynamic and inspiring lecturer, and a brilliantly clear expositor. Although he was opposed to publishing "every sneeze," his publication record is equally daunting and inspiring. His expository style, indeed, made each of his papers a joy to read.

Above all, Lee was a wonderful friend, husband, and father. His deep roots in Judaism, which he shared in every aspect with Ruthie and his children, led him to emigrate to Israel, and pervaded his character and his essence. A deeply spiritual person, he made all who interacted with him feel comfortable in who they were. Never judgmental, he led by example. With his passing, a piece of all of us has died. The field will never seem the same.

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Prof Lee Segel (right) with Prof Philip Maini and Rachel Levi-Drummer at the Israeli Society for Theoretical and Mathematical Biology 2002 Meeting (Photo courtesy of Ramit Mehr)

Biophysical Society Meeting 2005

My-Hanh T. Nguyen and Hena R. Ramay

Every year, we look forward to attending the Biophysical Society conference. This year, the 49th annual meeting was held in Long Beach, CA, on February 12-16. Our third attendance at this meeting was funded by the SMB through the student travel grant for other meetings. Our contribution to the program this year was poster presentations.

This conference is a major one, with approximately 5000 attendees. The first day of the meeting had a light schedule comprising mainly panel discussions and award ceremonies. However, the following days consisted of a vast array of research presentations, mostly targeted at topics of interest to biophysics-related research. The schedule of talks and posters was strenuous, starting as early as 8:15 AM with simultaneous sessions, about 700 posters a day, and workshops until 9:00 PM. Overall the meeting has a wide selection of activities and it was hard to keep up if one had not planned beforehand which sessions to sacrifice and which to attend.

Every day in the conference, the breakfast was organized for a specific group: Sunday was the postdoctoral breakfast, Monday was the new member breakfast, and Tuesday was reserved for the graduate student breakfast. These morning events allow new attendees to meet people and interact. Some highlights of the meeting for us were: the Cole dinner with the Membrane Biophysics Subgroup, Committee for Professional Opportunities for Women (CPOW) career luncheon, the grant writing workshop, the national lecture, and the reception dance. At the Cole dinner, a talk was given by Dr. Barbara Ehrlich from Yale University, honored as the Cole awardee, highlighting the major steps in her illustrious career, from contributions with her early mentors to her current work at the Laboratory of Molecular Hermeneutics, as well as her love for baking blueberry pies and wearing crazy socks. The agenda for the CPOW luncheon was similar to the women's luncheon at SMB, but just on a bigger scale. The grant writing workshop attracted a large number of young scientists who were eager to get a head start. Grant review committee members from NIH and NSF were invited to discuss some general proposal dos and don'ts and in the end a question-and-answer session was also held to entertain individual concerns. The major event of the conference is the national lecture. This year, it was given by Joachim Frank on cryo-electron microscopy of the ribosome. The reception dance afterwards was, to some, a rare sight to see fellow scientists unwind, relax, and show off their dance moves, while to the others, it was another chance to discuss research and collaborative opportunities.

In our view, the poster session was a very valuable asset of the meeting because it provided a very relaxed atmosphere for discussions, although it can be tiring for the presenter to usually speak non-stop for about three hours (more than the duration of the poster session). Over all, the poster session is more beneficial in terms of research discussions and interaction than platforms at this meeting, facilitating better opportunities for questions, challenges, and collaborative discussions.

As the conference is held in a different city each year, the attendees get a glimpse of life in that city. Long Beach, CA had a lot of good food to offer and an unforgettable whale watching expedition that included sightings of dolphins, seagulls, grey whales, and fin whales.

All in all this conference was once again a very educational as well as enjoyable experience for us. We would like to thank Dr. Saleet Jafri and Dr. Eric Cytrynbaum for sponsoring our application for this grant, and SMB for making our attendance at this conference possible.

AIBS Council Meeting
May 7 - 9, 2005
Raymond Mejía

The Society for Mathematical Biology, a member of the American Institute of Biological Societies, was represented at the Council Meeting held in Washington, DC. A report of the AIBS Annual Awards, the Council Meeting and an Open Access Journal Publishing Meeting is available at http://www.aibs.org/announcements/050519_now_online_report_on.html.

The keynote lecture was given by Cristian Samper, Director, National Museum of Natural History, Smithsonian Institution, Washington, DC, on "The Millennium Ecosystem Assessment". In addition to material available at the AIBS website, a report of the Millennium Ecosystem Assessment may be found at http://www.maweb.org.

