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Dear Colleagues,

After more than 10 years of "Biomathematics Newsletter" – its tiny issue Number 1 appeared June 6, 1988 – this current issue, together with the updated version of the "Address Booklet" got ready just before the TMBM conference in Amsterdam end of June (see page 27) and it will be the first Newsletter that is not only printed and shipped out in the traditional (and expensive) way but also available on the internet, via

<http://www.theobio.uni-bonn.de/newsletter>

About 250 scientists have responded during the last two years and sent their personal updates to us or to the ESMTB (European Society for Mathematical and Theoretical Biology; our list contains about 120 Society members, see also Treasurer's report page on 3).

Out of those, who answered the Newsletter form (these were about 130 people), 89 have voted for the possibility to *download* the BMN from the web page. They have received a corresponding e-mail message from us.

However, all of the those whose updates appear in the newest (third!) issue of the ADDRESS BOOKLET 1999 will obtain this by ordinary mail, because we think there is no other way to centrally distribute such details of personal information. (There might be a discussion in Amsterdam whether this service should be continued.)

We hope that both, Newsletter and Address Booklet, fulfill the purpose of documenting the growing importance of a fruitful scientific exchange within the European and world wide community of Biomathematicians and Theoretical Biologists by

1. reporting or announcing activities and events, and activities of the European Society,
2. presenting detailed information about research areas, results or problems offered by young (doctor) students, local interdisciplinary working groups, larger institutions or by journals and book series.

Some of these purposes and, in particular, the open market of offering free positions or announcing short-term events might be better achieved by using the Society Web Page (see report on ESMTB web page on page 2). It would be a good idea to find out, during the discussions at the Amsterdam Conference, in which form the Newsletter should persist. For example, the Newsletter could get the shape of a small magazine, with more pictures, with short but attractive articles or, say, with a historical section.

Meanwile, we are very grateful that Andrea De Gaetano from Rome has agreed to join the editorial team starting from the next issue. We hope that this will decrease the work load per editor, bring fresh ideas into the Newsletter and assure persistence.

At the Amsterdam Conference there will be a "ESMTB Newsletter Stand", where we will not only show (and eventually sell) our Newsletters and Address Booklets to interested participants but also like to discuss about future tasks and projects (looking for help and suggestions) and where one can also apply for ESMTB membership.

Last but not least, the figure on this BMN's title page has been offered by Broder Breckling: it shows a simulation of movement patterns of certain insects (see page 7 for details and page 8 with the complete, i.e. square, figure).

The editors for # 19: Wolfgang Alt, Edith Geigant, Hans Heesterbeek.

The **closing date** for the next issue BMN # 20 will be **September 30, 1999**. Please send, preferably by e-mail, information, scientific reports and other material to one of the editors:

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Society news

ESMTB webpage

The ESMTB-webpage is open now. You can find it under:

<http://www.mis.mpg.de/esmtb/>

It is located at the Max-Planck-Institute for Mathematics in the Sciences (MIS) in Leipzig, Germany, <http://www.mis.mpg.de>.

It contains and will contain information and links to

- meetings and conferences,
- other societies and groups,
- the ESMTB Newsletter
- and additional interests you express.

Please contact the Webmaster of this homepage at

email: esmtb@mis.mpg.de

if you have any information you would like to see posted on this webpage, like job offers, announcements, etc.

Angela Stevens, Responsible Board Member

Secretary and Treasurer's Report

Dear Colleagues,

after issuing several calls for 1999 Membership Fees (letter, e-mail, SMB e-mail net, Biomathematics Newsletter etc), I can tell you that the response this year has been excellent and we have now over 125 fully paid Society members. This means that the Society is in a fairly healthy financial position with regard to paying some of the costs for the Newsletter. If membership continues to hold steady at this number (and, of course, hopefully increase), then we will be able to start to commit money to fund projects such as an ESMTB Graduate Student Travel Fund and offer some financial support to fund small meetings, workshops and conferences. In addition to Membership Numbers being increased greatly, there has also been a very good response (globally) to journal subscriptions with 35 members subscribing to the various journals. I hope that this figure will also continue to rise in the coming years.

Concerning future membership fees and journal subscriptions, more details will be given in issue #20 (September/October 1999), but I intend to make payment of fees easier by setting up a EURO BANK ACCOUNT which should make payment more straightforward. I will also be contacting the various publishers so that journal subscriptions can be paid directly to the publishers without having to come through me. This should speed things up greatly.

The final point I have to bring to your attention is that of the annual plenary meeting of ESMTB Members. This will take place during the TMBM99 Conference in Amsterdam and will overlap with the SMB Annual Meeting. Please note that only fully paid members are permitted to attend the meeting which is an open forum for a discussion of the Society's business. The following arrangements have been made:

The plenary meeting will take place on the evening of Wednesday 30th June during the TMBM99 Amsterdam Conference. The precise location will be given in the conference programme and the schedule is as follows:

- The SMB annual meeting will be held on Wednesday June 30th starting at 6pm and lasting till 7pm.
- After that, from 7pm until 8pm, there will be a reception for members of SMB and ESMTB only (paid members only). Remember there is already a welcome reception the evening before, where everybody is invited. This reception for members is only planned because it is custom with the SMB and because there has to be some food served between the SMB annual meeting and the ensuing ESMTB plenary meeting of members.
- At **8pm** the **ESMTB plenary meeting** will start and last until 10pm at the latest.

Mark Chaplain, ESMTB Secretary and Treasurer

Report of the journal committee

A committee was founded within the board of the ESMTB for investigating the desired level of association between ESMTB and the scientific press. The members of the committee are Z. Agur, P. Auger and A. Goldbeter. Our discussions and surveys were conducted at the level of the committee and the board, with members of ESMTB, as well as with editors of Biomaths journals and with publishers. Now time is ripe for moving forward, from the conceptual phase to to the operative phase of activity. Since we feel that endorsement by

ESMTB members is mandatory at this stage, we present below a brief interim report, which will hopefully aid in shaping your views of the issue at hand.

Clearly, publication in the scientific literature is the ultimate vehicle for disseminating scientific ideas. No wonder then that the committee treats this subject with great prudence. In our discussions there has emerged the notion that a good affiliated journal will aid in establishing a feeling of identity among ESMTB members, and will provide us with an instrument for influencing science also at the meta-level, by making an impact on the directions of science and on its quality. Therefore we believe that a good affiliated journal can be an asset to the society, worthy of our endeavours.

The majority of ESMTB members (72%) chose none of the existing European Biomaths journals to be their ESMTB affiliated journal. Still, some of us, at the board, felt that the exploration of familiar avenues, such as existing European journals or enlarging the Bulletin, has not been exhausted yet. Therefore, we checked the possibility of "increasing the profile" of one of the existing journals to fit the society's prerequisites. Our conclusion is that this task is trickier than starting anew. Moreover, many of us who believe in Darwinism do not share the view that the "more than plenty" existing biomathematical journals do not justify the establishment of a new one. Rather, one believes that "survival of the fittest" also holds good for intellectual creatures, such as scientific journals, and that competition improves quality.

Founding a new journal: a publisher, Cambridge University Press (CUP), has been selected by us, and preliminary discussions with its head of the scientific journals section have been initiated by our representative, A. Goldbeter. The initial answer from CUP was one of keen interest. CUP requested further information as to the format, content, potential audience, competing journals, and envisaged composition of the editorial board. They were ready to examine questions related to subscription prices for Society members. However, they first wished to have sufficient information about the prospective journal in order to submit the project to their scientific board for approval.

It is the view of the journal committee, and the board as a whole, that these initial contacts with the publisher can be further pursued only upon receiving full endorsement by the members of ESMTB. The journal committee has already discussed the possible structure, title, editors and an advisory board of the new journal. These issues will be detailed at the forum once if the principle of a new journal is accepted.

Zvia Agur, Board Member

The Fifth Framework Programme of the EU

In a recent issue of this Newsletter Dr. Edward Whitehead had announced the launching of the Fifth Framework Programme. In order to apply we have to consider some relevant changes with respect to previous programmes of the EU. More than fundamental research (for which about only 20% of the total resources will be devoted), a multidisciplinary approach will be favoured for research activities of relevant socio-economic value. Special attention will be devoted to projects which involve Small and Medium Enterprises (SME's).

The evaluation of a project will occur in two ways:

- those who do not match minimal requisites will receive a fast "NO";

- those projects which are eligible may receive a " LONG YES", via a procedure which includes the following:
- correct prediction of costs,
- innovative character of the proposed research,
- feasibility,
- correct info's regarding the management of the project.

Similar projects may be joined in a cluster (unless already anticipated by a network of proponents).

The criteria of substantial evaluation of a project include:

- quality of the proponents and scientific innovation
- added value for the EU
- contribution to the social objectives of the 5FP (health of citizens, quality of life, etc.)
- economic development due to the results of the project
- resources, structure of the network, management.

Novelties for fellowships (Marie Curie):

- individual fellowships
- return fellowships ; to favour return to less favoured regions
- industry host fellowships; to support research at a company, partially supported by the host company.
- development host fellowships; for those who intend to spend a period at a less favoured region (to be defined by a list of the EU).
- training sites; the EU will select centres of excellence which may host PhD students for one year.

New participating countries:

From the start the following countries may participate to the projects, as for states members of the EU: Bulgaria, Romania, Poland, Hongrie, Czech Republic, Slovakia, Latvia, Estonia, Lithuania, Slovenia, Cyprus. Possibly from 2001 Switzerland.

On March 6, 1999 the Call for the Thematic Programme on *Quality of Life and Management of Living Resources* ("LIFE") has been launched. For the call text (and deadlines) please consult the following

<http://www.cordis.lu/life>

Key actions:

1. Food, Nutrition and Health
 - 1.1. Food technologies to improve product quality
 - 1.2. Safe food: tests to detect and processes to eliminate infectious and toxic agents
 - 1.3. The role of food in promoting and protecting health
2. Control of Infectious Diseases
 - 2.1. Development of vaccines, especially against viral diseases
 - 2.2. New strategies to identify and control infectious diseases
 - 2.3. Improvement of public health systems and care delivery
3. The "Cell Factory"
 - 3.1. Cell factory engineering
 - 3.2. Development of new processes and products
 - 3.3. Exploitation of new raw materials

4. Environment and Health
 - 4.1. Research into diseases and allergies related to the environment
 - 4.2. New methods of diagnosis, risk assessment and prevention of harmful environmental health effects
5. Sustainable Agriculture, Fisheries and Forestry
 - 5.1. New and/or improved systems of production and exploitation
 - 5.2. Integrated production and exploitation of biological materials from non-food uses
 - 5.3. Support for common policies
 - 5.4. New tools for the development of rural and other areas
6. The Ageing Population and Disabilities
 - 6.1. Age-related illnesses and health problems with high morbidity
 - 6.2. Biological, psychological, social and economic determinants of healthy ageing and the mechanisms leading to disability
 - 6.3. Demographic and epidemiological research on trends in the fields of ageing and disability
 - 6.4. New approaches to delaying the onset of disability, reducing the difficulties experienced by older people in their social and physical environment
 - 6.5. Effective and efficient delivery of health and social care services to older people, including comparative research on the financing of long term care and pensions

These will absorb 77% of the budget of LIFE; a 23% will be devoted to generic research and activities.

Vincenzo Capasso, email: capasso@elanor.mat.unimi.it

Reports of past activities

Polish National Conferences on Mathematics Applied in Biology and Medicine

September 15 - 18, 1998, Zwierzyniec, Poland

Polish National Conferences on Mathematics Applied in Biology and Medicine are held annually since 1995. The aim of the meetings is to stimulate the applications of mathematics in biology and medicine. New results in biomathematics as well as new solutions to problems in life sciences, which are obtained using known mathematical methods, are welcome. Proceedings include all papers accepted for presentation, and are published in English.

The meetings were initiated by Mariusz Ziolkowski (Department of Electronics, University of Mining and Metallurgy, Krakow), Jan Kozłowski (Institute of Environmental Biology, Jagiellonian University, Krakow) and Jacek Pietrzyk (Collegium Medicum, Jagiellonian University, Krakow), and the first two conferences (1995, 1996) were held in Zakopane. The third meeting (1997) was organized by Janusz Uchmanski (Institute of Ecology, Polish Academy of Sciences, Warszawa) and Tomasz Wyszomirski (Institute of Botany, Warsaw University) in Madralin near Warszawa. The fourth conference (September 15 - 18, 1998), was organized by Jacek Waniewski (Institute of Biocybernetics and Biomedical Engineering, Polish Academy of Sciences, Warszawa) and by Urszula Forys and Mirosław Lachowicz (Institute of Applied Mathematics and Mechanics, Warsaw University).

Over sixty participants, mainly from universities, technical universities and institutes of the Polish Academy of Sciences, gathered in Zwierzyniec (near Zamosc) - a capital of a national park in south-east Poland. Twenty seven presentations covered so wide and diverse applications of mathematical, statistical and computer methods in biology and medicine, that it was not possible to classify them in any "one-topic" sessions. Plenary lectures were given by Janusz Uchmanski: "Individual based modeling in ecology", Andrzej Swierniak: "Tumor cell cycle as the object of control", and Ryszard Rudnicki: "What mathematics is due to biology, that is about Wazewska & Lasota model of haemopoiesis". A special session was devoted to the memory of Professor Wieslaw Szlenk, a pioneer of biomathematics in Poland. During a long evening discussion the participants tried to evaluate the role of classical mathematical modeling versus new computer based models, which use Cellular Automata & Co methods, but, of course, no conclusion could be reached.

