The Society for Mathematical Biology

SMB Newsletter

Volume 21 #2 - May 2008

Society for Mathematical Biology Annual Meeting

July 30-August 2, 2008
http://www.smb.org/meetings/annual.shtml

hosted by the Centre for Mathematical Medicine,
Fields Institute
held at University of Toronto, Medical Sciences Bldg

Local Organizing Committee
M. Kohandel (Waterloo), I. Pressman (Carleton),
F. Skinner (Toronto Western Research Inst.),
S. Sivaloganathan - Chair (Waterloo),
Hongmei Zhu (York)

Contributed talk proposals will be accepted until May 15, 2008. Poster proposals will be accepted until July 15, 2008. Plenary speakers include M. Golubitsky (Houston), M. Knothe Tate (Case Western), N. Komarova (UC Irvine), H. Levine (UC San Diego), M. Lewis (Alberta), L. Mahadevan (Harvard), T. Secomb (Arizona) and Y. Zhou (China).

Inside this Issue:

2008 SMB Election Results

Congratulations to the newly elected President-elect and Board Members!

President-elect: Michael Mackey

New Board Members:

Mary Myerscough

Renee Fister

Santiago Schnell

Dear SMB Members:

I am looking forward to meeting many of you at the annual SMB conference in Toronto, July 30 - August 2. The plenary speakers represent a broad range of mathematical biology and the themes of the conference, like in previous years, will cover all areas of biology where mathematical modeling and simulation are actively pursued.

As you must have noticed, the SMB Newsletter now appears in a very nice format. Content wise, it now includes autobiographical profiles of career paths of mathematical biologists. We hope these profiles will inspire young people to pursue research and careers in biomathematics. The SMB Newsletter also now includes "nuggets" or "highlights;" these are short articles that describe a success story in mathematical biology. I encourage any one who wishes to contribute a personal success story to send this to me in the form of a "nugget," and, if appropriate, we shall publish it in the Newsletter.

The World Outreach Committee, newly formed last autumn, has been very active. In January 2008, Aziz Yakubu (the committee's chair) and I participated in a mathematical biology conference in Marrakech, where we witnessed the official formation of the African Society of Biomathematics. Both Aziz and I are serving on the liaison committee of this newly formed society. There are current discussions among the members of the World Outreach Committee on extending activities to other countries.

The Springer publication of the Bulletin of Mathematical Biology has been proceeding very smoothly, thanks to the hard work of Philip Maini, the Editor, and the excellent coordination with Achi Dosanjh from Springer.

Renewal of the annual SMB membership is now available online. This will make it much easier for you to renew your membership, as well as for those who wish to become new members. Holly Gaff has done a great job in putting the membership renewal procedure online, as well as in setting up the new improved format of the SMB Newsletter; she deserves our thanks.

On a personal side I am happy to inform you that, after seven years, I will step down this September as the Director of the Mathematical Biosciences Institute (MBI). Marty Golubitsky will become the new Director. Marty is a world leader in dynamical systems; he served as the President of SIAM, and he is one of the plenary speakers in the Toronto conference. His wife, Barbara Keyfitz, will join the mathematics department at Ohio State University. She is currently serving the last year as Director of the Fields Institute in Toronto; she is organizing a program on mathematical and quantitative oncology at the Fields Institute following the SMB conference.

I wish you all a great Spring and I am looking forward to meeting you in Toronto.

Sincerely,

Avner Friedman

SMB President

BIO SIGMAA

Janet L. Anderson Prize

The MAA's special interest group in mathematical and computational biology (BioSIGMAA) has recently established an award in honor and memory of our late colleague, Janet L. Andersen.

Until her untimely death in November 2005, Janet Andersen was Professor of Mathematics at Hope College in Holland, Michigan. She joined the Hope faculty in 1991 after completing her master's and doctoral work in algebraic geometry at the University of Minnesota.

Janet was a beloved and dedicated teacher of mathematics and served the profession in myriad ways, from her role as director of the Pew MidStates Science and Mathematics Consortium to her service as chair of the MAA's committee on the teaching of undergraduate mathematics.

Half a dozen years ago or so Janet became actively interested in mathematical biology, and was Principal Investigator for an NSF grant to develop a mathematical biology course, which she then taught at Hope College several times. In conjunction with that course, she mentored many student undergraduate research projects. Through activities of the BioQUEST curriculum consortium, the Society for Mathematical Biology and in many other ways, she was untiring in her efforts to promote the inclusion of mathematics in biology education (and vice versa) and encouraged broad collaboration among mathematicians and biologists in both research and teaching.

The Janet L. Andersen prize is awarded annually at MAA MathFest by "for excellence in mathematical and/or computational biology exhibited in a presentation by an undergraduate student," and was given for the first time at the San Jose Mathfest. We are writing now to ask if you would like to contribute to this fund.

We hope that, with your assistance, we will be able to offer two prizes each year, one to a Pi Mu Epsilon speaker and one to an MAA student speaker, as is customary for the other student prizes.

We are grateful for any contribution you may care to make. Checks should be directed to: The Janet L. Andersen Prize Fund, c/o Lisa Kolbe, Development Manager, The Mathematical Association of America, 1529 18th Street NW, Washington, DC 20036

Upcoming Meetings

Mathematical Tools for Multi-Scale Biological Processes

Call for abstracts for the International Conference: Mathematical Tools for Multi-Scale Biological Processes at Montana State University, Bozeman, MT, June 4 to June 6, 2008.

