E C MTB
Communications

TU**M**OUR

GROW**T**H

& T**H**ERAPY

E**∫**MT**B** European Society for Mathematical and Theoretical Biology

The scheme on the front cover represents the icon of the European *Marie Curie Research Training Network (MC-RTN) project*

Modelling Mathematical Methods and Computer Simulation of

Tumour Growth and Therapy

(for more details see pages 34/35)

ECMTB January 2005, No. 7 : CONTENTS

EDITORIAL

Dear readers.

"Systems Biology" is on the way to become one of the strong (pro-)motors of Mathematical and Theoretical Biology, as can be seen from the report on a recent Systems Biology Conference at Heidelberg in September 2004 (see page 19). Not only that acquisition and evaluation of data gained by ever more complex molecular assessment techniques require new statistical and combinatorical methods, now-a-days experimental biologists as well as "data miners" in the field of bioinformatics call for new methods in system modeling and analysis, in order to master their far-reaching projects of proteomics or whole-cell modeling. This is a good chance for the steadily growing community of Applied Mathematicians working in Biosciences – and for a potential revival of the more general field of *"Systems Theory"*, founded almost 70 years ago in the USA (mainly initiated by Ludwig von Bertalanffy) and now 'coming back' to Europe in a more modern constitution.

It seems worth to notice that there are other 'old traditions' which now do experience similar processes of revitalization – see, for instance, the historical article on the oldest Journal in Theoretical Biology, namely *Acta Biotheoretica*, founded 1935 at Leiden in the Netherlands, thus now 70 years ago (see page 13). The *Journal of Mathematical Biology (JMB)* with its age of 30 years is comparatively young, founded 1974 by H. Bremermann, F.A. Dodge and K.P. Hadeler (see the announcement of a special issue on page 3). In both journals, the current editors are successfully engaged in opening their spectrum of scientific contributions towards the interdisciplinary 'buisiness' or 'art' of developing, analysing and evaluating quantitative models and adequate numerical simulations of biological structures and processes.

Thus, we are glad to announce that now, after a not so easy and long lasting inauguration period, whereby *JMB* became the *Official Journal of our Society*, **each member of the ESMTB** will be automatically subscribed to obtain **free paper copies of the *Journal of Mathematical Biology*** (for details see the agreement with Springer Verlag on page 10).The submission fee will be paid by the Society out of the regular membership fees. Therefore – if not yet member of the ESMTB – take the chance and register soon (visit www.esmtb.org or use form on the following page)!

With best wishes for a good year 2005, and with the hope to meet you at the *European Conference on Mathematical and Theoretical Biology ECMTB 2005* in Heidelberg, Germany, during July 18 – 22 (for more details see page 30)

Wolfgang Alt, Hans Heesterbeek, Frithjof Lutscher

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The **closing date** for submissions to the next issue *COMMUNICATIONS # 8* will be **August 30st, 2005.** Please send, preferably by e-mail, information, scientific reports and other material to one of the editors:

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Those who are interested in the Society or want to have more information, please use the Society web site:
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JMB Special Issue in Honour of K.P. Hadeler at the occasion of his 70th Anniversary

The editors of the Journal of Mathematical Biology (JMB) are pleased to announce a special issue to be published on the occasion of the 70th anniversary of Professor Dr. Karl Peter Hadeler (University of Tuebingen) in 2006.

In 1974, H.J. Bremermann, F.A. Dodge, and K.P. Hadeler founded the Journal of Mathematical Biology. Since then, its high quality and international recognition have made this publication a leading journal in Mathematical Biology. JMB was started with the leitmotif
"Experimental Results Motivated by Theory –
Theoretical Work Disciplined by Biological Facts".

In the first volume, the editors write "the standard method of mathematical biology is to consider simplified descriptions of the biological reality, that is, mathematical models. A model should be as realistic as possible yet simple enough that inferences can be drawn from it." "Consequences must be derived by logical-analytical deductions or through computations or through a combination of both". These words are as relevant now as they were in the 70's.

All colleagues, friends, and collaborators of Karl Hadeler are invited to submit a paper for this special issue. All manuscripts will be subject to the usual review process to ensure the high scientific standard of JMB.

We would greatly appreciate your letting us know now (as soon as possible after January 2005) whether you intend to contribute even if it will still take some time before your manuscript is ready. This will facilitate our planning.

This special issue is scheduled to appear in summer 2006, the deadline for submission of contributions is *August 31, 2005*. With your submission, please indicate clearly that the manuscript is intended for the special issue dedicated to Karl Hadeler.

Former co-editor-in-chief Simon Levin as well as three former students of Karl Hadeler, namely Thomas Hillen, Frithjof Lutscher and Johannes Müller, will serve as guest editors for the special issue.

Odo Diekmann and Alan Hastings
The editors of JMB

JAMES D. MURRAY - Laurea Honoris Causae in Matematica

The laurea honoris causa for James D. Murray took place in the "Sala di Rappresentanza" at the Università degli Sudi di Milano on June 3, 2004

Magnifico Rettore, Illustrissimo Preside, Chiarissimi Colleghi, Gentili Signore e Signori, Cari Studenti, it is a great honour for me to propose in the name of the Department of Mathematics and the Faculty of Science of our University, the Laurea Honoris Causa to James Dickson Murray.

To start with, I like to quote some thoughts by a couple of the most influential Italians who, from remote to modern times, have tried to express a simple concept about the role that mathematical reasoning plays and may play even more in the development of Science and Technology.

Galileo Galilei, in 1623, wrote: *"...l'universo e' scritto in lingua matematica e i caratteri sono triangoli, cerchi ed altre figure geometriche…; senza questi é un aggirarsi vanamente per un oscuro laberinto."* – *… the universe is written in a mathematical language, and its characters are triangles, circles and other geometric figures …; without these it would be a vane odyssey through an obscure labyrinth – .*

Vito Volterra in 1901 said: *"Non con soverchie speranze…, né avendo nell'animo illusioni spesso dannose, ma nemmeno con indifferenza, deve essere accolto ogni tentativo di sottoporre al calcolo fatti di qualsiasi specie."* – *Not with over-expressed hope, nor with so often dangerous illusions, nor with pure indifference, there must be accepted each trial of subjecting to calculations the known facts on any species.* –

Still, while such an interaction has been so much fruitful to Physics, Chemistry, and Engineering, a robust bridge between mathematicians and life scientists cannot be said it has been established. Offering to James D. Murray an honorary degree in Mathematics is a sign of appreciation of his long lasting contribution to establish such a bridge.

An image may well represent how much visible has been his work, the front cover dedicated by Scientific American in 1988 to his work on the mathematical modelling of how the leopard gets its spots. This is just a symbol of his achievements in the development of a coherent theory of morphogenesis.
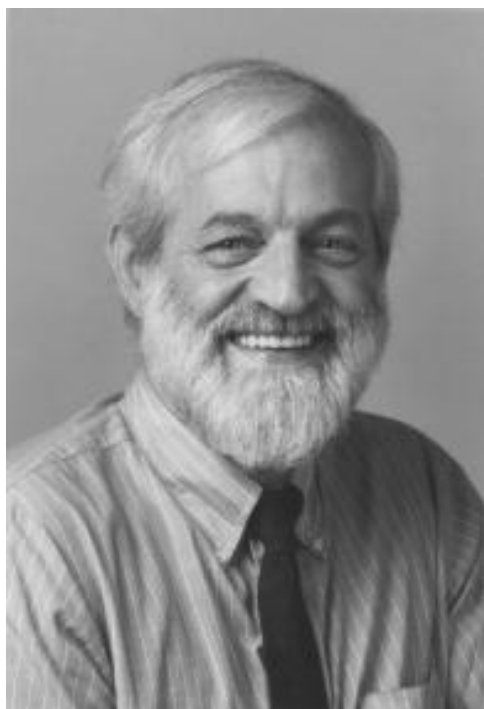

Figure 1: J. D. Murray

But let us start from the beginning. James Dickson Murray was born in Moffat, Scotland, on the 2nd of January 1931, and educated at St. Andrews where he received with honours a Bachelor Degree in Mathematics in 1953, and his PhD in 1956, under the supervision of Professor Mitchell.

Later he received an MA, and a DSc at Oxford University. His first post was in England at King's College in Durham; later he has held positions at Harvard, London, Oxford, Harvard again, and in 1965, at the age of 34, he became Professor of Mechanical Engineering at the University of Michigan. Afterwards he was Professor of Mathematics at the New York University, after which he returned for a long period to Oxford, where he was Professor of Mathematical Biology, and founder and Director of the Centre for Mathematical Biology. He left Oxford, in the late 80's, for the University of Washington at Seattle, where he spent all his time up to retirement, as Professor of Mathematics and Adjunct Professor of Zoology.

In the meanwhile he has been Visiting Scholar at various universities such as National Tsing Hua University; University of Florence; University of Utah; Massachusetts Institute of Technology; University of Texas at Dallas, University of Heidelberg, Caltech, Los Alamos National Laboratory, University of Paris, and others. Now he is Professor Emeritus at both Universities of Oxford and Seattle. As someone said, he can be really mentioned as a living example of a peripathetical scholar, like Erasmus.

James Murray began his career in fluid dynamics, and had already established his name in that field, before moving into mathematical biology and ecology thirty years ago. One of the early examples of his capabilities as an applied mathematician is related to his fundamental contribution to the biomechanics of the human body within the ejection mechanism of aircrafts; before he had discovered a resonance phenomena due to the ejection system, many pilots had been injured. Later he moved more deeply in the development and practical application of mathematical models in several diverse areas in the biomedical sciences. Recent and current topics of research, all of which involve the modeling, analysis, and biological interpretation of mathematical models, are:

wound healing, with a view of understanding and preventing severe scarring; fingerprint formation; tooth formation; sex determination and evolutionary survival in alligators; modeling of animal coat and butterfly markings, development and analysis of mechanochemical models and tissue-tissue interaction models for embryological pattern formation, with application in skeletal patterning; territory formation in wolf-deer interacting populations; patterning in plankton communities;

analysing the risk of spread of genetically engineered organisms; modeling alcohol metabolism and breath-analyser predictability; brain tumor growth; modeling and control of bovine tuberculosis in badgers and cattle; spread of diseases such as rabies and HIV, herd immunity to parasite infection; oscillatory phenomena and spiral waves in biology; analysis of enzyme-substrate kinetics; skin organ development, post-fertilization waves, and analysis of cell cortex dynamics, and, more recently, modeling of psychological processes, such as marriage breakdown; and colonization aspects of competing populations.

Murray's contributions to mathematical biology have been profound. In the early seventies, while most of the mathematicians were analysing stabilities for Reaction-Diffusion systems, he revisited and revitalized the ideas of Turing on diffusion induced instabilities, that may give rise to pattern formation. One should take into account that in those times the computational power was far from the one available nowadays, confirming the pioneering role played by Jim.

Among other fundamental results, his work with G. Oster on morphogenesis has led to new mechanisms for generating biological patterns and to the notion of morphogenetic rules. In the modeling and analysis of the factors determining the spread of rabies he introduced concepts that advanced the field in important ways. He has identified novel areas of research in a variety of fields within mathematical biology and brought them to the attention of the community through ground-breaking publications (he is author of more than 250 publications).

In his spare time, Professor Murray enjoys medioeval art and architecture, photography, 19th century English watercolour paintings.
His manual hobbies include a rare capability of reproducing antique furniture.

In addition to his seminal work in pattern formation and morphogenesis, Jim has written, in 1989, one of the most influential book on Mathematical Biology, now in its second and enlarged edition in two volumes.

During the 1980s, under his direction, the Centre for Mathematical Biology at Oxford became recognized throughout the world as the pre-eminent locale for research in mathematical biology. It was the first centre for mathematical biology in the UK, and was set up with the aim of fostering interdisciplinary research in the area and promoting it throughout the UK. The fact that there are now countless universities in the UK that have thriving research groups in mathematical biology is due almost entirely to Jim Murray's influence.

During the 1990s he established a large group at the University of Washington in Seattle, and collaborated with researchers in several departments there. From the mid 1990s, he has been involved in collaborations with various French universities and has played a pivotal role in encouraging the field there.

But not only has he been a great scientist; his dedication to teaching has made him capable of attracting scholars from all over the world in his Biomathematics Seminar, at any place he has held an academic chair. I still have in my mind the way Jim shared his enthusiasm with students from all over the world at the "coffee time" of his seminar on Biomathematics in Oxford.

Nowadays, his students (in a wide sense) are spread in many prestigious universities, from US to Europe, to Japan etc. and many of them are still continuing research at the interface between Mathematics and Life Sciences, and occupy relevant positions in Editorial Boards of scientific journals, in the Scientific Committees and Boards of the most influential national and international scientific Societies, that Jim himself has contributed to establish.

Out of the crowd I like to mention Masayasu Mimura, a world expert in pattern formation with reaction-diffusion systems, and a recognized leader of Applied Mathematics in Japan; Philip Maini, now Director of the Centre for Mathematical Biology in Oxford, and Editor in Chief of the Bulletin for Mathematical Biology; Mark Lewis from Canada, a former President of the Society for Mathematical Biology; Toshio Sekimura, Director of the Centre for Mathematical Biology at the Nagoya University, in Japan.

