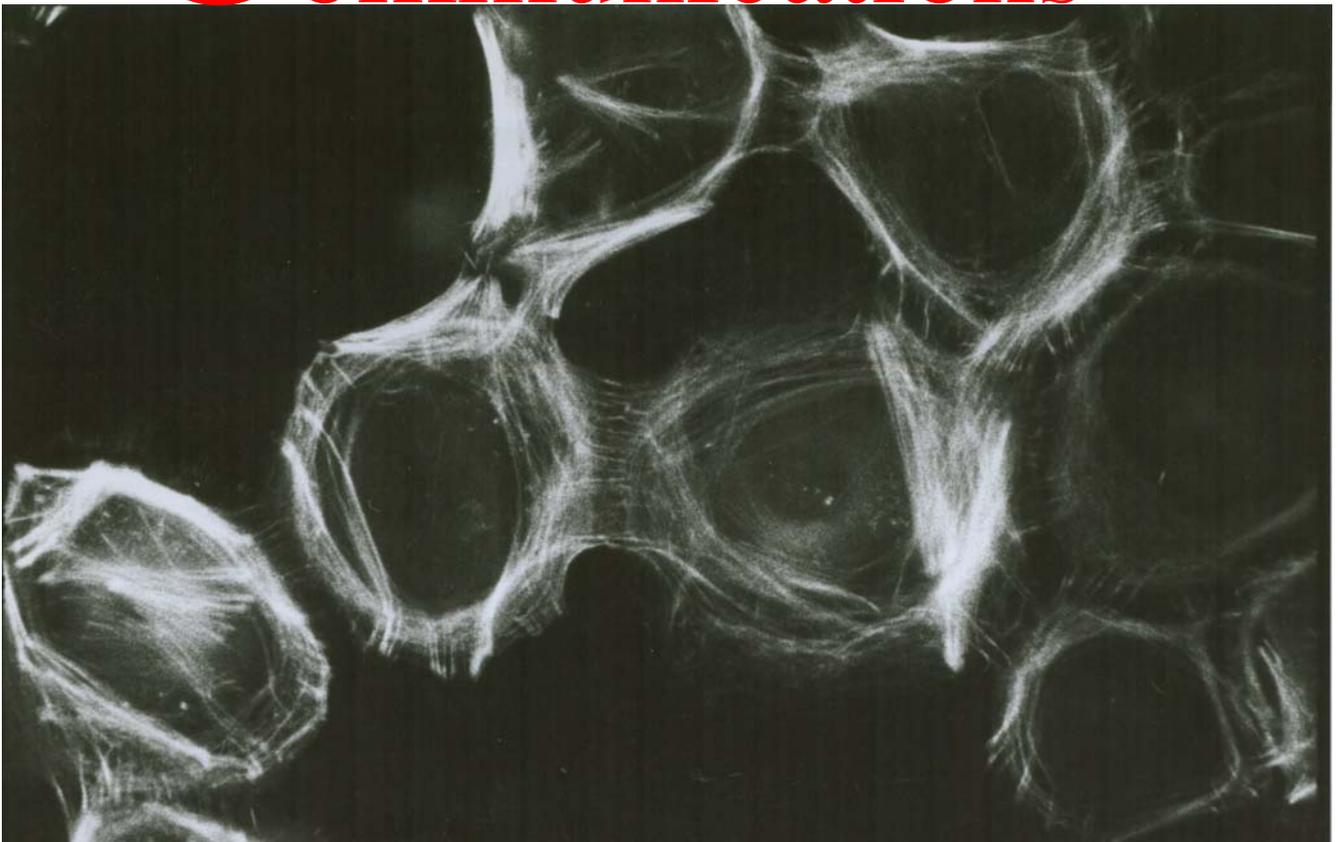


European Communications in Mathematical and Theoretical Biology  
December 2006, No. 9

# *ECMTB* Communications



ECMTB Editorial Board

Wolfgang Alt  
Helen Byrne  
Andreas Deutsch  
Luigi Preziosi



**A European Forum for Information, Presentation and Exchange**  
**Official Communication Bulletin of the ESMTB**  
**European Society for Mathematical and Theoretical Biology**

Picture on the front cover:

**„Cellular Proto-Tissue”**

**Monolayer of Human Epidermal Keratinocytes stained for Filamentous Actin**

(Group of Theoretical Biology / Dermatology Laboratory, University of Bonn, Germany)

Notice: The distributed printed issue contains an advertisement by the Royal Society for two Special Volumes of its Philosophical Transactions on “*Biomathematical Modelling*” (published May 2006)

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## LETTER to the President

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Dear Professor Alt,

President of the European Society for Mathematical and Theoretical Biology (ESMTB).

Let me introduce myself. My name is *Ari Laptev* and I am Professor of Mathematics at Imperial College London and at KTH in Stockholm. I have been elected as the *President of the **European Mathematical Society (EMS)*** for the period January 2007 - December 2010. EMS is a relatively new Society, which still needs to attract many more individual members, by providing a service which will meet the needs of every European mathematician.

Many important aims have already been achieved. Among them is the establishment of the EMS Publishing House, a non-profit organization, to which six journals and several book series are already contracted. It has been responsible for all the publications related to this year's International Congress of Mathematics in Madrid. The EMS plays an increasingly important role in relation to the governing bodies of the European Union. In particular, it is able to act as an intermediary for all European mathematicians, in contrast to the more limited possibilities of National Mathematical Societies.

The EMS promotes the quadrennial European Congress of Mathematics, which awards ten prizes to young European Mathematicians. It also runs a series of mathematical weekends and supports European Summer Schools. Many EMS Committees are involved in a large spectrum of activities.

The EMS Newsletter continues to improve in content and is now a valuable source of information concerning job opportunities, new publications, European Conferences, etc. It regularly publishes interviews with prominent mathematicians as well as articles of general interest.

Among our ambitions today is the encouragement of a closer collaboration between Pure and Applied Mathematics. We also plan to actively draw the attention of the younger generation of mathematicians to the beauty, diversity and importance of Mathematics. Our concern is to make the EMS more visible and more efficient in its promotion of Mathematics within Europe. We must highlight the significance of Mathematics as a field of competence, which is absolutely crucial to almost all areas of future Science and Engineering.

The creation of the European Research Council is an important step forward for Science in Europe and we all hope that the ERC will ultimately be financially self-sufficient and independent of Brussels' bureaucratic structure. Please pay attention to the web page: <http://erc.europa.eu>. There is a call for grant applications to young mathematicians, see documents <http://ec.europa.eu/research/fp7/> [http://cordis.europa.eu/fp7/home\\_en.html](http://cordis.europa.eu/fp7/home_en.html)

It could be also useful to look at [http://cordis.europa.eu/fp7/ideas/home\\_en.html](http://cordis.europa.eu/fp7/ideas/home_en.html) and click on "ERC Starting Independent Research Grant" [PDF]. As far as I understand the most important cite for us is: <http://cordis.europa.eu/fp7/dc/index.cfm>; click on: Ideas: 2006-12-22: ERC-2007-StG

I would like to use this opportunity to advertise Zentralblatt (ZB). EMS is one of the three owners of ZB. It recently became clear that ZB is about to launch an Author Data base of high quality, which could be a good alternative to MathSciNet. We have agreed with Springer that this data base will be available, free of charge, to all users for three months starting from April 2007. Moreover, it also has been agreed that all EMS individual members will have free access to this Data Base for at least two years. All members will be provided with a password and be able to log-in from any computer.

It is my strong wish to have a closer contact with your Society members and I would be very grateful if you forward this letter to them.

Finally, I wish you a very Happy New Year.

Yours sincerely,  
*Ari Laptev*

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## EDITORIAL

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Dear Society members, dear friends of mathematical and theoretical biology.

Wishing you a healthy and prosperous New Year 2007 gives a good opportunity to address the ***Perspectives in Mathematical and Theoretical Biology*** that can be envisaged for the current and future activities – within our own scientific community as well as by outreaching neighboring fields. After a long preparatory phase, we finally have started to fill 2 pages in the regular issues of ***JMB*** (*Journal of Mathematical Biology*) with a series of special contributions which, after an initial article on the state and goals of our Society, are going to highlight most important perspectives in our field: So far have appeared *Mathematical and Theoretical Biology for Systems Biology, and then ... vice versa* by Hans Westerhoff, *Hybrid and Multiscale Modelling* by Luigi Preziosi, and *Mathematical Neuroscience* by Stephen Coombes. More articles are pending, please, pay attention to them!

The last Board meeting (May 2006) took place in Amsterdam in order to thoroughly discuss the involvement of ESMTB into our “official society journal” JMB with one of the editors-in-chief, namely *Odo Diekmann*. The main outcome was a pledge for continuing joint activities to use and recommend this journal as one major ***medium for scientific publications within our interdisciplinary field*** – thereby reflecting both the mathematical and biological aspects in an open manner, emphasizing the development of new methods and theories for modeling, analysing or simulating biological phenomena, particularly those arising in modern biological research fields (*see Minutes Pages 6-9 and the Appendix on Page 10*). One of the topics that has special importance for the fast developing field of Systems Biology, but also for other more classical fields as Neurophysiology or Evolutionary Ecology, is ***Computational Biology***. It will be the general theme of a series of *special issues of JMB* starting this year. The forthcoming volume will be on ***“Computational Cell Biology”***, which is also the topic of an Embedded Meeting of our Society at the International Conference on Industrial and Applied Mathematics (ICIAM) during July 2007 in Zürich (*see Page 5 and the front cover depicting a “cellular proto-tissue”*). We cordially regret the sudden death of our friend *Reinhart Heinrich*, who was one of the leading scientists in our Society and a great promoter of Systems Biology (*see Obituary on Page 3*).

By pointing to the contributions on *Research Groups* in Hungary (*Page 12*) and on the 10-years *History of ITB* in Berlin (*Page 17*) let me express the hope, that joint activities within our Society will continue to flourish and support a fruitful further development of our field.

*For the Editorial Board,  
Wolfgang Alt (president of ESMTB)*

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The **closing date** for submissions to the next issue *COMMUNICATIONS # 10* will be **September 30<sup>th</sup>, 2007**. Please send, preferably by e-mail, any information, reports and other material to the managing editor

*Wolfgang Alt, Theoretische Biologie, IZMB, Universität Bonn, Kirschallee 1, D-53115 Bonn, Germany,  
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Those who are interested in the Society or want to have more information, please visit our Society web site at <a href="http://www.esmtb.org">www.esmtb.org</a>
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The following page can be used by members to pay their fee, or, by not-yet-members to register. Thanks!
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**CALL FOR MEMBERSHIP FEES 2006 and 2007**



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ESMTB membership includes automatic and free subscription to the **print edition** of the  
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-- The official journal of the Society --

Please register at [www.esmtb.org](http://www.esmtb.org) and send your payment of the required annual fee for 2006 and/or 2007 by bank draft transfer or electronically (PayPal).

**Membership Fees per year:**

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- 25 Euro (student, developing country or Eastern European member)
- 20 Euro (student SMB member)

b. The **Institutional Annual Membership Fee** is:

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## Obituary for REINHART HEINRICH

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Fully unexpectedly, Professor Reinhart Heinrich passed away in the night of October 22/23 at the age of 60. With great sadness, we must realize that we lost an excellent academic teacher, a very ambitious scientist, and a good friend. This is hard to believe, since just a few days before, he has been lively as ever. When I met him the last time on the International Conference on Systems Biology in Yokohama 10 days before, he was full of plans and developed ideas for new projects.

