Prioriteitenprogramma

Niet Lineaire Systemen

Populatiedynamica

News Letter

A newsletter for the project 'Population dynamics, including epidemiology' being part of the NWO priority program 'Nonlinear Systems'.

March 1, 1999

Visit the Home Page on:
`http://www.bio.vu.nl/thb/users/nls`

This newsletter will appear once every three months during the course of the project. Its content will mainly consist of announcements of activities, such as seminars and workshops. Moreover, information about foreign visitors being in the Netherlands as part of the program will be given.

To make this newsletter as informative as possible we ask you to let us know about activities that are planned and the date visitors are coming and give lectures. Also addresses of persons (in the Netherlands or abroad) who might be interested in receiving this newsletter are welcome.

All correspondence should be sent to: Bob Kooi
Theoretical Biology
Vrije Universiteit
De Boelelaan 1087
1081 HV Amsterdam

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Contents

Contributions to this newsletter were made by: Lia Hemelrik, Fleur Kelpin, Mirjam Kretzschmar, Eline Korenromp.

1 Editorial

The URL of the home-page for the NLS Population Dynamics and Epidemiology project is: `http://www.bio.vu.nl/thb/users/nls` Activities of the programme as well as useful links are given in a Calendar. You can down-load from this home-page the **Newsletter** (4 issues per year) in PostScript and DVI format. For the time being the newsletter will also be send by ordinary mail.

This home-page will be updated four times a year when also the new newsletter is issued. Only the calendar is updated more frequently. Please do not hesitate to contact for updates, improvements, suggestions and so on.

NLS mail-list

If you want to be notified by email when the NLS homepage `http://www.bio.vu.nl/thb/users/nls/` is updated, please send your:

Name + Title	Name company
Name Dept.	Street + number
Zip-code City	Country
E-mail address	Telephone number
Fax number	

to Karin Uyldert, Vrije Universiteit, de Boelelaan 1087, 1081 HV, Amsterdam or email: (`uyldert@bio.vu.nl`)

2 ACTA BIOTHEORETICA

Call for papers 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.

Acta Biotheoretica is abstracted and/or indexed in: Current Awareness in Biological Sciences (CABS), Biological Abstracts, Reference Update, CAB international, GEOBASE and Ecological Abstracts, Science Citation Index, Science Citation Index Expanded, Research Alert and Current Contents/ Agriculture, Biology and Environmental Sciences.

Quality: Acta Biotheoretica publishes papers of high quality from all parts of the world.

Originality: Besides clarity of exposition, the most important criterion for publication is the originality of the paper.

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 the web site: `http://www.wkap.nl/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.

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, e-mail:`SBQHAR@RULSFB.LEIDENUNIV.NL`

3 Job at London School of Hygiene & Tropical Medicine

Information sheet: Senior appointment in infectious disease modelling The London School of Hygiene & Tropical Medicine has an internationally excellent reputation in public health and tropical medicine, is a leading postgraduate medical institution in Europe and is Britain's national school of public health. A special strength of the School's research is its multi-disciplinary nature: leading researchers have backgrounds in public health medicine, epidemiology, clinical medicine, infectious diseases, chemotherapy, biochemistry, immunology, genetics, molecular biology, entomology, statistics, demography, health economics, public health engineering, medical anthropology, health promotion, environmental health management, and health policy.

Department of Infectious and Tropical Diseases The Department of Infectious and Tropical Diseases is newly formed and encompasses all of the laboratory-based research in the School as well as that on the clinical and epidemiological aspects of infectious and tropical diseases. It is headed by Peter Smith, who is Professor of Tropical Epidemiology. The range of disciplines represented in the department is very broad and inter-disciplinary research is a feature of much of our activity. The spectrum of diseases studied is wide and there are major research groups with a focus on malaria, tuberculosis, HIV/AIDS and other sexually transmitted diseases, vaccine development and evaluation, and vector biology and disease control. The Department is organised into five large research units comprising: Immunology, Pathogen Molecular Biology and Biochemistry, Disease Control and Vector Biology, Infectious Disease Epidemiology and Clinical Research. There is close interaction between scientists in different research teams. The Department has strong overseas links which provide a basis for field studies and international collaborations in developed and developing countries. The teaching programme includes MSc courses, which are modular in structure, a variety of short-courses and an active doctoral programme (PhD and DrPH). In addition, new distance-based learning (DBL) courses are now available, leading to MSc degrees in Infectious Diseases and Epidemiology.