Let me mention one of the most relevant cases that involved my personal experience; in 1988, while I was Visiting Professor at the Centre of Mathematical Biology established by Jim at Oxford University, he strongly supported, within the international community, my "embryo" idea of founding a European Society for Mathematical and Theoretical Biology in order to influence recognition of this scientific area within the new programmes of

Brussels on European cooperation. Together with Jim, Willi Jaeger, Karl Hadeler, Jacques Demongeot, Albert Goldbeter, Lee Segel (and myself), the ESMTB was officially founded in France during its first conference in 1991, and he accepted to be the first President of the Society; thanks to the contagious enthusiasm of which he has always been identified, well recognized scientists, and young ones from all over the world have been attracted to this interdisciplinary forum.

It was upon his pressure that later I took direct responsibility of continuing the job, so that two years ago 500 hundred delegates gathered from all over the world in this university to participate in the 5th General Conference of the Society.

I take the opportunity here to thank Jim for offering his support and encouragement in building up such a successful enterprise, that has given home to many young scientists in this field. [Let me mention that the current President of the Society, Professor Mats Gyllenberg has come here from Finland, as a witness of the appreciation of Jim's contribution on behalf of the whole Society].

To more relate Jim Murray to the scientific life of our university, let me also mention the time spent about thirty years ago in Oxford where, as a young researcher, Jim hosted me at the Mathematical Institute, and gave me a fundamental encouragement to continue and deepen my interest in the development and analysis of mathematical models in Biomedicine. In particular, I am indebted to Jim for his encouragement to pursue my studies on reaction-diffusion systems, modelling a class of infectious disease, that led to one of my most influential papers on the mathematical theory of infectious diseases, and eventually to my book on the Mathematical Structures of Epidemic Systems.

Thanks to Jim, the starting model on cholera epidemic proposed by Paveri-Fontana and myself, now together in this same university, has been made visible to the relevant scientific community. It was then that I learned his lesson to capture the essential features of a natural system, without making it obscure with unnatural "academic" complicacies.

Nowadays a group of experts in applications of Mathematics to the Life Sciences is active within the Department of Mathematics of our university, and has actively contributed in the establishing of MIRIAM, the Milan Research Centre for Industrial and Applied Mathematics, and the PhD programme on Mathematics and Statistics for the Computational Sciences.

We have an established group studying problems of pattern formation related to self-organization of systems of individuals/cells subject to random fluctuations; the so called ant colonies, or agent based models. And we are still taking advantage of the contacts with the School of Jim Murray; recently a student of Biology of our University, now Doctor Silvia Boi, spent a period at the Centre of Mathematical Biology in Bath to study the social behaviour of ants. The centre had been founded by Nick Britton, another former student of Jim.

Overall, Jim Murray's contribution to the field of mathematical biology is unparalleled. He has made concrete the message by Galileo and Volterra about the successful impact of mathematical reasoning in the Biological and Biomedical Sciences. [Professor Ferguson will show us an example of what this means.]

We are in presence of a scientist who combines a unique creativity and profound vision of real phenomena, to a capability of proposing mathematical models as simple as possible though capturing the essence of the phenomena. And when the mathematical methods are too sophisticated, he is still capable of communicating the results in clear understandable terms to a wide audience. It is so much so that once, after a general lecture at a conference on Biology, a colleague approached him asking where he had learned so much mathematics.

Professor Murray holds a large number of honors, a selection of which are: Guggenheim Fellow 1968; Fellow of the Royal Society (Edinburgh) 1979; Ulam Visiting Scholar, Los Alamos National Laboratory 1985; Fellow of the Royal Society (London) 1985; Fellow of the Institute of Biology (Great Britain) 1988; Foreign Member of the Academy of Sciences (France) 2000; London Mathematical Society Naylor Prize for Applied Mathematics 1989; President of the European Society for Mathematical & Theoretical Biology, 1991-1994; invited speaker at ICIAM 1991; Honorary D.Sc. degrees by University of St. Andrews 1994, and University of Strathclyde (Scotland) 1999. Honorary Fellow, Corpus Christi College, University of Oxford 2001.

On the basis of his outstanding achievements in building a bridge between Mathematics and a number of other disciplines, it is a great honour for me to submit to the Committee for the conferral of

the Laurea Honoris Causa in Mathematics the case of James Dickson Murray.

Milano, June 3, 2004

Laudatio by

Vincenzo Capasso
Dipartimento di Matematica
MIRIAM Research Centre for Industrial and Applied
Mathematics
Universita' degli Studi di Milano

SOCIETY NEWS

Minutes of the ESMTB Board Meeting

Utrecht, February 16th, 2004

Meeting starts 9.30 am

Present: Mats Gyllenberg (MG, chair), Marcelle Kaufman (MK), Vlastimil Krivan (VK), Philippe Tracqui (PT), Andreas Deutsch (AD), Wolfgang Alt (WA), Hans Heesterbeek (HH; minutes).

Absent with apology: Helen Byrne (HB), Rafael Bravo de la Parra (RB), Luigi Preziosi (LP)

Before starting the meeting proper, the chairman requests a moment of silence to commemorate the death of our colleague Ovide Arino.

1. *Adoption of the agenda*

Two items are added to the agenda: Request for financial support of PhD-student meeting (item 4A); Offer from IMA (item 4B).

2. **Minutes of the previous board meeting (Bonn, September 19th, 2003)**

The minutes of the board meeting that were already approved by e-mail by all board members, are now approved formally, and can be printed in the 6th issue of the Communications.

The points of action for the various board members, to be found in the minutes of the Bonn meeting have almost all been dealt with. Most will be mentioned at appropriate places in the minutes below. The other points of action were: update list of curricula in Europe (LP): this has been done and will appear on the agenda at the next board meeting.

3. **Report from the President**

- The European Commission organized a meeting for presidents of European scientific societies to discuss NEST (New and Emerging Science and Technology). MG attended the meeting and reported by e-mail to all board members afterwards. The outcome is that for societies themselves there is not much to gain from the initiative, which is aimed at researchers and research groups.
- MG informs the board that he is a member of steering group on systems biology (cellular level), as representative of the Finish Academy of Sciences. The steering group is for a European Science Foundation "Forward Look" on Systems Biology, initiated by Hans Westerhoff in January 2004 in The Hague. There are three workshops planned for 9 + 10 September 2004 and one conference. The aim is to discuss future directions in this field, leading probably to a future ESF program. The workshops will most likely be in the Netherlands and one of the workshops will have mathematical modeling as its theme. Participation is by invitation only. Members interested in attending can approach MG. **MG will send the minutes of the meeting in The Hague to all board members**.
- MG received a letter from a consulting firm, proposing to evaluate the next ESMTB conference; they would write a report, as an independent agency, on matters that can be improved. It is

decided not to do this. The letter is passed on to AD.

4. Report from the Treasurer

- AD shows charts that give details of the membership and points out that since June 2003 there has been a steady increase in paying membership. The registration and the system of tracking payments is now very efficient and well set-up. After a transition phase this now no longer seems problematic. In 2004 it is expected that all names on the membership list correspond with payments having been made. A reminder of payment will be send out in March 2004.
- There are currently 120 members, expected to reach 150 this year. It is projected that this will generate an income of about 5000 Euro.
- The balance at the end of 2003 was 300 Euro, after the 10.000 Euro fee for Springer had been paid (see item 5 on the agenda). In order to avoid a negative bank balance until payments for 2004 come in, the ESMTB kindly accepts a loan from WA and AD for 4.500 Euro (to be re-paid by the end of 2004). **AD will prepare papers concerning the finances for the two auditors Daniela Morale and Kalle Parvinnen. AD will present an official audit report for 2003 at the next board meeting.**
- Currently members can pay by bank transfer, credit card and Paypal. The latter is a very efficient and safe method of paying electronically. The company Paypal registers users and supplies them with a password. Upon supplying a credit card number or a bank account number once, registered users can then make easy payments to each other. The company charges 4% for this service. The costs of this are borne by the ESMTB for payment of ESMTB membership fees. The link can be accessed on the ESMTB web site.
- AD urges everyone to approach institutions and organizations for Institutional Membership.
- The "sleeping members" list now stands at 700 people. Some discussion ensues about possibilities to attract these people

again to the society; all have responded to several newsletter activities in the past. **AD has approached them previously and will do so again**, outlining the benefits of membership and upcoming meetings for which discounts are given. Individual approaches by board members of selected people on the list might work (WA) but seems a lot of work. Board members, however, see it as their work to promote the society continuously. **AD will circulate the list of 700 names among the board members for further action**.
- WA suggests to approach the Francophone, Dutch and Israeli societies for theoretical biology and discuss with them reciprocal membership. MG proposes to have the reduced rate on the same terms as those currently holding with SMB. This means a reduction of 20% in the fees, both ways. This idea is approved. **PT will discuss with the SFBT, HH will discuss with the NVTB and the Israeli society.** Final results will be communicated to the board by e-mail and AD will then take the steps necessary for speedy implementation.
- Finally, it is suggested to keep the membership fee for 2004 the same level as in 2003. This is approved.
- The board expresses many thanks to AD for his activities.

4A: Application for support. AD has received an application for financial support of the 10th Annual meeting of PhD students in Evolutionary Biology, to be held in the UK in August/September 2004. About 100 PhD students will attend. The draft program that accompanies the request shows a very biological and experimental focus of the meeting. Since we are a society of theoretical and mathematical approaches to biological problems, and since modeling is an important part of the evolutionary field, we propose to suggest to the organizers to reflect this influence of mathematics as a tool in their program. If needed, we can make suggestions. VK will be contact person. It is decided to sponsor this event with 1000 Euro (given our limited budget for 2004) + 50% of the ESMTB fee paid to the organizers for each new member (10 Euro per student). In return we make the above suggestion and require three things: a reduction in fees for PhD students that are

ESMTB members; a report of the meeting for the Communications; and mentioning of the society as sponsor. **AD will react to the organizers in this vein**.

4B: Offer of IMA Journal. AD has received a letter from Oxford University Press offering electronic access to the IMA journal *Mathematics in Medicine and Biology*. The journal has recently been given its new name, accompanying new managing editors and a new editorial board. The offer is that each ESMTB member can get free electronic access to the journal and its archive for six months and after that pays 59 pound Sterling for an extension of that period to the rest of 2004. The board feels that this is expensive for mere electronic access and does not see how many members would be interested in this offer. If it turns out that there is no obligation after the free trial period, then we can inform our members of this possibility. **AD will enquire as to the precise terms**.

5. Relation with Springer and *Journal of Mathematical Biology*

For an overview of the situation we refer to the **explanations by the president MG and the secretary HH** in the previous issue of the Communications (issue 6 March/April 2004). It is clear from the discussion that we wish to continue our relation with Springer and our association with JMB as the official ESMTB journal. After discussion many options it is decided that **MG, HH and AD will take the task of starting new negotiations with Springer**. It is expected that initial negotiating can be done by e-mail and that later in the year these board members will go to Heidelberg for formalizing the new agreement [see next page].

6. Summer schools after Ovide Arino

HH has received a letter from Andrea de Gaetano and Rafa Bravo de la Parra in which they outline plans for a funding proposal under the Marie Curie program in the 6th Framework of the EU. One of their aims is to fill the void that is left by the passing away of Ovide Arino, who for years tirelessly invested time and effort into the organization of ESMTB and other summer schools. The deadline for application is mid April 2004. Since the ESMTB (HB, RB and LP) also announced plans for a series of events in education at the board meeting in Bonn, the question of de Gaetano and Bravo de la Parra is to join forces

in order to prevent two competing proposals. The board supports this idea and decides to react positively to the proposal. **HH will send a reply and some suggestions on workshop topics and names of people for the intended Promoting Committee to the main organizers**.

7. ESMTB Conference 2005, Dresden

AD presents an update on the progress of organizing the 2005 ESMTB Conference in Dresden. The board is very satisfied that all is going well and is grateful to AD and the local organizing committee for doing all this work. A large part of the board meeting is spent finalizing, as far as the ESMTB is concerned, the list of topics for the conference and the list of proposed names for the Scientific Committee. AD will now discuss these lists with the SMB president Louis Gross to give him the opportunity for additions. He will then approach the names for the Scientific Committee and ask them to suggest at most two names for invited speakers. **AD will supply this list to the board by e-mail by March 18, 2004, together with a suggested top 15.** The board will then finalise their choice by April 1st, 2004, for discussion with SMB. Suggestions for names by the organizing committee are discussed and names are added in discussion. AD will incorporate these in the long list that will ensue. The time schedule for the conference has abstracts being submitted before February 1, 2005. The next board meeting should be scheduled shortly after that period, but before the program is finalized.

8. Report on the Communications

Fitjof Lutscher (Canada) is currently editing issue 6 of the Communications. The issue will probably be back to its original size after the reduced issue 5. 250 copies will be printed of which 150 go to paying members and of which 100 will be used for marketing purposes. WA proposes to symbolically value each issue at 20 Euro as the price to buy a hard copy for non-members. The contents will be placed on the ESMTB web-site for personal downloading.

9. Advisors to the board

WA suggests to appoint advisors to the board in order to more efficiently communicate with neigbouring fields of which the current board members do not have a good overview (e.g. biophysics, biotechnology, bio-engineering, bio-informatics). His initial idea is to invite them occasionally to board meetings. The board feels it is

a good idea to discuss scientific issues in the board (and in fact would like to stimulate this) and, for example, science policy and the future of mathematical and theoretical biology in Europe (and in general). However, one feels that board meetings are not the right set-up for these discussions. It is proposed to hold a special one-day workshop in 2005 to host such discussions. An option would be to have it as a **satellite meeting of the Dresden conference**. **AD will look into this possibility**. MG proposes to not make a list of formal advisors, but to appoint and approach ad hoc advisors whenever the need arises.