There is limited financial support for graduate students and postdoctoral researchers. For more information, see: http://www.math.ufl.edu/~deleenhe/montana/index.html

Confluence of Biology and Mathematics in the Commonwealth of Kentucky

The Biology and Mathematics in Population Studies (BioMaPS) group at Murray State University, invites you, graduate students and especially your undergraduate students to attend a workshop entitled "The Confluence of Biology and Mathematics in the Commonwealth," May 16-17, 2008. There is no registration fee. The target deadline for registration is Friday, May 2, 2008. This is for us to get an approximate number for planning. Please send us email if you are interested after this date. There will be funds available for 30 undergraduate students for housing. If you need more info, email christopher.mecklin@murraystate.edu or go to http://campus.murraystate.edu/biomaps for the registration form and more information about the workshop.

Highlights in Mathematical Biology

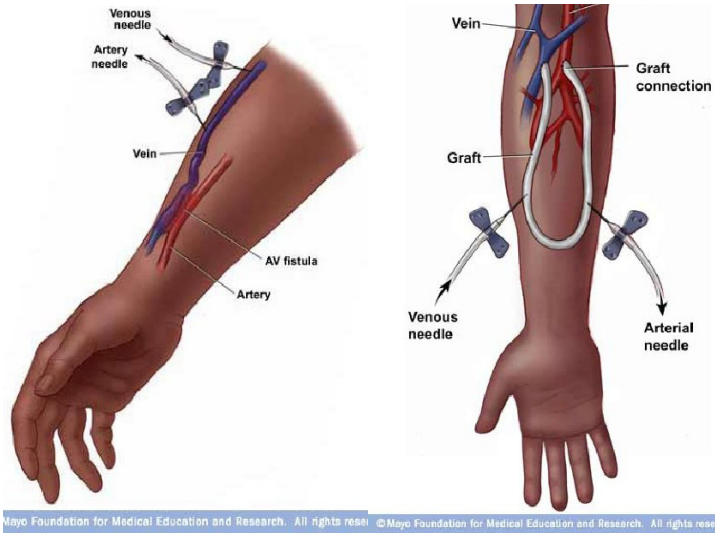
Mathematical Insights into Biological Processes

Submit your story to: editor@smb.org

The LifeLine: Vascular Access for Hemodialysis

Paula Grajdeanu

Healthy kidneys filter wastes from blood and keep body chemicals in balance. When the kidneys fail to perform their functions to full capacity, one cannot live long without some form of renal replacement therapy. One available treatment is hemodialysis, in which the patients' blood is pumped into an artificial kidney where metabolic waste products diffuse out of the blood, and the cleansed blood is then returned back to the body. Most people have 3 dialysis sessions every week, each session for about 3 to 4 hours.

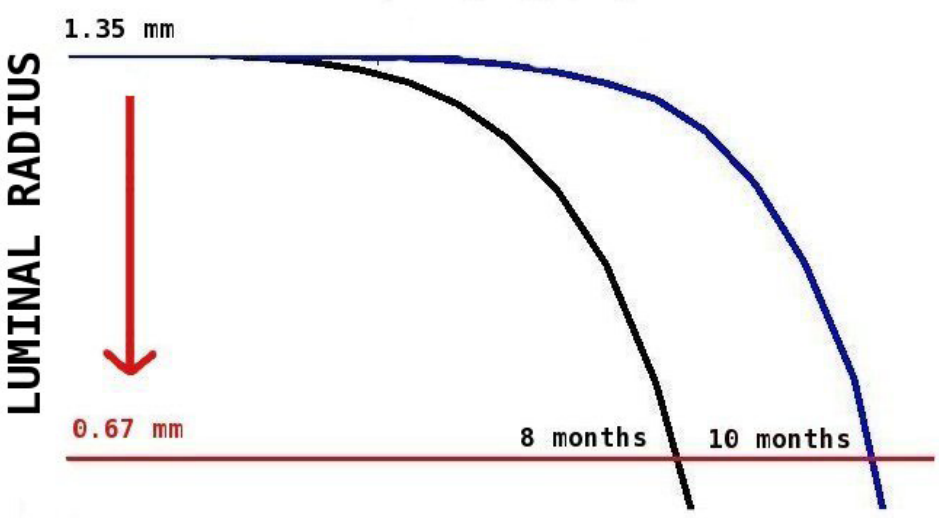


In order to perform hemodialysis, the patient must have suitable vascular access to allow adequate flow of blood to the hemodialysis circuit. The most common types of vascular access used for hemodialysis are the arteriovenous (AV) fistula and the expanded polytetrafluoroethylene (ePTFE) graft. A surgeon creates an AV fistula by directly connecting an artery to a vein, usually in the forearm. The increased blood flow causes the vein to hypertrophy so that it can be used for repeated needle insertions. A graft connects an artery to a vein by using a synthetic tube of ePTFE, usually in the shape of a loop. It does not require as much time to mature as a fistula, so it can be used soon after placement.