Reinhart studied physics at the Technical University Dresden from 1964-1968. He received his PhD in Theoretical Physics in 1971. In the early 1970s, he joined the Institute of Biochemistry at Humboldt University, Berlin, where he started to work about networks of enzymatic reactions. Together with *Tom Rapoport*, he established the Metabolic Control Theory. This theory, which was independently and simultaneously set up also by *Kacser* and *Burns* in Edinburgh (Kacser and Burns, 1973),

greatly influenced quantitative biochemistry worldwide. Their seminal paper (Heinrich and Rapoport, 1974) about control and effector strength, which belong to a series of papers concerning the linear steady-state treatment of enzymatic chains, is one of the most frequently cited papers ever published by scientists in the former GDR. In the 1980s, he moved to the department of Biophysics at the same university. In 1990 he became full professor and head of the Theoretical Biophysics. From 1990 to 1994 he was director of the Institute of Biophysics and from 1996 to 1998 director of the Institute of Biology of the Humboldt University. In 1991 he stayed as Visiting Professor at the University of Bordeaux with Prof. *Jean-Pierre Mazat*. Together with *Christine Reder* from Bordeaux, he developed an extension of Metabolic Control Theory for relaxation processes (Heinrich and Reder, 1991). In the period from 2000 to 2001 he was Visiting Professor at the Harvard Medical School in Boston. There, he worked about dynamic properties of signaling cascades (Heinrich *et al.*, 2002).

Reinhart initiated and organized the DFG-funded Graduate School “*Dynamics and Evolution of Cellular and Macromolecular Processes*” (1997-2006), which comprised about 20 research groups and provided doctoral education for 37 students. Based on collaborations that he had established with Boston University and with Kyoto University, he set off a series of common workshops with participants from all three schools at changing locations, including Dresden, Boston, Kyoto, and Berlin. This immensely inspired the dialog between partners coming from bioinformatics, database development and biological modeling. These endeavors eventually let to the successful application for an International Research Training Group (IRTG) “*Genomics and Systems Biology of Molecular Networks*”, the spokesman of which Reinhart was.

Reinhart can be considered a forefather of a field for which, later, the term Systems Biology was coined. He was investigating various subjects, such as modeling metabolic networks and metabolic control theory, modeling of signal transduction networks, nonlinear dynamics as applied to biological systems, protein translocation, lipid translocation, vesicular transport, and even DNA repair. When I started working with him, he was interested in the evolutionary optimization and design of cellular networks. Together, we first studied the properties of enzymatic reactions in states of maximal reaction rates. We found out that such optimal properties are not unique, but depend on the actual substrate and product concentrations. Then we also investigated the problem of optimal distribution of enzymes in metabolic pathways to ensure flux maximization, initially for steady states, then also for processes in which cells have to adapt to changes. We predicted a temporal order of enzyme production, showing that each enzyme must be only provided when it is needed, i.e. when its substrate is available (Klipp *et al.*, 2002). Later and independently, this scenario has been experimentally confirmed and termed “Just-in-time transcription”(Zaslaver *et al.*, 2004).

Reinhart was always searching for the principles behind our observations, looking for different perspectives, and connecting abstraction with biological evidence. This way he inspired me and his other students, and he taught us a way of thinking. But science was not Reinhart’s only interest. He also played the violin and he wrote poems and even a novel. “*Jenseits von Babel*” appeared in the late 80’s. I happened to read the chapter describing a journey to Tula in Russia when I was sitting in a train from Moscow to Tula in 1988 ...

Among the large number of his students, many are now very active in Biophysics, Bioinformatics or Systems Biology in several countries. With his ability to develop theoretical concepts and apply them to biological questions, Reinhart founded and run what can be considered a "Berlin school". He organized a large number of memorable conferences where he brought together many researchers from all over the world. The conference in Holzhau just after the fall of the Berlin wall in 1989 and the

workshops on the island of Hiddensee are mentioned again and again in the community.

Over the years, the number of under-graduate and PhD students in his group has grown remarkably. Some of them started only recently and they will badly miss their doctoral father. Thus, his colleagues and friends readily agreed that the best way to honor Reinhart is to try to continue his projects in his sense and to support his students.



Reinhart was a grand academic teacher, but moreover, he was an extremely sympathetic, understanding and humorous person. After this tragic loss, we will always remember the unique smile in his eyes, his large pool of entertaining stories, his hospitality and his warm-hearted personality.

*Edda Klipp*  
MPI Molecular Genetics, Berlin

Heinrich, R., Neel, B.G. and Rapoport, T.A. 'Mathematical models of protein kinase signal transduction' (2002) *Mol Cell* 9, 957-70

Heinrich, R. and Rapoport, T.A. 'A linear steady-state treatment of enzymatic chains. General properties, control and effector strength' (1974) *Eur J Biochem* 42, 89-95

Heinrich, R. and Reder, C. 'Metabolic Control Analysis of Relaxation Processes' (1991) *J Theor Biol* 151, 343-350

Kacser, H. and Burns, J.A. 'The control of flux' (1973) *Symp Soc Exp Biol* 27, 65-104

Klipp, E., Heinrich, R. and Holzhütter, H.G. 'Prediction of temporal gene expression. Metabolic optimization by re-distribution of enzyme activities' (2002) *Eur J Biochem* 269, 5406-13

Zaslaver, A., Mayo, A.E., Rosenberg, R., Bashkin, P., Sberro, H., Tsalyuk, M., Surette, M.G. and Alon, U. 'Just-in-time transcription program in metabolic pathways' (2004) *Nat Genet* 36, 486-91

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## SOCIETY NEWS

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### **ICIAM '07: ESMTB Embedded Meeting on “Computational Cell Biology”**

Next summer, from July 16th to July 20th, Zürich will host the International Congress on Industrial and Applied Mathematics (ICIAM). In this framework the ESMTB was asked to organize an embedded meeting with the goal to foster interdisciplinary collaboration between mathematicians and bioscientists and to act as a forum for the presentation of recent research results and new research directions in computational cell biology.

This is a wonderful opportunity to present the activity of the community, represented by the Society, to applied researchers who will be present at the meeting, working in different adjacent fields as engineering, informatics and physics.

The ESMTB embedded meeting will last two full days (with dates not yet known at present) covered by 40 minute review lectures on topics as:

- molecular motors, actin and microtubule dynamics, cytoplasm motion
- cell traction, cell adhesion
- chemotaxis, collective motion of cells
- cell imaging, cell based models, multiscale and hybrid modeling
- system biology, protein networks

The invited speakers are: Davide Ambrosi, Vincenzo Capasso, Andreas Deutsch, Richard Dickinson, Jorge Galle, Thomas Hillen, Peter Hunter, Janis Kalaitzidis, Esa Kuusela, Claude Verdier, Michael Mackey, Alex Mogilner, Francois Nedelec, Valdur Saks, and Hans Westerhoff.

*Luigi Preziosi, Wolfgang Alt  
Board of ESMTB*

### **Minutes of the ESMTB Board Meeting**

*Amsterdam, May 29, 2006*

Meeting starts at 9:15 am.

Present: Wolfgang Alt (WA, chair), Andreas Deutsch (AD), Christine Jacob (CJ), Eva Kisdi (EK; minutes), Luigi Preziosi (LP; from 10:15 am), Hans Westerhoff (HW), Attila Csikász-Nagy (ACs, non-voting counselor).

Odo Diekmann (OD, editor-in-chief of the *Journal of Mathematical Biology*) is present during the discussion of the first main point of the agenda.

Absent with apology: Carlos Braumann (CB), Rafael Bravo de la Parra (RB), Helen Byrne (HB), Jean-Christophe Poggiale (JP).

### ***Review of the last Board meeting in Bonn, February 18, 2006***

WA briefly summarizes the previous board meeting, the minutes of which have already been accepted via email. The elected cash auditors, Daniela Morale (University of Milan) and Alexander Anderson (University of Dundee) have agreed to perform the 2006 audit. The elected East-European representatives, Attila Csikász-Nagy (Hungary) and Oleg Demin (Russia) have also agreed to join the Board as non-voting counselors. Unfortunately, it was not possible for Oleg Demin to obtain visa in time to attend this board meeting. WA reminds the board members that their reports for the Communications are due in September.

### ***Adoption of the agenda***

The proposed agenda is accepted. Suggestions for the Proceedings of the next Conference (Edinburgh 2008) placed under #6.

## 1. Scopes and publishing policy of the *Journal of Mathematical Biology* (JMB)

The Board welcomes Odo Diekmann (OD), one of the two editor-in-chiefs of JMB. OD gives a status report on JMB as follows.

- The aim of JMB is to obtain biological insight by mathematical approach. This is to be taken in a broad sense, giving time for emerging ideas to develop: e.g. methodologies promising future biological potential can be included. JMB puts emphasis on obtaining high-quality, in-depth reviews and gives more time to referees than usual in the biological sciences.
- In 2004, OD received 115 submissions, 37 of which were accepted. (Unfortunately, no statistics are available on the manuscripts submitted to A. Hastings, the other editor-in-chief.) In 2005, OD received 164 submissions; the rise is partly due to the special issue congratulating K. Hadeler. 36% of the submissions were rejected prior to formal review. These fast rejections include those papers that have no clear biological relevance.
- JMB starts a sequence of double special issues on computational biology, which appear annually. The special issues will be added as extra pages without affecting the space available for regular papers. The first such issue is planned for 2006/2007 and is edited by P. Clote on computational molecular biology (RNA). This will be followed by a special issue on computational cell biology in 2007 (edited by WA and LP) and a special issue on computational oncology in 2008 (edited by Mark Chaplain). Future special issues could focus on the computational aspects of physiology, sequence analysis, neurology, immunology, etc.
- Guest editors of the special issues will be asked to develop guidelines on how to review material involving massive computational efforts, where falsification is possible only by essentially repeating the whole work. The special issues will also introduce the possibility of posting supplementary material on JMB's website,

and will place color figures at no charge if they are essential.

- The present Editorial Board of JMB ensures stable operation. Molecular cell biology is somewhat lacking in the editorial board, and there is an increasing number of submissions on networks. In general, JMB has no difficulties handling all submissions properly, but this puts a large workload on OD. New editor-in-chiefs will have to be appointed from 2008/2009.
- The impact factor of JMB is increasing since 2001 and its latest (2004) value is pretty high in its field, 1.762.

Following OD's report, the Board asks a few quick questions from which the following points arise:

- Since JMB has become the official journal of ESMTB, there is a shift towards intra-individual (molecular, biochemical, physiological, etc.) topics. According to a quick count of WA (based on the 2004 volumes and part of 2006), papers relating to biochemical, physiological, medical, developmental, and regulatory aspects together comprise somewhat less than half of published papers, and about the same as papers on population dynamics, evolution, and epidemiology together.
- The number of submissions has considerably increased. This implies that the workload should now be more distributed among the members of the editorial board.

After the free questions period, the discussion concerning JMB is organized around three main topics, listed below as 1a, 1b, and 1c.

### 1a. Readership and the Mission Statement

OD and the Board agree that JMB should be a bridge between biology and mathematics, and each paper should clearly explain what the relevance of the results to biology is. As OD points out, JMB editors already encourage the authors to do this. He argues that direct applications to concrete biological problems cannot always be demanded, as JMB should provide space for building up extended mathematical theories.

The Board would like to make the papers more accessible to biologists (without sacrificing mathematical rigor). The abstract should state the biological results; the biological perspective should be described in the introduction in a non-technical way; the conclusions should include clearly formulated messages to biology as well as to mathematics. Explanatory material, such as a glossary, may also help and may be placed on the website. Review articles addressed to biologists would be useful as bridges. ACs remarks that JMB is indexed, with abstracts available, in biological databases such as PubMed; it is therefore important to make the abstracts accessible for biologists. OD agrees with the intentions but cautions that most institutional subscribers are mathematics libraries rather than biologists, and that JMB should not constrain authors by diminutive requirements. Review articles are welcomed by the present "Aims and scope" of JMB, but it is hard to get such submissions; here the Society's help would be appreciated.

[LP arrives during this discussion.]

Next, the Board finalizes the Mission Statement of JMB, which is an Appendix to the contract between ESMTB and Springer Verlag. The Mission Statement is to be sent to both editors-in-chief and to Springer Verlag for agreement, and subsequently published in the Communications (*see Id. and the Appendix on Page 10*).