10. Any other business
Two items should be included in the next board meeting: a discussion about the curricula inventory of LP and WA, also in the light of the recent Bologna Agreement; discussion about a preliminary list of candidates for the five places on the board that become vacant at the 2005 General Assembly of the ESMTB during the Dresden conference.

11. Next meeting
PT has kindly offered to organise the next board meeting in his new office in Grenoble. The meeting is scheduled for March 7th, 2005. This gives the board the opportunity to discuss the program of the Dresden conference in detail: the proposed sessions, mini-symposia, the abstracts received.

MG thanks HH for hosting the meeting in Utrecht and ends the board meeting at 5.15 pm.

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New agreement with Springer Verlag:
Automatic and free subscription to print edition of the Journal of Mathematical Biology (JMB)

As discussed in detail in ECMTB issue # 6 (March 2004), the ESMTB board, in the interest of sound financial management, had no other option than to cancel the contract with Springer Verlag before the end of 2003, using the escape clause built into that contract. As you know, Springer Verlag was very kind in continuing to honour their side of the contract during the transition period in 2004 in which new arrangements could be discussed. After discussion in the board, Mats Gyllenberg, Andreas Deutsch and I had a meeting in Heidelberg on October 19th, 2004, with dr. C. Byrne, Executive Editor Mathematics of Springer, and Ms. M. Weisleber, Societies Liaison Officer of Springer. This meeting was very open and constructive, and conducted in a very good atmosphere. As a good rendering of the fruitful

outcome of the meeting, I provide below parts of a letter from dr. Byrne outlining the new agreement.

Dear Mats, Hans, and Andreas.

You came to Heidelberg in October to discuss with us the options for continuing a collaborative and mutually beneficial arrangement between the ESMTB and Springer. I would like to thank you again for helping us to keep our discussion very open and very straightforward.

With this letter, we would like to confirm that Springer accepts the conditions that you proposed in that discussion, namely, that our previous arrangement for electronic access to the "Journal of Mathematical Biology" for all paying members of the ESMTB be dropped from further consideration, as this was not perceived by the members as a privilege of membership, a majority of them having electronic access already through their institution or affiliation; and that in place of this, we arrange a subscription to the print edition of JMB for all paying members of ESMTB, at a standard rate inclusive of mailing costs, that will be set for 2005 at EURO 20,00.

It is understood by both parties that the agreed subscription fee per member, barely covering expenses, is agreed in goodwill and in anticipation of significant growth in membership numbers and dues in the coming 3-5 years.

It is agreed that progress in this respect will be reviewed at the ESMTB Congress in Dresden in the summer of 2005.

I propose that we consider it as an interim, modified continuation of our earlier contractual agreement and, if we are all happy with the progress made between now and the addressed congress, rewrite the contract of 2002 correspondingly at that stage for signature in the latter part of 2005.

It remains for me to wish you a restful and happy Christmas, and all the very best for yourselves, your families, and, of course, the Society, in 2005.

I hope you agree that this is a very good deal for our society. It now becomes very attractive to be a member, also if one is already a member of a sister society through reciprocal membership. This is also good news for the Journal of Mathematical Biology, which will now see an increased readership, but more importantly a broader readership; this will strengthen the journal in its aim to grow towards increased biological content of the mathematical and theoretical papers it publishes. The board is confident that this new agreement will signal a long a productive collaboration with Springer Verlag and the Journal of Mathematical Biology.

Hans Heesterbeek (Secretary ESMTB), Utrecht

Mathematics in Medicine Study Group:
The Early Years
School of Mathematical Sciences, University of
Nottingham, England

A rapidly developing field of mathematical modelling involves its application to medicine. It is extremely desirable that such mathematical developments do not take place in isolation from real experimental and medical issues. For the field to attain its full potential, with significant impact on medical practice, it is, therefore, essential that close contact between mathematical and medical researchers takes place.

Through EPSRC (Engineering and Physical Sciences Research Council) funding awarded to the Centre for Mathematical Medicine at the University of Nottingham, a series of meetings - Mathematics in Medicine Study Groups (MMSGs) - was organised.
The main aim of these meetings was to establish collaborations between mathematical and biomedical researchers by exposing the mathematical modellers to medical problems requiring the development of new models and providing the biomedical participants both with quantitative results specific to their interests and with broader insight into the scope for applying modelling techniques.

Four week-long MMSGs have now taken place (three in Nottingham, England; one in Strathclyde, Scotland). Meetings were typically attended by between 40 and 50 participants, the majority of whom were applied mathematicians (including PhD students and PDRAs, many of whom had little or no previous experience in working on biomedical problems!). The format of the meetings was based on that successfully developed in the Study Groups in Industry (information about European Study Groups in Industry is contained elsewhere in the Communications). Prior to each meeting, discussions between the organisers and a number of potential biomedical participants took place in order to identify a number of issues that would benefit from mathematical investigation. Short descriptions of the problems were then circulated to all participants prior to, or at, the meeting. On the first day of the Study Group, each topic was presented by the relevant biomedical expert(s) to all the participants. On subsequent days, multi-disciplinary teams worked on

each problem. Interim progress reports were presented midway through the meeting, thereby enabling participants to contribute to progress with each project. Conclusions were presented on the final day and written reports compiled and circulated subsequent to the meeting (these reports may be downloaded from the Network's web pages, see below).

In addition to the problems under consideration, several invited lectures were given during each MMSG. The aim of these lectures was three-fold: (i) to showcase areas with potential for multidisciplinary collaboration and (ii) to illustrate ways in which mathematical modelling has been used successfully to provide insight into specific biomedical problems; (iii) to train young researchers to apply their mathematical skills to modelling biomedical problems.

While MMSGs are still in their infancy (certainly in comparison with the Study Groups with Industry), we believe there are many good reasons why they should continue. Firstly, they provide a stimulating environment within which experimentalists, clinicians and mathematicians can foster new collaborations and joint research interests. Second, they can help to train a new generation of mathematicians who are equally at ease working with theoreticians and biomedical researchers. Finally, based on the outcome of the MMSGs that have already taken place, the collaborations that develop have a strong likelihood of securing research funding - in excess of £1.5million of UK research council funding has already been secured from proposals developed by participants at the MMSGs.
So, what is the current status with regard to future MMSGs? With colleagues from Oxford, Southampton and Strathclyde, we are seeking funding to organise future UK-based MMSGs. In addition, we are applying to host a student-focused MMSG with funding from the EU. This meeting would function as a summer school, with a predominantly pedagogical nature, and form one of a series of summer schools in a proposal to the EU which is being coordinated by Andrea de Gaetano.

For details of upcoming activities of a similar nature, please contact Helen Byrne
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or refer to the following web address:

http://www.maths.nottingham.ac.uk/Cmm

Helen Byrne
Centre for Mathematical Medicine
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Research group on Mathematical Biology
Max Planck Institute for Mathematics in the Sciences, Leipzig, Germany

The research group focuses on structure formation and function in cellular systems by means of modeling, mathematical analysis and simulations.

Pattern formation and emergence of structure in interacting cell systems are not only of principle theoretical interest but are important means to reveal information on underlying functional mechanisms, especially when mutant populations show defined changes in structure in comparison to wild-type populations.

A major aim is to try to detect underlying robust mechanisms and to understand which of the biological information on the various involved small scales is needed to describe macroscopic quantities of interest correctly and to avoid the explicit resolution of microscopic structures and processes where not necessary.

Biological phenomena we are analyzing are, among others, self-organization of microorganisms as observed in populations of *Myxococcus xanthus*, *Dictyostelium discoideum*, and *Escherichia coli*. In this context we deal with micro-, meso-, and macroscopic models for chemotaxis and pattern formation due to surface bound signals, and the modeling of bacterial flagella.

Further on we are interested in tumor growth, wound-healing, and the dynamics and restructuring of the cellular cytoskeleton. Traveling waves in inhomogeneous media are a focus we are generally interested in, for example also in the context of ecology and epidemiology.

Mathematically we are dealing with non-linear partial- and integro-differential equations, with interacting stochastic many particle systems and limiting procedures.

The group is involved in the RTN Programme *Fronts-Singularities*, and in the DFG Focus Programme *Analysis, Modeling, and Simulation of Multiscale Problems*. Recently a DFG Graduate College was granted, *INTERNEURO*, where the group will take part in 3 PhD-projects on structure formation in neural tissues, jointly with groups from biophysics, biotechnology and neurophysiology [see also page 33].

At the time one research associate, 2 PhD-students and 4 Diploma students are working in the group. Two postdocs recently got outside offers, one for a permanent position. This year several summer inter-ships joined the group on projects related to simulations of tumor growth and the dynamics of the cytoskeleton.

Further information about other research groups at the MPI can be found under http://www.mis.mpg.de/
about the research group Mathematical Biology
http://www.mis.mpg.de/as
about open positions at the MPI:
http://www.mis.mpg.de/mpi/positions.html

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The history of *Acta Biotheoretica:*
The world's oldest theoretical biology journal

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Introduction

Since the beginning of the twentieth century, theoretical biology in The Netherlands grew into an important biological discipline. *Acta Biotheoretica* is an international journal of Dutch origin on the mathematical and philosophical foundations of biological and biomedical science and exists 70 years in 2005. Here we briefly describe the history and scope of the journal *Acta Biotheoretica* in connection with the history of theoretical biology in The Netherlands.

What is Theoretical Biology?

Within science, biology is generally not considered to be a "hard" science. Nevertheless, theoretical biology has existed as long as researchers have been interested in investigating the living world. Most of the time, subjects we now consider to be part of theoretical biology were incorporated in the different biological disciplines. At first, theoretical biology comprised a general investigation into the nature of life and its development on Earth. Later on however, theoretical investigations kept pace with the distinction of disciplines in biology. Therefore, theoretical biology was included in all biological disciplines studying entities and phenomena on different levels of organization, from molecular biology to ecology.

Founding a Dutch journal on theoretical biology.

The international journal on theoretical biology that was founded by Dutch scientists has its origins in the 1930s. Three professional friends decided to issue a journal in 1934. These were C.J. van der Klaauw (fig. 1, zoologist at Leiden University), J.A.J. Barge (medical anatomist at Leiden University) and A. Meyer (biologist at the University of Hamburg). In

that part of the twentieth century the number of researchers working in the field of theoretical biology strongly increased.

Figure 1: Prof. Dr. C.J. Van der Klaauw (1893-1972)
One of the founders of Acta Biotheoretica

Moreover, communication between researchers was not as easy as nowadays, due to the mailing system and the difficulties of traveling. The three scientific friends wanted to create a platform for communication that promoted the scientific contacts within the field of theoretical biology itself and between theoretical biology, the other biological fields and areas outside biology. In addition, the platform they had in mind should enable students and scholars to always return to the study of questions and problems in theoretical biology. One of the prerequisites for issuing a journal on theoretical biology was the existence of an extended network of scientist. Therefore, van der Klaauw, Barge and Meyer approached many researchers spanning almost the entire academic field of biology. Because they proposed to publish articles in three modern European languages, namely French, English and German, they received a very positive cooperative response. According to their ideas, every publication in the journal should be written in one of these three languages and be accompanied by summaries in the

two other languages (Van der Klaauw *et al.* 1935: 3). About fifty excellent scientists agreed to support the three friends in issuing the journal, recommending new contributions, refereeing and editing submitted manuscripts. In the early years, the Board of the journal consisted of the three founders, and seven other scientists from different countries formed the Editorial Board. An advisory team was composed from the other cooperating scientists.

Acta Biotheoretica, the story continues

The new journal was called *Acta Biotheoretica* and started with support of the Jan van der Hoeven Foundation for theoretical biology of animals and humans. In the first volume the *Acta Biotheoretica* was defined as being "(…) an international biological journal for the promotion of theoretical biology, being exclusively devoted to investigations on biological theories, particularly also the special mathematics and logic of biology" (*Acta Biotheoretica* 1 (1935): first printed page, no page number). This journal, first published in 1935 (see title page of Volume 1 in figure 2), is one of the oldest international journals publishing on theoretical biology.
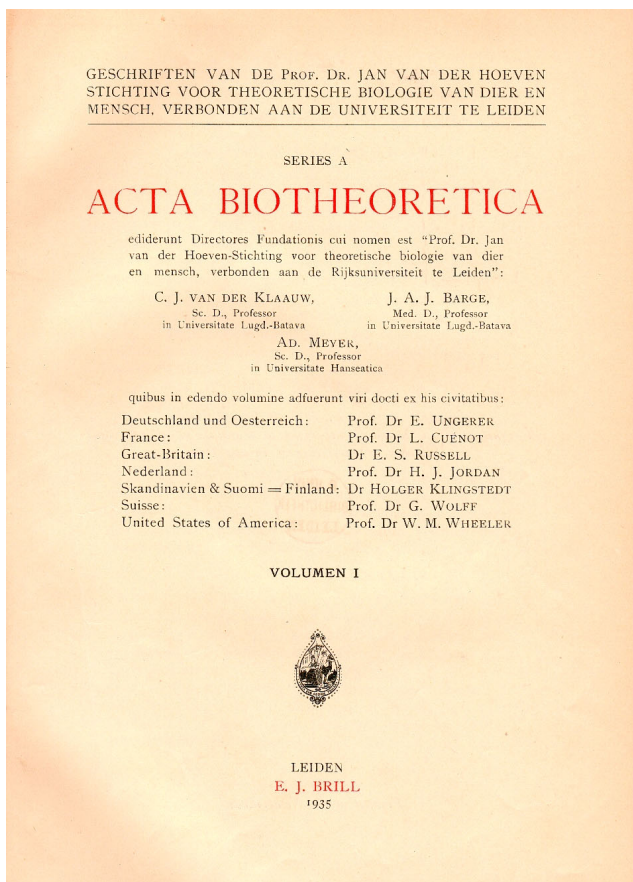

Figure 2: The title page of the first volume of the Acta Biotheoretica in 1935

From its foundation the journal has been devoted to the development and promotion of the field of theoretical biology. The journal has continuously operated from a broad understanding of the nature of theoretical biology and has reflected the particular character of theoretical biology as it existed and still exists in The Netherlands. In this view, theoretical biology covers the entire spectrum of theoretical investigation of the living world, ranging from the philosophy of biology to mathematical biology. Therefore, the journal allows the process of biological theory formation to range from purely verbal argumentation to the mathematical analysis of biologically based models.

