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'.

December 18, 1998

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

Email: `kooi@bio.vu.nl`

Contents

Contributions to this newsletter were made by: Hans Heesterbeek, Geertje Hek, Hans Metz.

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 Summer school Spatio-Temporal Patterns, June '98, Univ. Twente

A report by Geertje Hek (Mathematics Department Utrecht University).

A mixed group of about 25 Master Class and Ph.D. students from different countries attended this summer school. Four speakers gave lectures about different topics in spatio-temporal patterns. A brief survey is given here:

Rick Durrett from Cornell gave a view of oriented percolation and contact processes, from the basic theory to recent results. He discussed contact processes with one species, without and with fast stirring (leading to a dynamical system) and ended up with contact processes with two species and fast stirring. With ODE and phase plane theory he derives conditions for coexistence. In an epidemic model and a competing contact process, both with large homogeneous mixed populations, he showed that conditions for invasability and coexistence depend strongly on the ratio of birth rate and death rate.

Nick Ercolani from Arizona told about singularity and defects, patterns far from threshold. By means of examples (Rayleigh-Bénard convection, Swift-Hohenberg) he showed a method to give a good description of patterns with different régimes and a kind of boundary layers. A phase equation was derived, and solvability conditions leaded to a universal 'phase gradient form'. Solutions were constructed via Legendre transform and a Hodograph equation. These solutions appeared to give a good description of certain patterns found in experiments.

Yasamasa Nishiura from Sapporo told about patterns in singularly perturbed problems and order parameter equations. By means of examples he gave a new approach to understand singularly perturbed problems (without the knowledge of scaling): the renormalisation method or envelope approach. The knowledge that a solution is given by the envelope of local approximations leads to a renormalisation group equation or map. This method, invariant manifold theory and bifurcation theory gave (stable) patterns which were also found in numerical and real experiments. A video showed us the results.

Satya Majumbar gave a survey of self-organized criticality in sandpile models. A square lattice with piles of particles with certain maximum height formed the model. Adding particles and toppling at one site let particles leave other sites. This gives a matrix that describes the model. One can find stable configurations, recurrent and transient ones. Avoiding any forbidden subconfiguration a class of allowed configurations can be found. The number of allowed configurations appeared to be the determinant of the matrix describing the process.

The lectures were interesting and the group was interested, so there was a lot of discussion. But mathematics were not the only topical items: different cultures, music, the food and world-problems also filled important parts of conversations. The campus of the U.T. served as a place to eat, sleep, walk, go out, sing, etc. One night we however left the campus for pizza and beer in the city of Enschede, where the lecturers turned into coin-football players and great laughers. The mixture of mathematics and joy made this week a very nice one.

3 Report of visit by Mark A. Lewis

Mark A. Lewis (Department of Mathematics, University of Utah Salt Lake City, UT 84112, USA) visited Utrecht and Leiden, December 2–8, 1998, reported by Hans Metz.

The main purpose of the visit was to let Mark interact and collaborate with those researchers in the Netherlands that specialize in the modelling and mathematical analysis of spatial ecological processes and in particular invasion waves, to wit Hans Metz (Leiden), Odo Diekmann (Utrecht) and Frank van den Bosch (Wageningen) and their collaborators. The Dutch researchers and Mark have at some points quite different approaches, which meant that considerable time was spent comparing the approaches and discussing how the differences could be put to the test. All parties found the contacts most enjoyable, and some good amount of information was exchanged.

During the visit Mark gave three talks:

On the asymptotic speed of a stochastic invasion (Utrecht, December 3, and Leiden, December 4, 1998): Despite the recognized importance of stochastic factors, models for ecological invasions are almost exclusively formulated using deterministic equations. Stochastic factors relevant to invasions can be either extrinsic (quantities such as temperature or habitat quality which vary randomly in time and space and are external to the population itself) or intrinsic (arising from a finite population of individuals each reproducing, dying, and interacting with other individuals in a probabilistic manner). It has been long conjectured that intrinsic stochastic factors associated with interacting individuals can slow the spread of a population or disease, even in a uniform environment.

The Leiden talk gave an introduction to this problem from an overall perspective. The Utrecht talk was devoted to a mathematical analysis of the conjecture for the case where individuals interact locally over small spatial neighborhoods. A set of equations describing the dynamics of spatial moments of the population is formulated. Although the full equations cannot be expressed in closed form, a mixture of a moment closure and comparison methods can be used to derive upper and lower bounds for the expected density of individuals. Analysis of upper and solution gives an bound on the rate of spread of the stochastic invasion process. The stochastic process spreads more slowly than the corresponding deterministic model would predict. The slow spread situation corresponds to invaders occurring in widely spaced high density foci. In these cases spatial correlations between individuals mean that density dependent effects are significant even when expected population densities are low. Finally a heuristic formula for estimating the rate of spread was proposed, based on a scaling argument for moments.