### **1b. Expanding the scope of JMB**

The Board identifies the following areas where JMB could expand its coverage (several areas are already covered to some extent):

Networks

metabolic systems

signal transduction

gene regulation and organization

Systems biology (integrative biology)

molecular biology, molecular dynamics

cell biology

Neurobiology

Developmental biology

Evolutionary biology including game theory

Control theory

OD emphasizes that JMB is open to submissions on all parts of biology and the Society can promote submissions in the above areas. JMB already receives an increasing number of submissions on networks.

### **1c. Changes to the editorial board**

In conjunction with the area expansion and to decrease the work load, the Society Board recommends to add new members to the editorial board of JMB. OD agrees that handling the increasing number of network papers would benefit from an expert on the editorial board. He also agrees that molecular cell biology is underrepresented among the editors, but currently there are not many submissions in this area. For the rest, OD argues that JMB can handle the submissions smoothly with its current editorial board.

Before leaving, OD expresses his appreciation for the recommendations and promises feedback after he could investigate the recommendations in detail.

The Board will now invite proposals from both editors-in-chief for the names of the new editors-in-chief taking office from 2008/2009. The next board meeting will discuss the candidates. In cooperation with the editors-in-chief currently in office and in consultation with Springer, the Board appoints the editors-in-chief next to take office. In addition, the Board will make recommendations for the composition of the renewed editorial board of JMB.

### **1d. Other issues related to JMB**

The Board votes for the finalized Mission Statements: 6 vote yes, 0 no, 0 abstentions.

*(See the Appendix on Page 10 with the revised text taking into account the responses by Springer and both editors-in-chief of JMB.)*

Finally, the Board reviews its plans concerning the 2-page material it can place in every issue of JMB. The *Letter of the President* is finalized and will be placed first along with the standard advertisement material of ESMTB. The "*Perspectives in Mathematical and Theoretical Biology*" should follow (see the minutes of the last board meeting in Bonn 2006).

Guest editors and the special issues of JMB as well as recommendations for the review process will be discussed at the next board meeting.

## **2. Report by the Treasurer**

AD announces that the ESMTB Newsletter will soon be launched. This electronic service will be dedicated to fast information exchange, including for example job openings, conference and workshop announcements, and the current contents of JMB. The ESMTB Newsletter will be available on the Society's website, and a brief email with the appropriate link will be sent to every member.

**Submissions to the Newsletter** can be sent to AD by email: [andreas.deutsch@tu-dresden.de](mailto:andreas.deutsch@tu-dresden.de); online submission will be available later.

According to the balance sheet of May 24, 2006, 13,040 Euros are on the Society's bank account. Expected members' dues are about 10,000 Euros in 2006. This year's expected expenditures total about 11,000 Euros, which include our support to CMPD2 (see Page 26), to the Euroconference in Crete and to the Sarajevo summer school Mathematical Techniques in Modeling Physiological Systems (see *minutes of the Bonn meeting, ECMTB 8*), payment to Springer, and the production and mailing costs of the 2006 flier and the Communications. The assets of the Dresden 2005 Conference, which are the property of the Society, will be added later.

## **3. ESMTB support for summer/winter schools**

WA reads the letter of support he wrote for the Marie Curie Summer School proposal of Mostafa Bachar, Jerry Batzel and Franz Kappel (Univ. Graz). ESMTB offers (i) financial support

of a maximum of 1500 euros; (ii) to participate in the scientific committee; (iii) to co-organize events; (iv) to communicate the series of summer schools to members; and (iv) to support the organization of the network associated with the summer schools. The Board approves the letter and makes several suggestions to improve details.

HW describes the Second FEBS Advanced Course on Systems Biology, a 1-week winter school in March 2007 organized in Austria. All present Board members agree to support this school with a lump sum of 1000 euros plus the yearly membership fees of new members who join the Society in connection to this event.

## **4. Embedded ESMTB meeting on Computational Cell Biology at ICIAM 2007**

LP lists contributors to be invited to the embedded meeting on computational cell biology organized by ESMTB at ICIAM 2007 in Zürich. HW proposes several more names to add. The same authors will be invited to contribute to the Computational Cell Biology special issue of JMB with review-type articles submitted by May 2007 (i.e., before the conference). The Board has no objections and leaves further details to LP, WA and AD.

## **5. Improvement of East-European participation in ESMTB**

ACs is asked to summarize specific difficulties East European colleagues experience nowadays. Obviously, lack of money e.g. for traveling is still a big problem. Lack of communications is another focal problem: East-European groups do not know enough of each other and so cannot collaborate. East-Europeans tend not to take leadership in EU-grant applications.

The *Communications* will invite East-European research groups to introduce themselves and will invite articles reviewing mathematical and theoretical biology in East-European countries. ACs is asked to write the first such article also as a model for the future ones.

HW proposes that ESMTB should recognize excellent research groups with an official title, thereby helping them e.g. in application procedures.

East-European groups should be brought together at regional meeting(s) to discuss their specific difficulties and to foster collaboration in research and education. Following such smaller meetings, the ECMTB Conference in 2011 could be held in (or near) Eastern Europe.

## 6. ECMTB 2008 in Edinburgh

The Society's next triennial conference will be in Edinburgh and organized by Mark Chaplain (see minutes of the Dresden board meeting in 2005, Communications 8:11). SMB has unfortunately withdrawn from the 2008 Conference: They expressed their interest in organizing joint conferences also in the future but not every three years. ECMTB 2008 will thus be a conference of ESMTB and is now planned for a maximum of 500 participants.

WA urgently writes to Mark Chaplain to request his extended proposal, including the scientific committee, plenary speakers, conference topics, and plans for the eventual Proceedings. The Board intends to advise on these matters. The Board also proposes to include previous organizers and ESMTB board members in the organizing committee, and to inform the board about communications with the scientific committee. Experiences of the highly successful Dresden 2005 conference must be exploited.

By email, EK has collected opinions of the board members concerning what form of the conference proceedings would ensure the highest quality and best representation of the scientific results. Two possibilities gained support within the Board: (i) A substantial part of the Proceedings consists of invited chapters; (ii) Each conference contributor submits a short (e.g. 4-page) paper. LP and RB propose a modification to (i) such that symposium organizers write a review of their sessions and papers based on the talks appear in special journal issues.

## 7. Communications

WA reminds of the September deadline of the coming issue of the Communications (#9). Conference reports, descriptions of working groups and dissertations are welcome. The first East-European survey article (see above) will appear. Minutes of the board meetings and the reports by the board members will be included. HW and LP set out to compile a research program list.

## 8. Diverse

V. Capasso has agreed to act as the representative of ESMTB at ICIAM; M. Gyllenberg continues to be the representative at EMS.

To improve cooperation and exchange of information, CJ will establish contact with the International Biometric Society (IBS), WA with the European Biophysical Societies' Association (EBSA), and EK with the European Society for Evolutionary Biology (ESEB).

The Board thanks HW for his generous hospitality in Amsterdam. The next meeting of the Board is scheduled for March 2, 2007 in Torino, Italy.

The meeting ends at 4:15pm.

*Eva Kisdi*  
*Secretary of ESMTB*

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## **Appendix:**

### **Mission statement for a suitable ESMTB-affiliated journal** *Revised version (December 2006)*

Note: In this document solely for convenience, we use the word “biology” when we mean “biology and medicine” and similarly we write “mathematical” when we mean “mathematical and theoretical”. We start with a number of statements of principle and end with a series of points that discuss the consequences of these statements.

1. The journal must in principle reflect all parts of biology and must not be biased either for or against any biological sub-discipline.
2. The basis for accepting suitable papers must be quality.
3. Papers in the journal should have a relevant biological question/problem as their basis and should apply mathematical reasoning to study this question. There are two categories of suitable papers:
  - i) The mathematical reasoning leads to new insight or relevant conclusions about the original biological question (i.e. there is feedback to biology);
  - ii) The mathematical approach or methodology, as inspired by the biological question, is new, or new to the field, and interesting in a broader context (i.e. there is methodological feedback to the community so that the approach can be used in the future to answer biological questions).
4. The managing editors and their editorial board should be able to decide whether a paper is biologically relevant and contains sufficient feedback (of one of the two kinds). Manuscripts that do not meet these conditions or are obviously of insufficient quality will be returned immediately and will not be admitted to the reviewing process. The editorial board safeguards quality and a good mix of biological topics in the journal.
5. Papers must be written in good English.
6. The reviewing procedure should be fast. A decision for rejection of a manuscript should be made within 3 months.

Some consequences:

- This is not an applied mathematics journal: there must be relevant biology in each paper by addressing biological concepts, experimental assays or data.
- This is not a biology journal: there must be mathematical reasoning in each paper by addressing aspects of Mathematical Biology such as development of new theory, modeling, analysis, and data evaluation. All this is to be judged by the (managing) editors.
- A consequence of the above two points is that, for each manuscript admitted to review, the choice of reviewers should represent both the biological and mathematical aspects.
- Likewise, the editorial board should represent the mathematical and the biological aspects and should be large enough to reflect the diversity of both fields. Members with broad expertise and a good overview of several sub-disciplines will help to reach this goal.
- There will be no issues devoted to conference proceedings. There may however be special issues devoted to important areas of interdisciplinary research in the field.
- Manuscripts and reviews should be submitted preferentially in electronic version to speed up the reviewing process.

*The Board of ESMTB*

## New EU Framework Programme (FP 7)

The new European Union Framework Programme is slowly shaping up and we hope to inform you on the actions of interests for the bio-mathematical community in the next issue of the Communications

In principle, it is stated that FP7 will try to simplify instruments and procedures for funding and participation. Collaborative research will be based around broad research themes, rather than instruments, with much continuity from FP6 as well as the addition of two new topics, space and security.

The broad objectives of FP7 have been grouped into four categories: **Cooperation, Ideas, People** and **Capacities**. For each type of objective, there is a specific programme corresponding to the main areas of EU research policy. All specific programmes work together to promote and encourage the creation of European poles of (scientific) excellence.

The specific programme on **“Cooperation”** supports all types of research activities carried out by different research bodies in trans-national cooperation. Eligible actions range from collaborative research projects and the creation of networks to the establishment of European Technology Platforms and the coordination of non-EU research programmes. International cooperation with non-EU countries is also included. Accounting for over half FP7's total budget, the 'Cooperation' Programme aims to gain or consolidate leadership in key scientific and technology areas.

The programme will be sub-divided into the following nine distinct themes.

- Health
- Food, agriculture and biotechnology
- Information and communication technologies
- Nanosciences, nanotechnologies, materials and new production technologies

- Energy
- Environment (including climate change)
- Transport (including aeronautics)
- Socio-economic sciences and the humanities
- Security and space

The specific programme for **“Ideas”** aims to support frontier research at the existing borders of knowledge, carried out by individual teams in all scientific and technological fields, including engineering, socioeconomic sciences and the humanities. The investigator-driven programme will be carried out by an independent European Research Council (ERC) to stimulate creativity, excellence and the discovery of radical, new knowledge.

The Specific Programme on **“People”** provides support to researchers, supporting their career development and mobility by means of an expansion of the existing 'Marie Curie' exchange programme. These actions will be reinforced and refocused on key aspects of skills and career development, while also strengthening the links with national research systems. The overall aim is to strengthen, qualitatively and quantitatively, human resources in the European research sector.

The specific programme on **“Capacities”** will focus on improving research capacities throughout Europe. The main actions include support to research infrastructures, research for the benefit of SMEs, regional research-driven clusters, help for convergence regions to unlock their full research potential, 'Science in Society' (activities aimed at strengthening the link between science and society in general) and horizontal activities of international cooperation.