Just after the successful start of their journal, the editors started *Folia Biotheoretica*, *Bibliographia Biotheoretica* and *Bibliotheca Biotheoretica*. Each of these publication series served a different goal. The *Folia Biotheoretica* was, "(…) a series of introductory studies regarding theoretical biology. (…) Each number treats a certain subject and appears in connection with a symposium held at the University of Leyden" (Acta Biotheoretica 11 (1953-1956): inside front cover). The *Bibliographia Biotheoretica* originated to help students and scholars to gain an overview of the available literature in their field. The references to typically theoretical papers were collected by the editors and published in the *Bibliographia Biotheoretica*. The *Bibliotheca Biotheoretica* was established as "(…) a series of monographs on certain subjects of theoretical biology (…) [not aimed] at giving reviews in the manner of a pure compilation, but bearing the personal stamp of the author and having a scientific, objective and critical character" (Acta Biotheoretica 11 (1953-1956): inside front cover). From 1971 the "editor in chief" Prof. Jeuken (1971) announced that lists of new titles in theoretical biology continued to appear in *Acta Biotheoretica* itself. With the publication of Current Contents this service was abolished. In more recent years, Current Contents has been replaced by classified on-line literature search facilities covering almost all the literature in (theoretical) biology. Nowadays, *Acta Biotheoretica* is the only one of these four series that still continues to be published on a regular basis (see also Dullemeijer 1976: 57-59). The Editorial Board of this journal has been changed frequently as is shown in Table 1. Jeuken (figure 3) and Dullemeijer (figure 4) were predecessors that we have known personally.

Piet Dullemeijer, the managing editor of *Acta Biotheoretica* in the periods 1966 – 1969 and 1987 – 1998, recently co-authored the first chapter of our

book (Reydon *et al.* 2004). Before the appearance of this book, Dullemeijer passed away. In his honour we include a short sketch of his life and work (see boxed section).

From the start of *Acta Biotheoretica*, researchers attempted to bring forward the specific character and value of biological investigation in the published articles. These investigators agreed upon the view that the majority of biology cannot be reduced to physics, chemistry or mathematics. They admitted however, that these other scientific disciplines had an added value for their own work. The journal provided a platform for publications on a wide variety of topics: these spanned the entire spectrum of theoretical biology ranging from philosophy of biology (for example, there were two papers on the question whether biology could be considered an autonomous science; Sapper 1935 & 1936) to the mathematical foundations of biological science (e.g. Volterra 1937). The purpose of the journal was adapted to include the publication of articles from other disciplines that could help biologists in their work, because the specific character and value of biological investigation required the input from scientific disciplines outside biology (at the time, biologists frequently acquired training in fields outside biology).

Table 1: Editors of *Acta Biotheoretica*

| Volumes	years	Editors				
I-VIII	1935-1948	Van der Klaauw	Barge	Meyer		
IX-X	1949-1951	Van der Klaauw	Barge			
XI-XII	1953-1956	Van der Klaauw	Van der Vaart			
XIII-XVI	1958-1960	Van der Vaart	Duijff			
XVII	1967	Van der Vaart	Duijff	Dullemeijer		
XVIII	1968	Van der Vaart	Dullemeijer	Verveen		
XIX	1970	Van der Vaart	Jeuken	Verveen		
XXIV-XXXII	1975-1983	Jeuken	Van Laar	Verveen		
33-35	1984-1986	Van Laar	Verveen			
36-37	1987-1989	Dullemeijer	An der Heiden	Ludwig		
38-46	1990-1998	Dullemeijer	Demongeot	An der Heiden	Ludwig	
47-49	1999-2001	Hemerik	Demongeot	An der Heiden	Stevens	
50-52	2002-2004	Reydon	Hemerik	Demongeot	An der Heiden	Stevens
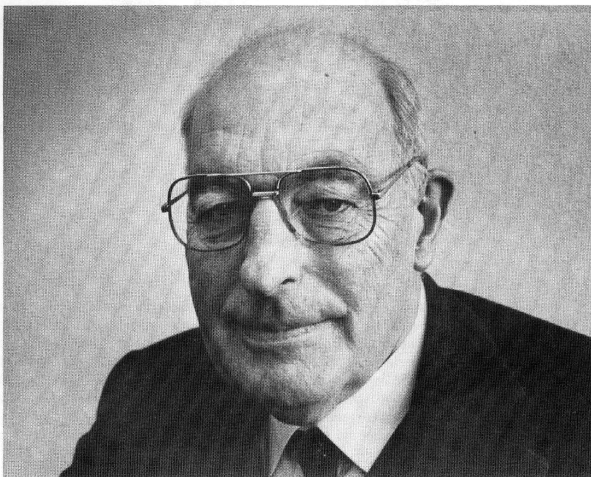
Figure 3: Prof. Dr. M. Jeuken (1916 -1983)

Despite the successful start of *Acta Biotheoretica*, the outbreak of the Second World War unfortunately hampered the main efforts to build bridges between various areas of scientific investigation. The journal barely survived the war due to reinforced language barriers and the state of the founding editors. The Germans imprisoned Van der Klaauw, Meyer was physically unable to travel and Barge had become an old man. Young co-workers tried to consolidate the journal, but the communication system was almost fully broken down: the need for a completely new editorial system arose. Meanwhile, researchers in theoretical biology in different countries got organised differently and were going their own way, among other things, because they were working in different disciplines between which there was not much contact.

The end of World War II marked the start of a new policy. The original intent had been to publish one volume of the journal per year (see Acta Biotheoretica 1 (1935): first printed page, no page number). However, most of the volumes that were published from 1939 onward covered two to four years per volume (volumes 5 to 13). After 1960 the publication frequency increased, but it was not until the late 1960s that *Acta Biotheoretica* was again published annually. Due to the damaged connections between the scientist that originally gave their support, the journal's editors were (directly after the war) unable to achieve the journal's aim "(…) to

bring into the sphere of international thought theories and views which at present are too much restricted to certain schools and certain countries" (Acta Biotheoretica 1 (1935): first printed page, no page number), hoping to "(…) put an end to the terrible fragmentation of biotheoretical thought" (Van der Klaauw *et al.,* 1935: 2; translation TR). After the war the publications in the *Acta Biotheoretica* reflected the existing fragmentation of biological thought by containing mostly papers stemming from particular schools of theoretical research and symposia reports of specialised disciplines. Thereafter, the published papers show a restoration of the original aims of the journal. From Volume 33 (1984) onward, the journal's official policy is that papers should be written in English (Instructions for authors, Acta Biotheoretica 33 (1984): 63-66). Nevertheless, in later volumes papers in French have occasionally entered the journal's pages, for instance in special issues on the annual meeting of the Société Francophone de Biologie Théorique. Only since 1999 all publications in the *Acta Biotheoretica* are bound to be written in English.

The scope of *Acta Biotheoretica*
In 1938, Van der Klaauw observed that theoretical biology "(…) has not yet developed into a universally acknowledged department of biology, a fact which gives rise to a good deal of confusion in the application of the term (…)". He expressed the view that theoretical biology should be understood "(…) on as broad a basis as possible, so that the subject may later be able to develop itself freely along its own lines" (Van der Klaauw 1938: vii). In the second part of the twentieth century theoretical biology had become a mature field of investigation worldwide, with its Dutch branch occupying a special position in the international scholarly landscape. The philosopher Michael Ruse acknowledged in 1988 in an overview of the state of affairs at that time in philosophy of biology:
"Holland has a small subdiscipline which seems virtually unique to that country. So-called theoretical biology runs the gamut from hard-line mathematical modeling to serious study of the philosophical foundations of biology. To date, the subject's practitioners have perhaps been more successful at the mathematical end of the spectrum (…). Now, however, (…) a new generation of philosophically trained biologists is producing work on ethics, ecology, theory structure, and more (…)" (Ruse 1988: 86)." Today, theoretical biology in The Netherlands still covers this entire spectrum. *Acta Biotheoretica*'s founding editors adopted the aim of the Jan van der Hoeven Foundation to develop "(…)

a theoretical biology within, and strictly in the service of the science of practical biology" (Van der Klaauw 1938: viii). They however, did not see theoretical biology as subordinate to the gathering of empirical data, but as a field of work that was of value in itself. This becomes clear from the quote: "Facts are regarded as parts of knowledge having eternal truth and validity, while theory is regarded rather as a necessary evil, a means by which facts may be deduced. (…) However, it is not true that theory is a necessary evil. It is only to secure the joy of knowledge that it [i.e., theory] gives us, that we search for the facts that can verify it" (Van der Klaauw et al. 1935: 1-2).
Thus, theoretical biology should not only serve the practical biology, but it should also develop general theories that account for the phenomena studied in biological practice. This is expressed in the description of the character of theoretical biology that the journal's founding editors adopted: "By 'Theoretical Biology' is meant, in the first place theories and views of a general character regarding the biologcal sciences, in the second place the mathematical foundations of these sciences (…), in the third place the philosophical and logical foundations of the biological sciences (…)" (Acta Biotheoretica 11 (1953-1956): inside front cover).
This broad view of the field is maintained in the present day scope of the journal. Minor changes occurred as new areas of investigation were opened up. Some of these new areas were included into the journal's scope. Biochemistry, for instance, became a promising new area of investigation, but researchers in this field never used *Acta Biotheoretica* for publication of their theoretical results. Similarly, physiological genetics and developmental biology did not find their way to the journal's pages. Bioinformatics, however, was a field that explicitly entered into the journal's scope. As the editor, M. Jeuken, asserted in an editorial in Volume 25 of the journal: "Originally theoretical biology was only philosophy of biology. About 1940 biomathematics came into the field. (…) Bioinformatics is a new part of theoretical biology (…)" (Jeuken, 1976: i; cf. Instructions for authors, Acta Biotheoretica 30 (1981)).
At present, the journal is conceived primarily as an international journal publishing on the mathematical and philosophical foundations of biological and biomedical science, as its subtitle since 2002 conveys.

In conclusion
Nowadays, the papers in the *Acta Biotheoretica* reflect the diverse nature of theoretical biology

worldwide. Due to severe cutbacks in research funding, philosophy of biology in The Netherlands is at present in far from good shape, but we still believe that a mature theoretical biology should essentially encompass research into both the mathematical and philosophical foundations of biological science. Moreover, *Acta Biotheoretica* should in our opinion continue to publish in both fields of work, as well as on topics that lie in between these two.

Figure 4: Prof. Dr. P. Dullemeijer (1925-2004)

Short biography of Pieter Dullemeijer
(based upon Dubbeldam *et al.* 1989)
Dullemeijer started his biological education in 1945 at Leiden University. In 1956 he defended his PhD. Thesis in the field of animal morphology. At that time he was associate professor in the Department of Zoology at Leiden University. Since 1970 he has been Professor of Animal Morphology. Van der Klaauw, one of the founders of *Acta Biotheoretica*, was his teacher and thesis adviser.
Within the field of Animal Morphology, Dullemeijer extended the concept of functional elements in the skull as proposed by van der Klaauw (1945). He developed the idea of hierarchical relationships between functional morphological components that can be distinguished at various levels of organization.

Throughout his scientific career he was always interested in biological theory formation, ethics and philisophy of biology. Therefore he really had his heart in the editorship of *Acta Biotheoretica.*

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CMPD - Computational and Mathematical Population Dynamics
(MPD'7 and Destobio'3 joint meeting)
June 21-25, 2004, Trento, Italy

The White Rabbit put on his spectacles.
"Where shall I begin, please your Majesty?" he asked.
"Begin at the beginning," the King said, very gravely, "and go on till you come to the end; then stop."
(by Lewis Carroll)

It is perhaps not quite in the current fashion but still it does seem to be a good idea to begin at the beginning. Although the name CMPD has not been heard before this year, the conference already has a long history. The whole story actually began in 1986 when the 1st Mathematical Population Dynamics (MPD) conference was organized by *Marek Kimmel*, *Ovide Arino* and *David Axelrod* in the University of Mississippi. Eleven years after that remarkable event, the series of DeStoBio conferences (Deterministic and Stochastic Models for Biological Interactions) was launched by *Tanya Kostova* in Sofia in 1997 on the other side of the Atlantic. These two respectable "parents" (it was not without a good reason that Tanya Kostova received a title of "godmother" at the CMPD opening ceremony) gave life to this nice "baby" conference that uttered its first words on June 21, 2004 in a beautiful town of Trento in the heart of Italian Alps.