Both types of vascular access can have complications that require further treatment or surgery. As a well-functioning vascular access is essential for hemodialysis, extensive morbidity exists among end-stage renal disease (ESRD) patients. How long can someone live on dialysis and how well can someone do, depend heavily on the quality of the medical care. The expense of creating and maintaining vascular access for patients on dialysis accounts for a significant portion of any health care system. In the US alone, more than 20% of patients with ESRD are hospitalized for vascular access procedures, at an annual cost of 1 billion dollars.

The leading cause of access failure is from loss of patency due to venous stenosis (50% narrowing of the blood vessel), as the result of neointimal hyperplasia formation either at the site of venous anastomosis or in the downstream vein. It is then of critical importance to detect access stenosis in a timely manner so that appropriate corrective steps can be undertaken prior to thrombosis (total occlusion of the blood vessel). However, while the occurrence of stenosis is well recognized, the pathogenesis of it is complex and still not well understood. The process involves a number of growth factors, migration and proliferation of different types of cells, and excessive production of extracellular matrix. The release of growth factors due to oxidative stress and turbulent flow has been suggested as a possible mechanism for neointimal hyperplasia formation.

At the Mathematical Biosciences Institute, postdoctoral researchers Paula Budu-Grajdeanu and Richard Schugart, together with mathematician Avner Friedman, work closely with the Interventional Nephrology Team of The Ohio State University Medical Center, Anil Agarwal, Chris Valentine and Brad Rovin, to analyze the biological mechanisms that lead to vascular access



stenosis and direct attention to potential therapies to prevent and treat stenosis. Using partial differential equations to describe the complex pathogenic network relevant to neointimal hyperplasia formation, they have developed a mathematical model, in which all growth factors (TGF-beta, PDGF, ET-1) are lumped together into one generic chemical species and all cellular species (smooth muscle cells, fibroblasts) are lumped together into one generic cell type. The model accounts for oxidative stress by having the growth factors increase as the luminal radius decreases.

This relatively simple model captures some of the main features of intimal hyperplasia formation and it realistically predicts the stenotic event (red line) as a function of the initial concentration of the growth factors inside the intimal-luminal space (black curve). It also shows that a drop in the initial concentration of growth factors delays the access stenosis, prolonging the lifespan of the vascular access (blue curve).

The results imply that one mechanism by which the functional state of the hemodialysis vascular accesses can be extended is to control the concentration of the growth factors in the proximal vein. In particular, interventions aimed at specific chemical mediators involved in VNH formation may be successful in reducing the human and economic costs of vascular access dysfunction. With cooperative efforts, i.e., interplay between computational experiments and data, the mathematical model can be expanded and used by clinical researchers as a testbed for exploring and evaluating various therapies that can target both the traditional and the alternative pathways that are involved in the pathogenesis of vascular stenosis. As only limited empirical data for various parameters is available at present, clinical studies need to be conducted in parallel with the development of the model to improve its reliability.

SMB World Outreach Committee Update

The newly appointed World Outreach Committee (WOC) of SMB consisting of Abdul-Aziz Yakubu (Chair), Daniel Bentil, Abba Gumel, Yi Jiang and Jorge Velasco-Henandez has already started exploring research and educational activities in developing/emerging communities. For the next two years, WOC will focus more on promoting world mathematical biology.

On January 4, 2008 SMB President, Avner Friedman, and Abdul-Aziz Yakubu witnessed the formation of the African Society of Biomathematics (ASB) at the January 3-8, 2008 International Conference on Biomathematics at Marrakech-Morocco. The steering committee of the newly formed ASB consists of Joseph Mugisha (Uganda), Hassan Hbid (Morocco), Ogana Wandera (Kenya), Edward Lungu (Botswana) and Henry Laurie (South Africa). The assembled group also approved a Liaison Committee consisting of Abba Gummel (Canada), Odo Diekmann (The Netherlands), Pierre Auger (France), Abdul-Aziz Yakubu, Avner Friedman and Carlos Castillo-Chavez (USA). The Steering Committee is charged with developing the structure of ASB (officers, membership, etc.) and the Liaison Committee is to help ASB with connections and support from the international community, including other societies of mathematical biology.

SMB President and WOC are also planning on a China-SMB conference in 2009. Avner Friedman will be visiting China in the spring of 2008 to finalize discussions for the international meeting. Also, WOC is exploring locations in Mexico and Africa for joint meetings/workshops in 2010 and 2011.

SMB World Outreach members and other SMB members celebrate the formation of the African Society of Biomathematics in January 2008. (See additional picture on page 7.)

My Career in Mathematical Biology
A Personal Journey

Philip Maini

I was first exposed to mathematical biology in the final year of my undergraduate degree in mathematics when I went to a course on ordinary differential equations given by Jim Murray. The course motivated modelling and mathematical techniques by examples in ecology, biology and epidemiology and I was struck not only by these novel (to me) examples but also by the fact that here was a lecturer who genuinely seemed excited by the subject he was teaching.

I was very happy when Jim took me on as a graduate student – it was the early days of the mechanochemical models and of the Centre for Mathematical Biology (CMB), which opened in 1983. It was very exciting for a graduate student to have the chance to meet many of the major names in the field and to watch them at work during the morning coffee break. I worked on investigating the Oster-Murray-Harris mechanochemical model in the context of feather germ formation. I also got to visit Los Alamos National Laboratory and the University of Utah in my third year when Jim was on sabbatical in those places.