The **next conference** will be organized in

Ustrzyki Gorne (Bieszczady Mountains), September 14 - 17, 1999.

More information (in Polish) at

<http://wavelet.elektro.agh.edu.pl/kkzmbm>.

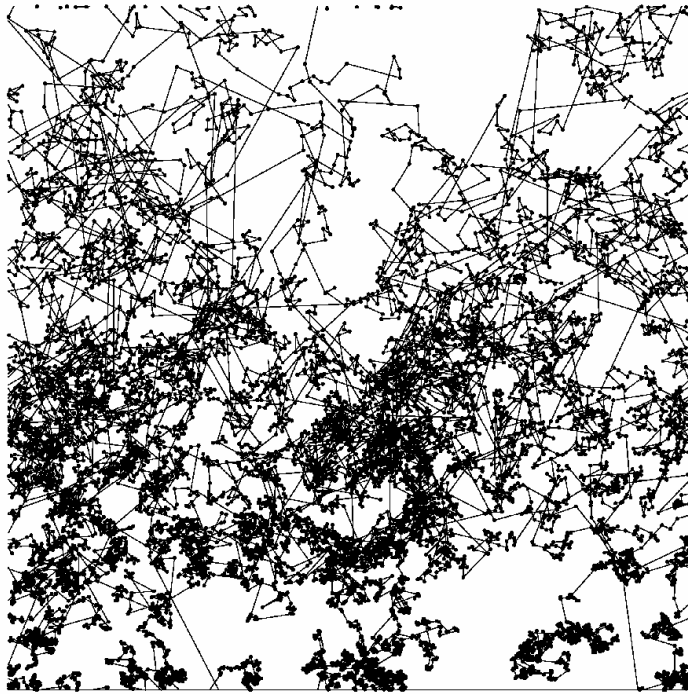
Jacek Waniewski, email: jacekwan@ibib.waw.pl

Object Oriented Modelling and Simulation of Environmental, Human and Technical Systems, Report on the 24th Conference of the Association of Simula Users (ASU)

30. Sept - 2. Oct. 1998, Salzau (Schleswig Holstein, Germany)

Simula has the well-established fame of being one of the more elegant programming languages which was developed in the "ancient times" of early information technology during the 1960s. Is it still in use? Unbelievable, but the Association of Simula Users continues to organize annual meetings since a quarter century to discuss new developments concerning basic aspects as well as new applications of the Simula programming language. Being a small user group however has the advantage of an intense and direct exchange. Who has experienced the personal and "mutualistic" style of communication will like to join it again. In 1998, the ASU meeting was held at Salzau Castle, a historical place, mentioned in documents already 1000 years ago, and nowadays famous for the cultural events which take place there. Organizer of the conference was the Ecology Center at the University of Kiel, and this was the reason to provide a presentation of a variety of ecological applications done in Simula.

Simula is the programming language which is currently used at the Ecology Center for the purpose of biocenotic modelling. Modelling the interaction of biotic entities is a part of a wider range of modelling activities also using other approaches. The Ecology Center runs the Project "Ecosystems Research in the Bornhoeved Lakes Region", which investigates typical ecosystems of the Northern German moraine landscape (beech forest, pasture, farmland, wetland, lake) in a spatio-temporal context. It is one of the large ecosystem research initiatives sponsored by the Federal Ministry of Research and Technology. The project employed 120 scientists from various disciplines during its main field-investigation phase (1992 - 1996). Being now in its evaluation-phase (1997 - 1999), model applications are developed for different purposes. Especially biocenosis modelling faces problems, which have proven difficult to be included in conventional differential equation based models. Many organismic interac-



Dispersal study for Carabus sp. (Insecta, Coleoptera). Movement pattern (daily positions) of 18 individuals for 630 d (approx. 3 annual activity periods) on an area of 420 x 420 m are simulated. The effect of a local spatial resistance gradient can be seen. From above to below the mean daily migrating distance decreases by the factor 2.1. This causes (a) a higher probability to meet individuals in the area with higher spatial resistance and (b) a higher variability of occurrences in this area. (Simulation by Jopp, Reuter and Breckling)

tion effects cannot be explained using homogeneous dynamics of average population density calculations. In particular, this includes the role of

- spatial heterogeneity
- individual variability
- interaction on different hierarchical levels (esp. organ - individual - population - metapopulation)
- structure-function relationships
- self-organization and emergent properties in organismic interactions.

The current state of the project's object-oriented model development was presented at the ASU conference and is now available as a proceedings volume. In the following, we give a short overview of some of the 17 papers presented during the Salzau meeting.

Two contributions introduce (a) the general modelling concept of the Bornhoeved Project and (b) the use of the facilities of object orientation in Simula for modeling biocenotic processes.

Further papers deal with particular applications:

Hauke Reuter presents simulations of the population interactions of small rodents. Under certain conditions periodic cycles of population outbreaks occur, which are empirically well investigated during previous decades, but which still are not fully understood. It has proven difficult to distinguish the interaction of food-limitation, the mutual impact of individual activity and physiology, population age structure, density dependant behavioural changes,

mobility and predator influences. Using an object-oriented individual based approach this interaction can be studied. The model supports the conclusion, that the rodent cycles are not a one-factor phenomenon. It can be shown, that outbreak dynamics are driven by an overlay of various factors, which can change their relative importance to a large degree.

Hoelker and Breckling present a study of fish cohort development. Using field- and laboratory data of roach (*Rutilus rutilus*), a dominant species in many Northern German lakes, the models provides a synopsis of eco-energetics and the consequences of movement pattern and facultative shoaling for resource use, food composition and spatial population distribution. (See picture.)

Spatial distribution dynamics in a different context is the focus of the paper by *Jopp et al.* They use empirical data of carabid beetles to investigate the role of spatial heterogeneity and migration distances on an individual base. For several species an inverse relation of frequency and walking distance per day was found: The shorter the distance the more frequently it occurs, and the larger the distance the rarer it is. Long term consequences of this migrating pattern for several years and the role of local spatial resistances can be estimated, while field studies applying telemetric tracking of single organisms only cover time ranges of 2-3 weeks.

Two papers deal with investigation of black alder trees (*Alnus glutinosa*). *Ulrike Midelhoff* presents a spatially explicit model for the dynamics of the fine-root system and how it is modified by heterogeneous distribution of nutrients, interaction of the coarse root system of different individuals and also the influence of above-ground interaction (photosynthesis, mutual shading). *Christiane Eschenbach* mainly deals with the shoot architecture and how it is generated by the interaction of physiological processes on the level of leaves, internodes, meristems and roots. Both papers show, how morphological aspects and physiological processes interact to let the modular organization of the plant individual and stand interaction effects emerge.

The ecological contributions demonstrate, how it is possible to connect quantitative dynamics in simulation models with qualitative interrelations when using the object oriented programming approach. It extends the the range of interactions, which are accessible for model representation.

Further contributions to the proceedings volume address industrial and technical applications. E.g. *Michel Gourgand et al.* describe a "Generic Hybrid Flow-Shop Simulation Model Using Simula". A non- Simula contribution is by *Freudenberg and Herper*, presenting a paper on "Worker Simulation using HLA" (High Level Architecture).

Another five conference contributions deal with basic aspects of Object Orientation. One focus of interest in this context is the simulation of nested quasiparallel systems. In this context, it is possible to run simulations which start internal sub-simulations, which use specifications from the upper processes. This is interesting for studying cooperations or antagonisms of actors, who evaluate alternatives of what to do by internally representing (the potential intentions of) co-actors to determine next steps to take. The contributions by *Islo* ("Application of Transplanted Object References in Nested Quasiparallel System Models") and by *Kindler* ("Transplantation - What Causes it in MS-Dos Simula") show, how this type of situations can be dealt with in Simula and explain several implications on the programming level.

The next ASU meeting will be held

23rd - 27th of August 1999 in Hungary at Lake Balaton.

For the year 2000 there is a meeting planned in Malta. Further information on coming

Simula-events as well as the proceedings volume of the 1998 meeting is available through the ASU Secretariat c/o H. Islo, AF Industri-Teknik AB, Box 35, SE-164 93 Kista, Sweden, Tel: +46 8 657 15 10, Fax: +46 8 657 3701, email: hio@ind.af.se.

Price: SEK 250, DM 60, EUR 30, US\$ 40 (includes postage and handling charge) This price applies when paying by major credit card. Payment by bankcheck or bank transfer incurs an extra fee of SEK 100, DM 22, EURO 11, US\$ 16 for bank transfer fees.

For further information about the Ecosystem Research in the Bornhoeved Lakes Region contact

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Broder Breckling, Kiel, Germany, *Henry Islo*, Sollentuna, Sweden.

Workshop on “Mathematical Problems in the Modeling and Control of Tumor Immune System Interactions”

February 21 - 26, 1999, Oberwolfach, Germany

From the 21st until the 26th of February we were - being a group of twelve - happy to experience a generous interpretation of the “Research in Pairs” program, offered by the Mathematical Research Center in Oberwolfach and sponsored by the “Volkswagen Stiftung”. Thus, we tried “to pair” mathematical knowledge and biological expertise.

Distortions in the cell cycle, tumor immune cell interactions and growing tumor masses are major points of interest in modeling cancer; each of these points requires different mathematical methods, such as dynamical system theory, diffusion reaction equations, cellular automata and kinetic theory. Talks on topics of neighbor disciplines such as modeling wound healing and pattern formation were intended to suggest alternative methods that could be applied to the modeling of tumor growth as well.

Participants came from England, Germany, Israel, Italy, Poland and from the US. The sessions were devoted to microscopic modeling, macroscopic modeling and cellular signaling, leaving enough room for extended discussions after each talk. Macroscopic modeling is mainly based on diffusion models and free boundary problems. Cellular automata, on the other hand, have been successfully applied to various problems of pattern formation in biology, and it seems to be promising to integrate the discrete theory of cellular automata and continuum models.

Presented microscopic models focused mainly on the distortion of the cell cycle. The question was heavily discussed to what degree time delays and stochasticity have to be an integral part of possible models, or if they are just useful excuses for hiding missing biological information. A talk on the role of cell signaling in wound healing provided indications in how to treat this phenomenon mathematically in the case of growing tumor masses.

A consensus was reached, that no model can be totally satisfactory, being based on properties of a cell alone. Rather, an integration of cell properties and environmental conditions is required. The kinetic cellular theory, deriving macroscopic variables such as tumor size from modeling microscopic interactions, could be a first step in that direction.

Extra sessions were devoted to the proposal on an European network “Improving Cancer Therapy through Mathematical Modeling and Simulation” and to the presentation of a WEB

page on research in modeling tumor immune system dynamics

<http://calvino.polito.it/~preziosi/bioweb.html>.

We hope that our meeting was just the beginning of a fruitful and extensive cooperation.

Italian and broken English were the official languages of the congress; Polish, Hebrew, English and French were also admitted. Mechanical models of cell interactions were discussed in the basement of the “Hotel Hirschen” in an international bowling tournament: Italy vs. the rest of the world.

Sabine Stöcker, Dipartimento di Matematica, Politecnico di Torino.

Workshop of the Graduate Programme ”Dynamics and Evolution of Cellular and Macromolecular Processes”

March 17–19, 1999, Hiddensee

Since 1997, the interdisciplinary graduate programme (Graduiertenkolleg) of the Deutsche Forschungsgemeinschaft “Dynamics and Evolution of Cellular and Macromolecular Processes” connects theoretical and experimental groups in Berlin with a common interest in the quantitative analysis of cellular structures. Problems under study span a wide range from the determination of protein structure to the development of the nervous system. Researchers from the Humboldt and Free Universities, from the Max-Delbrück-Center for Molecular Medicine, and from the Max-Planck-Institute for Molecular Genetics participate in the programme.

The diversity of topics and approaches in the programme was brought together in our most recent annual workshop held at the island of Hiddensee in the Baltic Sea. Unlike the previous two conferences which mainly consisted of contributions from established scientists, this year’s workshop primarily gave PhD students and young researchers the opportunity to present their work. In addition, a small number of invited guests from the United Kingdom, Spain, Russia and Germany gave overviews of their research areas, while the group leaders made up a substantial part of the audience.

The workshop was opened by the session on *Enzyme Networks and Transport*. That enzymes and transport processes are fundamental to almost all cellular processes and interact in intricate ways was well illustrated by the presentations on cell volume regulation, response times in complex transitions, metabolic oscillations in yeast cultures, evolutionary optimization of metabolism, and lipid transport and fusion dynamics of biological membranes, involved in such diverse processes as bile formation in the liver and influenza infection.

As more quantitative information on gene expression is becoming available, the integration of genetic regulation and cell function is developing into a focus of intense research, as witnessed in the session on *Genes and Networks*. Contributions encompassed the structural basis of the genetic code, DNA sequence analysis, the prediction of protein structure and function from genome data, and the establishment of structural properties of metabolic systems in the course of evolution.