And good and meaningful words they were, too. The conference started with a welcome ceremony followed by the first plenary lecture to the memory of Ovide Arino delivered by *Hassan Hbid*, one of his former students. The closing lecture on June 25 was given by Simon Levin who provided a wide and in many ways impressive overview of the state-of-the-art in ecosystem management. More plenary lectures were given by distinguished scientists such as *Helen Byrne*, *Albert Goldbeter*, *Peter Jager*, *Mercedes Pascual* and others. Over two hundred contributed talks that were organized into 28 oral sessions and two poster sessions. The topics addressed in the talks and lectures covered virtually all aspects of contemporary theoretical population dynamics, from evolution and ecology of animals, plants and pathogens to modeling tumors and cells, genetics and adaptation The conference turn-out was equally impressive: about three hundred participants came from almost forty countries from different parts of the world.

Apart from outstanding scientific merit, it should be mentioned that the conference was very well organized. In particular, computer facilities were provided in abundance and everything worked perfectly. All necessary information was readily available, and help was provided immediately when required. Also, it was a good idea to place some of the plenary lectures, for which high turn-out was to be anticipated, into the closing session. Most of the conference participants stayed until the end and maintained the exciting atmospere until the very last moment.

This success was made possible by the excellent work of the local organizing committee led by *Mimmo Iannelli* and *Andrea Pugliese*. Together with all the local volunteers they managed to create an atmosphere of hospitality and effectiveness, providing generous help, that made participants feel welcome and free to engage in scientific discussion and discovery. It is this atmosphere combined with the wonderful surroundings of Trento (pleasant weather, many restaurants and bars, everything in walking distance) that facilitate interactions, such as one participant put it: "I managed to get in touch with a few people who I wanted to meet for a long time!"

On behalf of all the CMPD participants, I would like to thank the conference organizers, especially Mimmo Iannelli and Andrea Pugliese, for the wonderful work they did to make everything go so smoothly. This joint meeting hopefully initiate another good tradition in the field, as *Odo Diekmann* put it in his closing remarks. Neither the date nor the place of the next conference in the series has been specified at CMPD but we hope it will take place soon enough.

Program and abstracts are still available at http://www.unitn.it/events/mpd

Sergei Petrovski

ECMI Modelling Week
August 13-22, 2004, Lappeenranta University, Finland

The European Consortium for Mathematics in Industry (ECMI) organises annual Modelling Weeks to get mathematics students from all over Europe into contact with each other and with realistic problems in the context of industrial research and development. The 18th Modelling Week since 1985 took place at Lappeenranta University in Finland in August 2004. The attending 48 students from 13 countries formed 9 well mixed teams, each coached by an academic colleague who posed a problem from industrial collaborations of his home institute. Among these there was one problem from biotechnology (Ethanol Production with Microorganisms) that required to analyse known mechanisms of intracellular metabolic oscillations and their synchronisation within a cell culture in order to devise methods to prevent such oscillations from reaching macroscopic scales. By the end of the week, each team presented its approach(es) and often a first solution to the problem thanks to great motivation which the students also gained from nightly 'Wihta' session in the nearby Sauna on Lake Saimaa.

Lutz Brusch

EPSRC Summer School "Cell adhesion and migration: the interface with tissue engineering"
September 6-10, 2004, University of Nottingham, England

In September this year, the Centre for Mathematical Medicine (CMM) at the University of Nottingham hosted the second EPSRC-funded Summer School "Cell adhesion and migration: the interface with tissue engineering". While the first School, held in 2002, focussed on cell-scale phenomena, the second School covered the behaviour of cell populations. The School attracted graduate students and post-doctoral researchers wishing to learn about cell adhesion and migration and the role of these fundamental processes in the rapidly developing field of tissue engineering. The particpants included biologists, physical scientists, engineers and mathematicians. They gained an overview in the relevant biological background, experimental techniques and theoretical models through a series of lectures, tutorials and laboratory tours. The participants also gained first-hand experience of multi-disciplinary research by pooling their expertise

to develop mathematical models of some simple tissue engineering problems. We were particularly fortunate to have several distinguished guest lecturers from around the UK, and we also welcomed Professor *Steve Cowin* from the City University of New York who gave two lectures on bone remodelling. The CMM comprises members of the University of Nottingham who use mathematics to provide insight into biomedical phenomena. We are always keen to develop new collaborations with biomedical scientists both within the University of Nottingham and elsewhere. For further details of activities and forthcoming events run by the CMM please see

http://www.maths.nottingham.ac.uk/Cmm/index.cgi
or contact any or the three authors:

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5th International Conference on Systems Biology
October 9-13, 2004, Heidelberg

The annual ICSB conferences represent one of the most important international academic conferences with focus on systems biology. The purpose of these conferences is to bring together a forum of scientists working in interdisciplinary, quantitative, systems-oriented bio-medical research and to provide a review of the current stage in this area of science.

This year, the conference was attended by more than 400 participants (among them 43 speakers and about 240 posters) from all over the world and took place from 9 to 13 October 2004 in the beautiful city of Heidelberg, on the banks of the Neckar River, where in 1386 Count Ruprecht I founded the oldest University of Germany.
The guide-line session topics for the conference were chosen in order to cover the present understanding of various complex biological processes such as metabolic and signal transduction systems, bacterial systems biology, methods and software for systems biology, spatial models and systems biology for medicine.
The two days October 9th and 10th were reserved for tutorials and workshops related to systems biology topics. Among them was the community effort to identify "Live standards in European Systems Biology" organised by *Hans V. Westerhoff* (Amsterdam) and *Dietmar Schomburg* (Köln). 11 speakers (predominantly from but not limited to

Europe) introduced the most pressing needs for standardisation in their fields including experimental protocols, enzyme assays, model repositories and computational/mathematical methods of analysis. A draft for Standard Operating Procedures in systems biology was compiled after discussions among the 140 participants at that workshop and will be promoted by the EUSYSBIO project, www.eusysbio.net. Many of the participants reassembled later on October 14th and 15th to discuss further steps at a SBML Forum meeting, where SBML denotes a standard for exchange of mathematical models, and the 3rd workshop of the Yeast Systems Biology Network.

The conference started with *Y. Lazebnik's* (Cold Spring Habour Laboratory, NY/USA) opening lecture: *Systems Biology - a user's view*: a brilliant and personal opinion about the systems biology research approach and ended with the keynote lecture of *M. Kirschner* (Harvard Medical School, Boston, MA/USA), which represented a review of the current understanding on regulatory and core processes that are relevant to generate heritable phenotypic variation.

The plenary talks, which introduced each session, together with the other talks featured experimental, computational and theoretical advances in a variety of fields that range from technologies to detect gene expression, gene expression data analysis, metabolomics, to mathematical modelling and analysis of kinetic networks, functional analysis of biological control systems, signal transduction and others.

Although the topics discussed and the structure of the conference have been selected in order to give more importance to the *Metabolic Systems* and *Signal Transduction* sessions, the *Methods and Software* session interlinked computer scientists and biologists at the cutting side computational biology and research findings.

After the plenary lectures I found also of particular interest, the lectures of *S. Klamt* (MPI for Dynamics of Complex Technical Systems, Magdeburg), which presented a novel modeling approach (minimal cut sets, MCSs) for studying the stoichiometry of (metabolic) complex reaction systems; *M. L. Blinov* (J.R. Faeder, W.S. Hlavacek, Los Alamos National Laboratory, NM/USA) whose work combine general-purpose software development software (BioNetGen) and rule-based modeling of signal transduction; and the lecture by *M. Bentele*, (I. Lavrik, P.H. Krammer, R. Eils, German Cancer Reseach Center (DKFZ), Heidelberg), which introduced a new stochastic-deterministic approach for simulation and analysis of large signal transduction networks.

In my opinion, systems biology has developed fast in the last years, and this approach will be more and more adopted for studying metabolic systems and signal transduction also in eucaryotic cells. For modeling complex systems different mathematical approaches have been presented showing a trend to develop mathematical tools for applications on particular biological studies.

The location and size of the conference provided many opportunities for personal contacts and professional exchange. I think that the very good work of the conference chair *Robert Eils*, organizing and scientific committee contributed to the success of the conference and that many of the participants look forward to the next ICSB.

Further information: http://www.icsb2004.org/

Perla Del Conte-Zerial

Three important conferences specially targeted at linking the paradigm of biological/natural processes with computation were held in the months of September and October, 2004. The conferences are

(a) **3rd International Conferences on Artificial Immune Systems (ICARIS)**
September 13-16, Catania, Sicily, Italy

(b) **8th International Conference on Parallel Problem Solving from Nature (PPSN VIII)**
September 18-22, 2004, Birmingham, UK

(c) **6th International conference on Cellular Automata for Research and Industry (ACRI)**
October 25-27, 2004, Amsterdam, Netherlands

(a) **The Conference on Artificial Immune Systems, ICARIS,** was held for four days; tutorials were offered on the first day, while contributed papers were presented during the remaining three days. The tutorials discussed the possibility of using concepts from immune systems to develop efficient algorithms for different applications as well as using different

computational techniques for modeling immune systems. Notable among the tutorial speakers was *Filippo Castiglione* (Consiglio Nazionale delle Ricerche (CNR), Rome, Italy), who discussed the ways of simulating immune systems and related pathologies on a computer and thereby improving the understanding of their functions. The contributed papers explored different immunological mechanisms, and their relation to information processing and problem solving. The main immunological mechanisms which have been used to model applications are self-nonself models, network models (e.g., of B-cells), clonal selection and hypermutation etc. The applications, which have been developed using the above mechanisms, ranged from robotics, optimization, anomaly detection and search algorithms in networks. *Alan Perelson*, well-known for his ground-breaking work in immune network theory during the late-80's and early-90's, as well as his continual input into the Sante Fe group and their development of negative detection algorithms based on the negative selection of T-cells, was the keynote speaker of the conference. A special session on *immunoinformatics*, acting as a bridge between the area of immnoinformatics and the emerging area of artificial immune systems (AIS), was also held.

(b) The International Conference on Parallel Problem Solving from Nature (PPSN) has been one of the most respected high-quality international conferences in natural computation since 1990. The conference was held for five days - the first two days were dedicated for workshops and tutorials respectively, while contributed papers were presented in form of posters for the remaining three days. The contributed papers covered a wide range of applications, which have derived inspiration from natural systems, including biological, ecological, physical, chemical and social systems. Some of the natural system inspired techniques, which were discussed are evolutionary computation, quantum computation, neural computation, artificial life, swarm intelligence, artificial ant systems, artificial immune systems etc. A number of specialist workshops were run on the first day to focus on some of the areas of natural computation; worth mentioning is the *Workshop on Nature Inspired Approaches to Networks and Telecommunications*. The tutorials also highlighted the various possibility of using nature inspired techniques for computation. *Michael Vose's* (University of Tennessee, USA) discussion on genetic algorithm theory and *Richard Watson's* (Harvard University, USA) tutorial on population genetics were particularly interesting.

Mandyam V. Srinivasan (Research School of Biological Sciences, Australian National University) in his keynote talk wondered how insects possess fast, reliable and accurate visual systems, despite possessing a brain that carries fewer than 0.01% neurons as ours does. He explored the secrets of their success, by describing research aimed at understanding the mechanisms underlying visual perception, navigation, learning, memory and 'cognition' in honeybees.

(c) The ACRI Conference focused on how emergent behavior arises from local behavior or local rules executed by a system. Different models concerning environment (pollution models, biomass evolution, desertification, erosion processes, landslides, etc.), biological systems (ecological models, species evolution, immune systems, contamination processes, artificial life), socio-economical systems (vehicular and pedestrian traffic, urbanism, social models, economical and financial processes, etc.) reflect this behavior. The conference spanning three days, comprised presentations of contributed papers, poster sessions and several invited talks. The presentation sessions discussed different recent tools and theory developed in the area of cellular automata research. Moreover, there have been several sessions describing applications of Cellular Automata in the field of ecology, bio-medicine, traffic management etc. Several leading scientists - *Tommaso Toffoli, Paulien Hogeweg, Jim Crutchfield, Andrew Adamatzky etc*. highlighted on different aspects of development of Cellular Automata research. Keeping in mind the 100th birth anniversary of John von Neumann, detailed discussions on his contributions in the field of computation were made. *Paulien Hogeweg* (Theoretical Biology and Bioinformatics group, Utrecht University) discussed the advantages and possibilities of studying biological development and evolution with multilevel particle systems. She reviewed results in which larger scale spatial patterns formed by local interaction between model particles and by feedback, via Darwinian evolution, on the local interactions. Moreover, she examined 'particle' models which are defined as multilevel systems and pointed their advantages over single level systems.

Niloy Ganguly
Technical University of Dresden, Germany

Don't Panic! A functional response to Hans Metz

December 9-10, 2004, Leiden University, The Netherlands

To celebrate the 60th birthday of Hans Metz a two-day symposium on theoretical biology was organized at Leiden University. The symposium is financially supported by the University of Leiden, the Netherlands Society for Theoretical Biology (NVTB), and the Netherlands Organisation for Scientific Research (NWO). There were 70 participants.