In fact, I went back to the University of Utah in 1988 as an assistant professor before returning to Oxford in 1990 as a lecturer in mathematical biology. I have worked on a number of areas of application of modelling, for example, pattern formation, wound healing and tumour growth. Presently I am Director of the CMB, Professor of Mathematical Biology and Editor of the Bulletin of Mathematical Biology.

I never intended to become a university academic as I always wanted to be a high school teacher. In fact, in 1986 Jim Murray very kindly let me take a "sabbatical" from my postdoc at the CMB to work as a teacher at Eton College. Despite its austere appearance I found the school to be very warm and friendly and I was very tempted to stay on permanently. However, 26 seemed a very early age to have a real job so I went back to being a postdoc and sort of ended up in a permanent job in university without really planning it.

I have been very lucky to have as my mentors Jim Murray and Hans Othmer, both of whom have always given me great support and excellent advice. I think that it is very important to have experienced people you can trust to discuss not only science but also all the other aspects of being a university academic.

What do I like about my job? I find the applications to biology very exciting indeed. Biology never ceases to fascinate and surprise me. I enjoy working together with colleagues from other disciplines. I have been lucky to work with a lot of bright people and learn from them. One of the highlights is seeing, both at undergraduate and graduate level, students develop and mature into mathematicians and independent scientists. I also enjoy travelling, learning about new areas (biological and geographical) and having friends from many different cultural backgrounds. Mathematical biology seems to be a very friendly subject and the atmosphere at conferences and summer schools is something very special.

What don't I like about my job? Politics, metrics and the

fact that we have allowed the importance of one aspect of our job (research) to grow out of all proportion at the cost of all the other important things we do (teaching, general service).

What about the future? This is a very exciting time for mathematical biology. When I started out in 1982 one actually knew everything that was going on in the subject. Now, it is a challenge to keep up to date with the latest findings in one's own specialised area of research. I think that there has been a change over the past 5-6 years as more biologists now feel that mathematical and computational approaches are necessary. The boom in systems biology has been astonishing and while this means that the immediate future is very bright, we have to be careful longer term. There has been a lot of hype and while we are presently reaping the benefits of that, we could suffer long term if we do not deliver.

Overall, I think that being a university academic is a great privilege. I do not know of many other jobs where by and large you are left to get on with whatever interests you at the time (and can take time off to play football!). The variety is enormous and the intellectual challenges stimulating. It is a pleasure to be consistently working with young people who are at a formative time of their life. However, my mum is not convinced and still asks me when I am going to get a real job, but I am having too much fun to worry about that.

Selected publications of Philip Maini:

E.J. Crampin, E.A. Gaffney and P.K. Maini, Mode-doubling and tripling in reaction-diffusion patterns on growing domains: A piece-wise linear model, J. Math. Biol., 44, 107-128 (2002)

T. Alarcón, H.M. Byrne, P.K. Maini, A multiple scale model for tumour growth, SIAM J. Multiscale Modelling and Simulation, 3(2), 440-475 (2005)

R.E. Baker, S. Schnell, P.K. Maini, A clock and wavefront mechanism for somite formation, Dev. Biol., 293, 116-126 (2006)

S. McDougall, J. Dallon, J. Sherratt, P.K. Maini, Fibroblast migration and collagen deposition during dermal wound healing: mathematical modelling and clinical implications, Phil. Trans. R. Soc. A, 364, 1385-1405 (2006)

S. Schnell, R. Grima, P.K. Maini, Multiscale modeling in biology, Amer. Sci., 95, 134-142 (2007)

M.D. Johnston, C.M. Edwards. W.F. Bodmer, P.K. Maini, S.J. Chapman, Mathematical modeling of cell population dynamics in the colonic crypt and in colorectal cancer, PNAS, 104, 4008-4013 (2007)

R.A. Gatenby, K. Smallbone, P.K. Maini, F. Rose, J. Averill, R.B. Nagle, L. Worrall, R.J. Gillies, Cellular adaptations to hypoxia and acidosis during somatic evolution of breast cancer, Brit. J. Cancer, 97, 646-653 (2007)

SMB World Outreach members and other SMB members celebrate the formation of the African Society of Biomathematics in January 2008. (See additional picture and story on page 5.)

Highlights in Mathematical Biology

Mathematical Insights into Biological Processes

Submit your story to: editor@smb.org

Modelling Cancer Invasion: "Let's Stick Together"

Mark Chaplain

In vivo cancer growth is a complicated "multi-scale" phenomenon involving many inter-related biochemical and cellular processes at many different spatial and temporal scales. Although there are many different types of cancers (e.g. carcinoma, sarcoma, melanoma, leukaemia, glioma), solid tumours (carcinoma, sarcoma) make up a large fraction of all clinically observed cancers. The growth of solid tumours occurs in two distinct phases: the initial growth being referred to as the relatively harmless avascular phase and the later growth as the vascular phase.