Current work in infectious disease modelling The School has a long history of research on transmission models, and there are a number of current projects involving modelling, most of which are being conducted in the Department of Infectious and Tropical Diseases.

A particular strength of this research is that most of the modelling work benefits from the availability of extensive empirical data from the School's many epidemiological field studies.

Vaccination policy Felicity Cutts is involved in a range of projects using deterministic models to evaluate alternative vaccination strategies. Current work focuses on measles, rubella and hepatitis B vaccination, based on serological data from Ethiopia, India and other populations. Some of this research is carried out in collaboration with scientists at the Communicable Disease Surveillance Centre (CDSC, Colindale) and Warwick University. Paul Fine has been working with Ilona Carneiro and Emilia Vynnycky on the problem of oral polio vaccine persistence in the population in the context of polio eradication. Felicity Cutts and Andy Hall have also worked on cost-benefit modelling of hepatitis B vaccination in the UK, and a new Wellcome Trust grant will fund work with Punam Mangtani and Jenny Roberts on adult vaccination policy in the UK. The Infectious Disease Epidemiology Unit is a WHO Collaborating Centre for the Evaluation of Vaccines in Developing Countries.

HIV prevention strategies Charlotte Watts has been working on deterministic models to evaluate the effectiveness of four intervention strategies for HIV prevention in Africa: (i) school-based sex education; (ii) condom promotion; (iii) improved STD treatment; (iv) interventions among sex workers. Cost information will also be incorporated so that cost-effectiveness can be modelled. This work has been sponsored by UNAIDS.

Richard Hayes, Heiner Grosskurth and Susie Foster have secured DFID funding for a project to apply the STDSIM stochastic simulation model of HIV and four other STDs to empirical data from three randomized trials conducted in East Africa (in Mwanza, Tanzania; and Masaka and Rakai, Uganda). These trials have evaluated the impact of four different HIV control strategies in three different populations. The model will be used to predict the relative effectiveness of the four strategies in the differing conditions of the three study populations. Comparative cost data will also be collected so that cost-effectiveness can be evaluated. This project will be conducted in collaboration with Erasmus University Rotterdam and the research teams of the three East African trials. A research fellow and research student will be working full-time on this project over the next three years. This project follows on from previous research conducted by Jamie Robinson and Richard Hayes using SimulAIDS to model the HIV epidemic in rural Uganda.

Tuberculosis Emilia Vynnycky is working with Paul Fine on deterministic transmission models of tuberculosis. The main emphasis is on modelling the natural history of infection and disease, and analysing case reproduction rates. Initially the project is using empirical data from the UK, but it is planned to apply the model also to data from developing countries including Malawi and India.

Rabies Chris Dye and Rupert Quinnell have worked on deterministic models of rabies, looking particularly at vaccination policy for dogs, and drawing on empirical data from Tanzania and Kenya.

Leishmaniasis Clive Davies and Chris Dye have worked on models of the transmission and control of cutaneous and mucosal leishmaniasis, with funding from the European Union and the Wellcome Trust, using data from Peru and Bolivia.

New Variant CJD Peter Smith and Simon Cousens are members of the committee advising the government on policy with regard to BSE and new variant CJD. With Emylia Vynnycky and Louise Linsell they are using models to predict future numbers of CJD cases in order to provide advice to the Department of Health.

Malaria David Bradley and Brian Greenwood are advising Klaus Dietz on a large malaria model which is being developed as an EU collaboration. Paul Coleman has also been working with Anne Mills on modelling the cost-effectiveness of malaria intervention strategies in Africa, with special reference to drug resistance and treatment policies.

Strategic initiative in disease modelling Transmission models are likely to play an increasingly important role within public health and epidemiology over the next decade, and it would be desirable for the School to build up solid strengths in this area to the benefit of both its research and teaching programmes. The Department of Infectious and Tropical Diseases has identified the strengthening of its work on transmission models as a strategic priority, and as part of this initiative wishes to appoint a senior academic to promote and develop this area of research.

The main aim of this initiative is to build an effective critical mass of modellers, working on a range of infectious diseases. Having developed effective collaboration and networking between scientists working in this area, the medium-term aim would be to attract substantial external funds to increase the volume of disease modelling work within the School.