Hans Metz pairs an in-depth knowledge of mathematics with a vast knowledge of biology and he has the rare ability to merge the two disciplines to the benefit of both. In addition he has an uncanny ability to conjecture deep relations between biological processes, which very often, but sometimes only after many years, can be rigorously proved. He has worked in statistics/ethology, spatial spread of populations, epidemic theory, physiologically structured population models and adaptive dynamics, but his interest is even broader. He has successfully imprinted his conviction that insight into opulation phenomena can be obtained by modelling, combining and integrating mechanisms that operate on the level of individuals, on PhD students working in many different areas. Also

through his influence on other researchers originating in Leiden, and now in prominent positions in other universities in the Netherlands, and his many other activities (for example as a founding father of the Netherlands Society for Theoretical Biology), Hans Metz can truly be said to have a large catalysing influence on theoretical biology in the Netherlands. The influence of Hans continues to be felt in the PhD students upervised by the relatively many students of Hans that have obtained senior research positions and professorships in the Netherlands and abroad.

The six main speakers addressed research that was either close collaboration with Hans (structured population models, adaptive dynamics) or presented their own view of areas of research close to the interest of Hans, such as evolution, structured populations and feedback mechanisms. These speakers were *Mats Gyllenberg*, *Ulf Dieckmann*, *Maus Sabelis*, *Bas Kooijman*, *Paulien Hogeweg* and *Roger Nisbet*. Interspersed with these speakers were short and longer contributions by former PhD students of Hans Metz and speakers with lectures on topics of special interest to Hans; the PhD student lectures were often a mix of serious science and anecdotal material. The speakers, the audience and, what is all-important, Hans Metz himself, enjoyed the two-day meeting very much.

Hans Heesterbeek, Utrecht

NEW BOOKS

Zoological Physics: *Quantitative Models of Body Design, Actions, and Physical Limitations of Animals*
Boye K. Ahlborn

Springer-Verlag, 2004, 430 pp. 259 illus., ISBN: 3-540-20846-1 (hb), USD 79.95

"This book presents a physicists view of life. The primary life functions of animals, such as eating,

growing, reproducing and getting around all depend on motion: Motion of materials through the body, motion of limbs and motion of the entire body through water, air and on land. These activities are driven by internal information stored in the genes or in the brain and by external information transmitted by the senses. This book models these life functions with the tools of physics. It highlights the role played by physics in the animal kingdom."

Cellular Computing
Martyn Amos, *University of Exeter*

Oxford University Press, 2004, 238 pp., ISBN 0-19-515539-4 (hb), £45.00, ISBN 0-19-515540-8 (pb), £25.00

"The completion of the first draft of the human genome has led to an explosion of interest in genetics and molecular biology. The view of the genome as a network of interacting computational components is well established, but researchers are now trying to reverse the analogy, by using living organisms to construct logic circuits. The potential applications for such technologies are huge, ranging from biosensors, through industrial applications to drug delivery and diagnostics. This book deals with the implementation of this technology, describing several working experimental demonstrations using cells as components of logic circuits, building toward computers incorporating biological components in their functioning."

Bioterrorism: Mathematical Modeling Applications in Homeland Security
H. T. Banks and **C. Castillo-Chavez** (Editors)

SIAM, 2003, 240 pp., ISBN 0-89871-549-0 (pb), USD78.00

"Globalization and the possibility of bioterrorist acts have highlighted the pressing need for the development of theoretical and practical mathematical frameworks that may be useful in our systemic efforts to anticipate, prevent, and respond to acts of destabilization. This book collects the detailed contributions of selected groups of experts from the fields of biostatistics, control theory, epidemiology, and mathematical biology who have engaged in the development of frameworks, models, and mathematical methods needed to address some of the pressing challenges posed by acts of terror. The ten chapters of this volume touch on a large range of issues in the subfields of biosurveillance, agroterrorism, bioterror response logistics, deliberate release of biological agents, impact assessment, and the spread of fanatic behaviours."

Advanced Distance Sampling - Estimating abundance of biological populations
S.T. Buckland, *University of St Andrews*, **D.R. Anderson**, **K.P. Burnham**, *Colorado Cooperative Fish and Wildlife Research Unit*, **J.L. Laake**,

National Marine Mammal Laboratory, **D.L. Borchers**, **L. Thomas,** *University of St Andrews*

Oxford University Press, 2004, 434pp., ISBN 0-19-850783-6 (hb), £50.00

"This advanced text focuses on the uses of distance sampling to estimate the density and abundance of biological populations. It addresses new methodologies, new technologies and recent developments in statistical theory and is the follow-up companion to Introduction to Distance Sampling (OUP, 2001). In this text, a general theoretical basis is established for methods of estimating animal abundance from sighting surveys, and a wide range of approaches to the design and analysis of distance sampling surveys is explored."

An Introduction to Continuous-Time Stochastic Processes: *theory, models, and applications to finance, biology, and medicine*
V. Capasso, D. Bakstein

Birkhäuser, 2004, 352 pp., ISBN: 0-8176-3234-4 (hb), USD 79.95

"This book is an introduction to the theory of continuous-time stochastic processes. It features concrete examples of modelling real-world problems from biology, medicine, finance, and insurance using stochastic methods. No previous knowledge of stochastic processes is required. Key topics covered include: Interacting particles and agent-based models (ant colonies) Population dynamics: from birth and death processes to epidemics Financial market models: the non-arbitrage principle Contingent claim valuation models Risk analysis in insurance. Prerequisites include knowledge of calculus and some analysis; exposure to probability would be helpful but not required since the necessary fundamentals of measure and integration are provided.

Part I: The Theory of Stochastic Processes.- Fundamentals of Probability.- Stochastic Processes.- The Ito Integral.- Stochastic Differential Equations.
Part II: The Applications to Stochastic Processes.- Applications of Finance and Insurance.- Applications to Biology and Medicine.
Part III: Appendices.- Measure and Integration.- Convergence of Probability Measures on Metric Spaces.- Maximum Principles of Elliptic & Parabolic Operators.- Stability of Ordinary Differential Equations"

Recent Developments in Biologically Inspired Computing
Leandro N. de Castro, *Universidade Católica de Santosm,* **Fernando J. Von Zuben**, *State University of Campinas*

Idea Group Publishers, 2005, 456 pp., ISBN 1-59140-313-8 (pb), USD 74.95

"This book deals with problem solving techniques inspired by nature. It covers areas in computational intelligence, including evolutionary algorithms, artificial neural networks, artificial immune systems and swarm systems. It also brings together novel and philosophical trends in the fields of artificial life and robotics."

Cellular Automaton Modelling of Biological Pattern Formation: ***characterization, applications, and analysis***
A. **Deutsch**, **S. Dormann**

Birkhäuser, 2005, 334 pp. 131 illus., ISBN: 0-8176-4281-1 (hb), USD89.95

"This book focuses on a challenging application field of cellular automata: pattern formation in biological systems, such as the growth of micro-organisms, dynamics of cellular tissue and tumours, and formation of pigment cell patterns. These phenomena, resulting from complex cellular interactions, cannot be deduced solely from experimental analysis, but can be more easily examined using mathematical models, in particular, cellular automaton models. The book is divided into three parts: Part I deals with general principles, theories, and models of pattern formation; Part II examines cellular automaton modelling; and Part III explains various applications. The models and analytic techniques described may be extended to other exciting applications in biology, medicine, and immunology. Key topics and features: * Provides an introduction and historical account of the principles of biological pattern formation (morphogenesis) * Gives an overview of mathematical modelling approaches to morphogenesis, and an introduction to cellular automata and analytic techniques * A supplementary web-based Java applet---"Cellular Automaton Simulator"---enables interactive simulation of various cellular automaton applications described in the book; available on the internet at www.biomodeling.info ."

Computation in Living Cells: Gene Assembly in Ciliates
Ehrenfeucht, A., Harju, T., Petre, I., Prescott, D.M., and G. Rozenberg

Springer-Verlag, 2004, 201 p. 92 illus., ISBN: 3-540-40795-2 (hb),
USD 49.95

"Natural Computing is concerned with computation that is taking place in Nature. The investigation of computations in living cells is one of the central and fastest growing areas of research in this field. Gene assembly in ciliates (unicellular organisms) is a splendid example of such computations, and it is fascinating from both the biological and the computational viewpoints. As a matter of fact, both biology and the science of computation have benefited from the interdisciplinary research on the computational nature of gene assembly ~V this work has helped to clarify important biological aspects of gene assembly, yielded novel insights into the nature of computation, and broadened our understanding of what computation is about. This monograph gives an account of both the biology and the formal analysis of the gene assembly process."

Introduction to Mathematical Methods in Bioinformatics
A. Isaev

Springer-Verlag, 2004, 294 pp., ISBN: 3-540-21973-0 (pb), USD 59.95

"This book looks at the mathematical foundations of the models currently in use. This is crucial for the correct interpretation of the outputs of the models. A bioinformatician should be able not only to use software packages, but also to know the mathematics behind these packages. From this point of view, mathematics departments throughout the world have a major role to play in bioinformatics education by teaching courses on the mathematical foundations of the subject. Based on the courses taught by the author the book combines several topics in biological sequence analysis with mathematical and statistical material required for such analysis.

Content: Introduction: Biological Sequences.- Sequence Alignment.- Markov Chains and Hidden Markov Models.- Protein Folding.- Phylogenetic Reconstruction.- Elements of Probability Theory.- Significance of Sequence Alignment Scores.- Elements of Statistics.- Substitution Matrices.- Exercises."

Compact Handbook of Computational Biology
Andrzej K. Konopka, *BioLingua Research*, **M. James C. Crabbe**, *University of Reading* (Editors)

Marcel Dekker, 2004, 650 pp., ISBN: 0-8247-0982-9 (hb), USD 195.00

"As computational methods continue to extend the reach of traditional study designs in biological research, this interdisciplinary handbook emerges as the first of its scale and calibre to synthesize foundational concepts, techniques, and challenges distinctive to bio-molecular sequence analysis, biopolymer structure analysis and prediction, and genomic analysis and evolution—presenting descriptions backed by over 975 works cited as well as practical guidelines direct from more than one dozen field luminaries."

Introduction to Mathematical Immunobiology of Cancer
V. A. Kuznetsov, *Institute of Chemical Physics, Russia*

World Scientific, 2005, 300pp., ISBN 981-02-2316-1, USD 85

``In this book, actual problems of immune cells interaction with tumours are discussed for the first time in terms of biological kinetics, theoretical biophysics, nonlinear systems and pattern recognition principles. On the basis of the detailed analysis of experimental and clinical data, mathematical models of tumour cells immune recognition mechanisms, cooperative phenomena, immune response dynamics as a whole are described and investigated. Modern mathematical methods are involved in the analysis of the models. Attention is paid to the determination of temporal and quantitative parameters of the ligand–receptor interactions, the processes of tumour cell interaction with different classes of immune cells and monoclonal antibodies. This book is divided into three parts and each part is subdivided into various chapters. The parts are: Basic Immune Reactions and Mathematical Modelling; Analysis of Kinetic Recognition and Damaging of Target Cells at the Effector Stage of Immune Response; Dynamics of Local and Distributed Interaction Processes of Immune and Target Cells in Vivo; Structural Functional Reconstructions of Immune Homeostasis at the Tumour Progression."

Applied Mathematical Models in Human Physiology
Johnny T. Ottesen, Metta S. Olufsen, and **Jesper K. Larsen**

SIAM, 2004, 298 pp., ISBN 0-89871-539-3 (pb), USD 71.00

"This book introduces mathematicians to real applications from physiology. Using mathematics to analyze physiological systems, the authors focus on models reflecting current research in cardiovascular and pulmonary physiology. In particular, they present models describing blood flow in the heart and the cardiovascular system, as well as the transport of oxygen and carbon dioxide through the respiratory system and a model for baroreceptor regulation. Some of the models treated are simple "real-time" models that can be directly used in larger systems, while others are more detailed "reference" models that show the underlying physiological mechanisms and provide parameters for and validation of simpler models. The book also covers two-dimensional modelling of the fluid dynamics in the heart and its ability to pump, and includes a discussion of modelling wave-propagation throughout the systemic arteries.

The first two chapters of the book provide an introduction to the physiologic concepts necessary for understanding the modelling assumptions and methodologies. The remaining chapters describe six different models of the cardiovascular and pulmonary system. Each model is introduced by a case study and can be studied individually

Chapter 1: Introduction; Chapter 2: Cardiovascular and Pulmonary Physiology and Anatomy; Chapter 3: Blood Flow in the Heart; Chapter 4: The Ejection Effect of the Pumping Heart; Chapter 5: Modelling Flow and Pressure in the Systemic Arteries; Chapter 6: A Cardiovascular Model; Chapter 7: A Baroreceptor Model; Chapter 8: Respiration; Appendix A: The SIMA Simulator; Appendix B: Momentum Equation for a Small Artery."

New Visions on Growth and Form: fingered growth, dendrites, and flames
Pierre Pelcé, *Université de Provence*

Oxford Unversity Press, 2004, 398 pp., ISBN 0198527012 (hb), £49.95

"This book deals with the patterns observed during the growth of a diverse range of systems in nature. It presents a search for the universal phenomena that govern growth, and discusses their implications on the observed structures.