Yet another level of cellular activity is cell signalling, reflected in two sessions on *Enzyme Networks and Signalling*, and *Waves and Calcium Signalling*. Topics too numerous to list in detail ranged from the mathematical modelling of protein translocation to the organization of the visual system. A particular focus was calcium signalling with two experimental and four theoretical contributions. Interestingly, some of the calcium concentration patterns observed

in cells are quite reminiscent of chemical waves in inanimate nature that formed the topic of an overview talk.

The first part of the session on *Protein Structures and Patterns* was devoted to the determination of protein conformation and activity with a variety of theoretical and experimental methods. In the second part, a number of systems were introduced that require the elucidation of the interaction of many different protein molecules, such as adhesion and movement of fibroblasts and growth cone guidance in developing neurons.

Many lively discussions were generated by the overview presentations and in particular by the work of the PhD and diploma students. One point stressed by many participants to be quite unique to the workshop was the exposure of experimentalists and theoreticians to each others work at such an early stage. It sometimes proved to be rather demanding for both sides, and hopefully serves to stimulate new collaborations.

Thomas Höfer and Reinhart Heinrich, Humboldt University Berlin
<http://www.biologie.hu-berlin.de/GK>

Recent theses

Dynamics of Weed Populations: Spatial Pattern Formation and Implications for Control

Jacco Wallinga, Wageningen Agricultural University, December 1998

Why are annual weeds patchily distributed over arable fields, even if these fields provide a spatially homogeneous environment? In this PhD thesis an explanation is given, based on spatial models of plant population dynamics and percolation theory. According to this explanation, the spatial pattern of annual weeds is expected to be scale-invariant. The expected scale-invariance is indeed observed for a spatial pattern of the annual weed *Galium aparine* L. (cleavers) in a field of winter wheat.

An important aspect of population dynamics of weeds is that weeds are subject to population control by farmers in order to avoid excessive crop yield losses. The effect of weed control is that the density of weed plants is larger than zero (because it is impossible or too costly to eradicate weeds), but much lower than the equilibrium density without control (because at high densities the weeds would cause excessive crop yield losses).

If weed control is such that weed population density is held fixed at a very low level, there are no dynamics at a global level, but the spatial dynamics at a local level are quite interesting. In order to study these spatial dynamics at a local level, a model of weed population dynamics is used that is very similar to the basic contact process and to a model which is known to physicists as directed percolation in 2+1 dimensions. Space is conceived as a 2-dimensional lattice, and the state of each lattice node indicates whether a weed is present at that site or not. Time is discrete, with time steps corresponding to one growing season. Each time step weeds can be killed by weed control or they can propagate by sending seeds to adjacent nodes. The fraction of weeds that are killed is chosen at each time step such that the number of remaining plants is exactly constant, and this means that the fraction of weeds that are killed approaches a critical value (this is a so-called "self-organised" formulation of the standard directed percolation process). Monte Carlo simulations show that the relations between some

quantities of interest can be described by power laws, with exponents that do not depend on the exact model details (this is the so-called "universal behaviour" pertinent to the critical point). For instance, the number of weeds in a cluster varies with the radius of that cluster according to a power law. The exponent of that power law is a fractal dimension of the spatial weed pattern.

The reason for being interested in spatial dynamics of weed populations is that the growing public concern about use of chemical weed control in agriculture has provided an impetus to design alternative weed control strategies. It is nearly impossible to test these control strategies for their herbicide use in long-term field experiments. As an alternative, modelling studies are used to analyse spatio-temporal dynamics of annual weed populations and to identify the key factors that determine the long-term herbicide use of weed control programmes. In this thesis, three different weed control programmes were studied.

In the first weed control programme, herbicides are applied to the whole field only if the weed density exceeds a threshold value, otherwise there is no control at all. The dynamics of a weed population subjected to such a threshold control programme is characterised by aperiodic (quasi-periodic or chaotic) cycles, whereas the long-term herbicide use does not depend on the threshold value.

In the second weed control programme, the optimum herbicide dosage is determined and applied to the whole field. In this case the density of the weed population will approach a low equilibrium value. The herbicide use of such an "optimum dose control programme" is determined by the herbicide dose required to keep the weed population at a low density.

In the third weed control programme, the spatial scale of weed control decision making is reduced such that only weed patches are sprayed. The herbicide use of such a "patch control programme" is determined by the spatial pattern of weeds as well as the spatial resolution of the patch sprayer. The patch control programme is only of interest if weeds are heterogeneously distributed over space. If the spatial pattern of weeds is scale-invariant, the fractal (Hausdorff) dimension is helpful in relating the scale at which weeds are controlled (which indicates the spatial accuracy of weed control) to the area that is to be sprayed (which indicates the amount of herbicides that is required for control).

Thus the finding that weed patch formation may be regarded as a "self-organised critical phenomenon", can be applied to answer very practical questions about the herbicide use of patch control programmes.

Some parts of this PhD thesis have been published as:

Wallinga, J. 1995 The role of space in plant population dynamics: annual weeds as an example. *Oikos* 74, 377-383.

Wallinga, J. & Van Oijen, M. 1997 Level of threshold weed density does not affect the long-term frequency of weed control. *Crop Protection* 16, 273-278.

Wallinga, J. 1998. Analysis of the rational long-term herbicide use: evidence for herbicide efficacy and critical weed kill rate as key factors. *Agricultural Systems* 56, 323-340.

Wallinga, J., Groeneveld, R.M.W., & Lotz, L.A.P. 1998 Measures that describe weed spatial patterns at different levels of resolution, and their applications for patch spraying of weeds. *Weed Research* 38, 351-359.

Wallinga, J., Grasman, J., Groeneveld, R.M.W., Kropff, M.J., & Lotz, L.A.P. Submitted to *Journal of Applied Ecology*. Prediction of weed density: the increase of error with prediction interval, and the use of long-term predictions for weed management.

Copies of this thesis are available upon request.

Jacco Wallinga, Department of Infectious Diseases Epidemiology, National Institute of Public Health and the Environment (RIVM), P.O. Box 1, 3720 BA Bilthoven, The Netherlands, tel fax: +31-30-2744409 email: jacco.wallinga@rivm.nl

New Journals and books

Whenever the information on books in this section is taken from the book itself or from promotional material furnished by the publisher/author, the text will be in "quotation marks" (overtly commercial statements from the blurb have been removed). If the information is not in quotation marks, then it constitutes a review.

Mathematical Modeling in the Environment

Charles R. Hadlock, Bentley College

Cambridge University Press, 1999, 316 pp., ISBN: 0 883 85709 X, Price: £29.95 (paperback)

"This book has a dual objective: first to introduce the reader to some environmental issues of the day; and second to illustrate the role played by mathematical models in investigating these issues. The subjects covered are ground water contamination, air pollution, and hazardous materials emergencies. These issues are presented in their full real-world context and are used to develop classical mathematical themes. The emphasis throughout is on fundamental principles and concepts, not on achieving technical mastery of state-of-the-art models.

Chapter contents: 1. Introduction; 2. Ground water; 3. Surface water; 4. Air quality; 5. Emergency planning and response; 6. Risk analysis; 7. Public health; 8. Waste management; 9. Policy making and government decision making."

Spatial Pattern Analysis in Plant Ecology

Mark R. T. Dale, University of Alberta

Cambridge University Press, 1999, 326 pp., ISBN 0 521 45227 9, £45.00

"The predictability of the physical arrangement of plants, at whatever scale it is viewed, is referred to as their spatial pattern. Spatial pattern is a crucial aspect of vegetation which has important implications not only for the plants themselves, but also for other organisms which interact with plants, such as herbivores and pollinators, or those animals for which plants provide a habitat. This book describes and evaluates methods for detecting and quantifying a variety of characteristics of spatial pattern. As well as discussing the concepts on which these techniques are based, examples from real field studies and worked examples are included, which, together with numerous line figures, help guide the reader through the text.

Chapter contents: Preface; 1. Concepts of spatial pattern; 2. Sampling; 3. Basic methods for one dimension and one species; 4. Spatial pattern of two species; 5. Multispecies pattern; 6. Two-dimensional analysis of spatial pattern; 7. Point patterns; 8. Pattern on an environmental gradient; 9. Conclusions and future directions; References; Index."

Epidemic Modelling, An Introduction

Daryl J. Daley, Joe Gani, Australian National University

Cambridge University Press, 1999, 226 pp., ISBN 0 521 64079 2, £30.00

"This general introduction to the ideas and techniques required to understand the mathematical modelling of diseases begins with an historical outline of some disease statistics dating from Daniel Bernoulli's smallpox data of 1760. The authors then describe simple deterministic and stochastic models in continuous and discrete time for epidemics taking place in either homogeneous or stratified (non-homogeneous) populations. A range of techniques for constructing and analysing models is provided, mostly in the context of viral and bacterial diseases of human populations. These models are contrasted with models for rumours and vector-borne diseases like malaria. Questions of fitting data to models, and their use in understanding methods for controlling the spread of infection, are discussed. Exercises and complementary results at the end of each chapter extend the scope of the text. Intended for students taking courses in mathematical biology who have some basic knowledge of probability and statistics.

Chapter contents: Preface; 1. Some history; 2. Deterministic models; 3. Stochastic models in continuous time; 4. Stochastic models in discrete time; 5. Rumours: modelling spread and its cessation; 6. Fitting epidemic data; 7. The control of epidemics; References; Index."

Advanced Theoretical Ecology, Principles and Applications

J. McGlade (editor)

Blackwell Science Ltd, 1999, 368 pp., ISBN 0 865427348, £34.95

"*Advanced Ecological Theory* is intended for both postgraduate students and professional researchers in ecology. It provides an overview of current advances in the field as well as closely related areas in evolution, ecological economics and natural resources management, familiarising the reader with the mathematical, computational and statistical approaches used in these different areas.

Contents: Individual-based models in Ecology (McGlade); Stochastic effects in population models (Renshaw); Spatial models of interacting populations (Keeling); Correlation equations and pair approximations for spatial ecologies (Rand); Theoretical aspects of community assembly (Law); The dynamics of the flows of matter and energy (Pimm); Population and evolutionary dynamics of consumer-resource systems (Getz); Understanding the ecological and evolutionary reasons for life history variation: mammals as a case study (Harvey); Species diversity (Rosenweig); Ecological economics (Milner-Gulland); Ecosystem analysis and the governance of natural resources (McGlade)."

Community Ecology

P. Morin

Blackwell Science Ltd, 1999, 432 pp., ISBN 0 865423504, £25.00

"Community ecology – the study of the patterns and processes involving two or more species – has developed rapidly in the last two decades, driven on by new and more sophisticated research techniques, advances in mathematical theory and modeling, and the increasing pressure on the environment wrought by humans. Morin guides us through the main tenets and central concepts of community ecology - competition, predation, food webs, indirect effects, habitat selection, diversity, and succession. Morin includes examples drawn from both the aquatic and terrestrial realm and from both plant and animal species. Balancing theory with experimentation and drawing on new studies to complement the historical foundations of the discipline, he also stresses that both the empirical and theoretical approaches are necessary to drive ecology forward. The final chapter on applied community ecology demonstrates how

community ecological processes have a wide environmental relevance. Although in its infancy, the application of community ecology to emerging problems in human-dominated ecosystems could mitigate problems as diverse as management strategies for important diseases transmitted by animals and the restoration and reconstruction of viable communities.

Contents:

Part I: Communities: Basic Patterns and Elementary Processes; Communities; Competition: Mechanisms, Models and Niches; Competition: Experiments, Observations and Null Models; Predation and Communities. Empirical Patterns; Models of predation in simple communities; Food Webs; Mutualisms; Indirect Effects;

Part II: Factors Influencing Interactions Among Species; Temporal Patterns: Seasonal Dynamics, Priority Effects, and Assembly Rules; Habitat Selection; Spatial Dynamics, Recruitment-Limited Patterns, and Island Biogeography;

Part III: Large Scale, Integrative, Community Phenomena; Causes and Consequences of Diversity; Succession; Applied Community Ecology; Appendix; Bibliography; Index."

Ecological Dynamics

W. S. C. Gurney, University of Strathclyde, *R. M. Nisbet*, University of California, Santa Barbara

Oxford University Press, 1998, 350 pp., ISBN 0 19 510443 9, £29.95

"This textbook will introduce readers to the use of dynamic mathematical models in environmental problem solving and in the study of ecology. The focus of the book is modelling rather than specific models. Starting at an elementary mathematical level, concentrating on simulation as an experimental skill, the text then moves to a more formal treatment using more powerful and general methods of analysis, and then explores a number of current research topics to show applications of modelling to current ecological theory. There is extensive software, called SOLVER, to be made available in executable versions on Internet, to facilitate the laboratory component of this course.

Contents:

I. Methodologies and Techniques: 1. Ecological Modelling; 2. Dynamics; 3. A Dynamicist's Toolbox;

II. Individuals to Ecosystems: 4. Modelling Individuals; 5. Single species populations; 6. Interacting populations; 7. Ecosystems; 8. Physiologically Structured Populations; 9. Spatially Structured Populations. Bibliography, Index."