*Luigi Preziosi  
Board of ESMTB*

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## RESEARCH GROUPS

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### Central and Eastern Europe come into view

The last issue of “*Communications*” featured the ESMTB membership statistics. Altogether, 33 members from 7 Eastern/Central European countries were listed. This is less than Germany, UK, or Italy single-handedly. This anomaly was also seen in the new board elections of the ESMTB. Not a single member from the Eastern/Central Europe was represented in the board. This led the newly established board to invite **Oleg Demin (Russia)** and myself, **Attila Csikász-Nagy (Hungary)**, as non-voting counselors of the board. Our duty was to act in the board on behalf of the scientists from the Eastern/Central part of the continent and be recognized by Western European colleagues. As an initiative, we decided to invite scientists from Eastern/Central European countries to present current state of research in the field of mathematical and theoretical biology in their homeland. Here I present the first piece of this series:

### Mathematical and Theoretical Biology in Hungary

Hungarians are famous for great mathematicians and physicists (i.e. Erdős, Rényi, von Neumann, Szilard, Wigner, etc.). One of the “Martians of science” [1], **Leo Szilard**, changed his carrier from atomic physics to theoretical biology later in his life. We can continue the list of great theoretical biologists with Hungarian roots: **Ludwig von Bertalanffy**, and the tragically forgotten **Ervin Bauer**, whose work was banned by the Russian KGB for more than 40 years [2]. A lack of scientific fund during the communist regime forced researchers to delve into theoretical fields, which led to prosperous outcomes in the disciplines of physics, chemistry and biology.

The current state of Hungarian theoretical and mathematical biology is bright. In the last 5 years, 58 papers appeared in related journals [3]

by Hungarian authors. Some of the theoretical works were published in high impact journals. Hungarian authors with highly cited papers include, **Eörs Szathmáry** on evolution, **Géza Meszéna** on ecology and evolution, **Tamás Vicsek** on collective behaviour, and **Béla Novák** on cell cycle dynamics [4]. Others work is on theoretical and mathematical aspects of neurobiology, population dynamics, enzyme kinetics and biological networks. Hungarian researchers from other disciplines are also attracted to the emerging field of systems biology.

It is worth to mention that many Hungarian groups are involved in the EU funded networks. The **Collegium Budapest**, a theoretical institute for advanced studies, is located in the capital and facilitates networking among scientists. The Collegium hosts ‘focus groups’ on special research projects, which are often led by a Hungarian expert in the field.

Below I list the details of 17 research groups that work on mathematical and theoretical biology in Hungary. The future seems promising, since the average age of principal investigators is just above 50 years (including well established investigators). Hopefully, new labs under the leadership of young talents will open in near future, and promote this exciting field of mathematical and theoretical biology.

[1] I. Hargittai (2006): The Martians of Science.

*Oxford University Press, USA*

[2] M. Müller (2005): Ervin Bauer a Martyr of Science. *Hungarian Quarterly* XLVI.178

[3] Theoretical biology journals collection at:

<http://www.bio.vu.nl/nvtb/JournalsTB.html>

[4] Thomson ISI Web of Sciences retrieved results

*Attila Csikász-Nagy, [csikasz@mail.bme.hu](mailto:csikasz@mail.bme.hu)  
Molecular Network Dynamics Research Group  
of the Hungarian Academy of Sciences and  
Budapest University of Technology and  
Economics, Budapest, Hungary*

**Institution:**  
**Eötvös University, Pázmány P. Stny. 1A, H-1117 Budapest**

<b>Group name, department</b>	<b>Leader(s) # researchers</b>	<b>Research topics</b>	<b>Web address</b>
Theoretical ecology and evolution group; Department of Biological Physics	Géza Meszéna + 4	theoretical ecology & evolution, adaptive dynamics, speciation	<a href="http://niche.elte.hu">niche.elte.hu</a>
Neural Information Processing Group; Department of Information Systems	András Lőrincz +15	Modelling the hippocampal entorhinal loop, neocortical information processing, basal ganglia thalamocortical loops and higher cognitive functions, Data-mining in fMRI and EEG/ERP experiments	<a href="http://nipg.inf.elte.hu">nipg.inf.elte.hu</a>
Laboratory for Chemical Kinetics; Institute of Chemistry	Tamás Turányi +4	Enzyme kinetic simulations, Spatial patterns, chemical waves, Combustion simulations, Femtochemistry, Atmospheric chemistry	<a href="http://garfield.chem.elte.hu/">garfield.chem.elte.hu/</a>
Biological Physics Research Group of the Hungarian Academy of Sciences; Dept. of Biological Physics	Tamás Vicsek +3	collective behaviour (modelling of group motion, synchronization of organisms, including birds and humans) networks (growth and restructuring of large networks, including protein interaction, and various social networks, such as collaboration or phone calls)	<a href="http://angel.elte.hu/kutcsop/">angel.elte.hu/kutcsop/</a>
Biological Nanosystems Group Dept.of Biological Physics	Imre Derényi +4	molecular motors, membrane nanotubes, complex networks, population dynamics and evolution	<a href="http://angel.elte.hu/~derenyi">angel.elte.hu/~derenyi</a>
Theoretical biology group; Department of Plant Taxonomy and Ecology	Eörs Szathmáry/ János Podani +9	origin of life, RNA world, evolution of cooperation / communication / metabolic networks / viruses, major transitions in evolution, spatial population dynamics, cellular automata, community dynamics and species borders, comparative genomics, yeast systems biology, virus dynamics, theoretical immunology, classification, sampling theory, pattern analysis, numerical taxonomy, Martian life	<a href="http://ramet.elte.hu/~ramet/indexe.html">ramet.elte.hu/~ramet/indexe.html</a>
Theoretical biology and ecology research group of the Hungarian Academy of Sciences	Eörs Szathmáry +7	Origin of life, evolution of replicators / bacteria / cooperation, spatial population dynamics, cellular automata, quorum sensing, biological activity in chaotic flows, discrete state population dynamics, evolutionary game theory, discrete mathematical methods in sequence analysis	<a href="http://ramet.elte.hu/~ramet/indexe.html">ramet.elte.hu/~ramet/indexe.html</a>

**Institution:**  
**Budapest University of Technology and Economics, H-1521 Budapest**

Group name, department	Leader(s) # researchers	Research topics	Web address
Department of Mathematical Analysis	János Tóth +3	Deterministic and stochastic models of reaction kinetics with applications in biochemistry, neurobiology, toxicokinetics, signal transduction etc. reducing the number of variables.	<a href="http://www.math.bme.hu/~jtoth">www.math.bme.hu/~jtoth</a>
Molecular Network Dynamics Research Group of the Hungarian Academy of Sciences	Béla Novák +6	Mathematical modeling of cell cycle, cell morphogenesis, microtubule dynamics, circadian rhythm. Phaseplane and bifurcation analysis	<a href="http://www.cellcycle.bme.hu">www.cellcycle.bme.hu</a>

Institution, Group name, department	Leader(s) # researchers	Research topics	Web address
Szent István University, <b>Gödöllő</b> Institute of Mathematics and Informatics	Zoltán Varga +4	Applications of mathematical systems theory in biology, evolutionary games, ecological modelling, management of renewable resources	
Szent István University, <b>Budapest</b> Department of Physiology and Biochemistry	Tibor Bartha +6	Energy metabolism (thyroid hormones, leptin, ghrelin), neuroendocrinology (estrogen, gonadotropins, UCP)	<a href="http://www.vetphysiol.hu">www.vetphysiol.hu</a>
Szent István University, <b>Budapest</b> Department of Biomathematics and Informatics	János Fodor +5	Epidemiology, applied statistics, dynamical and statistical analysis of agricultural systems, fuzzy logic and its applications, modelling biological and social systems	<a href="http://www.univet.hu/english/units/math/">http://www.univet.hu/english/units/math/</a>
Semmelweis University <b>Budapest</b> , LINK-Group, Dept.of Medical Chemistry	Péter Csermely +19	Network topology and dynamics, biological networks, network stability, network modules	<a href="http://www.weaklink.sote.hu">www.weaklink.sote.hu</a>
Berzsenyi Dániel College, <b>Szombathely</b> Dept. of Zoology	János Izsák	Statistical ecology, diversity indices and abundance models. Epidemiology statistics.	<a href="http://allattan.bdf.hu/oktatok/ji.htm">allattan.bdf.hu/oktatok/ji.htm</a>
KFKI Research Institute for Particle and Nuclear Physics <b>Budapest</b> Computational Neuroscience Group, Department of Biophysics	Péter Érdi +11	EURESIST - Integration of viral genomics with clinical data to predict response to anti-HIV treatment; ICEA - Modelling goal-directed navigation of the rat; Model-based source localization of extracellular action potentials; Generation and control of septo-hippocampal oscillations; Study of sensory systems	<a href="http://cneuro.rmki.kfki.hu/">cneuro.rmki.kfki.hu/</a>
<b>BudapestTech</b> Biotechnology Group	Miklós Kozlovsky +1	Microarray (DNA/Protein) and Bioinformatics data analysis, Algorithms in Bioinformatics	<a href="http://www.nik.bmf.hu">www.nik.bmf.hu</a>
Computer and Automation Research Institute, Hungarian Academy <b>Budapest</b> Theoretical Computer Science Research Group	Erzsébet Csuha-Varjú +2	Molecular computing, DNA computing, membrane computing, bio-inspired models of computation, computational models of biological networks, collective behaviour of bio-inspired agents	<a href="http://www.sztaki.hu/tcs">www.sztaki.hu/tcs</a>

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## RECENT THESES

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### **Deciphering living networks: Perturbation strategies for functional genomics**

***Alberto de la Fuente***

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*Free University Amsterdam*

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Advisors:

Prof.Dr. H.V. Westerhoff

Prof.Dr. J.L. Snoep

Supervisor:

Dr. P.J. Mendes

Using modern experimental techniques it is possible to measure the concentrations of a great many, and ultimately all, cellular constituents such as mRNAs, proteins and metabolites. Given these experimental technologies, astronomical amounts of new data will appear. To enable us to see the forest for the trees, we need to find ways in which best to analyze data so as to obtain better understanding of biochemical systems and predictive power. When those new ways of analyzing the data are found, this may even lead to a preference for a certain type of data or certain experimental methodologies. This may then help direct experimentation towards the highest possible impact for understanding of biochemical systems. Ideally, the three levels of biochemical organization, *i.e.* mRNAs, proteins and metabolites, are studied all together in an integrated fashion. However, due to the number of components and complexity of such integrated systems it is reasonable to try to decompose the system and to study the subsystems or to use simplified descriptions of the whole system. It will be important to decompose the system into subsystems that behave in isolation in much the same way as they do when they are embedded in the whole system.

This is exactly what I deal with in my dissertation; on the one hand I show how and when it is possible to study systems properties of metabolism *in vivo*, ignoring the effects of gene and protein expression, and on the other hand I develop a quantitative concept in terms of Metabolic Control Analysis to describe the properties of the whole system in a simplified form, *i.e.* as a gene network a description of only the dynamics of gene expression without explicit accounting for metabolites and proteins. This concept enables the inference of the topology of such gene networks from experimental data. The analysis guides the experimenter towards the specific experiments that need to be done in order to be able to infer interactions between genes on a genome scale.

After introducing the relevant preliminaries in Chapter 1, in Chapter 2 I introduce the concept of hierarchical biochemical systems and show how to express their properties in terms of properties of the individual flux-disconnected modules of which they are composed. In particular, I focus on the study of metabolic systems. I propose several methods with the goal of distinguishing regulation that takes place at the metabolic level only from regulation that involves transcription or translation, thus quantifying the relative importance of each of these processes to the global systems behavior. I verify the experimental applicability of these methods by analyzing data obtained by simulation of a biochemical system.

In Chapter 3 I introduce the concept of gene network. ‘Gene networks’ are network models in which the nodes represent gene activities (mRNA levels) and the edges correspond to regulatory interactions between them. Such models are highly phenomenological because they do not represent explicitly the proteins and metabolites that mediate those interactions. I show the use of Regulatory Strengths to quantify gene-gene interactions and show how to express these coefficients in terms of the biochemical

system underlying these interactions. This approach establishes a clear and formal link between phenomenological gene network modeling and more detailed approaches considering the hierarchical structuring of biochemical networks as introduced in Chapter 2.