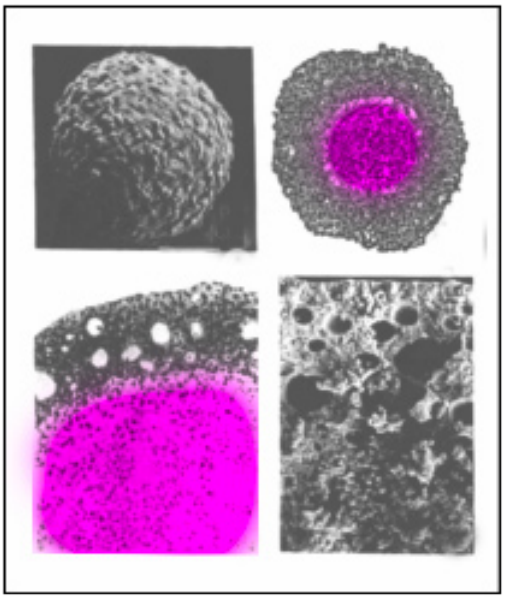


Figure 1: Images of avascular multicellular spheroids. The coloured interior region shows the necrotic core of dead cells through lack of nutrient (oxygen).

During the early avascular stage of solid tumour growth there may be an immune response to the cancer from the host, with cells of the immune system, most notably T-lymphocytes, responding to and attacking the cancer cells. However, unfortunately solid tumours do not always remain avascular and localised. The transition from avascular growth to vascular growth depends upon the crucial process of angiogenesis which is necessary for the tumour to attain nutrientsand dispose of waste products. To achieve vascularization, tumour cells secrete a diffusible substance known as tumour angiogenesis factor (TAF) into the surrounding tissue. This has the effect of stimulating nearby capillary blood vessels to grow towards and penetrate the tumour, re-supplying the tumour with vital nutrient.

Invasion and metastasis can now take place. Indeed, invasion, the ability of cancer cells to break out of tissue compartments and spread locally, is one of the hallmarks of cancer and gives solid tumours a defining deadly characteristic. Cancer cells achieve this through the secretion of matrix degrading enzymes,

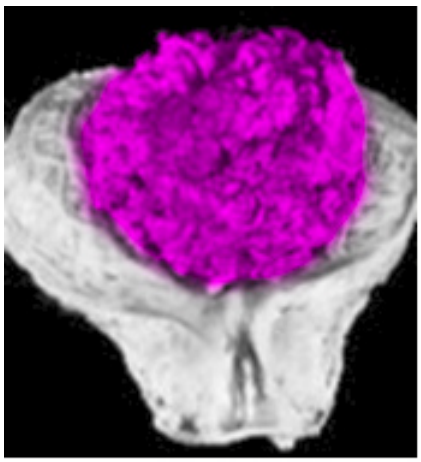


Figure 2: Image of an invasive bladder cancer

cell proliferation, loss of cell-cell adhesion, enhanced cell-matrix adhesion and active migration. Invasion of tissue by the cancer cells is one of the key components in the metastatic cascade, whereby cancer cells spread to distant parts of the host and initiate the growth of secondary tumours (metastases).

Recent new work by A. Gerisch and M.A.J. Chaplain (Mathematical modelling of cancer cell invasion of tissue: Local and non-local models and the effect of adhesion. J. Theor. Biol. 250, 684-704) formulates a novel continuum model of cancer cell invasion of tissue which explicitly incorporates the important biological processes of cell-cell and cell-matrix adhesion. This is achieved using non-local (integral) terms in a system of partial differential equations where the cells use a so-called "sensing radius" R to detect their environment. A numerical exploration of this model using computational simulations shows that for certain parameter sets, the cancer cells "split" into two sub-populations, with one sub-population actively invading the tissue, the other sub-population remaining close to the initial spatial location. The computational results of the model provide experimentally testable hypotheses regarding the relative strengths of cell-cell and cell-matrix adhesion i.e. how well cancer cells "stick together".

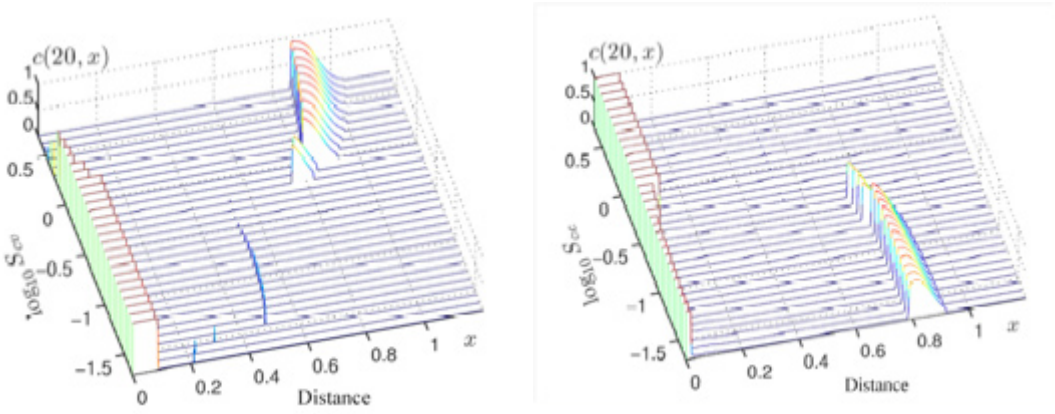


Figure 3: Plots showing the effect on invasion of varying the cell-matrix adhesivity Scv and the cell-cell adhesivity Scc. As the cell-matrix adhesivity is increased the cancer cells eventually break away and invade (left). As cell-cell adhesivity is increased the invading cancer cells remain localised (right). Adapted from Gerisch and Chaplain (2008).