The Geometry of Ecological Interactions: Simplifying Spatial Complexity

U. Dieckmann, IIASA, *R. Law*, University of York, and *J.A.J. Metz*, University of Leiden (eds.)

Cambridge University Press, 1999, 450 pp., ISBN 0 521 64294 9 (hb), £50,00 (approx.)

"We give the table of contents of this book:

1. Introduction: Richard Law, Ulf Dieckmann, and Johan A.J. Metz

A. Empirical and Statistical Background.

2. A Neighborhood View of Interactions among Individual Plants: Peter Stoll and Jacob Weiner;

3. Spatial Interactions among Grassland Plant Populations: Jonathan Silvertown and J. Bastow Wilson;

4. Spatio-temporal Patterns in Grassland Communities: Tomáš Herben, Heinjo J. During, and Richard Law;
 5. Statistical Modeling and Analysis of Spatial Patterns: D.R. Cox, Valerie Isham, and Paul Northrop.
- B. When the Mean-Field Approximation Breaks Down.*
6. Grid-based Models as Tools for Ecological Research: Christian Wissel;
 7. Coexistence of Replicators in Prebiotic Evolution: Tamás Czárán and Eörs Szathmáry;
 8. Games on Grids: Martin A. Nowak and Karl Sigmund;
 9. The Interplay between Reaction and Diffusion: Mikael B. Cronhjort;
 10. Spirals and Spots: Novel Evolutionary Phenomena through Spatial Self-structuring: Maarten C. Boerlijst;
 11. The Role of Space in Reducing Predator–prey Cycles: Vincent A.A. Jansen and André M. de Roos.
- C. Simplifying Spatial Complexity: Examples.*
12. Spatial Scales and Low-dimensional Deterministic Dynamics: Howard B. Wilson and Matthew J. Keeling;
 13. Lattice Models and Pair Approximation in Ecology: Yoh Iwasa;
 14. Moment Approximations of Individual-based Models: Richard Law and Ulf Dieckmann;
 15. Evolutionary Dynamics in Spatial Host–parasite Systems: Matthew J. Keeling;
 16. Foci, Small and Large: A Specific Class of Biological Invasion: Jan-Carel Zadoks;
 17. Wave Patterns in Spatial Games and the Evolution of Cooperation: Regis Ferriere and Richard E. Michod.
- D. Simplifying Spatial Complexity: Techniques.*
18. Pair Approximations for Lattice-based Ecological Models: Kazunori Satō and Yoh Iwasa;
 19. Pair Approximations for Different Spatial Geometries: Minus van Baalen;
 20. Moment Methods for Ecological Processes in Continuous Space: Benjamin M. Bolker, Stephen W. Pacala, and Simon A. Levin;
 21. Relaxation Projections and the Method of Moments: Ulf Dieckmann and Richard Law;
 22. Methods for Reaction–diffusion Models: Vivian Hutson and Glenn T. Vickers;
 23. The Dynamics of Invasion Wave:s Johan A.J. Metz, Denis Mollison, and Frank van den Bosch;
 24. Epilogue: Richard Law, Ulf Dieckmann, and Johan A.J. Metz.”

Game Theory and Animal Behavior

Lee Alan Dugatkin, University of Louisville, *Hudson Kern Reeve*, Cornell University (eds.)
Oxford University Press, 1998, 334 pp., ISBN 0 19 509692 4, £55.00

”Contents: 1. P. Hammerstein: What is Evolutionary Game Theory?; 2. L.A. Giraldeau: Game Theory and Social Foraging; 3. L.A. Dugatkin: Game Theory and Cooperation; 4. S. Riechert: Game Theory and Animal Contests; 5. R. Johnston: Game Theory and Communication; 6. H. Kern Reeve: Game Theory, Reproductive Skew, and Nepotism; 7. D. Mock, et al: Game Theory, Sibling Rivalry, and Parent-Offspring Conflict; 8. M. Gross & J. Repka: Game Theory and Inheritance in the Conditional Strategy; 9. J. Brown: Game Theory and Habitat Selection; 10. A. Sih: Game Theory and Predator-Prey Response Rqces; 11. D. Stephens & K. Clements: Game Theory and Learning; 12. D.S. Wilson: Game Theory and Human Behavior; 13. R. Gomulkiewicz: Game Theory, Optimization, and Quantitative Ge-

netics; 14. H.K. Reeve and L.A. Dugatkin: Why We Need Evolutionary Game Theory.”

The Philosophy of Biology

David L. Hull, Northwestern University, Michael Ruse, University of Guelph (eds.)

Oxford University Press, 1998, 782 pp., ISBN 0 19 875213 X (hbk), £45.00, ISBN 0 19 875212 1 (pbk), £18.99

”The latest in the Oxford Readings in Philosophy series, *The Philosophy of Biology* brings together articles from the past decade, looking at such issues as the nature of evolutionary theory, the social implications of biology today (particularly the Human Genome Project), and the ongoing debate between biblical literalists and the defenders of biological science. The 36 articles in this collection are divided into 10 parts, each with an introduction by the editors. Throughout the volume an attempt is made to offer positions from different perspectives, so that the reader will be challenged as well as informed.

Contents:

David L. Hull and Michael Ruse: Introduction;

Part I: Adaptation: Introduction to Part I; 1. Mary Jane West-Eberhard: Adaptation: Current Usages; 2. Richard Dawkins: Universal Darwinism; 3. D. C. Dennett: The Leibnizian Paradigm; 4. Stephen Jay Gould and Elisabeth S. Vrba: Exaptation - A Missing Term in the Science of Form; 5. Elliott Sober: Six Sayings About Adaptationism;

Part II: Development: Introduction to Part II; 6. Ron Amundson: Two Concepts of Constraint: Adaptationism and the Challenge from Developmental Biology; 7. P. E. Griffiths and R. D. Gray: Developmental Systems and Evolutionary Explanation;

Part III: Units of Selection: 8. Kim Sterelny and Philip Kitcher: The Return of the Gene; 9. Robert N. Brandon: The Levels of Selection: A Hierarchy of Interactors; 10. Elliott Sober and David Sloan Wilson: A Critical Review of Philosophical Work on the Units of Selection Problem;

Part IV: Function: Introduction to Part IV; 11. Ron Amundson: Function Without Purpose: The Uses of Causal Role Function in Evolutionary Biology; 12. Philip Kitcher: Function and Design; 13. Peter Godfrey-Smith: Functions: Consensus Without Unity;

Part V: Species: Introduction to Part V; 14. Brent D. Mishler and Robert N. Brandon: Individuality, Pluralism, and the Phylogenetic Species Concept; 15. Kevin de Queiroz and Michael J. Donoghue: Phylogenetic Systematics and the Species Problem; 16. Marc Ereshefsky: Eliminative Pluralism;

Part VI: Human Nature: Introduction to Part VI; 17. John Maynard Smith: Science and Myth; 18. David L. Hull: On Human Nature; 19. Evelyn Fox Keller: Gender and Science: Origin, History, and Politics; 20. Susan Oyama: Essentialism, Women, and War: Protesting Too Much, Protesting Too Little; 21. Edward Stein: Essentialism and Constructionism about Sexual Orientation;

Part VII: Altruism: Introduction to Part VII; 22. Alexander Rosenberg: Altruism: Theoretical Contexts; 23. Elliott Sober: What Is Evolutionary Altruism?; 24. David Sloan Wilson: On the Relationship Between Evolutionary and Psychological Definitions of Altruism and Selfishness;

Part VIII: Human Genome Project: Introduction to Part VIII; 25. Marga Vicedo: The Human Genome Project: Towards an Analysis of the Empirical, Ethical, and Conceptual Issues Involved; 26. Philip Kitcher: Who’s Afraid of the Human Genome Project?; 27. Diane B. Paul: Is Human Genetics Disguised Eugenics?; 28. Elisabeth A. Lloyd: Normality and Variation: The Human Genome Project and the Ideal Human Type; 29. Alexander Rosenberg;

The Human Genome Project: Research Tactics and Economic Strategies;
Part IX: Progress: Introduction to Part IX; 30. Robert J. Richards: The Moral Foundations of the Idea of Evolutionary Progress: Darwin, Spencer, and the Neo-Darwinians; 31. Michael Ruse: Evolution and Progress; 32. Daniel W. McShea: Complexity and Evolution: What Everybody Knows; 33. Stephen Jay Gould: On Replacing the Idea of Progress with an Operational Notion of Directionality;
Part X: Creationism: Introduction to Part X; 34. Alvin Plantinga: When Faith and Reason Clash: Evolution and the Bible; 35. Ernan McMullin: Evolution and Special Creation; 36. Alvin Plantinga: Reply to McMullin.
Notes on the Contributors, Further Reading, Index.”

Metapopulation Ecology

Ilkka Hanski, University of Helsinki

Oxford University Press, 1999, 324 pp., ISBN 0 19 854066 3 (hbk), £45.00, ISBN 0 19 854065 5 (pbk), £22.50

”*Metapopulation Ecology* aims to present a synthesis of current research in this rapidly expanding area of population biology. It encompasses both the essential theory of metapopulations and a wide range of empirical studies - including the author’s own research on the metapopulation biology of the Glanville fritillary butterfly - and includes discussion of practical applications to conservation biology.”

Asymptotic Methods for the Fokker-Planck Equation and the Exit Problem in Applications

J. Grasman, O.A. van Herwaarden, University of Wageningen

Springer-Verlag, 1999, 219 pp., ISBN 3 540 64435 0, DM 79 (hbk)

”This book deals with the diffusion approximation of stochastic processes. For the probability density of the state variables of a stochastically perturbed dynamical system one derives a linear diffusion equation: the so-called Fokker-Planck equation. In particular the problem of exit from a domain of the state space is studied. Using singular perturbation techniques one obtains an estimate for the probability that exit takes place through a part of the boundary and for the corresponding expected exit time. The problem is singular because of the fact that an asymptotic solution is made with respect to a small parameter indicating the order of magnitude of the diffusion compared to the deterministic change. There are classes of problems that require a special treatment, such as the problem of escape from a neighborhood of a stable equilibrium and the problem of exit through a boundary where deterministic drift and diffusion vanish. Various examples of application of the method to problems in the natural sciences are given. In much detail dispersive groundwater flow and the pollution of pumping wells is analysed. Other topics are stochastic oscillation and preferent weather regimes in the atmospheric circulation.

The application of the method to problems in stochastic population biology plays a prominent role in the book. First the stochastic logistic system is analysed and an approximation for the expected extinction time of a population is derived from it. Next systems of two interacting populations are analysed and the expected extinction time of one of them is computed with mixed analytical-numerical techniques for a prey-predator system and for a SIR-model of an infectious disease.

As a result of the approach that is taken to analyse the Fokker-Planck equation, concepts as resilience and persistence of biological populations are considered from a different point of

view and are quantified accordingly. Moreover, it is shown that if one wishes to study the risk extinction of one population being part of a system of interacting populations, one may as well consider that single population modelled as a stochastic logistic system. This result holds for a large class of problems; it is applied a.o. to metapopulations.”

DNA Computing: new computing paradigms

G. Paun, Romanian Academy, *G. Rozenberg*, University of Leiden, *A. Salomaa*, University of Turku

Springer-Verlag, 1999, 402 pp., ISBN 3 540 64196 3, DM 89.00

”This is the first text and monograph about DNA computing, a molecular approach that might revolutionize our thinking and ideas about computing. Although it is too soon to predict whether computer hardware can change from silicon to carbon and from microchips to DNA molecules, the theoretical premises have already been studied extensively. The book starts with an introduction to DNA-related matters, the basics of biochemistry and language and computation theory, and progresses to the most advanced mathematical theory developed so far in the area.

Contents: *Part I. Background and Motivation*: DNA: The power of complementarity; Beginnings of molecular computing; *Part II. Mathematical Theory*: Introduction to language theory; Sticker systems; Watson-Crick automata; Insertion-deletion systems; Universality by finite H systems; Splicing circular strings; Distributed H systems; Splicing revisited.”

An Introduction to Structured Population Dynamics

J. M. Cushing

SIAM, 1998, 193 pp., ISBN 0 89871 417 6, \$ 36.00

”Interest in the temporal fluctuations of biological populations can be traced to the dawn of civilization. How can mathematics be used to gain an understanding of population dynamics? This monograph introduces the theory of structured population dynamics and its applications, focusing on the asymptotic dynamics of deterministic models. This theory bridges the gap between the characteristics of individual organisms in a population and the dynamics of the total population as a whole.

In this monograph, many applications that illustrate both the theory and a wide variety of biological issues are given, along with an interdisciplinary case study that illustrates the connection of models with the data and the experimental documentation of model predictions. The author also discusses the use of discrete and continuous models and presents a general modeling theory for structured population dynamics.

Cushing begins with an obvious point: individuals in biological populations differ with regard to their physical and behavioral characteristics and therefore in the way they interact with their environment. Studying this point effectively requires the use of structured models. Specific examples cited throughout support the valuable use of structured models. Included among these are applications chosen to illustrate both the mathematical theories and biological problems that have received attention in recent literature.