In Chapter 4 I review previously proposed approaches to use Metabolic Control Analysis to infer properties of the biochemical constituents from observations of the whole system, *i.e.* “the inverse MCA”. In the “conventional MCA” it has been shown that when the *local* properties of the components of the system have been experimentally determined (elasticities) one can calculate the *systemic* properties of the system as a whole (control coefficients). Inverse MCA establishes the exact opposite; one measures the properties of the global system and calculates the properties of the components. Then, I develop an inverse MCA approach to enable the inference of the regulatory structure of gene networks from gene expression data. The proposed methodology relies on systematic perturbations in gene expression rates and measurements of the genome wide steady state responses. The method is evaluated by applying it to data produced with several mathematical models of gene networks. Finally, a large set of simulated data on large gene networks is analysed in order to thoroughly evaluate the proposed method.

In Chapter 5, the general discussion, I describe the place of my work in current functional genomics and systems biology research. I compare the gene network inference method to

recent variants that have appeared in the literature and generalize the approach to deal with other types of biochemical systems. At the end, I suggest improvements which could be made to the method, in particular in light of the limited quality of currently produced data sets.

The thesis can be downloaded at:  
[http://www.bioinformatica.crs4.org/Members/alf/phd\\_thesis.pdf](http://www.bioinformatica.crs4.org/Members/alf/phd_thesis.pdf)

Further reading:

de la Fuente A, Brazhnik P, Mendes P. ‘Linking the genes: inferring quantitative gene networks from microarray data’.  
Trends Genet. 2002 Aug; 18(8):395-8.

de la Fuente A, Mendes P. ‘Quantifying gene networks with regulatory strengths’.  
Mol Biol Rep. 2002; 29(1-2):73-7.

Brazhnik P, de la Fuente A, Mendes P. ‘Gene networks: how to put the function in genomics’.  
Trends Biotechnol. 2002 Nov; 20(11):467-72.

de la Fuente, A., Snoep, J. L., Westerhoff H. V. & Mendes, P. ‘Metabolic control in integrated biochemical systems’. European Journal of Biochemistry, 2003 Sep; 269 (18): 4399-4408

de la Fuente A, Mendes P. ‘Integrative modelling of gene expression and cell metabolism’.  
Applied Bioinformatics, 2003;2(2), 79-90.

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**More theses should be sent to us – since we want to award prizes !**

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**In order to promote the circulation of RECENT THESESES in our scientific community by publication of abstracts within the *European Communications*, we want to collect more of during each year and then select the most challenging ones concerning innovative ideas or tools. To these selected authors we think to award an annual price (which we might name *Reinhart Heinrich Price* for “Guiding young scientists in the field of mathematical and theoretical biology”) by the ESMTB.**

Thus, please, feel responsible to encourage graduate students and PhD finishers to participate in this yearly round and to send their THESESES ABSTRACT as soon as possible (but before end of October)!

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## HISTORY: 10 YEARS ITB “Institute of Theoretical Biology” in Berlin

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### Tenth Anniversary of the ITB: "Where is Theoretical Biology heading?"

October 12 - 14, 2006, Berlin

This year the Institute of Theoretical Biology (ITB) in Berlin celebrated its 10 years anniversary. On occasion of this anniversary the staff of ITB organized a nice symposium on current trends of theoretical biology. Thematically, the talks were divided into Evolutionary Biology, Neuroscience, Immunology, Systems Biology and Bioacoustics. The talks were held in a general and interdisciplinary fashion. Famous researchers like *J. Hopfield*, *T. Kirkwood*, *S. Pääbo*, *T. Fitch* and others tried to convey to the audience some of their main contributions in this exciting scientific field.

For me personally it was a great pleasure to be there, since I spent almost a year at ITB, working with *Prof. H. Herzel* and I now had the chance to meet old friends. I wish all the best to ITB and I hope to keep up the good work.

*Babis Hatzikirou*  
ZIH, TU Dresden

### Happy birthday ITB – and many happy returns!

On the occasion of the 10<sup>th</sup> Anniversary of the Institute for Theoretical Biology (ITB) at Humboldt University Berlin, the organizers put together a gem of a conference programme bridging many of the specialist disciplines of biology, thereby underpinning the claim of Theoretical Biology as the unifying foundation for all of Biology. Whereas the usual conference, even with a biomathematical orientation, is specialized, this meeting was different: the talks about neurobiology could be understood by and inspire an ecologist and *vice versa*.

The common theme of the talks – *building bridges between disciplines* – was nicely illustrated by *Tecumseh Fitch*, who showed historical pictures of the Tyne Bridge Construction (1928) in his talk on “Communication”.



Building bridges in 1928: the Tyne Bridge

The speakers, the audience, and the organizers can be commended – the speakers for keeping the attention of the audience throughout the one-hour-long talks designed to give a broad and understandable overview of the field – the audience for the lively and insightful discussions that followed and enriched each talk – and the organizers for having formed an institutional attractor over the first 10 years of the ITB’s existence that pulled in so many internationally renowned speakers to this well-attended meeting with about 180 participants from 10 countries.



In the following, we give a brief overview of the talks presented at the meeting.



The Symposium opened with some lessons on how to found a new institute. **Bernd Ronacher** reconstructed the ‘prehistory’ of the ITB. The starting point was a program of the DFG to initiate interdisciplinary research and teaching programs, so-called “Innovationskollegs”, at the universities of the former GDR. As early as 1992 the zoologist *Rüdiger Wehner*, the biochemist *Cornelius Frömmel*, the physicist *Werner Ebeling* and others realized that the time was ripe for an Institute for Theoretical Biology. The strong support from the Biology Department, the Medical Faculty, the Wissenschaftskolleg Berlin and the Berlin Senate lead finally to a novelty in the scientific landscape – the parallel hiring of three professors in Theoretical Biology (*Peter Hammerstein*, *Andreas Herz*, *Hanspeter Herzel*) representing the diversity of biological research. Such an overcritical mass was essential to attract many guests, excellent students, and, until now, four independent junior research groups. The ITB later initiated various collaborative grants such as the SFB Theoretical Biology or the Bernstein Center for Computational Neuroscience. Moreover, a comprehensive teaching program was established ranging from biomathematics in the first year to more than 20 specialized courses in many fields of theoretical biology. These activities have been accompanied by yearly schools on specific topics such as Theoretical Immunology (2002), Circadian Clocks (2003), Memory (2004), Molecular Medicine (2005), or Aging (2006). The symposium 10 years after the foundation of the ITB also reflects the diversity of modern biology and the need to discuss unifying concepts.



The first speaker of the symposium was **Svante Pääbo** from the Max Planck Institute of Evolutionary Anthropology in Leipzig. He addressed a most intriguing question – what distinguishes humans from non-human primates? Besides genetic differences such as the ‘language gene’ *FOXP2* he focussed on gene-expression profiles in

various organs. In testes and the brain, indications of positive selection have been found. He finished his talk by presenting first steps of a Neandertal genome project. This idea triggered a hot debate about the reliability of ancient DNA sequences.



While **Tom Kirkwood** spoke one hour on “Aging”, our life expectancy increased by about 12 minutes. Quite pleased with this, we learned about the Disposable Soma Theory’s idea that ageing is caused by damage, and less enchanting news of trade-offs between longevity and competitiveness or reproduction. Hungry mice live longer because resource allocation is shifted away from reproduction towards maintenance and repair, reducing cellular damage during periods of famine; the same difference in resource allocation also exists between germ line and somatic cells.



**Stanislas Leibler** focused on population diversity as a mechanism for survival in a changing environment when the new environment cannot be predicted or identified by sensing, and showed how the optimal rate of switching between the phenotypes either best adapted to environment  $E_i$  or  $E_j$  is coupled to the probability of transitions between the respective environments, and that the distribution of environments can be measured by the entropy or information content of the environment. He built one bridge between ecology and economics after the other, demonstrating that economists had known all about portfolio diversity as a mechanism for optimizing returns before us biologists and that we really should be reading the economics literature first. We bet this will pay off in such rapidly changing times.



**Rolf Hoekstra** spoke about “Threats from within”, the conflict between the genome and selfish genetic elements within the genome. The list of such selfish elements is long, including Homing Endonuclease Genes, Transposable Elements, and Killer Genes (Meiotic Drive). Transposable

elements have been ‘domesticated’ for the vertebrate immune system where they are used to generate the huge diversity of antibody genes. Since selfish elements would tend to decline in clonal (asexual) populations, they have to jump to another lineage by horizontal gene transfer. Sex could have evolved because it can prevent the spread of selfish elements.



**Manfred Laubichler** bridged the past with the present in his talk on the “History of Theoretical Biology”, showing that Theoretical Biology was born about 100 years ago out of a data crisis, an overwhelming accumulation of data without a theoretical framework for their interpretation, that sounds all too familiar in the age of ‘-omics’. The reassuring message for the audience was that Theoretical Biology will also lead out of the current data crisis.



**Tecumseh Fitch** first explained the bioacoustics of animal vocalizations in his talk on “Communication” and then went on to play soundtracks and amazing x-ray movies of the larynx in action in various animals ‘willing’ to participate. He explained many intriguing examples of animals faking larger body size by anatomical changes leading to a ‘deeper’ voice (actually, formants, the peaks in the frequency spectrum, correlate better with body size than the pitch, the perceived fundamental frequency). This proves that animal vocalizations are used as a cue for body size.



When we recollect the name of a person that we met in our childhood, or the name of a small city visited many years ago, we are sometimes absolutely confident when we finally got the right name. **John Hopfield** addressed the question of how this process could be implemented in a simple associative neural network by including ‘check bits’ into the neural code. He also showed that forgetting, i.e. the degradation of a stored memory, can be slowed down by spike-time-dependent learning rules,

for which (luckily!) experimental evidence has been accumulating over the last few years. Finally, Hopfield presented a related model for spatial navigation that predicts hysteretic effects when an animal is brought to a new environment – the experimental neuroscientists in the audience took busy notes...



**Christian Machens** focused on working memory. He demonstrated that previously separated ‘black boxes’ – information storage, memory and decision making – can be realized within the same elementary feedback network. He focused on the task of discriminating between two successively presented stimuli and showed that the uploading of the first stimulus into short-term memory can be seen as the creation of a fixed-point attractor; during the waiting period until the second stimulus arrives, the system operates as a line attractor; the second stimulus then generates a repeller that automatically drives the network to the correct solution. Supported by experimental results, this model nicely illustrates that dynamical-systems theory can even help to bridge cellular neurobiology and psychology.



**Jorge Carneiro** spoke about the “Immune System” that has to solve the problem of generating a comprehensive set of antibodies capable of binding to the diversity of target structures of the rapidly evolving microbial pathogens while discriminating these alien targets from self. Good old Clonal Selection Theory postulates that the growth and multiplication of a clone of immune cells producing a particular antibody targeting non-self antigens is stimulated when the antigen is present, while self-reacting immune cells are eliminated. This can be exploited by pathogens using self-antigen mimicry, eventually leading to autoimmune diseases. He then explained Version 2 of the Clonal Selection Theory, which is based on competition between effector and regulatory cells for antigen presenting cells and cross-regulation of the two competing cell types, which can better explain the causes of

autoimmune diseases as an imbalance in these interactions.



**Uri Alon** presented his ideas on ‘motifs’ in gene transcription and other networks. Motifs are those ‘building blocks’ of a network that occur more often than in a randomized network. For example, of the 13 possible 3-node motifs only the feed-forward loop occurs more frequently than expected in *E. coli* and yeast transcription networks. As networks build bridges, they make for an ideal unifying and theoretical perspective in Biology, occurring on different scales and in different functions: food webs, social, neuronal, signal transduction, regulatory, metabolic networks, etc. This facilitates the comparison of disparate fields from the perspective of network topology, which Alon used in his talk to point out that, for example, food webs have other motifs than gene transcription networks.



In the talk of **Alexander Borst**, “Theoretical Biology took off to Fly”, motion processing in the blow fly was presented as a fascinating case study of neural signal processing. Evidence for gap junctions (electrical synapses) between adjacent motion detecting cells

responsible for neighbouring spatial input ranges was surprising since one would expect this to reduce the spatial resolution of motion detection. Indeed, gap junctions result in linear interpolation between adjoining input ranges, but this was found to be essential for detecting motion in natural images correctly.