The Department seeks to recruit a senior modeller, to help take forward this initiative. For details of the post and person specification please contact:

Prof.dr. Richard Hayes, London School of Hygiene and Tropical Medicine, Keppel Street London WC1E 7HT Tel. 0044 171 636 8636 / 0044 171 927 2243 Fax. 0044 171 436 4230 email: `richard.hayes@lshtm.ac.uk`

or Eline L. Korenromp, MSc. Center for Decision Sciences in Tropical Disease Control (CDTDC) Department of Public Health, Faculty of Medicine, Erasmus University Rotterdam P.O. box 1738 3000 DR Rotterdam The Netherlands Fax ++31 10 436 9449/9455 Tel ++31 10 408 7985/7714 Internet: `http://www.eur.nl/fgg/mgz/` email: `korenromp@mgz.fgg.eur.nl`

4 Modelling of Contact Structure and the Spread of Infectious Diseases

A report by Mirjam Kretzschmar (RIVM). Organizers: Dr. M. Kretzschmar (RIVM), Dr. M.C.M. de Jong (ID-DLO).

On September 24, 1998, a workshop took place in Bilthoven, The Netherlands, about "Modelling of Contact Structure and the Spread of Infectious Diseases". The aim of the workshop was to bring together researchers who have worked on different approaches in modelling contact patterns, epidemiologists who have studied actual contact patterns in specific populations, and modellers who are applying epidemic models to public health and veterinary questions. The speakers were Lisa Sattenspiel (University of Missouri, Columbia, USA), Minus van Baalen (University of Amsterdam & Universite M. et P. Curie, Paris), Gianpaolo Scalia-Tomba (Universite La Sapienza, Rome, Italy), John Edmunds (University of Warwick, United Kingdom), Mart de Jong (ID-DLO, Lelystad), Nico Nagelkerke (RIVM, Bilthoven

& KNCV, The Hague), and Tom Snijders (University of Groningen). In the first lecture Lisa Sattenspiel gave an account of the spread of influenza between settlements in Canada in 1918, and showed the importance of understanding the social structure and contact patterns between those settlements for explaining the observed mortality patterns. Next, Minus van Baalen talked about the application of the pair approximation approach in modelling the invasion of new strains of a pathogen depending on the contact structure of the population. His simulation results showed that in a population where every individual only contacts a small number of neighbors, it is possible that a less virulent strain of a pathogen may invade and establish itself locally, whereas globally a more virulent strain is dominant. Gianpaolo Scalia-Tomba succeeded in intuitively explaining some mathematically intricate results about the spread on an infectious disease in a population with two levels of contacts: local contacts that take place in small groups such as households, and global contacts with other parts of the population. John Edmunds then gave us some insight into the contact patterns of the Warwick student population with special reference to his own research group. He showed results of an empirical study about contact patterns pertaining to contacts of varying intensity, ranging from "having a two-way conversation" to "having sex". Then Mart de Jong talked about the interpretation of different threshold quantities and showed how the basic reproduction ratio R0 depends on the average number of aquaintances in a contact network. Nico Nagelkerke demonstrated how molecular epidemiology can contribute to the study of tuberculosis transmission. From the clustering of DNA-fingerprints of TB and their relationship to different ethnic groups in the Netherlands he drew conclusions about the contact patterns among and between those groups. Finally, Tom Snijders gave an introduction into the main concepts of social networks and discussed the possible applicability of those concepts in modelling transmission dynamics of infectious diseases in networks. He also talked about some statistical approaches in connection with the sampling of networks.

The workshop was continued on September 25, 1998, in a small group consisting mainly of the speakers of the day before. In an open discussion several of the problems that had been mentioned in their talks on the day before, were discussed in more detail. Although the background of the participants of this discussion group was very diverse, the discussion was fruitful for all. In total, the workshop was perceived as stimulating and as an inspiration for future work.