Contents: Preface. Chapter 1: Discrete Models. Matrix Models; Autonomous Single Species Models; Some Applications; A Case Study; Multispecies Interactions; Chapter 2: Continuous Models. Age-Structured Models; Autonomous Age-Structured Models; Some Applications; Multispecies Interactions; Other Structured Models; Chapter 3: Population Level Dynamics.

Ergodicity and Nonlinear Models; The Linear Chain Trick; Hierarchical Models; Total Population Size in Age-Structured Models; Appendix A: Stability Theory for Maps. Linear Maps; Linearization of Maps; Appendix B: Bifurcation Theorems. A Global Bifurcation Theorem; Local Parameterization; Appendix C: Miscellaneous Proofs. Bibliography. Index.”

Models of Adaptive Behaviour: An Approach Based on State

Alasdair I. Houston, John M. McNamara, University of Bristol

Cambridge University Press, 400 pp., ISBN 0 521 65539 0, £20.95

”*Models of Adaptive Behaviour* sets out a framework for adaptive explanations of behaviour, and applies this to give analyses of a range of biological issues such as energetic gain, energy-predation trade-offs, dynamic games, state-dependent life histories, annual routines and fluctuating environments. It gives an account of this new field, summarizing previous research, presenting new material and suggesting directions for future research. Organisms differ in terms of their state - for example in their size, energy relations or temperature - which often affects their behaviour. The framework adopted in this book takes this into account, and provides a common current for comparing diverse actions. Ultimately this could lead to the development of state-dependent dynamic models.

Contents: Acknowledgements; 1. Introduction; 2. States, actions and tradeoffs; 3. Dynamic optimization, 4. Maximizing the energy gained from foraging; 5. Risk-sensitive foraging; 6. The energy-predation trade-off; 7. Dynamic games; 8. State-dependent life history theory; 9. Routines; 10. Life histories in fluctuating environments; References; Index.”

Theoretical Morphology: The Concept and Its Applications

George R. McGhee, Jr., Rutgers University

Columbia University Press, 1998, 378 pp., ISBN 0 23110617 3, \$ 26.50 (pbk)

”Theoretical morphology—which seeks to sketch the range of forms that biological entities could take, with the ultimate goal of discovering why certain forms exist but others do not—is among paleontology’s most significant contributions to the understanding of evolution. Today, with the aid of computers in developing conceivable morphologies, the discipline has been able to advance into a remarkable tool for the study of evolution. Yet despite these advances, the field remains largely untapped and ripe with research potential. In this volume, paleontologist George McGhee presents the first overview of the field, its advancements in recent years, and the challenges ahead.

McGhee describes the steps involved in defining the geometric parameters (theoretical morphospaces) for an organic form in order to generate a spectrum of other possible forms that have never actually appeared. He also addresses the simulation of actual processes of morphogenesis, with the goal of attaining a more nuanced comprehension of how evolutionary processes work. *Theoretical Morphology* takes readers through a variety of theoretical morphospaces including those for univalved, bivalved, discrete, and branching growth systems.

Contents: Preface; What is Theoretical Morphology?; The Concept of the Theoretical Morphospace; Twists and Twigs: Theoretical Morphospaces of Branching Growth Systems; Spiral and Shells I: Theoretical Morphospaces of Univalved Accretionary Growth Systems; Spirals and Shells II: Theoretical Morphospaces of Bivalved Accretionary Growth Systems; Step by Step: Theoretical Morphospaces of Discrete Growth Systems; The Time Dimension: Evolution and Theoretical Morphospaces; Theoretical Models of Morphogenesis: An Example;

Theoretical Models of Accretionary Growth Systems; Theoretical Models of Other Aspects of Morphogenesis in Nature; The Future of Theoretical Morphology; Glossary.”

Nonlinear Dynamics of Interacting Populations

Alexander D Bazykin, Russian Academy of Sciences

World Scientific, 1998, 216 pp., ISBN 981 02 1685 8, £52.00

”This book contains a systematic study of ecological communities of two or three interacting populations. Starting from the Lotka-Volterra system, various regulating factors are considered, such as rates of birth and death, predation and competition. The different factors can have a stabilizing or a destabilizing effect on the community, and their interplay leads to increasingly complicated behavior. Studying and understanding this path to greater dynamical complexity of ecological systems constitutes the backbone of this book. On the mathematical side, the tool of choice is the qualitative theory of dynamical systems - most importantly bifurcation theory, which describes the dependence of a system on the parameters. This approach allows one to find general patterns of behavior that are expected to be observed in ecological models. Of special interest is the reaction of a given model to disturbances of its present state, as well as to changes in the external conditions. This leads to the general idea of ”dangerous boundaries” in the state and parameter space of an ecological system. The study of these boundaries allows one to analyze and predict qualitative and often sudden changes of the dynamics - a much-needed tool, given the increasing antropogenic load on the biosphere. As a spin-off from this approach, the book can be used as a guided tour of bifurcation theory from the viewpoint of application. The interested reader will find examples of how known bifurcations occur in applications.

Contents: Ideas and Methods of Modeling Populations; Dynamics of Isolated Populations; Predator-Prey Interactions; Competition and Symbiosis; Local Systems of Three Populations; Dissipative Structures in Predator-Prey Systems.”

Quantitative Analysis of Movement

Peter Turchin, University of Connecticut

Sinauer, 1998, 406 pp., ISBN 0 87893 847 8, \$ 38.95

”In the last two decades it has become increasingly clear that the spatial dimension is a critically important aspect of ecological dynamics. Ecologists are currently investing an enormous amount of effort in quantifying movement patterns of organisms. Connecting these data to general issues in metapopulation biology and landscape ecology, as well as to applied questions in conservation and natural resource management, however, has proved to be a non-trivial task. This book presents a systematic exposition of quantitative methods for analyzing and modeling movements of organisms in the field.

Quantitative Analysis of Movement is intended for graduate students and researchers interested in spatial ecology, including applications to conservation, pest control, and fisheries. Models are a key ingredient in the analytical approaches developed in the book; however, the primary focus is not on mathematical methods, but on connections between models and data. Case studies have been selected from a wide variety of organisms, including plants (seed dispersal, spatial spread of clonal plants), insects, and vertebrates (primarily, fish, birds, and mammals).

Contents:

Preface;

1. Why Study Movement? Population Dynamics in Space and Time. Movement and Spatial Dynamics. Models, Data, Theory. Empirically Based Models.
2. Data for Measuring Movement Introduction. Methods for Recording Paths. Mark-Recapture Methods.
3. Modeling Movement Introduction. Linear Dispersal. Empirical Models. Diffusion. Individual-Based Movement Models. Passive Dispersal. Models of Spatial Population Dynamics.
4. Building Behaviorally Based Models The Problem. Movement without Directional Persistence. Movement with Persistence: 1D Space. Persistence and Directional Bias: 2D Space. Congregation.
5. Analysis of Movement Paths Introduction. Discrete Representation of Paths. Inferring the Rate of Population Spread. Effects of Spatial Heterogeneity. An Alternative Approach: Fractal Analysis. Measuring Attraction: Random Walk Approach. Measuring Attraction: Kinematic Analysis.
6. Mass Mark-Recapture Introduction. Estimating the Rate of Dispersal. Population Spread and Dispersal "Tails". Quantifying Effects of Spatial Heterogeneity. Seed and Pollen Dispersal in Plants. Measuring Attraction. A Worked Example: Population Redistribution in a Bark Beetle.
7. Individual Mark-Recapture Introduction. Rate of Dispersal. An Alternative Approach for Vertebrate Dispersal. A Worked Example: Dispersal of Juvenile Spotted Owls. Effects of Spatial Heterogeneity. Applications: Movement Corridors for Conservation. Attraction to Conspecifics. Maximum Likelihood Estimation.
Appendix: Diffusion for Ecologists Derivation of the Diffusion Equation. Time-Dependent Solutions. Time-Independent Solutions. Population Spread.
Bibliography; Glossary; Common Symbols; Index."

Call for papers: ACTA BIOTHEORETICA: a journal for understanding theories in biology and medicine

Acta biotheoretica was founded in the early fifties by the Prof. Jan van der Hoeven Foundation for Theoretical Biology, which is attached to the Leiden University. It is the journal of the Dutch Society for Theoretical Biology and of the French Society for Theoretical Biology. This year the editorial board has been renewed in order to reflect new developments in theoretical biology. At the conference 'Theory and Mathematics in Biology and Medicine' to be held in Amsterdam from June 29th, until July 3rd 1999 it will be decided whether Acta Biotheoretica can also serve as the journal of the European Society for Mathematical and Theoretical Biology.

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- French Society for Theoretical Biology: Publication of the Annual Proceedings.
- Special Features: - ideas section, - news, views and announcements.

Electronic Publication:

- Acta Biotheoretica will soon be available via the Internet. For more information please visit our web site: <http://www.wkap.nl/kaphtml.htm/JRNLHOME>
- An Internet subscription means that you can receive the Journal up to 4 weeks in advance of the printed version. Talk to your library about Internet subscriptions and have Acta Biotheoretica licensed for use within your institute.

Aims and Scope:

Acta Biotheoretica is a journal devoted to the promotion of theoretical biology, paying special attention to the methodology of formation of biological theory. Papers on all kind of biological theories are welcome. Interesting subjects include philosophy of biology, biomathematics, computational biology, genetics, ecology and morphology. The process of theory formation can be presented in verbal or mathematical form. Moreover, purely methodological papers can be devoted to the historical origin of the philosophy underlying biological theories and concepts. Papers should contain clear statements of biological assumptions, and where applicable, a justification of their translation into mathematical form and a detailed discussion of the mathematical treatment. The connection to empirical data should be clarified. The journal also welcomes critical book reviews and short notes directing attention to interesting new theoretical ideas. Finally, we would like to encourage you to submit manuscripts or ideas for special issues.

Editorial Board:

W.J. Bock, New York, NY, U.S.A.; J. Demongeot, Grenoble, France; D. von Engelhardt, Lübeck, Germany; A.C. Gittenberger-de Groot, Leiden, The Netherlands; U. an der Heiden, Witten-Annen, Germany; A.I. Houston, Bristol, England, U.K.; D.L. Hull, Evanston, IL, U.S.A.; E. Kisdi, Turku, Finland; H.B. Lück, Marseille, France; M.C. Mackey, Montreal, Canada; J.P. Mazat, Bordeaux, France; J.A.J. Metz, Leiden, The Netherlands; R.M. Nisbet, Santa Barbara, CA, U.S.A.; I. Olivieri, Montpellier, France; A.G. Petrovic, Strasbourg, France; P. Schuster, Wien, Austria; R. Thom, Paris, France; W.J. van der Steen, Amsterdam, The Netherlands.

Managing Editor: Dr. Lia Hemerik, Mathematics Department, Wageningen Agricultural University, The Netherlands

Editorial Office: Acta Biotheoretica, P.O. Box 9516, 2300 RA Leiden, The Netherlands, email: sbqhar@rulsfb.leidenuniv.nl

Call for Papers: **BIostatistics**

Oxford University Press

"Among the important scientific developments of the 20th century is the explosive growth in statistical reasoning and methods for application to studies of human health. Examples include developments in likelihood methods for inference, epidemiologic statistics, clinical trials, survival analysis, and statistical genetics. Substantive problems in public health and

biomedical research have fueled the development of statistical methods, which in turn have improved our ability to draw valid inferences from data.

The objective in creating 'Biostatistics' will be to advance statistical science and its application to problems of human health and disease with the ultimate goal for advancing the public's health. 'Biostatistics' is being developed as a companion journal to *Biometrika*, but will focus on methods and applications.

Co-Editors:

Scott Zeger (Johns Hopkins University, USA) and Peter Diggle (Lancaster University, UK)

Advisory Board:

D. Cox (chair), S. Zeger, P. Diggle, P. Armitage, M. Gail, N. Keiding."

Information: <http://www.biostatistics.oupjournals.org/instauth>

Communications and requests

Job Offer: Postdoctoral Research Position

Theoretical Biology and Biophysics Group at Los Alamos National Laboratory

A regular postdoctoral research position in *HIV Modeling* is available in the Theoretical Biology and Biophysics Group at Los Alamos National Laboratory. Work will involve working with Alan Perelson and collaborating with experimentalists in the development of models relevant to cutting edge HIV research. Familiarity with differential equations, computer simulations, and statistics is desirable. Knowledge of immunology and virology would also be helpful. Position is for two years (assuming satisfactory performance during the first year), but an extension to a third year is possible. The salary depends on years of experience since Ph.D. and typically will range between \$48k and \$53k. To qualify as a postdoc a Ph.D. must be obtained before the start of the position, and only candidates within three years of completion of their Ph.D. are eligible. Further details about the Los Alamos postdoc program can be found at <http://www.hr.lanl.gov/Postdoc/>.

Please send current cv and 3 letters of reference to Alan S. Perelson, Theoretical Biology and Biophysics Group, MS-K710, T-10, Los Alamos National Laboratory, Los Alamos, NM 87545. email: asp@receptor.lanl.gov, FAX: 505-665-3493, Telephone: 505-667-6829.

Postitions available

Max-Planck-Institute for Mathematics in the Sciences (MIS) in Leipzig

Project: Mathematical Biology

- one Postdoc position (3 years)
- one PhD-position (2 years)

Extension of both contracts is possible.