The relaxed format of the Symposium – only four talks per day with extensive discussion sections, long coffee and lunch breaks, and a splendid evening in the former lecture hall of *Rudolf Virchow* at the Charité – helped trigger many informal discussions between the different camps of Theoretical Biology – from Systems Biology to Evolution, from Neuroscience to Immunology, from Biomathematics to Computational Modelling.

Mark your calendar for a similarly illuminating meeting in Fall 2016 – the 20<sup>th</sup> Anniversary of the ITB!

*Jan-Ulrich Kreft*

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*Theoretical Biology, Bonn, Germany*



Photos of the meeting by  
*Ed Hagen and Samuel Glauser*  
(ITB, Berlin)

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## PAST ACTIVITIES

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### BIOMATHEMATICS

#### Cooperation agreement between University of Evora (Portugal) and University of Campinas (Brasil)

Last April, the Universities of Evora (Portugal) and the University of Campinas (Brasil) signed a cooperation agreement in the area of Biomathematics involving the Project on Stochastic and Statistical Applications in Life Sciences (Research Centre of Mathematics and Applications, University of Evora) and the Research Group in Epidemiology and Mathematical Physiology (University of Campinas). The coordinators are *Carlos A. Braumann* and *Russell Alpizar-Jara* (University of Evora) and *Hyun Mo Yang* and *Wilson Castro Ferreira Jr.* (University of Campinas). The purpose is the cooperation in research projects and an exchange visitors program.

By the way, the University of Campinas is the site of next CMPD 2: Conference on “Computational and Mathematical Population Dynamics” to be held in July 16-20, 2007. For information see announcement below (Page 26) and [www.cmpd2.ime.unicamp.br](http://www.cmpd2.ime.unicamp.br)

*Carlos A. Braumann*  
*Board of ESMTB*

#### 7<sup>th</sup> Frankfurter „Stochastik-Tage“ 2006: German Open Conference on Probability and Statistics

*March 14 - 17, 2006*

*Goethe-Universität, Frankfurt am Main*

Continuing the series of “Stochastik-Tage” taking place in a two year rhythm (the previous was hold in Karlsruhe 2004), the DMV-Fachgruppe Stochastik organized the Seventh Stochastik-Tage, this time jointly with the University of Frankfurt/Main. The Bernoulli society and the IMS acted as cosponsors of the event.

The Campus Westend with its impressive former ‘IG-Farben-Haus’ hosted more than 400 participants including many from outside Germany and provided an inspiring surrounding. In the tradition of the previous conferences, the Frankfurter Stochastik-Tage offered an international forum for scientists working in probability theory and statistics and can be viewed as major European event in this field.

In thirteen sections including traditional stochastic disciplines as Stochastic Processes, Random Fields, Stochastic Geometry and Limit Theorems, the conference committee (chaired by *Anton Wakolbinger*, Frankfurt) also installed the sections Stochastic Models in Physics and Biology as well as Statistics in Biosciences and Medicine. Each section consisted of an invited lecture and contributed talks. Moreover, five plenary talks were given by *Adrian Baddeley* (Perth), *David Cox* (Oxford), *Luc Devroye* (Montreal), *Mark Low* (Philadelphia) and *Sylvie L’el’eard* (Nantes). The organizers of the section Stochastic Models in Physics and Biology were *Ellen Baake* and *Friedrich Götze* from Bielefeld.

The contributed lectures captured a wide range of biologically inspired topics such as ‘Stochastic Modeling of Tropical Cyclone Track Data’ (*Jonas Rumpf*, Ulm), ‘How T cells use large deviations to recognize foreign antigens’ (*Natali Zint*, *Ellen Baake*, *Frank den Hollander*, Bielefeld), or ‘On rare mutations’ (*Andreas Greven*, Erlangen), and showed how questions in the field of Theoretical Biology can be tackled by a large variety of mathematical methods.

The next Stochastik-Tage in 2008 will take place in Aachen.

*Tobias Klauß*  
*TU Dresden*  
*Institut für Mathematische Stochastik*

**BIOMAT School:  
Mathematics and Life Sciences -  
Models of Development**

June 5 – 9, 2006

Facultad de Ciencias, Universidad de Granada,  
Spain

In June of this year the second edition of Biomat Schools was organized in Granada, Spain, by the maths department of UG (Universidad de Granada) and the applied maths department of UCM (Universidad Complutense de Madrid).

The central questions of the school were how mathematical theories and applications can be useful in biology, which problems they can solve and what does “the other side” of the biomathematical world (biologist and medical doctors) want and require from mathematicians. The school invited speakers from the field of mathematics and physics as well as from biology and medicine, so it was very well balanced between its “bio” and “mat” parts. The topics ranged from a new theoretical formulation for complex multicellular systems, by *Nicola Bellomo* (Turino University), to a very exhaustive background on growth and tumor growth in experimental systems in vivo and in vitro, by *Mercedes Villalobos* (University of Granada), including some applied subjects such as computational electrophysiology, namely on mathematical modelling of the hearts electrical activity, by *Victor Perez Garcia* (Castilla la Mancha University).

Despite the extreme weather (over 30 degrees), the not so comfortable accommodation and a very tight time schedule, the conference clearly represented a great opportunity to get a better understanding of the biological problems mathematicians can study, what approaches they can use, and to interact productively in a friendly environment with biologists, finding common paths of communication.

Finally I want to stress the importance of the lectures by *Hans Meinhardt* (Max Plank Institute, Tübingen, Germany), who devoted himself for many hours with passion talking about his whole life research on partial differential equation models for biological

pattern formation, showing how a good brain can develop very efficient mathematical models with a few good equations and minimal use of computational tools.

*Sebastiano de Franciscis  
TU Dresden, ZIH, Germany*

**SBMC 2006:  
The challenges of Systems Biology**

July 12 – 14, 2006

Heidelberg, Germany

The SBMC2006 conference took place in the heart of the beautiful Old Town Heidelberg, on the banks of the Neckar River and has been very well organized by HepatoSys, the Federal German research initiative on Systems Biology of hepatocytes supported by the German Ministry of Education and Research (BMBF) along with numerous industrial as well academic sponsors.

Because of the interdisciplinary collaborations between important institutions such as DKFZ, EMBL, EML, BIOQUANT, Heidelberg is now claiming a prominent role among the most important centers for Systems Biology.

The aim of the conference was to provide insights into some aspects of Systems Biology techniques for analyzing the mammalian cells behavior, in particular cell regulation of gene expression and signal transduction networks.

Areas of biology covered included quantitative life cell imaging, proteomics, dynamic modeling of signaling pathways in primary cells systems such as hepatocytes.

Among the speakers of high international profile are worth mentioning:

*Session Proteomics:*

**L. Cantley** (Division of Signal Transduction Harvard Institutes of Medicine, Boston).

It is becoming increasingly clear that Systems Biology will catalyze fundamental changes in the future of health care. Lewis Cantley’s recent research focuses on a systems biology analysis approach in order to understand the biochemical pathways that regulate normal mammalian cell

growth and the defects in signal transduction that cause cell transformation. A logical network and the regulation of metabolic energy lead to cell growth control in response to growth factors, nutrient availability and cellular energy status, and play a critical role in cancers.

*Session Life Cell Imaging:*

**N. Hiroi** (JST ERATO-SORST - Kitano Symbiotic Systems Project, Tokyo) presented a new reaction-diffusion modeling method (Dimension Restricted Reaction Kinetics) for modeling biochemical reactions in crowded spaces like in cytoplasm *in vivo*. The DRRK-analysis method enables to represent the fractal dimension of molecular movement in its ODE structure.

*Session Dynamic Modeling of Signaling Pathways:*

**B. Kolodenko** (Thomas Jefferson University, Philadelphia). Boris Kholodenko has made pioneering contributions towards the understanding of the spatio-temporal organization of cell signaling and its significance for cell fate determination. A highly combinatorial network generated by phosphorylations and binding forms of a large number of kinases and their substrate effectors at different states of the network can be described by a *domain oriented* macro model of the network.

This approach leads to an important result: the receptor-mediated membrane relocation of cytosolic proteins is very important for the spatial-temporal organization of the GPCR-and RTK- induced signaling (growth factors, RAS signaling).

**J. Ferrell** (Department of Molecular Pharmacology Department of Biochemistry Stanford). One way to understand the design principles of complex signaling networks is to identify feedback loops, which are involved in the regulatory schemes. In the example presented by James Ferrell a positive feedback loops triggers the *Xenopus* oocyte maturation and determine the function of the mitotic oscillator in *Xenopus* embryos.

**P.K. Sorger** (MIT, Cambridge). Cytokines and their receptors activate complex signal cascades controlling cell proliferation, cell death and differentiation. In order to understand cell-type variation and differences between normal and

disease cell states, Sorger and colleagues recently developed mechanistic and numerical models that encompass various aspects of cytokines signaling, and focus on pro-apoptotic (Tumor Necrosis Factor) and pro-survival cytokines (EGF and Insulin Growth Factor). Such models are numerical, but they have been formulated on the basis of experimental data and subjected to experimental verification. Systems biology based models, which focus equally on computation and experimentation, are going to play an important role in the development and use of drugs for major Human diseases in the immediate future.

*Session Hepatocytes:*

**H.V. Westerhoff** (University of Manchester). Living cells' primary processes are mostly chemical or physical reactions that are carried out by metabolic and other pathways. Each of these pathways has to be regulated in time and tuned according to the functional status of the other. Hans Westerhoff described a new method to dissect such regulation into various subtypes: metabolic regulation, gene expression regulation and regulation by signal transduction.

The quality of most of the conference talks show that significant progress has already been made in systems biology analysis of higher eukaryotes. However, as an increasing number of complex biological processes become amenable to quantitative analysis, this field has the potential and the responsibility to go much further. With new technological advances, both in theoretical and experimental approaches, systems biology can aim at rigorously reshaping various areas of biology, for example, in the field of data integration methodology, the formation of morphogen gradients during developmental processes and, evolutionary systems biology, to name a few. The years to come will hopefully demonstrate how models with increasing and more accurate predictive value can be generated.

*Perla Del Conte-Zerial  
TU Dresden*

Further information: <http://www.sbm06.de/>

**2<sup>nd</sup> Summer School of the MCRTN:  
Modelling, Mathematical Methods and  
Computer Simulation of  
Tumour Growth and Therapy**

*July 15-19, 2006*

*Orthodox Academy, Kolymbari, Crete*

In July this year, right after the Euroconference entitled “*Which mathematics for biology?*” also in Crete (in the small town of Anogia, near Crete's capital Heraklion) the Marie Curie Training Network “*Modelling, Mathematical Methods and Computer Simulation*” organised its second summer school. The aim of this summer school was to discuss discrete and continuous modelling approaches in the study of tumour growth, vascularisation and metastasis.

As it is usual in meetings of this kind, the audience was quite diverse (physicians, physicists, life scientists, computer scientists, etc.), though mathematicians were predominant. The scientific programme was quite intense and included talks by senior researchers (the first two days) as well as by younger scientists from the

network (the remaining three days). Of particular interest for people who have recently arrived to the field of mathematical and computational cancer research were the talks given by *Matthias Simon* (University Clinics Bonn) and *Georg Breier* (University Clinics Dresden), who presented introductory talks about tumour biology and reminded us mathematicians and computer scientists about the complexity of the matter that we tackle with simplified models.

The summer school took place in the premises of the Orthodox Academy of Crete in Kolymbari. This location, while probably not as unique as the one for the Euroconference in Anogia, was quite functional and comfortable with ample of space for meetings and wireless internet access.

*David Basanta  
Zentrum für Informationsdienste und  
Hochleistungsrechnen  
Technische Universität Dresden, Germany*

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## ANNOUNCEMENTS

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**The Marie 2<sup>nd</sup> International Symposium  
Dynamical Systems Theory and Its  
Applications to Biology and Environmental  
Sciences**

*March 14-17, 2007*

*Hamamatsu city campus of Shizuoka University,  
Japan.*

Symposium Objectives

Dynamical systems theory in mathematical biology and environmental science has been attracted much attention from many scientific fields as well as mathematics. Mathematicians should establish a mathematical basis on the various problems appeared in dynamical systems of biology and feed back their work to biology and environmental sciences. Biologists and environmental scientists should clarify/build the

model systems that are important in the global biological and environmental problems of their own. The purpose of "The International Symposium on Dynamical Systems Theory and Its Applications to Biology and Environmental Sciences" is to discuss many interests on the rich properties of dynamical systems appeared in biology and environmental sciences.