One may draw the general conclusion that the tumour microenvironment i.e. the oxygen/nutrient supply to the tumour, the biomechanical properties of the matrix and cell-cell and cell-matrix adhesion, has a major impact on invasion. This novel approach complements existing previous work in the area going back to the seminal paper of Greenspan (1976) and developed theoretically and analytically by Byrne and Chaplain (1996, 1997) and computationally by Lowengrub and co-workers (2003, 2007).

Unravelling and better understanding the complex processes involved in cancer invasion may ultimately lead to treatments being developed which can localise cancer and prevent metastasis.

References:

Anderson, A.R.A. (2005) A hybrid mathematical model of solid tumour invasion: the importance of cell adhesion. Math. Med. Biol. 22, 163-186

Byrne, H.M., Chaplain, M.A.J. (1996) Modelling the role of cell-cell adhesion in the growth and development of carcinoma. Math. Comput. Modell. 24, 1-17

Byrne, H.M., Chaplain, M.A.J. (1997) Free boundary problems associated with the growth and development of multicellular spheroids. Euro. J. Appl. Math. 8, 639-658

Cristini V., Lowengrub J., Nie Q. (2003) Nonlinear simulation of tumor growth. J. Math. Biol. 46, 191-224

Frieboes HB, Lowengrub JS, Wise S, et al. (2007) Computer simulation of glioma growth and morphology. Neuroimage 37, S59-S70

Gerisch, A., Chaplain, M.A.J. (2008) Mathematical modelling of cancer cell invasion of tissue: Local and non-local models and the effect of adhesion. J. Theor. Biol. 250, 684-704

Greenspan, H.P. (1976) On the growth and stability of cell-cultures and solid tumors. J. Theor. Biol. 56, 229-242

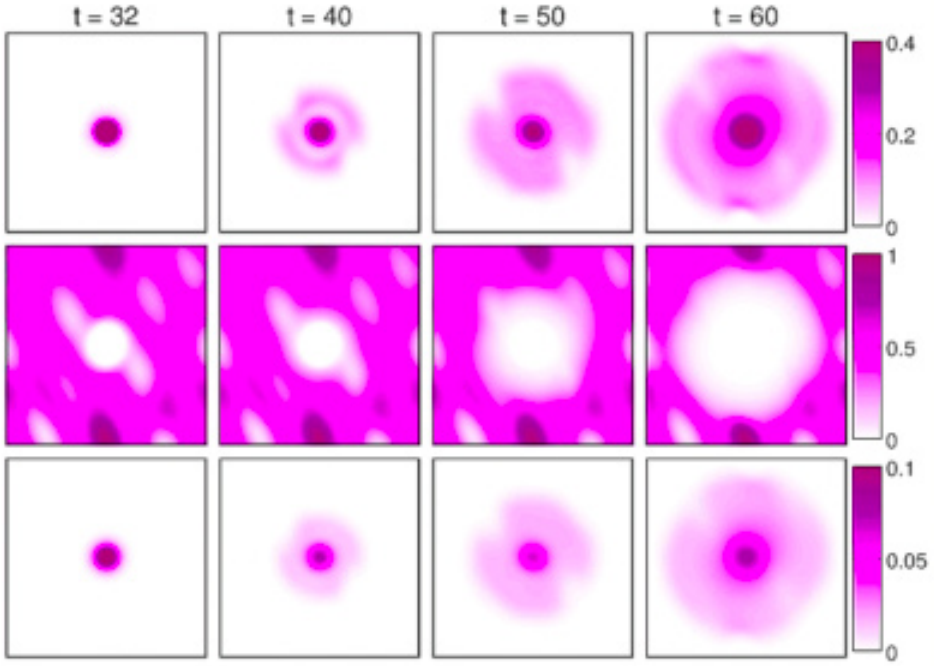


Figure 4: Plots showing an invasive cancer in 2D. Top row shows the invading cancer (density), middle row shows the extracellular matrix (density) while the bottom row shows the matrix degrading enzyme (concentration). See Gerisch and Chaplain (2008) for more details.

Positions Available

PhD Position, University of Strathclyde

We have been awarded a PhD studentship to study mathematical modelling of the spread of Hepatitis C amongst injecting drug users in Scotland, supervised by Dr. David Greenhalgh, University of Strathclyde, Glasgow, UK and Dr. Sharon Hutchinson (Health Protection Scotland (HPS)). The project aims to develop mathematical models for the spread of hepatitis C virus (HCV) amongst injecting drug users (IDUs). The models will use differential equations in the first instance. Models for the spread of HIV amongst IDUs will be adapted to HCV. We will concentrate on designing models to examine the effect of HCV prevention measures, such as the provision of needles/ syringes and other injecting equipment, methadone treatment and educational interventions. Heterogeneity in injecting risk behaviours among IDUs will be explored in the model. If time permits we would also explore individual-based stochastic Monte-Carlo simulation models to compare the results with the deterministic models and the effect of friendship networks and geographical dispersion on the spread of HCV. A very important part of this project is the link with HPS and we would use epidemiological data on HCV from HPS to estimate the parameters in our models as well as guidance from HPS staff (Dr. Hutchinson and Professor Goldberg) in the model formulation. We would also aim to link in with the detailed numerical computer simulation models of the spread of HCV used by HPS. This studentship is funded at standard EPSRC rates (£12,923 p.a. for 2008/9), plus home fees. The preferred start date is 1st October 2008, but other start dates may be possible. It is suitable for UK or EU-eligible students (fees and stipend) or other EU students (fees only) with a good or expected good (2i or above or equivalent) Honours degree in Mathematics, Statistics or other numerate subject. For further information please contact Dr. David Greenhalgh, Department of Statistics and Modelling Science, University of Strathclyde, Livingstone Tower, 26 Richmond Street, Glasgow G1 1XH, Scotland, UK, david@stams.strath.ac.uk