Candidates are expected to have good knowledge in Analysis and/or Stochastics and should be interested in Mathematical Modeling in Biology.

The Max-Planck-Society is an Equal Opportunity Employer and encourages applications of minorities and disabled.

Applications should be sent until June 25, 1999 to
Max-Planck-Institute for Mathematics in the Sciences (MIS), Personalabteilung
Inselstr. 22-26, D-04103 Leipzig, Germany.
phone: (+) 49-341-9959 718, fax: (+) 49-341-9959 658

Applications after that date are also welcome.

Information: Angela Stevens, email: stevens@mis.mpg.de

ECAL'99: Artificial Life Creator Contest ONLINE

Due to a strong demand, we decided to organize an online version of the Artificial Life Creators Contest associated to ECAL99 (European Conference on Artificial Life), see

<http://www.epfl.ch/ecal99>.

This online contest will be only simulation-based. Competitors can engage the competition by sending their name, affiliation and source code program to the organizers (only one program per competitor!). These source codes will not be disclosed to any third party. The organizers will run one-to-one matches between competitors and display the results on the Web (including top 10, scores, and some records of the matches that you can play back with Webots-ECAL).

This online contest will be held from

April 15th, 1999 to June 30th, 1999.

The winner will get a free entrance to the European Conference on Artificial Life as well as a airline ticket (up to a maximum of US\$1000) to come to Lausanne next September to enter the ECAL Artificial Life Creator Contest on both simulator and real robot. Other participants may profit from lessons learned during the online contest to modify their Alife creatures and participate to the contest in Lausanne where prizes in Alife software and hardware will be available.

More info is available on

<http://www.cyberbotics.com/indexContest.html>

Forthcoming events

International Uexküll Symposium

June 7-9, 1999, Tartu, Estonia

Jakob von Uexküll (1864-1944) was an important figure among the founders of theoretical biology in the beginning of the century. Rediscovery of Uexküll's works by semioticians since 1970s has played an important role in the paradigm change which has turned semiotics from a general theory of human language into an approach applicable to all living systems. In a similar way, the new interest in Uexküll's works in biology is a part of a current post-Darwinian paradigm shift in theoretical biology.

The symposium titled as "Uexküll and the living environment" will be held in Tartu, Estonia, June 7-9, 1999. The workshop will be organised by Jakob von Uexküll Centre

<http://www.zbi.ee/~uexkull>

together with the Department of Semiotics of the University of Tartu.

Tentative list of lectures at the Uexküll-symposium:

Thomas A. Sebeok (Bloomington, IN, USA) - Normal semiotics and Uexküll's paradigm shift.

Solomon Marcus (Bucuresti, Romania) - The logical and semiotic status of Umwelt.

Tuomo Jämsä (Savonlinna, Finland) - Jakob v. Uexküll's Bedeutungslehre from a perspective of linguistic semantics.

Bernard C. Patten (Georgia, USA) - Environ analysis: a mathematical system theory of environment descended from J. von Uexküll.

Alexei Sharov (Blacksburgh, VA, USA) - Umwelt and reality (about the relationship between Uexküll's views and pragmatism).

Kalevi Kull, Michail Lotman (Tartu, Estonia) - J.v.Uexküll and Juri Lotman.

Aleksei Turovski (Tallinn, Estonia) - On the biosemiotics of the well-parasitised hydrobiosis.

Sergei Chebanov (St. Petersburg, Russia) - Umwelt as living world: a biological analogue of wave-particle complementarity.

Sören Brier (Aalborg, Denmark) - Umwelten and anticipation in cognition: Umwelten / signification spheres, cognitive domains, idealized cognitive models, and language games as theories to understand the construction of interpretants in anticipatory bio-semiotic systems.

Urmias Sutrop (Konstanz, Germany) - On the term *Umwelt*.

The workshop in Tartu will be followed by a session "Uexküll and biosemiotics" at the International Summer Institute of Semiotics, in Imatra, Finland, June 11-13, 1999.

The selected contributions will be published in the special issue of the international journal *Semiotica* (guest editor of the issue - Kalevi Kull).

Further information about the symposium is available at

<http://www.zbi.ee/~uexkull/confanno.htm>

Kalevi Kull, email: kalevi@zbi.ee

Theory and Mathematics in Biology and Medicine

June 29 - July 3, 1999, Amsterdam, The Netherlands

This is an update on previous announcements (see e.g. BMN 18, p. 40/41). For the meeting 420 abstracts were submitted that have been carefully considered for either an oral contribution or a poster. Some of the sessions were heavily oversubscribed and choices had to be made. In total there will be 18 plenary lectures, 180 oral contributions and more than 200 poster contributions.

There are 6 day sessions and 12 afternoon sessions. The day sessions are:

1. Non-Linear Population Dynamics;
2. Epidemiology of Infectious Diseases;
3. Sequencing, Folding and Molecular Structure;
4. Evolution, Game Theory and Adaptive Dynamics;
5. Computational Neuroscience;
6. Immunology and Within-Host Dynamics of Pathogens;

Of the day sessions we list the the plenary speakers:

1. Non-Linear Population Dynamics. Invited speakers: D. Rand (University of Warwick, United Kingdom); H.L. Smith (Arizona State University, USA).
2. Epidemiology of Infectious Diseases Invited speakers: K Dietz (Tübingen University, Germany); V. Andreasen (Roskilde University, Danmark).
3. Sequencing, Folding and Molecular Structure Invited speakers: M.S. Waterman (University of Southern California, USA); P.G. Higgs (University of Manchester, United Kingdom).
4. Evolution, Game Theory and Adaptive Dynamics Invited speakers: J.A.J. Metz (Leiden University, the Netherlands); P. Hammerstein (ITB, Humboldt University, Berlin, Germany).
5. Computational Neuroscience Invited speakers: D. Willshaw (University of Edinburgh, United Kingdom); I. Segev (Hebrew University, Jerusalem, Israel).
6. Immunology and Within-Host Dynamics of Pathogens Invited speakers: L.A. Segel (The Weizmann Institute of Science, Israel); T.B. Kepler (North Carolina State University, USA)

Besides the invited speakers within these sessions the organising committee has invited six additional, plenary speakers:

1. Karl P. Hadeler (Tübingen University, Germany): Competition, Variability, and Exclusion: Elimination of some and survival for many;
2. Bruce R. Levin (Emory University, USA): Mathematical models of the within and between host population biology of antibiotic treatment and resistance;
3. Lila Kari (The University of Western Ontario, Canada): DNA computing in vitro and in vivo;
4. Karl Sigmund (University of Vienna, Austria): Reciprocal altruism, direct and indirect;
5. Bela Novak (Technical University Budapest, Hungary): Modelling the cell division cycle;
6. Eshel Ben-Jacob (Tel-Aviv University, Israel): Bacterial wisdom and the challenge of antibiotic resistance.

A final plenary lecture will be a distinguished lecture by the first Okubo Prize laureate. This prize is an initiative of the Society of Mathematical Biology, together with colleagues in Japan to honour the memory of Professor Okubo. The first Okubo prize laureate is Martin Nowak of Princeton University.

The subjects of the afternoon sessions are: Individual-Based Population Dynamics; Gene Networks; Pattern Formation and Morphogenesis; Education in Mathematical Biology; Parasites and Diseases in Wildlife; Metabolic Control Networks; Whole Heart Modelling; Metapopulation Dynamics; Particle Based Modelling; Networks, Cellular Signalling and Biological Rhythms; Classification Methodology; Miscellaneous.

Information: For registration and more details please visit the following web-site

<http://www.bio.vu.nl/tmbm99>

or contact the Conference Service of the Vrije Universiteit Amsterdam: VU Conference Service, De Boelelaan 1105, Amsterdam, The Netherlands, phone: +31 - 20 - 4445790, fax: +31 - 20 - 4445825, email: vu_conference@dienst.vu.nl.

PIms Thematic Programme on Mathematical Biology

June, July, August 1999, University of British Columbia, Vancouver, Canada

The Pacific Institute for the Mathematical Sciences (PIms) announces a Thematic Programme on Mathematical Biology to be held at the University of British Columbia, Vancouver, B.C., Canada during June, July, and August 1999. The purpose of this Thematic Summer is to bring together researchers at various levels of expertise in an environment where focussed talks will be given in several different areas of mathematical biology.

There are five workshops in this Thematic Programme on the topics of genomics, physiology, epidemiology, ecology, and cell biology. The organizers, invited speakers, and dates of each workshop are:

- Genomics (Michael Waterman, University of Southern California, and David Sankoff, Universite de Montreal) - May 31-June 11, 1999.
- Physiology (Robert M. Miura and Yue-Xian Li, University of British Columbia, and Gerda de Vries, University of Alberta) - June 14- 25, 1999.
- Epidemiology (Pauline van den Driessche, University of Victoria, and Fred Brauer, University of Wisconsin and University of British Columbia) - July 19-30, 1999.
- Ecology (Marc Mangel, University of California, Santa Cruz) - August 2-13, 1999.
- Cell Biology (Leah Keshet, University of British Columbia) - August 16-27, 1999.

Each two-week workshop will include tutorial and research talks. Formal talks by invited speakers will be interspersed with informal seminars, and there will be ample time for detailed discussions among the participants.

More details on the workshops, updates on the invited speakers, and registration and housing information can be found on the PIms website at

<http://pims.math.ca/sections/activities/bio.html>

There are no registration fees. Participants are encouraged to stay for the entire three months of the Thematic Programme.

Applications and further inquiries should be sent to:

The Director, Pacific Institute for the Mathematical Sciences, Attention: Thematic Programme on Mathematical Biology, University of British Columbia, Vancouver, B.C. Canada V6T 1Z2,

email: pims@pims.math.ca, Phone: 604-822-3922, Fax: 604-822-0883.

Stochastic Dynamics and Pattern Formation in Biological Systems

July 7-10, 1999, Korea University, Seoul, Korea

In recent years, a significant and exciting progress has been achieved toward the physical understanding of various biological phenomena. Two different approaches are emphasized: stochastic dynamics approach and nonlinear dynamics approach for the nonequilibrium nature of biological systems. This workshop would bring a group of experts in different disciplines (physics, biology, and physiology) to exchange the latest ideas regarding these newly emerging biological physics paradigms.

Subjects: Stochastic dynamics, nonequilibrium pattern formation, spatio-temporal chaos, synchronization, neural dynamics, protein and membrane dynamics, molecular motors

List of invited speakers:

D. Astumian (U. of Chicago), A. Baumgärtner (Jülich), E. Bodenschatz (Cornell U.), R. Goldstein (U. of Arizona at Tucson), R. Kapral (U. of Toronto), A. Kawana (NTT), A. Longtin (U. of Ottawa), A. Pikovsky (U. of Potsdam), J. Pine (Caltech), W. Sung (POSTECH), H. Swinney (U. of Texas at Austin), D. Thirumalai (U. of Maryland), E. Vicsek (Eötvös U.).

Advisory Committee:

K.-C. Lee (chair, Seoul Natl. U.), H. Swinney (co-chair, U. of Texas), B. L. Hao (Academia Sinica), A. Libchaber (Rockefeller U.), Y. Kuramoto (Kyoto U.), C.-I. Um (Korea U.).

Information: Consult the internet page at <http://turing.korea.ac.kr/workshop/> or Prof. Kyoung Jin Lee, Dept. of Physics, Korea University, Sungbuk-Gu, Anam-Dong 5-1, Seoul, Korea. Tel: (82-2) 3290-3104, Fax (82-2) 3290-3534, email: kyoung@nld.korea.ac.kr or Prof. W. Sung, Dept. of Physics, POSTECH, Pohang, Tel: (82-562) 279-2061, Fax: (82-562) 279-3099 email: sung@galaxy.postech.ac.kr

Design Principles for the Immune System and Other Distributed Autonomous Systems

July, 11-16, 1999, Santa Fe Institute

Rationale:

Distributed autonomous systems are collections of interacting entities (agents) that function without a "leader." Three biological examples of such systems – respectively molecular, cellular and community-wide – are metabolism, the immune system, and insect colonies. Other examples are found in robotics and artificial intelligence. In our view, at the operational level distributed autonomous systems are best regarded not as striving toward an overall goal (as is postulated in many approaches to complex systems) but rather as responding "appropriately" to continual overlapping challenges. The systems operate amidst a milieu that their actions alter. Agent activities are modified by numerous feedbacks that come from sensing both the milieu and messages from other agents.

Nature of the Workshop:

The central purpose of this workshop is to air and to discuss suggestions for principles that guide the effective operation of distributed autonomous systems, with a strong but not exclusive emphasis on the immune system. Because of its importance, its complexity, and the depth to which it is understood, the immune system is an ideal focus for this meeting. Thus about two-thirds of the conference will be devoted to immunological questions. Topics that are illuminated by a study of the immune system, or illuminate such a study, will be interspersed with immune topics. The former topics include task allocation in social insects, optimizing metabolism, using immune principles to improve computer security, and agent-based architecture in high level artificial intelligence.

The workshop will be organized in "Gordon Conference style". In general, the workshop will take place in the mornings and evenings, with afternoons free for participants to interact amidst the outstanding natural and cultural attractions of the Santa Fe area.