The symposium constitutes of the lectures by about 20 eminent mathematical biologists and contributed oral or poster sessions. Asian contributors are especially welcome to the symposium.

Collections of papers based on the presentations may appear as special issues of international journals. We already have agreements with Journal of Biological Dynamics.

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3-5-1 Johoku, Hamamatsu, Shizuoka, 432-8561,  
JAPAN.

<http://moon.sys.eng.shizuoka.ac.jp/~dstympo2nd>

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**Fourth International Conference  
on Mathematical Biology**

*May 29 to June 1, 2007*

*Inst. of Biology in Wuyishan  
Fujian, P. R. China*

This conference will bring together the world's leading experts in the field of mathematical ecology, epidemiology, biometrics, bioinformatics, mathematical neuroscience and related mathematical problems in biology and computational biology and rehabilitations to present their most recent work and provide a collegial atmosphere for the scientific discussion of the latest advances in the field.

We also plan to have exciting and beautiful excursions for sight seeing tours after the technical program. We sincerely hope that this will bring to you an unforgettable memory.

<http://icmb.mnkjxy.com>

Registration Form to be returned  
before January 28 to [Prof. Lansun Chen.](#)



**3rd NanoBio-Europe 2007**

*June 13-15, 2007*

*Münster/Germany*

[www.nanobio-europe.com](http://www.nanobio-europe.com)

Europe's leading congress on nanobiotechnology offers three days of high level plenary talks and an industrial exhibition including company presentations. 8 workshops on specific issues held by speakers of international reputation from academia as well as industry will offer extensive information to participants from science and industry. Following Grenoble in 2006, now for the second time Münster, a city of science and culture decorated with the International Awards for Liveable Communities (Livcom), will host the conference.

**Scientific Program**

The program consists of eight scientific sessions given by speakers of international reputation from academia and industry addressing the following topics:

- Nanobioanalysis in vitro
- Nanobioanalysis in vivo
- Nanoassemblies / Surfaces
- Drug Delivery / Theranostics
- Nanomaterials for Regenerative Medicine
- Integrated Systems / Sensors
- NBIC / Neurobionics
- Far Future Challenges

At the beginning of each session an invited speaker will highlight a special hot topic of the area addressed by the session, followed by several shorter papers selected from the proposals for oral presentations (Call for Papers is open now). Special time and a large area is dedicated to poster sessions allowing in-depth discussion of scientific results. The scientific sessions are accompanied by industry presentations and an exhibition of major companies and European clusters. They will highlight the current and future application areas and active locations in Europe in the area of nanobiotechnology.

**2<sup>nd</sup> Conference on Computational and  
Mathematical Population Dynamics  
(CMPD2)**

July 16 - 20, 2007

University of Campinas, Campinas, Brazil

The Organizing Committee is waiting for your contribution. We are also expecting your collaboration do spread the word about our conference among your partners/scientific societies.

<http://www.cmpd2.unicamp.br>

Please, do not hesitate to contact the Conference Secretariat at [cmpd2@ime.unicamp.br](mailto:cmpd2@ime.unicamp.br).

The Organizing Committee is looking forward to see you at Campinas.

*H. M. Yang  
Conference Chair*

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**International Conference on Artificial Neural  
Networks (ICANN 2007)**

September 9 - 13, 2007

Ipanema Park Hotel, Porto, Portugal

ICANN is an annual conference organized by the European Neural Network Society in co-operation with the International Neural Network Society, and is a premier event in all topics related to neural networks.

**Deadlines**

16 Feb: End of submission of special session and workshop proposals.

23 Mar: End of submission of full papers.

**Conference Proceedings**

Published by Springer-Verlag  
(Lecture Notes in Computer Science).

**Neural Networks Special Issue**

An extended version of selected ICANN 2007 papers will be published in a Special Issue of Elsevier's journal *Neural Networks*.

Sponsors: ENNS, INNS, JNNS, EURASIP,  
INEB, ISEP, UBI

Student support available (please see web page)

ICANN 2007 Secretariat

Gabriela Afonso, INEB, Campus FEUP, Rua Dr.

Roberto Frias, Porto, Portugal

([gafonso@fe.up.pt](mailto:gafonso@fe.up.pt))

<http://www.icann2007.org>

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**IEEE Congress on Evolutionary Computation  
(CEC)**

September 25-28, 2007

Swissôtel The Stamford, Singapore

**CALL FOR PAPERS**

The Congress is sponsored by the IEEE Computational Intelligence Society, and co-sponsored by the Evolutionary Programming Society and the IET.

The annual IEEE Congress on Evolutionary Computation is one of the leading events in the area of evolutionary computation. It covers all topics in evolutionary computation, including, but not limited to:

Ant colony optimization

Artificial immune systems

Artificial life

Autonomous mental & behavior development

Bioinformatics & bioengineering

Coevolution & collective behavior

Cognitive systems & applications

Combinatorial & numerical optimization

Computational finance & economics

Constraint & uncertainty handling

Evolutionary data mining

Evolutionary design

Evolutionary games

Evolutionary intelligent agents

Evolutionary learning systems

Evolutionary robotic & control systems

Evolvable hardware & software

Evolving neural networks & fuzzy systems

Memetic & hybrid algorithms

Molecular & quantum computing

Multiobjective optimization

Particle swarm intelligence

Real-world applications

Representation & operators

Theory of evolutionary computation

*CEC 2007* will feature a world-class conference that aims to bring together researchers and practitioners in the field of evolutionary computation and computational intelligence from all around the globe. Technical exchanges within the research community will encompass keynote speeches, over 30 special sessions, over 10 tutorials and workshops, panel discussions as well as poster presentations. On top of these, participants will be treated to a series of social functions, receptions and networking sessions, which will serve as a vital channel to establish new connections and foster everlasting friendship among fellow counterparts.

Singapore is a vibrant commercial and financial hub, which at the same time also serves its role as a melting pot for the fusion of a diverse mix of many different cultures. Visitors to this tropical island resort will be treated to a great array of interesting attractions, festival celebrations and cultural events, not forgetting the one-stop shopping and eating experience in this entertainment paradise. The conglomeration of all the different elements will definitely give visitors of Singapore an exciting and unforgettable experience.

#### Student Travel Support:

The IEEE/CIS Student Travel Grant Program offers a number of travel grants to assist IEEE/CIS Student Members presenting papers at IEEE CEC 2007.

For more information, please see the conference website at <http://www.cec2007.org>.

#### Accepted Tutorials:

- Adaptive Business Intelligence - Evolutionary Computation for Real World Problems: *Zbigniew Michalewicz*
- Artificial Immune Systems: *Dipankar Dasgupta*
- Evolution Strategies: *Thomas Baeck*
- Evolutionary Computation: A Unified Approach: *Kenneth A. De Jong*
- Evolutionary Computation in Bioinformatics: *Gary Fogel and Gwenn Volkert*

- Evolutionary Computation in Finance and Economics: *Edward Tsang*
- Evolutionary Multi-Criterion Optimization (EMO): Fundamentals, State-of-the-art Methodologies and Future Challenges: *Kalyanmoy Deb*
- Evolutionary Robotics: *Dario Floreano*
- Evolutionary Soccer Teams for RoboCup Simulation: *Tomoharu Nakashima*
- From Evolving Single Neural Networks to Evolving Ensembles: *Xin Yao*
- Genetic Programming Practice and Theory: *Riccardo Poli*
- Particle Swarm Optimization and Differential Evolution: *Ponnuthurai Nagaratnam Suganthan and Andries P. Engelbrecht*

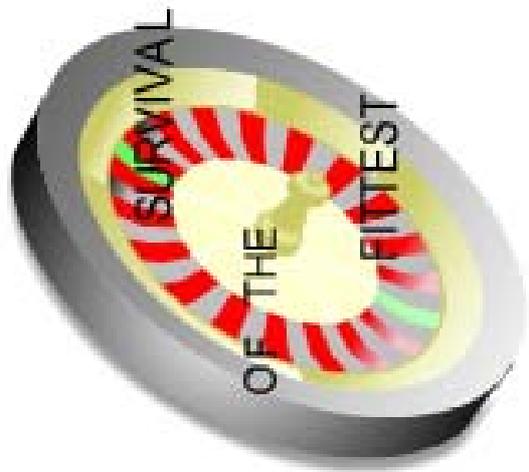
#### Important Dates:

Paper Submission Deadline: March 15, 2007

Decision Notification: May 15, 2007

Camera-Ready Submission: June 15, 2007

For more details, please visit the conference website at: <http://www.cec2007.org>



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## NEW JOURNALS AND BOOKS

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### **BIOLOGICAL THEORY** **Integrating Development, Evolution and Cognition**

New Journal from MIT-Press

Editor-in-Chief: **Werner Callebaut**  
*Konrad-Lorenz-Institute for Evolution and  
Cognition Research (KLI), Altenberg, Austria*  
[biot-office@kli.ac.at](mailto:biot-office@kli.ac.at)

Devoted to theoretical advances in the fields of evolution and cognition with an emphasis on the conceptual integration afforded by evolutionary and developmental approaches, *Biological Theory* aims to include a wide audience of scientists, social scientists, and scholars from the humanities among its readership.

Vol. 1, Issue 1: Selected examples of articles

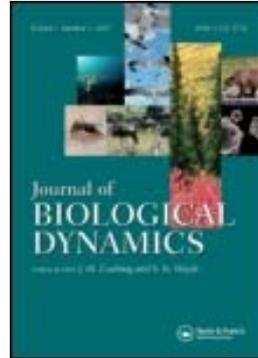
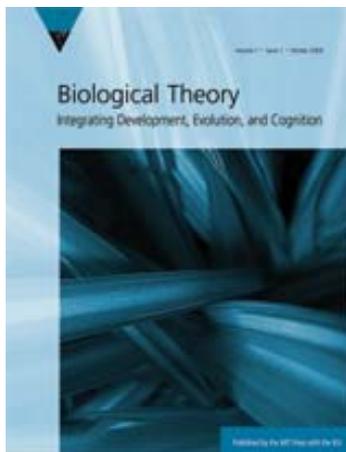
*Don Ross: Game Theory in Studies of Evolution and Development. Prospects for Deeper Use*

*Stephen C. Stearns: Theory and Data in the Evolutionary Approach to Human Behavior*

*Hiroaki Kitano, Kanae Oda: Self-Extending Symbiosis. A Mechanism for Increasing Robustness through Evolution*

*Fred L. Bookstein: My Unexpected Journey in Biomathematics*

*Eörs Szathmáry: Bird as Aeroplanes.  
Remembering John Maynard Smith*



### **Journal of BIOLOGICAL DYNAMICS**

New Journal from Taylor & Francis

Editors-in-Chief:

**J.M. Cushing**, *Univ. of Arizona, Tucson*  
**S.N. Elaydi**, *Trinity Univ., San Antonio*

[www.tandf.co.uk/journals/authors/tjbdauth.asp](http://www.tandf.co.uk/journals/authors/tjbdauth.asp)

*Journal of Biological Dynamics* publishes state of the art papers dealing with the analysis of dynamic models that arise from biological processes. The Journal focuses on dynamics phenomena, at scales ranging from the level of individual organisms to that of populations, communities, and ecosystems that arise in the fields of ecology and evolutionary biology, population dynamics, epidemiology, immunology, environmental science, and animal behavior.

In addition to papers that analyze original mathematical models and develop new theories and analytic methods, the Journal welcomes papers that connect mathematical modeling and analysis to experimental and observational data.

The Journal also publishes short notes, expository and review articles, book reviews and a section on open problems.