MSc/PhD/Post-Doctoral Trainees, Bar-Ilan

The Computational Immunology Lab of Prof. Ramit Mehr, Bar-Ilan University, Israel (http://repertoire.os.biu.ac.il/) needs Research Students (for the MSc or PhD degrees) and Post-Doctoral Trainees for several fascinating projects. More info: http://repertoire.os.biu.ac.il/Info-4-candidates.htm. If you are interested, please send email to mehrra@mail.biu.ac.il, stating the position you are interested in, and attach your CV, any publications or reports you have from your previous research projects, your grades in your previous studies (full lists), a statement of your research interests, career goals and plans, and names of people who will be willing to recommend you, e.g., advisors from previous studies, projects or jobs (please give names + phone numbers and/or email addresses of these persons).

Postdoctoral Position, U Kentucky

A postdoctoral position in computational physiology is available in the Center for Biomedical Engineering at the University of Kentucky. This NIH-funded research project involves: (i) development of signal processing methods to detect arousals and other transient events in EEG signals, and; (ii) mathematical modeling of oxygen delivery to the brain in healthy elderly subjects and in patients with sleep-disordered breathing. Candidates should have training in stochastic signal processing (e.g., spectral analysis, entropy, time-frequency analysis) and experience using simulation software for solving time-dependent differential equations. Basic knowledge of respiratory physiology and neurophysiology is necessary. The ideal candidate will be enthusiastic about participating in both aspects of the project. Additional information about the laboratory may be found at http://www.uky.edu/~ebruce/. Applications may be sent by email to ebruce@uky.edu. Candidates should submit the following (PDF attachments preferred): (1) current C. V.; (2) contact information for 3 references. Eugene N. Bruce, PhD, Professor, Center for Biomedical Engineering, University of Kentucky, Lexington, KY 40506-0070

PhD Position, INRIA

INRIA Grenoble-Rhône-Alpes is seeking a PhD student to work on: Methods for the reduction of large and complex models of biochemical networks. A description of the subject of the PhD project, as well as conditions for applicants, can be found on the INRIA web site: http://www.inrialpes.fr/jsp/fiche_actualite.jsp?CODE=1204618110974&LANGUE=1&STNAV=&RUBNAV=&RH=ACCUEIL. The application dead-line is

May 15, 2008. All further information can be obtained from Daniel Kahn, INRIA Grenoble-Rhône-Alpes and Laboratory of Biometry and Evolutionary Biology, CNRS/University of Lyon (Daniel.Kahn@inria.fr) or Hidde de Jong, INRIA Grenoble-Rhône-Alpes (Hidde.de-Jong@inria.fr).

PhD Student, Ghent

The research group Plant Systems Modeling of the Department Plant Systems Biology at the VIB in Ghent, Belgium, has an opening for a PhD student (f/m) Computational modeling of phytohormone cross-talk during lateral root initiation. The VIB Department Plant Systems Biology in Ghent, Belgium has an opening for an ambitious and energetic research assistant in the research group Plant Systems Modeling, which focuses on computational modeling of plant development. Computer modeling is a crucial pillar in systems biology, a relatively new approach in biology that shifts focus from individual molecules, genes and cells to their dynamic interplay: how do molecules, genes and cells form a working mechanism, behaving in a predictable way? Modeling the biological system in a computer simulation gives us insights into developmental mechanisms that suggest new experiments, which our experimental collaborators test in the wet-lab. What will be your task? You will be building and analyzing dynamic models of auxin transport and its cross-talk with other phytohormones including cytokynin, during lateral root initiation. The work will be carried out in close collaboration with the institute's experimental labs of Dr. Tom Beeckman, Dr. Eva Benková, and Prof. Dr. Jirí Friml. Lateral roots originate from cells in the root basal meristem, a proliferating tissue region just above the root tip, forming a regular branching pattern with evenly spaced lateral roots. The crucial signal for initiating the lateral root is most likely the phytohormone auxin. Auxin levels oscillate at a period of around 15 hours, precisely coinciding with the rhythm by which new lateral roots appear. Our modeling project aims at unraveling the mechanisms behind these oscillating auxin flows, which may be driven by a dynamic interaction between auxin, the production and cellular localization of its transporter proteins, and additional phytohormones that modulate the transporter proteins' localization. In the second part of your project you will also include root growth and the tightly orchestrated cell divisions following lateral root initiation. For this challenging PhD dissertation project we are looking for an MSc in mathematical or theoretical biology, or an MSc in physics, applied mathematics or computer science with interest and affinity for biology. Programming experience (C++) and experience in biological modeling are a big plus. This project gives the opportunity to get a PhD in systems biology, in an energetic, international, multi-disciplinary centre of excellence for plant systems biology. We have funding for four years, but we encourage you to apply for external funds. Interested? Have a look at our website, www.psb.ugent.be, and send your cv and motivated letter of application to: Dr. Roeland Merks, Plant Systems Modeling group, Department Plant Systems Biology, VIB, and Molecular Genetics, Ghent University, Technologiepark 927, 9052 Gent, Belgium, roeland.merks@psb.ugent.be.