Abstracts

Lisa Sattenspiel University of Missouri, Columbia (USA)

Furs, flus, and feather beds: or why Canadian fur-trappers should stay in bed when they have the flu

In recent years, many researchers in mathematical epidemiology have developed models that incorporate realistic contact structures to allow for nonrandom interactions among populations separated in time, space, or social behaviors. I describe here such a model for the geographic spread of infectious diseases, and, more importantly, describe how the model is actually being used to study the impact of the 1918-19 influenza epidemic among three communities of native Canadian fur trappers. This application is made possible because of an unusually rich data base of information on both the mortality rates from this epidemic and on the daily mobility patterns of the fur trappers throughout the region during the time of the epidemic. Computer simulations in combination with ethnohistoric analysis of parish and Hudson's Bay Company post records have been used to assess the importance of trapper mobility on disease spread, the possible impact of quarantine practices during the epidemic, and the potential effects of seasonality on the spread of influenza.

Minus van Baalen Universiteit van Amsterdam & Universite Pierre et Marie Curie, Paris (F).
Contact networks and the evolution of virulence: Implications for virulence management
Some parasites require close contact between their hosts for transmission. If the host population is 'well-mixed' standard epidemiological methods can be used to study their dynamics and evolution. If, however, the host population is socially structured other methods are necessary. When parasites can transmit themselves to their host's immediate neighbours, the parasite population becomes 'viscous': even if there is no large-scale subdivision in the host population, the parasite cannot spread immediately throughout the entire population. To what extent are parasites adapted to their host's social structure? How are parasites expected to respond when this contact structure changes? To address these questions, I will assume that the host population has a fixed contact network in which every host is socially connected to a fixed number of hosts. Using cellular automaton models and the correlation dynamics approach I will show that in a simple SIR model, less virulent parasites may be favoured in 'viscous' than in 'well-mixed' host populations. When a mutant parasite arises, it will form a local focus of infection (cluster). A cluster of less virulent parasites can invade and replace more virulent strain if it spreads locally more effectively, i.e. if the cluster can grow. In the particular model that I studied, based on the assumption that more infectious (virulent) parasites induced a longer period of immunity, virulent parasites tend to be surrounded by immune hosts, whereas avirulent parasites benefit from having more susceptibles in their neighbourhood. Effectively, this is an instance of kin selection among parasites across hosts. Any change in the host population that disrupts the pattern of relatedness among the parasites is therefore expected to favour more virulent strains.

Gianpaolo Scalia-Tomba Universita La Sapienza, Rome (IT)
Final size of epidemics in structured populations
Recently, many theoretical efforts to understand the effects of mixing heterogeneity on epidemic spread in a population have been made (see e.g. Andersson 1998). The relation between heterogeneity caused by two-level mixing, i.e. high infection probability within a small group (e.g. a family) and small infection probabilities with other individuals in the population, and the probability and size of a large epidemic has been studied by Ball, Mollison & Scalia Tomba (1997). While the mathematical machinery used in the proofs of results is slightly complicated and heavy, the main intuitions can still be recovered by heuristic considerations about the outgoing and incoming contact graphs (cf. Barbour & Mollison 1990) and about the initial imbedded renewal structure (cf. Heesterbeek 1992). However, these methods yield little information about the real time behaviour of the epidemic. Furthermore, the usual deterministic approach to the problem runs into difficulties because of the essentially discrete nature of the small groups composing the population. Further work will be needed to clarify these issues.

Andersson H. (1998) Epidemic models on graphs and lattices: a short survey. Research report no. 204, Inst. Actuarial math. and math. stat., Stockholm University, Sweden.

Ball F., Mollison D., Scalia Tomba G. (1997) Epidemics with two levels of mixing. AAP 7, 46-89.

Barbour A.D., Mollison D. (1990) Epidemics and random graphs, in Stochastic processes in epidemic theory, Gabriel J.P, Lefevre C., Picard P., Eds., Lecture Notes In Biomathematics 86, 86-89.

Heesterbeek J.A.P (1992) R_0, Ph.D. thesis, CWI, Amsterdam.