Awardees included: Tom Meersman, Minneapolis Star Tribune, Print Media Award for "Invaded Waters"; Elizabeth Pennisi, Science, Print honorable mention for "The Secret Life of Fungi"; Diane Toomey, NPR's Living on Earth, Broadcast Media Award for "A Little Known Planet"; Kenneth R. Miller, Brown University, President's Citation Award; Deidre Labat, Xavier University of Louisiana, Education Award; B. Rosemary and Peter R. Grant, Princeton University, Distinguished Scientist Award; Jay M. Savage (ret), University of Miami, Outstanding Service Award.

Open Positions
EPSRC CASE Studentships

Two EPSRC CASE studentships are available in the Department of Statistics and Modelling Science at Strathclyde University, UK. One is on spatial modelling of multiple time series of counts, concerning statistical methods for spatial time series analysis of infectious disease data in Scotland. This project is jointly supervised by Dr. E. McKenzie and Professor C. Robertson, Statistics and Modelling Science and Dr. John Cowden, Health Protection Scotland. The second is on modelling genetic effects in the transmission of pneumococcal carriage and infection. This is part of a long-term collaborative research project between Wyeth Pharmaceutics, the Scottish Pneumococcus Reference Laboratory and Health Protection Scotland to develop a realistic population model for pneumococcal carriage and infection incorporating genetic sequencing information. This project is supervised by Dr. D. Greenhalgh and Prof. C. Robertson, Statistics and Modelling Science, Strathclyde University and Dr. D. McIntosh, Wyeth Pharmaceutics, in collaboration with Dr. Claire Cameron, Health Protection Scotland. Further details are available at http://www.stams.strath.ac.uk/vacancies/index.php

Postdoctoral Position, National Chung Hsing University, Taiwan

One year postdoctoral position working on mathematical and statistic modeling of infectious diseases is available with funding from a National Science Council (NSC - Taiwan) research grant. The position is for one year starting August 2005 (with some flexibility and option to renew for two more years). For more information please contact Dr. Ying-Hen Hsieh, email: hsieh@amath.nchu.edu.tw. See also http://amath.nchu.edu.tw/~yhhsieh.

Mathematical Modeling, Evolutionary Biodemography

The Max Planck Institute for Demographic Research is seeking to expand further its activities in the field of Evolutionary Biodemography and is recruiting to PhD and Post-Doc level vacancies involving Mathematical Modeling of Life History Evolution in an Ecological Framework. See http://www.demogr.mpg.de for information.

NERC Studentship, University of Glasgow

Applications are being accepted for a NERC Studentship to be held at University of Glasgow. The focus of this will be the study of the stability of model ecosystems. The studentship will commence in October 2005. Complete information posted at http://www.gla.ac.uk/Acad/IBLS/DEEB/dth/studship.htm.

Postdoctoral Position, Computational Cell Biology

The research project, under the supervision of Dr Stephen Coombes, Dr Martin Bootman, and Dr Llewelyn Roderick will develop models of calcium release within a fire-diffuse-fire framework and use these to determine how cells can shape spatio-temporal calcium patterns. By considering the combined role of space, noise and heterogeneity in generating a variety of experimentally observed calcium signals we will explore the mechanisms which allow a simple ion such as Ca2+ to play such a pivotal role in cell biology. One specific application of this work will be to understanding the pathological behaviours of atrial myocytes that give rise to atrial arrhythmias. Further details are available at: http://www.maths.nott.ac.uk/personal/sc/postdoc.html.

Postdoctoral Fellowship Department of Mathematics University of Trento - Italy

One postdoctoral fellow is sought to join the Department of Mathematics at the University of Trento-Italy for a period of two years starting with September 2005. The Fellow will take part in the research activities of the EPICO Project (local director M. Iannelli), concerning models for the description and control of epidemics. Specifically, based on the observational data provided by the Italian Health Institute, he/she will contribute at modelling and analysing scenarios for influenza outbreaks in Italy; control and eradication of childhood diseases; and epidemic outbreaks and endemic presence other infectious diseases. A good basic knowledge on modelling population dynamics is required, as well as experience in programming and simulations, and especially an interest in interacting with people from different backgrounds, working with mathematical models and observational data. A form for applications has been posted at address http://www.unitn.it/dipartimenti/mate/index.php (please check through the "highlights"). The application form (available on the site) will have to reach the Department in paper form by the deadline of June 30, 2005. It is however suggested that people interested in this fellowship send a preliminary email to ianelli@science.unitn.it, with a CV and names and e-mails of three references. Questions and other information can be obtained by e-mail writing to the same address.