Post Doctoral Associate, University of Miami

Applications are invited for a postdoctoral fellowship in mathematical biology at the University of Miami. The position, funded in part by a grant from the Howard Hughes Medical Institute, is set to begin in the Fall of 2008 and is for two years. The primary responsibility of the fellow in the fall of each year will be to develop an upper level undergraduate course in mathematical biology suitable for a combined audience of mathematics and biology students that the fellow will teach in the spring semester. The fellow is also expected to conduct research at the interface of mathematics and biology in conjunction with University of Miami faculty. Position #036663. Currently the University of Miami has faculty with research interests in ecology, population dynamics, epidemiology, and bioeconomics. In addition, the University is also home to the Abess Center for Ecosystem Science and Policy and to the newly established Institute for Theoretical and Mathematical Ecology. Applicants should have received a PhD in the mathematical sciences and should have demonstrated interest in research at the interface of mathematics and biology. We offer a competitive salary plus benefits. Review of applications will commence May 1, 2008 and will continue until the position has been filled. Please send a letter of application, professional resume, teaching philosophy and contact information for 3 references to: Professor Stephen Cantrell, Chairman of Hiring Committee, P.O. Box 249085, Coral Gables, Florida 33124-4250.

PhD Student Position, Umeå University

We are looking for a PhD student in mathematical ecology, to study evolution in response to exogenous ecosystem changes such as exploitation and climate change. A major part of the work will consist of the development and use of mathematical and computational tools. The position is a joint appointment by the Department of Ecology and Environmental Science and the Department of Mathematics and Mathematical Statistics, and the PhD student is expected to work with and take relevant courses at each of these departments. Depending on the direction in which the PhD student takes his or her research, the position may lead to a degree in mathematics or ecology. For this position, strong quantitative skills and an interest in ecology and applied mathematics are required. Candidates need a university Bachelor degree, with a minimum of 120 ECTS in relevant fields such as mathematics, physics, computer science, or ecology. Your application should include a cover letter describing your interest in and suitability for the position, a Curriculum Vitae, relevant publications (if available), copies of degree certificates, and contact information of two academic references. The procedure for recruitment for the position is in accordance with the Higher Education Ordinance (Högskoleförordningen chpts. 5 and 7). The position is available for a four year period (48 months) with an estimated pre-tax salary from 20,700 SEK per month (first year) to 24,100 SEK per month (final year). For more information about this position, contact Åke Brännström ake.brannstrom@math.umu.se, +46-(0)90-786 78 62 or Lennart Persson lennart.persson@emg.umu.se, +46-(0)90-786 63 16. For a general presentation of the two departments, see www.emg.umu.se and www.math.umu.se. See also www.umu.se for a general presentation of Umeå and the University. Union information is available from SACO, +46-(0)90-786 53 65, SEKO civil, +46-(0)90-786 52 96 and ST, +46-(0)90-786 54 31. Your complete application, marked with reference number 313-1420-08, should be sent to the Registrar, Umeå University, SE-901 87 Umeå, Sweden to arrive May 15, 2008 at the latest.

Graduate Student Positions, Simon Fraser U

Fully funded PhD or masters graduate student positions in mathematical biology available at Simon Fraser University, Vancouver, Canada. For fall 2008 or spring 2009. Possible research projects are: Cell-cell signaling in Dictyostelium discoideum or possibly using a 3-D model to study the effect that cell adhesion and cell-cell signaling has on the movement and the sorting out of different cell-types. Other options are using the model to study wound healing, somitogenesis in Zebrafish, gastrulation and cancer cell invasion. Another project is studying the flow of Nitrogen, Phosphorus and Carbon between various Phyla in marine systems. We have a bare bone model that lets us study how the stoichiometry of various organisms in the system, combined with the availability of nutrients affects the loss and accumulation of organically available N and P. The project would involve improving existing model or designing a new model to study how stoichiometry affects competition in environments with varying nutrients and how a complete system could evolve. If you are a biologist with interest in some mathematical applications or if you are a mathematician or physicist with interest in biology and are interested in mathematical biology, please email me with a brief resume, and summary of research interests. Dr. Eirikur Palsson, Department of Biology, Simon Fraser University, 8888 University Dr., Burnaby, BC V5A1S6, epalsson@sfu.ca, http://www.sfu.ca/~epalsson

Editor's Notes:

We hope you are enjoying our "My Career in Mathematical Biology" column. We also hope you enjoyed our new "Highlights in Mathematical Biology" column. We welcome contributions from your own work for future columns.

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

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

Holly Gaff, Editor, editor@smb.org