W.J. Edmunds Department of Biological Sciences University of Warwick Coventry, UK.
Who mixes with whom? Measuring contact patterns for air-borne infections
The rates and patterns of host mixing are critical determinants of the transmission dynamics of infectious diseases. For microparasitic human diseases spread by close contact (e.g. measles, rubella and influenza) there have been remarkably few attempts to directly quantify the relevant patterns of mixing. Instead, analysts tend to make (strong) assumptions regarding mixing patterns then indirectly estimate the mixing parameter(s) from epidemiological data. In contrast, the existence of clearly defined and well understood at-risk events for sexually transmitted diseases (a sex act and/or a new sexual partnership) have allowed researchers in this field to obtain estimates of relevant mixing patterns directly from sexual behaviour surveys or from contact tracing. We have applied these same survey techniques to estimate mixing patterns for close- contact infections by defining simple at-risk events for these infections and asking individuals to record these events in diaries. For example, we assume one-to-one conversations to be sufficient for the transmission of some aerosol infections, while skin-to-skin physical contact is required for others. Thus, at-risk events are often hierarchically arranged. For instance, conversation is not an at-risk event for an STD but sexual contact is an at-risk event for close contact infections. The data provided by these surveys have allowed us to tentatively estimate the mean and variability in the numbers of contacts that individuals make for a range of possible infections. Since we record information on the study participants and ask them to note the characteristics of their contacts (age, sex, where the contact occurred etc) we have been able to estimate how individuals mix within and between age groups and across different social settings (home versus work etc). In addition, by asking individuals to identify their contacts (by name) and sampling individuals through time we are beginning to be able to identify the structure and dynamics of social networks through which close-contact infections spread. Though still in the pilot stage, we believe these techniques have wide applicability and may lead to significant improvements in parameter estimation, model formulation and epidemiological prediction.

Nico Nagelkerke National Institute of Public Health and the Environment, Bilthoven
Martien Borgdorff Royal Netherlands Tuberculosis Association, The Hague
The role of the population structure of The Netherlands in TB transmission
Population structure, in terms of age, gender, ethnicity and behaviour plays an important role in the transmission dynamics of many infectious diseases. Unfortunately, empirical epidemiology is complicated by the difficulty or impossibility to establish who infects whom. Molecular fingerprinting now provides new opportunities to explore transmission, by identifying "clusters" of individuals linked by (recent) transmission. Since 1993 molecular fingerprinting, using IS6110, has been carried out on all diagnosed cased of tuberculosis in The Netherlands. We will show two applications of this data: 1. Clusters of two patients of Dutch nationality are analysed to establish the role of (similarity in) age in TB transmission. 2. Using incidence on unclustered patients, a probabilistic approach to identifying "sources" of "clusters" was developed. Using this approach, we estimated the contribution of different nationalities to the Dutch TB burden.

Tom Snijders Department of Statistics, Measurement Theory, and Information Technology, University of Groningen

An introduction to social networks and their relevance to diffusion of disease

Patterns of contacts in groups of individuals have received much attention in sociology. This has led to the development of the field of "Social Networks" since the 1970s. Social networks appear to be an important bridge between individual behavior and macro-level consequences. In this presentation some concepts and methodological approaches of social network analysis will be presented, focusing on the role of social networks in research on diffusion.

5 Calendar

May 26-30 1999

The XIII Max Born Symposium "Statistical Physics in Biology" held in Wroclaw, Poland - May 26-30 1999, will be devoted to two main issues:

- perspectives in DNA analys
- population dynamics and ageing

The total costs per one participant, covering board, accommodation and conference fee is only 230 US $. Proceedings of the Conference will be published in the special issue of Physica A. Deadline for abstract is April, 2nd 1999. Full information you will find on the web page: `http://www.ift.uni.wroc.pl/~poff/symposia/max13.html`

The main purpose of the meeting is putting together all new ideas which have appeared recently during investigation of DNA in various fields of science. The main topic is discussion of the basic mechanisms of DNA evolution as well as population evolution where various methods of statistical physics have been used. In particular, hot topic of genome evolution will be widely discussed.

Organizers: Stanislaw Cebrat and Miroslaw R. Dudek

June 6 - 19, 1999

The second Summer School "Mathematics in Cell Physiology and Proliferation" of Mathematical Biology will take place in Termoli (CB, Italy) between June 6 and June 19, 1999. An updated description of the school may be found at the web page `http://space.tin.it/scienza/hjcas/biomasch.htm` For all email communications please use the address `biomath@tin.it`

29 June- 3 July, 1999

Second Announcement: Theory and Mathematics in Biology and Medicine 1999 Vrije Universiteit Amsterdam, The Netherlands June 29 - July 3, 1999.

Registration Registration is possible through our web-site. You can find the instructions on the following web-site: `http://www.bio.vu.nl/tmbm99`

Call for Abstracts We invite all participants to submit an abstract for an oral presentation or for a poster. Abstracts will be reviewed by the session organiser(s) and by a responsible member of the scientific committee. The abstract submission dead-line is March 1, 1999.