The University of the Basque Country Press has recently edited a Special Issue of its journal "*The International Journal of Developmental Biology*" entitled

**"Developmental Morphodynamics"**

Guest editors *Richard Gordon & Lev Belousov*

[www.ijdb.ehu.es/web/contents.php?vol=50&issue=2-3](http://www.ijdb.ehu.es/web/contents.php?vol=50&issue=2-3)

We believe that the contents of this Special Issue are of particular interest to members of the ESMTB and ask you to include this information on your web and in your Communications. Please note that we are a scholarly, independent journal, run by scientists, for scientists; not for profit.

In return, we would be happy to offer a **10% discount** for your members (larger discounts are available for bulk orders). Likewise, we would also consider including a full color page advertisement for the ESMTB, or events you would like to internationally promote, in our journal at no cost.

Please let me know if you would be interested in these or similar reciprocal measures, with a view to promoting both the ESMTB and making our journal available to its members.

Yours sincerely,

*Michael Ryan, Customer Services*  
Dept. Cell Biology, Faculty of Medicine,  
University of the Basque Country  
E-48940 Leioa (Vizcaya), Spain

The International Journal of Developmental  
Biology, [www.intjdevbiol.com](http://www.intjdevbiol.com)  
e-mail: [ubcpres@intjdevbiol.com](mailto:ubcpres@intjdevbiol.com)

Content:

**DEVELOPMENTAL MORPHODYNAMICS**

**Preface**

*Developmental Morphodynamics - bridging the gap between the genome and embryo physics*  
by Lev V. Belousov and Richard Gordon

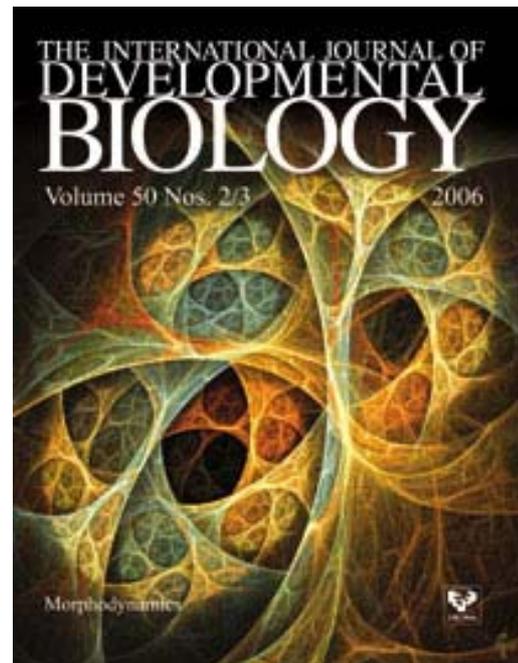
**Selected INTRODUCTORY PAPERS**

**Direct physical formation of anatomical structures by cell traction forces. An interview with Albert Harris**

by Lev Belousov

**From observations to paradigms; the importance of theories and models. An interview with Hans Meinhardt**

by Richard Gordon and Lev Belousov



**Selected CONTRIBUTIONS**

**Principles of branch formation and branch patterning in Hydrozoa**

by Stefan Berking

**Do lamellipodia have the mechanical capacity to drive convergent extension?**

by G. Wayne Brodland

**The dynamic geometry of mass cell movements in animal morphogenesis**

by Vladimir G. Cherdantsev

**Mechanical control of tissue morphogenesis during embryological development**

by Donald E. Ingber

**Morphodynamics of phyllotaxis**

by Alexander G. Malygin

**Before programs: The physical origination of multicellular forms**

by Stuart A. Newman, Gabor Forgacs and Gerd B. Müller

**Tissue morphogenesis: a surface buckling mechanism**

by Konstantin Y. Volokh

## **Dynamical Models in Biology**

by *Stephen P. Ellner and John Guckenheimer*.

Princeton University Press

From controlling disease outbreaks to predicting heart attacks, dynamic models are increasingly crucial for understanding biological processes. Many universities are starting undergraduate programs in computational biology to introduce students to this rapidly growing field. In *Dynamic Models in Biology*, the first text on dynamic models specifically written for undergraduate students in the biological sciences, ecologist *Stephen Ellner* and mathematician *John Guckenheimer* teach students how to understand, build, and use dynamic models in biology.

Developed from a course taught by Ellner and Guckenheimer at Cornell University, the book is organized around biological applications, with mathematics and computing developed through case studies at the molecular, cellular, and population levels. The authors cover both simple analytic models - the sort usually found in mathematical biology texts - and the complex computational models now used by both biologists and mathematicians

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## **Gender-Structured Population Modeling: Mathematical Methods, Numerics, and Simulations**

*M. Iannelli, M. Martcheva, and F. A. Milner*

<Frontiers in Applied Mathematics 31>

*Gender-Structured Population Modeling: Mathematical Methods, Numerics, and Simulations* gives a unified presentation of a mathematical framework for modeling population growth by couple formation. It provides an overview of both past and present modeling results. The authors focus on pair formation (marriage) and two-sex models with different forms of the marriage function — the basis of couple formation — and discuss which of these forms might make a better choice for a particular population (the United States). The book also provides results on model analysis,

gives an up-to-date review of mathematical demography, discusses numerical methods, and puts deterministic modeling of human populations into historical perspective.

The authors describe several models and derive the theoretical results that demonstrate the validity of these models. The numerical methods for approximating the solutions of the differential models — the equivalent of creating discrete simulators — are delineated. Simulation results are compared with actual demographic data to show some of the difficulties concerning the availability of data and to show that mathematical demography provides reasonable qualitative and quantitative estimates. The models in this book can be applied to different sets of data.

### Audience

This book is an excellent reference for demographers as well as graduate students and mathematicians interested in population dynamics, and is a great source for further research on the subject.

### Contents

- Chapter 1: Historical Perspective of Mathematical Demography;
- Chapter 2: Gender Structure and the Problem of Modeling Marriages;
- Chapter 3: Well-Posedness of the Fredrickson–Hoppensteadt Two-Sex Model;
- Chapter 4: Numerical Methods;
- Chapter 5: Age Profiles and Exponential Growth;
- Appendix: The Main Algorithm

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## **Complex Systems in Biomedicine**

*Quarteroni, Alfio; Formaggia, Luca; Veneziani, Alessandro (Eds.)*

2006, XX, 300 p., Hardcover.

ISBN: 88-470-0394-6

Mathematical modeling of human physiopathology is a tremendously ambitious task. It encompasses the modeling of most diverse compartments such as the cardiovascular, respiratory, skeletal and nervous systems, as well as the mechanical and

biochemical interaction between blood flow and arterial walls, or electrocardiac processes and the electric conduction into biological tissues. Mathematical models can be set up to simulate both vasculogenesis (the aggregation and organisation of endothelial cells dispersed in a given environment) and angiogenesis (the formation of new vessels sprouting from an existing vessel) that are relevant to the formation of vascular networks, and in particular to the description of tumor growth. The integration of models aimed at simulating the cooperation and interrelation of different systems is an even more difficult task. It calls for the set up of, for instance, interaction models for the integrated cardio-vascular system and the interplay between central circulation and peripheral compartments, models for the mid-long range cardiovascular adjustments to pathological conditions (e.g. to account for surgical interventions, congenital malformations, or tumor growth), models for the integration among circulation, tissue perfusion, biochemical and thermal regulation, models for parameter identification and sensitivity analysis to parameter changes or data uncertainty – and many others. The heart is a complex system in itself, where electrical phenomena are functionally related with the wall deformation. In its turn, electrical activity is related with heart physiology. It involves nonlinear reaction-diffusion processes and provides the activation stimulus to the heart dynamics and eventually the blood ventricular flow that drives the haemodynamics of the whole circulatory system. In fact, the influence is reciprocal, since the circulatory system in turns affects the heart dynamics and may induce an overload depending upon the individual physiopathologies ( for instance the presence of a stenotic artery or a vascular prosthesis). Virtually, all the fields of mathematics have a role to play in this context. Geometry and approximation theory provide the tools for handling clinical data acquired by tomography or magnetic resonance, identifying meaningful geometrical patterns and producing three-dimensional geometrical models stemming from the original patients data. Mathematical analysis, flow and solid dynamics, stochastic analysis are used to set up the differential models and predict uncertainty. Numerical analysis and

high performance computing are needed to numerically solve the complex differential models. Finally, methods from stochastic and statistical analysis are exploited for the modeling and interpretation of space-time patterns. Indeed, the complexity of the problems at hand often stimulates the use of innovative mathematical techniques that are able, for instance, to accurately catch those processes that occur at multiple scales in time and space (like cellular and systemic effects), and that are governed by heterogeneous physical laws.

Written for:

Reaserchers in Computer Applications in Life Sciences, Mathematicians who deal with applications in Medicine and Biology, Industries

Keywords:

cardiovascular modelling  
 mathematical modelling  
 medical imaging  
 modelling of cancer growth  
 physiological systems  
 population dynamics

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## **Mathematical Modeling of Complex Biological Systems.**

### **A Kinetic Theory Approach**

*Bellouquid, Abdelghani; Delitala, Marcello*

Birkhäuser 2006, Approx. 205 p., 47 illus., Hardcover. ISBN: 0-8176-4395-8

<Series: Modeling and Simulation in Science, Engineering and Technology>

This book describes the evolution of several socio-biological systems using mathematical kinetic theory. Specifically, it deals with modeling and simulations of biological systems — comprised of large populations of interacting cells — whose dynamics follow the rules of mechanics as well as rules governed by their own ability to organize movement and biological functions. The authors propose a new biological model for the analysis of competition between cells of an aggressive host and cells of a corresponding immune system.

Because the microscopic description of a biological system is far more complex than that of a physical system of inert matter, a higher level of analysis is needed to deal with such complexity. Mathematical models using kinetic theory may represent a way to deal with such complexity, allowing for an understanding of phenomena of nonequilibrium statistical mechanics not described by the traditional macroscopic approach. The proposed models are related to the generalized Boltzmann equation and describe the population dynamics of several interacting elements (kinetic population models).

The particular models proposed by the authors are based on a framework related to a system of integro-differential equations, defining the evolution of the distribution function over the microscopic state of each element in a given system. Macroscopic information on the behavior of the system is obtained from suitable moments of the distribution function over the microscopic states of the elements involved. The book follows a classical research approach applied to modeling real systems, linking the observation of biological phenomena, collection of experimental data, modeling, and computational simulations to validate the proposed models. Qualitative analysis techniques are used to identify the prediction ability of specific models.

The book will be a valuable resource for applied mathematicians as well as researchers in the field of biological sciences. It may be used for advanced graduate courses and seminars in biological systems modeling with applications to collective social behavior, immunology, and epidemiology.

Written for:

Graduate students, researchers and practitioners in applied mathematics, engineering, biomedicine, and biological sciences

Keywords:

complex biological systems  
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kinetic population models  
mathematical kinetic theory  
nonequilibrium statistical mechanics

**Modeling in Biopharmaceutics,  
Pharmacokinetics and Pharmacodynamics.  
Homogeneous and Heterogeneous  
Approaches**

*Macheras, Panos; Iliadis, Athanassios*  
2006, XX, 442 p.,

<[Interdisciplinary Applied Mathematics](#), 30>

The state of the art in Biopharmaceutics, Pharmacokinetics, and Pharmacodynamics Modeling is presented in this book. It shows how advanced physical and mathematical methods can expand classical models in order to cover heterogeneous drug-biological processes and therapeutic effects in the body. The book is divided into four parts; the first deals with the fundamental principles of fractals, diffusion and nonlinear dynamics; the second with drug dissolution, release, and absorption; the third with empirical, compartmental, and stochastic pharmacokinetic models, and the fourth mainly with nonclassical aspects of pharmacodynamics. The classical models that have relevance and application to these sciences are also considered throughout. Many examples are used to illustrate the intrinsic complexity of drug administration related phenomena in the human, justifying the use of advanced modeling methods.

This timely and useful book will appeal to graduate students and researchers in pharmacology, pharmaceutical sciences, bioengineering, and physiology.

Written for:

Graduate students and researchers in pharmacology, pharmaceutical sciences, bioengineering and physiology.