There exists a wide variety of patterns in nature, from inert matter such as crystalline dendrites and flames, to filamentous fungi and neurones in the living world. Their structural evolution during growth can be theoretically modelled in order to predict the shape of their forms, their dimensions and their growth rate. 'New Visions on Growth and Form' aims at answering such questions by employing different theoretical approaches and providing a critical appraisal. The book belongs to the wide field of non-equilibrium statistical physics, and explores different mechanisms such as transport, interfacial tension, and chemical reactions, which govern the growth of a material. It explains the fundamental equations relating different morphological quantities, as well as the relevant experimental control parameters. From the unifying concepts arising in the theoretical approach the author proposes a tentative description of cell morphogenesis as a further application of the theory."

Current Themes in Theoretical Biology: A Dutch Perspective
Thomas A. C. Reydon and **Lia Hemerik** (Editors)

Springer, 2004, ISBN: 1-4020-2904-7; approximately EURO 35.

When in 2001 the past and present Managing Editor and the publisher of *ActaBiotheoretica* realized that the following year the 50th volume of our journal would see the light, we felt that this milestone should not pass unnoticed and that the appropriate way to mark it would be the publication of a special volume of papers on theoretical biology. While editing this book during 2003 and early 2004, we realized that another milestone was not far off: in 2005 it will be 70 years ago that the journal was founded.
Current Themes in Theoretical Biology, which will be published in the second half of 2004, is the result of our efforts to make a book that could serve to mark both events. The papers collected in this book have been written on invitation by representatives of the theoretical biology community in The Netherlands. They are intended to reflect the entire spectrum of topics on which *Acta Biotheoretica* publishes, ranging from philosophy of biology at one end to mathematical biology at the other. Below, the

abstracts are given of the eleven chapters that are incorporated in this new publication.

1. The History of *Acta Biotheoretica* and the Nature of Theoretical Biology 2. Images of the Genome: From Public Debates to Biology, and Back, and Forth, 3. The Functional Perspective of Organismal Biology, 4. Infectious Biology: Curse or Blessing? Reflections on Biology in Other Disciplines, with a Case Study of Migraine, 5. The Composite Species Concept: A Rigorous Basis for Cladistic Practice, 6. The Wonderful Crucible of Life's Creation: An Essay on Contingency versus nevitability of Phylogenetic Development, 7. The Symbiontic Nature of Metabolic Evolution, 8. The Founder and Allee Effects in the Patch Occupancy Metapopulation Model, 9. Balancing Statistics and Ecology: Lumping Experimental Data for Model Selection, 10. Resilience and Persistence in the Context of Stochastic Population Models, 11. Evolution of Specialization and Ecological Character Displacement: Metabolic Plasticity Matters.

Evolutionary Theory: Mathematical and Conceptual Foundations
Sean H. Rice

Sinauer Associates Publishers, 2004, 348 pp, 100 illustrations, ISBN 0-87893-702-1 (pb), USD 49.95

"Evolutionary Theory is for graduate students, researchers, and advanced undergraduates who want an understanding of the mathematical and biological reasoning that underlies evolutionary theory. The book covers all of the major theoretical approaches used to study the mechanics of evolution, including classical one- and two-locus models, diffusion theory, coalescent theory, quantitative genetics, and game theory. There are also chapters on theoretical approaches to the evolution of development and on multilevel selection theory. Each subject is illustrated by focusing on those results that have the greatest power to influence the way that we think about how evolution works. These major results are developed in detail, with many accompanying illustrations, showing exactly how they are derived and how the mathematics relates to the biological insights that they yield. Roughly half of the book focuses on gene-based models, the other half being concerned with general phenotype-based theory. Throughout, emphasis is placed on the fundamental relationships between the different branches of theory, illustrating how all of these branches are united by a few basic, universal, principles."

Mathematical Modelling of Population Dynamics
R. Rudnicki (Editor)

Banach Centre Publications Vol. 63, 2004, ISSN 0137-6934, 266 pp., $60 ($30 for individuals)

The volume contains a collection of three survey papers and ten research articles devoted to mathematical methods in biology and medicine. They are an outcome of a conference and a school devoted to population dynamics, held at the Mathematical Center at Będlewo in 2002.

The survey papers: *Delays induced in population dynamics* (O. Arino and E. Sanchez), *Adaptive dynamics* (O. Diekmann) and *Structured population dynamics* (G. F. Webb) are an excellent introduction to the modern mathematical modelling in biology. The research articles indicate several current trends in population dynamics. They also illustrate the balance between adequate description of biological phenomena and mathematical methods and techniques. The contributions include a comprehensive mathematical article, *Semilinear perturbations of Hille-Yosida operators* by H. R. Thieme and H. Vosseler, as well articles devoted to specific biological problems, like *An age-dependent model describing the spread of panleucopenia virus within feline populations* by W. E. Fitzgibbon et al. and *Time delays in proliferation and apoptosis for solid avascular tumour* by U. Foryś and M. Kolev. The volume is addressed both to mathematicians and biologists.

Can be ordered from:
Institute of Mathematics, Polish Academy of Sciences
P.O. Box 21, PL 00-956 Warszawa, Poland
publ@impan.gov.pl

Protein Geometry, Classification, Topology and Symmetry: a computational analysis of structure
W. Taylor, *National Institute of Medical Research (UK)*, **A. Aszodi**, *Novartis (Austria)*

Institute of Physics, 2004, 380pp., ISBN 0750309857, USD 110.00

"In this book structural principals of proteins are reviewed and analysed from a geometric perspective with the aim on revealing the underlying regularities in their construction. Computer methods for structure analysis and the automatic comparison and classification of these structures are reviewed with an analysis of the statistical significance of comparing different shapes. Following an analysis of the current

state of the classification of proteins, more abstract geometric and topological representations are explored, including the occurrence of knotted topologies. The book concludes with a consideration of the origin of higher-level symmetries in protein structure."

Computational Biology of Cancer
Dominik Wodarz, Natalia Komarova, *University of California, Irvine*

World Scientific, 2005, 250pp., ISBN 981-256-027-0, USD 48

``The book shows how mathematical and computational models can be used to study cancer biology. It introduces the concept of mathematical modelling and then applies it to a variety of topics in cancer biology. These include aspects of cancer initiation and progression, such as the somatic evolution of cells, genetic instability, and angiogenesis. The book also discusses the use of mathematical models for the analysis of therapeutic approaches such as chemotherapy, immunotherapy, and the use of oncolytic viruses."

Modeling the Dynamics of Life - Calculus and Probability for Life Scientists (with iLrn Testing), 2nd edition
Frederick R. Adler
Brooks/Cole Publishing, 2005, 800pp., ISBN 0534404863 (hb)

Calculus for the Life Sciences
Greenwell, Ritchie and **Lyell**
Longman, 2005, ISBN 0582850045

WIE Calculus for the Life Sciences
A. Himonas
John Wiley & Sons, 2005, ISBN 0471661163

Calculus for Biology and Medicine, 2nd edition
Claudia Neuhauser

Prentice Hall, 2004, 822pp., ISBN: 0-13-045516-4 (hb)

FEBS Course: Systems Biology
March 12-18, 2005, Gosau, Austria

Advanced Lecture Course on Systems Biology
http://www.febssysbio.net

The workshop is generously supported by a number of science organizations, including FEBS, the BioCentrum Amsterdam, the German Ministery for Education and Research (BMBF), the Dutch foundation for Earth and Life Sciences/ALW-NWO, and the Austrian bm:bmk (the latter three through the transnational funding consortium SYSMO). It is clear that organizations supporting high-level scientific research are also eager to stimulate the development of human capital in this area.

At the meeting a network of young systems biologists will be established.
Registration is required through the above website.

**Thematic school : Modelling and Simulation of Biological Processes in the Genomic Context –
4th edition**
April 4-8, 2005, Montpellier France

Topics :
Artificial chemistry/virtual cell
Morphogenesis and development
Functions and robustness
Complex networks and evolution
Modelling complex biological systems and health care
                    Contact : thierrya@univ-montp2.fr
            or franck.molina@ibph.univ-montp1.fr

**Inaugural Physiological Flow Meeting:
"From Models to Man"**
April 11-12, 2005, University of Nottingham, England

This meeting will address issues in macro-scale physiological modelling and its interaction with vascular biology. This is the first meeting of the EPSRC-funded Physiological Flow Network, which aims to promote research interactions between experts in the field of physiological flow modelling. For details of network activities, and to register to become a member, please go to
http://www.physflow.net

At this first meeting, we will have presentations from UK experts in topics ranging from large scale vascular and respiratory modelling to small scale cell motility and extracellular matrix transport. Plenary presentations will be given by Professor Peter Hunter (Auckland, New Zealand) and Professor Peter Davies (U. Penn, USA). Further details of all presentations can be found under
http://www.physflow.net/inaugural.html

We would now like to invite contributed poster submissions, abstracts for which (max 200 words) should be submitted via the online application form at the web-site above. The deadline for submission is *25 February 2005*.

The meeting will be held at the University of Nottingham. A conference dinner will be held on the evening of April 11. To register for the meeting, please complete the online application form. Financial support for graduate students is available from EPSRC. If you wish to be considered for support, please fill in the "Case for Support" section in the application form by 25th February. Participants who do not qualify for support are also welcome to attend.

The cost to attend the meeting is as follows:
    Residential participants: 125 pounds
     (includes accommodation Monday 11 April
      and conference dinner)
     Daily rate for non-residential participants:
                                                35 pounds
     Conference dinner: 20 pounds

We look forward to seeing you in April 2005.

                    Spencer Sherwin and Sarah Waters

Workshop on "Modelling of Complex Systems by Cellular Automata 2005" (MCSCA 2005)
May 22-25, 2005, Atlanta, USA

International Conference on Computational Science (ICCS 2005),

http://www.c-mail.cz/kroc/workshops/MCSCA-2005/workshop-MCSCA-2005.html

The main goal of this workshop is to bring together researchers working with complex systems within diverse scientific fields as biology, physics, mathematics, engineering and many others. The restriction on papers is that a cellular automaton should express a complex system. Complex systems are proven to be the powerful computational concepts that help us to capture the essence of many real systems where other approaches and methods failed. Cellular automata enable us to define and to work with complex systems effectively and easily. This workshop is opened to other fields related to complex systems and/or cellular automata as well. The theme of this workshop lies in the heart of the conference main theme, i.e. it is designed to hit the community, which pioneer computational methods in a wide range of scientific fields. Our personal experience is that such contacts of researches from completely diverse fields could lead to a mutual cross-fertilization of all the above-mentioned fields and stimulate their own research!

Fields where systems exhibiting complex behaviour may include, but is not limited to the following:
Biomedicine and Biology,
Sociology and Psychology,
Physics,
Mathematics,
Informatics,
Econophysics,
and many other fields not mentioned here could be applied to present here. Applications from other neighbouring fields are welcomed but it should be discussed with organizers of this workshop.

For submission guidelines, see the above website.

Important Dates
- Full papers submission: January 7, 2005
- Notification of acceptance of papers: February 14, 2005
- Camera-ready papers: February 18, 2005
- Early registration: March 30, 2005

Mathematical Biology at the 2005 IAS/Park City Mathematics Institute
June 26 - July 16, 2005

Organizers: Mark Chaplain (Dundee); James Keener (Utah); Mark Lewis (Alberta); Philip Maini (Oxford).

Clay Senior Scholars in Residence: Simon A. Levin (Princeton); Charles S. Peskin, (Courant Institute).

The annual Summer Session is organized into six groups:

- Graduate Summer School
- Research Program in Mathematics
- Undergraduate Summer School
- Undergraduate Faculty Program
- Secondary School Teacher Program
- Mathematics Education Research Program

These groups meet simultaneously, pursuing both individual courses of study and a meaningful amount of interaction. The rich mathematical experience combined with interaction among all participants results in greatly increased understanding and awareness of the issues confronting mathematics and mathematics education today.

The Summer Session is a three week residential program held in Park City, Utah, from June 26 - July 16, 2005. Financial support is available.

Deadline for submission of applications is February 15, 2005.

For more information about application guidelines, please visit our website
www.ias.edu/parkcity.

The IAS/Park City Mathematics Institute is a program of the Institute for Advanced Study (IAS) in Princeton, New Jersey

Differential Equations in Mathematical Biology
Workshop, University of Le Havre, LeHavre, France,
July 11-13, 2005

We are organizing a workshop on "Differential Equations in Mathematical Biology" to be held at the University of Le Havre, LeHavre, France, July 11-13, 2005. The workshop will focus on

communication of current research results, ideas, and problems in differential equations and control theory in mathematical biology and initiating possible collaborations. The plenary speakers are Pierre Auger (IRD Bondy), Michel Langlais (Bordeaux 2), Hal Smith (Arizona State), Horst Thieme (Arizona State), Glenn Webb (Vanderbilt) and Jianhong Wu (York).

Further information on registration, hotel reservation, travel, etc. will be posted on the workshop website http://awal.univ-lehavre.fr/WORKSHOP/

Pierre Magal (Le Havre) magal.pierre@wanadoo.fr
Shigui Ruan (Miami) ruan@math.miami.edu

9th World Multi-Conference on Systemics, Cybernetics and Informatics
July 10-13, 2005

You can get the conference´s Call for papers in www.iiisci.org/sci2005/website/callforpapers.asp.

The best 10% of the papers will be published in Volume 3 of SCI Journal. Free subscriptions, for 2 years, are being considered for the organizations of the Journals´ authors.

We are emphasizing the area of Mathematical Modeling and Applied Mathematics which is related to your specific area.