Oral presentations: These are 15 minutes presentations (plus 5 minutes discussion). You can indicate in which session your presentation fits best. The first author has to give the presentation at the conference.

Poster presentations: Posters will be displayed for one day. You are required to be present at the poster viewing time for discussions with other participants.

Important Dates

- **March 1, 1999** abstract submission dead-line
- **April 1, 1999** early registration dead-line
- **May 15, 1999** notification of acceptance of abstract
- **June 1, 1999** deadline of cancellation with partial reimbursement
- **June 21, 1999** deadline of hotel cancellation with partial reimbursement

Important Addresses

- For the most complete source of the latest information: The conference web-site `http://www.bio.vu.nl/tmbm99/`
- For answers to some Frequently Asked Questions: `http://toranaga.bio.uva.nl/~aroos/tmbm99-faq.html`
- For information concerning registration, abstract forms, etc.:

VU Conference Service	Phone :	+31-(0)20-4446790
De Boelelaan 1105	Fax :	+31-(0)20-4445825
NL 1081 HV Amsterdam	Email :	`vu_conference@dienst.vu.nl`
The Netherlands		

- For contacting the organising committee: e-mail: `tmbm99@bio.vu.nl`

July 14 - 19, 1999

Biomathematics - Bioinformatics and Applications of Functional Differential Difference Equations Akdeniz University, Antalya, Turkey, July 14 - 19, 1999.

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.

Organizer	Special Sessions
Zvia Agur	The role of Discrete Models and Delay Differential Equations and in solving real lifeproblems 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
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
Hanna Parnas	Mathematical Modeling of Controlled Drug Release
Zia Taib	Probabilistic and Statistical Methods in Biology and Medicine

Proposed Parallel Sessions: 1. Theory of Differential Difference Equations 2. Discrete and Dynamical Modeling 3. Cell and Molecular Biology 4. Ecology and Evolutionary Dynamics 5. Neural Networks and Applications 6. Epidemiology and Theory of Epidemics

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 to: `akca@kfupm.edu.sa` or `ciplak@pascal.sci.akdeniz.edu.tr` or `fiskin@pascal.sci.akdeniz.edu.tr`

Further Information: Haydar Akca , King Fahd University of Petroleum and Minerals, Mathematical Sciences Department P.O.Box 1071 Dhahran 31261 Saudi Arabia

Telephone:	966 3 860 2279	(Office)
	966 3 860 6377	(Home)
Fax :	966 3 860 2340	
e-mail :	`akca@kfupm.edu.sa`	

January 5-9, 2000

Third Winter school on Population Dynamics Woudschoten, The Netherlands, January 5-9, 2000.
Please feel free to pass this message on to anyone you think would be interested in modelling population dynamics.

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 the BioMathematical Newsletter 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

More details will be announced in the next issue of the newsletter. Registration forms will become available in early 1999. If you wish to be put on a preliminary list of participants, please send an e-mail with your details (including area of research) to Fleur Kelpin at the address below. There is a limit of 55 participants.

Further Information:

Fleur Kelpin	Email : fleur@bio.vu.nl
Theoretical Biology	Vrije Universiteit
De Boelelaan 1087	NL 1081 HV Amsterdam
The Netherlands	http://www.bio.vu.nl/thb/users/nls

Application form NLS Winter school on Population Dynamics Woudschoten

I would like to participate in the Third Winter school on Population Dynamics Woudschoten, The Netherlands, January 5-9, 2000

Your application and payment should reach us **before October 1st, 1999**.

Name and address

Name :

Institution :

Address :

Phone :

Fax :

Email :

Description current work :

Special diet wishes

none yes/no

vegetarian yes/no

other :

Comments

Payment Participation in the winterschool costs NLG 600,- This includes all meals, lodging (double rooms) and lecture notes. Travel costs are not included. Non-Dutch participants are kindly requested to pay in NLG and to use an international money transfer.

Bank	Girokantoor Den Haag
Account	44719
In favour of	Faculteit Biologie, Vrije Universiteit
Address	De Boelelaan 1087, 1081 HV Amsterdam
Mention	Winterschool 2000 order 2375206

Please indicate your name and address clearly on all money transfers!