To provide essential background for those unfamiliar with immunology, a three hour pre-session is planned for Sunday during which basic immunological terminology and concepts will be presented. There will be a parallel "tutorial" for biologists in relevant mathematical concepts.

It is planned to incorporate material from the meeting in a book series by the Santa Fe Institute published by the Oxford University Press.

Organizers:

Irun Cohen, Immunology, Weizmann Institute

Stephanie Forrest, Computer Science, University of New Mexico

Alan Perelson, Theoretical Biology/ Biophysics, Los Alamos National Laboratory

Lee Segel, Applied Mathematics and Computer Science, Weizmann Institute

Alan Sher, Laboratory of Parasitic Diseases, National Institutes of Health

Approximately twenty junior participants (PhD students, postdocs) will be selected to attend, based on competitive applications. Travel support and living expenses will be provided, assuming success in grant applications. (Unfortunately application deadline was May 1, 1999 (ed.).)

Information: Questions can be addressed to email: cg@santafe.edu.

Updated information will appear at the SFI website <http://www.santafe.edu>.

The URL is <http://www.santafe.edu/sfi/research/workshops.html>.

International Conference on Biomathematics - Bioinformatics and Applications of Functional Differential Difference Equations

July 14 - 19, 1999, Akdeniz University, Antalya, Turkey

The conference on the Theory of Difference and Differential Equations with Applications to Biology and Medicine aims to stimulate collaboration between mathematicians and bioscientists and to act as a forum for the exchange of recent research results and new perspectives in those fields. In addition, the conference is devoted to a rapidly growing, interdisciplinary domain of science where experimental biology and medicine, biochemistry, functional differential and difference equations, stochastic functional differential equations and stochastic processing, functional analysis, evolution equations, operator theory, computational mathematics, and various fields of technology all come together.

Scientific program:

The scientific program will include one-hour plenary lectures, half-an-hour lectures and poster contributions. We also plan to publish the Conference Proceedings. The conference will cover the theory of difference and differential equations with applications to related disciplines within Biology and Medicine, including immunology, epidemiology, evolution, population dynamics and ecology, molecular biology, cell signaling, tumor growth and treatment, metabolic modeling, neuromodeling, computational biology, cardiovascular modeling, and biomechanics.

In addition, special sessions will be organized around focused topics that are particularly new or rapidly gaining importance. Participants are strongly encouraged to forward suggestions regarding the scientific program.

Honorary and advisory board:

R. Agarwal, N. Azbelev, D. Bainov, K. Cooke, A. Demirsoy, Yu. Domshlak, H. Freedman, I. Gyori, K.P. Hadeler, V. Kolmanovskii, V. Lakshmikantham, V. Maksimov, A. Myshkis, S. Saitoh.

Scientific committee:

Zvia Agur, Alfredo Bellen, Ovide Arino, Leonid Berezansky, Ludwik Byszewski, Valery Covachev, Jim Cushing, Odo Diekmann, Saber Elaydi, Efim Galperin, K.Gopalsamy, Gerry

Ladas, Marek Kimmel, Elena Litsyn, Michael C. Mackey, Rakhimberdiev Marat, Khashayar Pakdaman, Hanna Parnas, Andrejs Reinfelds, Hino Yoshiyuki, Glenn Webb

Organizing committee

Haydar Akca, Ovide Arino, Basem Attili, Ludwik Byszewski, Battal Ciplak, Kayahan Fiskin, Efim Galperin, Michael C. Mackey, Yaroslav Nartsissov Hanna Parnas, Ziad Taib

Organizers and Sessions:

- Zvia Agur : The role of discrete models and delay differential equations and in solving real life problems in cancer chemotherapy
- Elena Alekseeva : Nonlinear analysis of discrete interconnected systems and its applications to biology, medicine and economics.
- Ovide Arino, Moulay L. Hbid : State dependent delay equations arising from thresholds in population dynamics
- Leonid Berezansky, Elena Litsyn : Functional differential equations
- Olexander Boichuk : Normally resolvable boundary value problems and applications
- Ludwik Byszewski : Evolution equations, operator theory and functional analysis
- Odo Diekmann Physiologically structured populations
- Saber Elaydi, Gerry Ladas : Difference equations and applications
- Efim Galperin, D. Molodtsov and Q. Zheng : Set-theoretic methods in biomathematics
- K.Gopalsamy, Jim Cushing : Discrete and dynamical modeling
- Yoshiyuki Hino, Ryuichi Ishimura and Yutaka Kamimura : Abstract functional equations
- Michael C.Mackey, Glenn Webb : Modeling of cell replication and control
- Yaroslav Nartsissov: Mathematical modelling of metabolic processes in the living cell
- Hanna Parnas : Mathematical modeling of controlled drug release
- Angela Slavova, Valry Covachev: Neural networks-theory and applications
- Zia Taib : Probabilistic and statistical methods in biology and medicine

Further Information: H. Akca, email: akca@kfupm.edu.sa,

B. Ciplak, email: ciplak@pascal.sci.akdeniz.edu.tr,

K. Fiskin, email: fiskin@pascal.sci.akdeniz.edu.tr

Workshop on: Qualitative Behavior of Biological Systems

July 30 and 31, 1999, Max-Planck-Institute for Mathematics in the Sciences, Leipzig

With this workshop we would like to cover a broad spectrum of applications of mathematics in biology and encourage young people to join us and actively participate in the discussions following the talks. The workshop takes place just before the large EQUADIFF meeting in Berlin.

Organizers: Stefan Müller and Angela Stevens (MIS)

Invited Speakers: M. Bär (Dresden) P. Fife (Salt Lake City) K.P. Hadeler (Tübingen) P. Maini (Oxford) M. Mimura (Hiroshima) H. Othmer (Salt Lake City) J.J.L. Velazquez (Madrid)

Information: The organizers at email: stevens@mis.mpg.de or email: sm@mis.mpg.de or Ms. C. Grünewald (email: cgr@mis.mpg.de, secretary)

Address: Max-Planck-Institute for Mathematics in the Sciences (MIS), Inselstr. 22-26, D-04103 Leipzig, Germany, phone: +49-341-9959-50, fax: +49-341-9959-658.

The Seventh International Conference on Intelligent Systems for Molecular Biology (ISMB'99)

August 6 - August 10, 1999, Heidelberg, Germany

The ISMB conference provides a general forum for disseminating the latest developments in bioinformatics. ISMB was created in 1993 as what we believe was the first truly multidisciplinary conference series that brings together scientists from computer science, molecular biology, mathematics and statistics. Its scope includes the development and application of advanced computational methods for biological problems. Relevant computational techniques include, but are not limited to: machine learning, pattern recognition, knowledge representation, databases, combinatorics, stochastic modeling, string and graph algorithms, linguistic methods, robotics, constraint satisfaction, and parallel computation. Biological areas of interest include biomolecular structure, genomics, biomolecular sequence analysis, evolution and phylogenetics, biomolecular interactions, metabolic pathways, regulatory networks, developmental control, and molecular biology generally. Emphasis is placed on the validation of methods using real data sets, on practical applications in the biological sciences, and on development of novel computational techniques.

Organizing Committee:

Thomas Lengauer (Coordination), Reinhard Schneider, Peer Bork, Douglas Brutlag, Janice Glasgow, Hans Werner Mewes, Ralf Zimmer.

Please consult our website

<http://ismb99.gmd.de>

for

- the list of invited talks
- the list of accepted papers
- the tutorial program
- first information on the conference schedule and social events
- the registration form
- solar eclipse information

Early registration deadline is May 28, 1999.

Information: For further questions please contact email: ismb99@gmd.de

EU Advanced Course in Computational Neuroscience

August 23 - September 17, 1999, International Centre for Theoretical Physics, Trieste, Italy

Directors: Erik De Schutter (University of Antwerp, Belgium) Klaus Obermayer (Technical University Berlin, Germany) Idan Segev (Hebrew University, Jerusalem, Israel) Alessandro Treves (SISSA, Trieste, Italy)

The EU Advanced Course in Computational Neuroscience introduces students to the panoply of problems and methods of computational neuroscience, simultaneously addressing several levels of neural organisation, from subcellular processes to operations of the entire brain.

The course consists of two complementary parts. A distinguished international faculty gives morning lectures on topics in experimental and computational neuroscience. The rest of the

day is devoted to practicals, including learning how to use simulation software and how to implement a model of the system the student wishes to study on individual unix workstations. The first week of the course introduces students to essential neuro-biological concepts and to the most important techniques in modeling single cells, networks and neural systems. Students learn how to apply software packages like GENESIS, MATLAB, NEURON, XPP, etc. to the solution of their problems. During the following three weeks the lectures will cover specific brain functions. Each week topics ranging from modeling single cells and subcellular processes through the simulation of simple circuits, large neuronal networks and system level models of the brain will be covered. The course ends with a presentation of the students' projects.

The EU Advanced Course in Computational Neuroscience is designed for advanced graduate students and postdoctoral fellows in a variety of disciplines, including neuroscience, physics, electrical engineering, computer science and psychology. Students are expected to have a basic background in neurobiology as well as some computer experience.

A total of 30 students will be accepted. Students of any nationality can apply. We specifically encourage applications from researchers who work in less-favoured regions of the EU and from women. Travel grants and free accommodations are available for students from most countries in the world.

The EU Advanced Course in Computational Neuroscience is supported by the European Commission (4th Framework Biotechnology program), by the International Centre for Theoretical Physics (Trieste), by the Boehringer Ingelheim Foundation and by The Brain Science Foundation (Tokyo).

More *information* and *application forms* can be obtained:

http://www.bbf.uia.ac.be/EU_course.shtml

or

<http://www.ictp.trieste.it/cgi-bin/ICTPsmr/mklinks/mklist?smr1166>

Please apply electronically using a web browser if possible. email: eucourse@bbf.uia.ac.be or by mail: Prof. E. De Schutter, Born-Bunge Foundation, University of Antwerp - UIA, Universiteitsplein 1, B2610 Antwerp, Belgium, FAX: +32-3-8202669.

The First International Bioinformatics Summer School IBSS'99 — Information Systems and Network Analysis of Gene Regulation and Metabolism

September, 5 - 10, 1999, Magdeburg, Germany

Post-genomic methods in molecular biology generate large amounts of expression data, which require computational methods for their storage, management, and analysis. Knowledge databases with information on genes not only as genome constituents but also as the elements of regulatory, signaling, and metabolic pathways are essential resource for "reverse engineering" regulatory and metabolic networks in the cell. An updated illustrative list of different methodologies available in the internet can be obtained at (see

http://www.witi.cs.uni-magdeburg.de/iti_bm/dagstuhl/demos.html) .

The conclusion when looking at such a variety of approaches is that in order to support the analysis of gene regulation and metabolic network control we need distributed data access integrated with visualization, simulation, and analysis tools. Based on the experience of two international Dagstuhl Seminars on this topic (1995 and 1998 Schloss Dagstuhl with URL: <http://www.dag.uni-sb.de>) we invited scientists to prepare specific courses in:

- Basic Molecular Database Systems (R. Apweiler, EMBL Cambridge)
- Global Gene Expression Studies (A. Manson McGuire, Harvard Medical School)
- Gene Regulation (J. Collado-Vides, UNAM; E. Wingender, GBF)
- Metabolic Pathways (M. Kanehisa, University Kyoto)
- Cell Signaling (N. Kolchanov, Russia Academy of Science)
- Gene Expression and Cell Differentiation (J. Reinitz, Mt. Sinai Med. School)
- Modeling and Simulation of Metabolic Networks (M. Tomita, University Keio)
- Database Integration (T. Mück, University Vienna)
- Molecular Information Systems (R. Hofestädt, University Magdeburg)
- Metabolic Engineering (M. Reuss, University Stuttgart).

Organizing Committee: J. Collado-Vides (UNAM, Mexico), R. Hofestädt (University Magdeburg, Germany), J. Reinitz (Mt. Sinai Med. School, NYC, USA), M. Reuss (University Stuttgart, Germany).

Information: Prof. Dr. Ralf Hofestädt, Otto-von-Guericke University Magdeburg, Department for Computer Science, Universitätsplatz 2, D-39116 Magdeburg, email: hofestae@iti.cs.uni-magdeburg.de

First Annual University of Minnesota Computational Neuroscience Symposium
October 7-8, 1999, University Minnesota, Minnesota, USA

The Computational Neuroscience Program of the University of Minnesota in conjunction with the Department of Neuroscience, the Graduate Programs in Scientific Computation and Neuroscience, and the Supercomputing Institute for Digital Simulation and Advanced Computation will host a symposium on computational neuroscience on October 7 and 8 on the University of Minnesota campus. Topics include:

- molecular mechanisms in ion channels
- signal transduction
- neurotransmission and receptors
- computational models of vestibular and oculomotor control
- robotics and computer vision
- neural network models

Conference Administrator: Kathleen Clinton, email: clinton@compneuro.umn.edu.