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ECMTB 2005

OVERVIEW

The European Conference on Mathematical and Theoretical Biology brings together scientists and students 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. The conference is designed for researchers who are active in or interested in this fast-growing field where experimental biology and medicine, biochemistry, mathematics, computer science, physics and various fields of technology merge. Participants from Eastern European countries are particularly welcome. The conference will be held at the Dresden University of Technology (Germany), July 18-22, 2005.

The main conference goal is to show that mathematical and computational approaches are absolutely essential to solving central problems in the life sciences, ranging from the organizational level of individual cells to the dynamics of whole populations. Another

important goal is to provide a forum for young researchers by encouraging them to present their work, learn from others in the field and participate in the special mentoring program and introductory lectures on July 17, 2005.

Applications are invited for **contributed talks** and **poster** presentations. In addition, researchers are encouraged to submit **proposals for mini-symposia**. The conference will also feature selected exhibits by related companies.

The city of Dresden is located near both Berlin and Prague and is an ideal location for hosting ECMTB05. Dresden offers a rich cultural history and a high quality modern infrastructure. The surrounding Elbe valley is also famous for its natural beauty (UNESCO world heritage site).

KEY TOPICS AND CONFIRMED INVITED SPEAKERS

1. Cellular biophysics
   Christof Schütte, Berlin, DE
2. Regulatory networks
   Bela Novak, Budapest, HU
   Hans V. Westerhoff, Amsterdam, NL
3. Development
   Hans Meinhardt, Tübingen, DE
   Elly Tanaka, Dresden, DE
4. Evolution and ecology
   Andre M. de Roos, Amsterdam, NL
5. Neural systems and the brain
   Arjen van Ooyen, Amsterdam, NL
6. Immune systems
   Rob de Boer, Utrecht, NL
7. Biomedical applications
   Martin A. Nowak, Cambridge, USA
   Kristin Swanson, Seattle, USA
8. Biotechnology
   Bernhard O. Palsson, San Diego, USA
9. Innovative mathematical methods
   Odo Diekmann, Utrecht, NL
   Christine Jacob, Jouy-en-Josas, FR
10. Inter-disciplinary education
   Louis J. Gross, Knoxville, USA

ORGANIZERS

ECMTB05 is the sixth tri-annual conference of the European Society for Mathematical and Theoretical Biology (ESMTB) and the 2005 annual meeting of the Society for Mathematical Biology (SMB). The conference is organized by the Center for High Performance Computing (ZHR) at the Dresden University of Technology.

www.esmtb.org   www.tu-dresden.de/zhr
www.smb.org

ESMTB

The European Society for Mathematical and Theoretical Biology (ESMTB) was founded in 1991 during the first European Conference on "Mathematics Applied to Biology and Medicine" in l`Alpes d`Huez. ESMTB is a nonprofit organisation. The purpose of the society is to promote theoretical approaches and mathematical tools in biology and medicine in a European (and wider) context. This goal is pursued by organizing summer schools and conferences and by publishing the European Communications.

ESMTB Board

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Becoming a member of ESMTB

Online application at **www.esmtb.org**

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Mark Lewis	Edmonton	CA
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Michael Savageau	Davis	USA
Andreas Schierwagen	Leipzig	DE
Christoph Schmidt	Amsterdam	NL
Michael Schröder	Dresden	DE
Toshio Sekimura	Kasugai	JP
Joachim Spatz	Heidelberg	DE
Angela Stevens	Leipzig	DE
Andrzej Swierniak	Gliwice	PL
Denis Thieffry	Marseille	FR
Gerda de Vries	Edmonton	CA
Sebastian Walcher	Aachen	DE
Chris Wiggins	New York	USA

FEES

The conference fee covers admission to all sessions, program and abstract booklet, welcome reception, poster party, coffee breaks, conference dinner and participation in the social programme and company exhibition.

250 €	for members of ESMTB or SMB
180 €	for student members of ESMTB or SMB
310 €	for non-members
210 €	for student non-members
50 €	discount is given on each fee for early registration (May 1, 2005).

Cancellation before June 15, 2005 enables for refund of 80% of the paid fee, 20% will be refunded in case of later cancellation.

DEADLINES

Feb. 1, 2005	Submission deadline of abstracts for contributed talks and posters
April 1, 2005	Acceptance notification for abstracts
May 1, 2005	Early registration closes

CONTACT

ECMTB 2005
Centre for High Performance Computing (ZHR)
Dresden University of Technology (TU Dresden)
D-01062 Dresden
Germany

Fax:	+49-351 463 37773
e-mail:	info@ecmtb05.org
WWW:	**www.ecmtb05.org**

Dynamical Systems Master Class 2005-2006

We would like to draw your attention to the Master Class in "Finite and Infinite Dimensional Dynamical Systems" which will be held from September 2005 until June 2006 in The Netherlands. The lecturers include H. Broer, O. Diekmann, A. Doelman, S. van Gils, E.W.C. van Groessen, A.J. Homburg, J. Hulshof, Yu. A. Kuznetsov, M. Martens, M. Peletier.

We are looking for students in their last undergraduate year or recently graduated students (Master students, or beginning PhD students) that are interested in this subject. There will be a very limited number of fellowships that the Dutch Mathematical Research Institute will be able to offer.

More information, including a brochure about studying in The Netherlands, the presentation of our Master Class, and how to apply, can be obtained from our website:

http://mri.math.uu.nl/pagina/vervolg_education_master.html

For more information you can also contact Jean Arthur (MRI secretary) at: email: mri@math.uu.nl tel.: +31 30 2531472 fax.: +31 30 2518394

Odo Diekmann

EMPLOYMENT OPPORTUNITIES

The Research Training Group 1097
"INTERNEURO": Interdisciplinary Approaches in Cellular Neuroscience, Leipzig, Germany sponsored by the German Science Foundation invites qualified graduate students in mathematics and computer science to apply for two year PhD-fellowships with starting date in April 2005. Extension for a third year is possible. In addition, one postdoctoral scholarship is offered.

Each doctoral student will work on an interdisciplinary research project, and will be jointly supervised by two professors. The thesis will be related to one of the following 14 research projects, each situated at the interface of two scientific disciplines and aimed at resolving a current neuroscientific problem by employing state-of-the-art methodological tools including,

(1) Pathophysiology of macular edema
(2) Developmental mechanics of the fovea centralis
(3) Retinal angiogenesis/neovascularization: diabetic retinopathy
(4) Spatial/temporal pattern formation in retinal spheroid cultures
(5) Light guiding properties of retina cells
(6) GNDF-dependent photoreceptor cell maturation
(7) Active biomechanics of growth cone movement
(8) Microlocalization of trace elements in CNS
(9) Passive and active mechanics of neurodegeneration

(10) Molecular pathophysiology of central osmoregulation
(11) Regulation of the IP3 signal cascade by calbindin D28k
(12) Neuronal Ca2+ signals in vitro and in silico
(13) GABAergic and glycinergic inhibition in the auditory brain stem
(14) Excitation and inhibition in the auditory brain stem

The mathematical methods to be employed will include one or more of the following
Differential-equations and dynamical systems
Multigridmethods and other numerical methods
Stochastic analysis
Information theory
Neural nets

Applicants should sent their curriculum vitae, a detailed description of their university education and training together with copies of the corresponding documents, and future research and career plans (one page), if possibles, not later than January 31, 2005 to

Head of the Research Training Group
Prof. Dr. Andreas Reichenbach
Paul Flechsig Institute for Brain Research
University of Leipzig
Jahnallee 59
D-04109 Leipzig
GERMANY

reia@medizin.uni-leipzig.de
www.interneuro.de

The Marie Curie Research Training Network (MC-RTN) project

Modelling Mathematical Methods and Computer Simulation of Tumour Growth and Therapy

has been successful in obtaining funding from the European Community under its 6th Framework Programme.

The 12 partners of the Network cover 9 countries:

- **France** (Universite J. Fourier, Grenoble I, CNRS and Ecole Normale Supérieure, Paris)
- **Germany** (University of Dresden and University of Witten/Herdecke)
- **Greece** (Foundation for Research and Technology, Crete)
- **Israel** (IMBM: Institute for Medical Bio-Mathematics)
- **Italy** (Politecnico di Torino)
- **Poland** (University of Warsaw)
- **Spain** (Universidad Complutense de Madrid)
- **Sweden** (Goteborg University)
- **United Kingdom** (University of Nottingham and University of Dundee)

The aim of the Marie Curie Research Training Network is to develop the whole modelling process from phenomenological observation to simulation and validation, through the development of mathematical models and their qualitative and quantitative study, in order to simulate the different aspects of tumor dynamics within the full range of scales (sub-cellular, cellular and macroscopic), including multiscale aspects.

The primary objective is to promote training-through-research, especially of young researchers having less than ten years of research experience at the pre-doctoral and post-doctoral level, respectively denoted in the table below by ESR (Early Stage Researcher) and ER (Experienced Researcher). Community funding will cover the temporary appointment of young researchers coming from a country other than that of the team concerned and the organisation of summer schools and workshops.

Vacant Research Positions

Research unit	Type	mo	Contact
Paris (France)	ESR ER	11 22	benoit.perthame@ens.fr
Grenoble (France)	ESR ER	36 12	claude.verdier@ujf-grenoble.fr
Witten-Herdecke (Germany)	ESR ER	36 12	adheiden@uni-wh.de
Dresden (Germany)	ESR ER	18 18	deutsch@zhr.tu-dresden.de
Crete (Greece)	ESR ER	24 24	daphne@tem.uoc.gr
IMBM (Israel)	ESR ER	12 24	agur@imbm.org
Turin (Italy)	ESR ER	24 24	luigi.preziosi@polito.it
Warsaw **(Poland)**	ESR ER	36 24	lachowic@mimuw.edu.pl
Madrid (Spain)	ESR ER	36 18	miguel_herrero@mat.ucm.es
Goteborg (Sweden)	ESR	36	yem@fy.chalmers.se
Dundee (UK)	ESR ER	18 18	chaplain@maths.dundee.ac.uk
Nottingham (UK)	ESR ER	18 18	helen.byrne@nottingham.ac.uk

Developing mathematical models at all the scales mentioned above requires making use of a wide variety of theoretical tools from a range of disciplines (e.g., cellular automata, individual-based models, continuum mechanics, kinetic theory, stochastic processes, system theory, compartmental models, multiphase systems) and developing different mathematical tools to obtain both qualitative and quantitative results. For this reason and for the training objective, usually the applicants are not required to be an expert in a particular field or have an expertise in a particular method. However, the following table can be helpful to identify the type of research that each unit is going to develop.

More information can be obtained contacting the relevant group leader or Luigi Preziosi.

It follows a scheme of modeling aspects and scales:

Modelling Mathematical Methods and Computer Simulation of Tumour Growth and Therapy

Modeling Aspects	Modeling scales		
	Sub-cellular and Cellular	Macroscopic	Therapy
Mathematical Modeling and Computer Simulation	Paris, Grenoble Goteborg, IMBM Dresden, Warsaw	Turin, Madrid Paris, Grenoble Goteborg, IMBM Crete, Nottingham Dresden, Dundee	Turin, Madrid Paris, Grenoble Goteborg, IMBM Crete, Nottingham Dresden, Dundee Witten-Herdecke, Warsaw
Qualitative Analysis and Multiscale Methods	Turin, Paris, Warsaw Witten-Herdecke, Dresden		
Experimental Aspects and Validation	Grenoble, Paris, IMBM Nottingham, Goteborg		
High-Performance Algorithms for Tumor Simulations	Dresden, Turin, Dundee		

Detailed information can be found at the web page:
http://calvino.polito.it/~mcrtn/

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***Graduates Studies in Biocomplexity,
Systems Biology and Computational Biology***

The *NIH Roadmap* has identified Interdisciplinary Biosciences which combine Physical, Mathematical, Computational and Biological skills, as the key area of Biological training research for the next 20 years. Such research is essential if the results of the Human Genome Project are to translate into new medical, biotechnological and scientific results.

Indiana University is currently undertaking a major expansion in experimental, computational and theoretical Systems Biology and Biocomplexity.

Multiple departments have deployed new syllabi or programs in graduate training to support these areas. Substantial opportunities exist for co-supervision and cross-training between departments and with the School of Informatics, School of Medicine, the Center for Medical Genomics & Bioinformatics and the Centers for Computational Biology and Bioinformatics at Indiana University Bloomington and at Indiana University Purdue University Indianapolis. For more information, please visit http://www.biocomplexity.indiana.edu/prospective/.
Prospective students should apply to the department whose faculty most closely matches their interests and background.

International Congress of Mathematicians (ICM 2006) in Madrid

TO ALL MEMBERS OF EUROPEAN SOCIETIES OF MATHEMATICS

Dear colleague,
as you know we have already crossed the border of -2 years till the celebration of the ICM 2006 in Madrid.
All the up-to-date information about this event can be found in the Web page

http://www.icm2006.org

Very soon we will start distributing relevant information concerning the organization and registration for the ICM among all pre-registered people.

The pre-registration process is open and we want to invite you to pre-register through the web page to keep timely informed about the ICM. We want to make the ICM a big success and we cannot do it without the participation of as many mathematicians as possible. Thus we invite you to pre-register now for the ICM.

Looking forward seeing you in the ICM,

Manuel de Leon, President of the Organizing Committee of ICM
Carlos Andradas, Vicepresident