Additional information is also available on the World Wide Web at:

<http://www.compneuro.umn.edu/symposia.html>

Third Winter School on Population Dynamics

January 5-9, 2000, Woudschoten, The Netherlands

This will be the third edition of this event, organised by Odo Diekmann, Hans Heesterbeek, Fleur Kelpin and Bob Kooi. The previous schools in January 1996 and January 1998 each attracted more than 50 PhD-students from a broad range of countries and population biological subjects. Reports by participants about these schools can be found in BMN 13 and BMN 17.

As in the previous editions we emphasise the word ‘school’ and aim to give PhD students in population biology a good understanding of the way mathematics is applied to study problems in their field as well as a thorough background in relevant deterministic and stochastic mathematical techniques. Five lecturers who will each give a series of 4 or 5 lectures. These lecture series start at an elementary level and connect to recent research topics towards the end. Basic techniques receive attention, and lecture notes accompany the presentation.

In addition we retain a successful part of the 1996 and 1998 editions in that participants team up in small groups around one or two papers of their choice from a list we provide. The papers cover the same areas as the lecture topics but go beyond the basic material. We look for stimulating and challenging papers that are allowed to be more difficult than usual, provided they have a rewarding message once you understand them. The groups then study these papers together during several periods of a few hours scattered throughout the week (the idea being that five know more than one and one learns to read more advanced papers). On Saturday one person from each group then gives a short presentation about the findings, ideas, criticism, comments etc.

The speakers are:

- Fred Adler (ecology and evolution)
- Rob de Boer (immunology, virology)
- Bas Kooijman (dynamic energy budgets, ecotoxicology)
- Roger Nisbet (stage structured populations, numerics and applications)
- Horst Thieme (mathematics of physiologically structured population models)

The costs of the school are Dfl 600,00 (Euro 270,00). The school is made possible thanks to the support from the programme on Nonlinear Systems of the Netherlands Organization for Scientific Research (NWO). A registration form is available at the web-address given below. There is a limit of 55 participants.

Information: <http://come.to/winterschool2000>

Systems Science 2000 – Integrative Approaches to Natural and Social Dynamics

March 20 - 22, 2000, University of Osnabrück, Germany

Systems science has developed rapidly in recent years. Impetus was received from the investigation of the non-linear dynamics of complex systems, which occur in physical, chemical but also ecological and social systems. Theoretical systems science investigates the endogenous structure and the exogenous influences which effect the stabilisation, self-organisation, adaptation and emergence, etc. of systems. Applied systems science applies these concepts to various different systems, whether subject-specific or interdisciplinary. Mathematical modelling and simulation are core methods to investigate developmental paths of environmental systems and to recognise critical situations earlier. Systems science investigates the structure and function of complex systems in order to gain a better understanding of the dynamic behaviour of systems. Systems scientific investigations are carried out in numerous academic disciplines, as partly reflected in the name itself, e.g. ecosystems research, economic cybernetics, systemic psychology, etc. Often similar methods are used without the inclusion of experience from related disciplines.

Aims and Scope:

The international conference - Systems Science 2000 -, to be held in Osnabrück from 20 -

22 March 2000, intends to bring together scientists from various different fields in order to present and discuss the present position of systems science. Besides the main talks, to which internationally renowned scientists will be invited, we also plan to organise numerous sessions with brief talks and posters. The following fields could be discussed:

- General Aspects of Systems Science,
- Ecological and Environmental Systems,
- Social and Economic Systems,
- Sustainable Development,
- Technology and Risk Assessment,
- Biological Systems,
- Psychological and Cognitive Systems,
- Mathematical Systems Theory and Its Applications,
- Education in Systems Science.

Organising Committee:

H. Malchow, M. Matthies, K. Brauer, E. Umbach, M. Klein, S. Franz, T. Gehrs

Scientific Committee:

P. Allen (UK), H. Behncke (D), N. de Lange (D), W. Ebeling (D), O. Fränzle (D), T.G. Hallam (USA), F. Hinterberger (D), G. Jetschke (D), M. Jischa (D), S.E. Joergensen (DK), T. Klenke (D), A. Kratochwil (D), J. Kriz (D), D. Mackay (CAN), K. Mainzer (D), H. Malchow (D), M. Matthies (D), T.E. McKone (USA), H. Meinhardt (D), P. Milling (D), M. Peschel (D), O. Richter (D), B. Rieger (D), C. Rollinger (D), E. Rühl (D), M. Ruth (USA), R.W. Scholz (CH), K.H. Simon (D), K.G. Troitzsch (D), E. Umbach (D), C. Wissel (D)

Call for Papers:

We invite all potential participants to submit an abstract for an oral or poster presentation. Abstracts must be submitted by 1 September 1999 using the abstract online service offered under

<http://www.usf.uos.de/~sys2000>

All further information will be posted there as well.

Registration:

Please, register your interest now using the mentioned online service. Your name will be kept on the mailing list.

Information: University of Osnabrück, Institute of Environmental Systems Research, D-49069 Osnabrück, Germany. Tel/Fax +49-541-969-2575/2599,
email: sys2000@usf.uni-osnabrueck.de and on the web: <http://www.usf.uos.de>

Deterministic and Stochastic Modeling of Biointeraction (DESTOBIO 2000)

August 23-27, 2000, West Lafayette, Indiana, USA

We announce the Second International Conference on "Deterministic and stochastic modeling of biointeraction" organized by the Department of Mathematics of Purdue University August 23-27, 2000. The meeting will be held in West Lafayette, seat of the main campus of Purdue University.

Following the first DESTOBIO organized in Sofia (Bulgaria) in 1997, the aim of the meeting is again to bring together people from the deterministic and stochastic modeling worlds with

the expectation that something useful may come out. We hope this meeting, just like the one in Bulgaria, will turn out to be very exciting.

Topics of the Conference:

1. Deterministic and stochastic approaches to mathematical modeling in population dynamics, epidemiology, immunology, genetics, neurophysiology, molecular biology, cell biology, pattern formation, bioecology;
2. Computational biomathematics.

Information: Please check the Web page at

http://www.math.purdue.edu/~milner/DESTOBIO_2000.html

or ask Fabio Augusto Milner, email: milner@math.purdue.edu.

Send e-mail indicating your interest in participating to

email: destobio@math.purdue.edu

Short announcements of forthcoming events

5th International Work-Conference on Artificial and Natural Neural Networks

June 2-4, 1999, Alicante, Spain

This biennial meeting with focus on the interplay between neuroscience and computation, without disciplinary boundaries, has the topics:

- Foundations of Computational Neuroscience: Brain Organization Principles;
- Neural Modeling: Biophysical and Structural Models;
- Plasticity Phenomena (Maturing, Learning and Memory);
- Complex Systems Dynamics;
- Artificial Intelligence and Cognitive Neuroscience;
- Artificial Neural Nets Simulation, Implementation, and Evaluation;
- Methodology for Nets Design;
- Bio-inspired Systems and Engineering;

Information: <http://iwann99.umh.es>

Summer School on Mathematics in Cell Physiology and Proliferation

June 6-9, 1999, Termoli, Italy

The subject of the school will be mathematical methods applied to the study of cell and molecular biology. The goal of the school is to offer doctoral students and young post-doctoral researchers a presentation of some mathematical techniques widely used in modelling problems in cell physiology and proliferation, together with a review of a selection of some such problems of contemporary relevance. The target audience is mainly composed of advanced graduate students and post-graduates in the life sciences and in mathematical disciplines (math, applied math, physics, engineering).

Information: <http://space.tin.it/scienza/hjcas/biomasch.htm>

IX International Symposium on Applied Stochastic Models and Data Analysis

June 14 - 17, 1999, Lisbon, Portugal

The Symposium 1999 will focus on new trends in theory, applications and software of Applied Stochastic Models and Data Analysis. Provisional topics are: Human Resources; Environment; Management and Administration; Production; Inventory and Logistics; Marketing; Finance; Insurance; Planning and Control; Quality, Reliability and Safety; Information Systems and Official Statistics; Sample Surveys; Research and Development; and Travel and Tourism. Particular attention will be paid to the application of new technologies in business and industry such as Data Mining, Data Warehousing, Symbolic Learning, Neural Networks, Genetic and Fuzzy Algorithms, Computer Graphics, Knowledge-Based Systems, and Decision Support Systems.

Information: <http://www.di.fct.unl.pt/asmda99>

Fourth International Congress on Industrial and Applied Mathematics (ICIAM 99)

July 5-9, 1999, Edinburgh, Scotland

The Fourth International Congress on Industrial and Applied Mathematics will focus on mathematical and computational methods in the solution of real world problems:

- Mathematical modelling in industry and commerce
- Mathematics of biology and medicine
- Mathematics of finance, investment and banking. Risk theory.
- Mathematics in the Social Sciences
- Mathematics of Geophysical and Oil Sciences
- Mathematics of material science, fluid dynamics and combustion theory
- Environmental and Climate change
- Electromagnetism, including telecommunications, semi-conductors and electronics
- Cryptography, Coding and Computer Science
- Signal and Image Processing
- Computational differential equations

Information: <http://www.ma.hw.ac.uk/iciam99/>

EQUADIFF 99

August 1-7, 1999, Berlin, Germany

Equadiff 99 is one of a series of conferences devoted to all mathematical aspects of differential equations:

Dynamical Systems: Celestial Mechanics, Homoclinic Tangencies, Singular Perturbations, Stochastic Systems, Symmetry, Topological Methods and Conley Index.

Infinite Dimensions: Delay Equations, Geometric Dynamics, Hyperbolic Conservation Laws, Hyperbolic Wave Equations, Hysteresis, Large Domains, Lattice Dynamical Systems, Microstructure, Nonlinear Functional Analysis, Variational Methods, Viscosity Solutions.

Global Attractors and Stability: Global Attractors and Limits, Nonautonomous Attractors, Order Preserving Systems, Qualitative Theory of Parabolic Equations, Stability of Fronts and Pulses.

Computational Aspects: Computer Algebra Tools, Control and Optimization, Dynamics and Algorithms, Exponentially Small Phenomena, Geometric Integrators, Numerical Ergodic Theory, Numerics of Dynamics.

Applications: Chemistry, Chemotaxis, Cross-Diffusion, and Blowup, Industrial Applications,

Mechanics, Models in Biology, Medicine, and Physiology, Molecular Modelling, Patterns, Semiconductors, Steady Water Waves, Unsteady Hydrodynamic Waves.

Information: <http://www.math.fu-berlin.de/~equadiff>

Mathematische Biologie

October 24-30, 1999, Mathematisches Forschungsinstitut, Oberwolfach, Germany

Organizers: Odo Diekmann, Utrecht and Karl Peter Hadeler, Tübingen

The Third World Congress of Nonlinear Analysts

July 19-26, 2000, Catania, Italy

The attempt to understand the nonlinear world is dominating large parts of mathematics which is bound to increase in the next century. Thus, there is a definite need to have a forum, on a global basis, to forge unity in diversity and for bringing more cooperation and collaboration into the world community of nonlinear analysts.

Topics: Aerospace Sciences, Atmospheric Sciences, Biological Sciences, Chemical Sciences, Cosmological Sciences, Economics, Engineering & Technological Sciences, Environmental Sciences, Geophysical Sciences, Medical & Health Sciences, Numerical & Computational Sciences, Oceanographic Sciences, Physical Sciences, Social Sciences & Mathematical Sciences.

Address: WCNA-2000, Florida Institute of Technology, Applied Mathematics Program, Melbourne, FL 32901, USA, email: dkermani@winnie.fit.edu, fax: +1-407-674-7412.

<http://www.fit.edu/AcadRes/math/wcna2000.htm>

Application for 1999 ESMTB Membership:

Please fill in this application form for 1999 ESMTB Membership, indicate your choice of journal (if any) and send your payment of the required annual fee for 1999 to Dr. M.A.J. Chaplain at the address below. The annual membership fee is \$ 25 per year (full member) and \$ 15 (student member). Members from Eastern European countries should pay at the **student rate**.

Please note that there will be a reduction in the registration fee for the 1999 TMBM Amsterdam Meeting for those paid-up members of the Society.

Name:

Address:

Phone/FAX:

E-mail:

would like to be a member of the European Society for Mathematical and Theoretical Biology.

The prices for subscription to the journals are given below. We would like to encourage as many members as possible to take advantage of these special rates which we have negotiated with the publishers. Please try to subscribe to one (or more!) of the journals as well as paying your annual membership fee for 1999.

1. No journal (membership only)
2. *Acta Biotheoretica* (Kluwer) £ 40.00 per year
3. *Journal of Biological Systems* (World Scientific) £ 40.00 per year
4. *Journal of Mathematical Biology* (Springer Verlag) £ 70.00 per year

Send this form, with payment of your annual membership fee, to:

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Scotland, UK

email: chaplain@mcs.dundee.ac.uk

Methods of Payment (see also Treasurer's report):

- 1) By CASH (i.e. POUNDS STERLING)
- 2) By CHEQUE: If paying by cheque, please make the cheque payable to "ESMTB" (in POUNDS STERLING ONLY). Please note that payment by EUROCHEQUE is acceptable.
- 3) BANK DRAFT TRANSFER: Payment may be made directly to the ESMTB account, details of which are:

Bank:	The Royal Bank of Scotland, Balfour Street, Dundee, Dundee University Branch
Account Name:	ESMTB
Sort Code:	83 18 38
Account Number:	00 145 384