Wolf home ranges and prey survival (Leiden December 7, 1998): Wolves are now recolonizing much of North America. It is not yet clear how they will impact the ecosystems to which they return. Data from established wolf populations indicate that they when wolves are close to prey they interact strongly with them. However, much of the time wolves are far from their prey: radio tracking data shows wolves moving around their large home ranges in complex spatial patterns, using scent marks, trails and other features as movement cues.

With new spatial modeling methods it is possible to describe wolf movement, behavior and impact on prey. Here the home ranges arise through the interactions between scent-marking and detailed spatial movements. When incorporated into a mechanistic model, these interactions result in distinctive territories with 'walls' of scent marks defining the edges the territory, and the 'buffer zones' found between territories. Such mechanistic models are an improvement on traditional statistical models for home ranges and can also be used to predict the effects of changing conditions on the wolf home ranges. Finally, the model results can be compared with radio-tracking data. For example, data from northeastern Minnesota that indicates buffer zones between wolf territories act as refuges for their primary prey species, white-tailed deer.

4 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.

Information: Fleur Kelpin, e-mail: `fleur@bio.vu.nl` Theoretical Biology, Vrije Universiteit, De Boelelaan 1087, 1081 HV Amsterdam, The Netherlands.
See also `http://www.bio.vu.nl/thb/users/nls`

5 Calendar

June 6 and June 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.

A meeting organised under auspices of:

- The European Society for Mathematical and Theoretical Biology (ESMTB)
- The Society for Mathematical Biology (SMB)
- The Netherlands Society for Theoretical Biology (NVTB)

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Welcome The international conference on Theory and Mathematics in Biology and Medicine 1999 will be held in Amsterdam, the Netherlands from Tuesday June 29 through Saturday July 3, 1999. The organising committee is pleased to invite colleagues all over the world to join this conference.

Theoretical and mathematical biology and medicine is a diverse field in which interdisciplinary collaboration is essential for progress. The field ranges from experimental research linked to mathematical modelling to the development of more abstract mathematical frameworks in which observations about the real world can be interpreted and with which new hypothesis for testing can be generated. More recently, much attention is also paid to the development of efficient algorithms for complex computations and visualisation, notably in molecular biology and genetics (i.e. genome mapping).

The TMBM99 conference aims to stimulate interdisciplinary collaboration between mathematicians and the bioscientists and to act as the main forum for the exchange of recent research results and new research directions to the widest possible community in theoretical biology and medicine. The meeting is unique in that it is the fourth official tri-annual congress of the European Society for Mathematical and Theoretical Biology (ESMTB) joined with the annual conference of the Society for Mathematical Biology (SMB) for 1999. The conference is organised by the Netherlands Society for Theoretical Biology, the oldest society for theoretical biology in the world. Through these links, this will be the first World Congress devoted to one of the fastest growing domains in science where experimental biology and medicine, biochemistry, mathematics, computational science, physics and various fields of technology come together to attack many problems of great relevance to society.

In this second and final announcement you will find information about the scientific program and about the possibilities to present oral and poster contributions. In addition we provide some information on registration and submission of abstracts and we guide you to our web page for actual registration and submission.

Scientific Program The scientific program is organised on the basis of a subdivision into specific subjects. Oral and poster contributions by participants are possible.

There will be several parallel sessions each day. Three different types of sessions are planned:

(i) Day sessions: These sessions cover an entire day. They include two invited speakers in the morning and shorter contributions (15 min.) during the rest of the day.

(ii) Afternoon sessions: These sessions consist exclusively of a series of shorter contributions (15 min.).

(iii) Poster sessions: Poster sessions will be organised in the central hall of the Free University. During the afternoon there will be time to visit the poster sessions and discuss the research presented with the author.

Invited Speakers A number of speakers have been invited to give plenary presentations at the conference. The majority of the invited speakers are scheduled in sessions with a particular topic. Below you will find a list of these sessions with the invited speakers and some information about the session contents.

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

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

The closing lecture of the conference 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 honor the memory of Professor Okubo.

Day Sessions

1. Non-Linear Population Dynamics

Organisers:
M. Kirkilonis (Utrecht University, The Netherlands)
M.P. Boer (Centre for Biometry Wageningen (DLO), The Netherlands)
Invited speakers:
D. Rand (University of Warwick, United Kingdom)
H.L. Smith (Arizona State University, USA)
Abstract:
Mathematical population dynamics is one of the oldest disciplines of theoretical biology, and has become a major subject in the study of ecological and other related problems. Different

biological situations are described by a wide range of models, mathematically formulated as non-linear dynamical systems. Solutions of such systems show a rich variety of behaviour hinting at the possible complexity of biological interaction between individuals, populations and their environment.

2. Epidemiology of Infectious Diseases

Organisers:

M. Kretzschmar (National Institute of Public Health and the Environment (RIVM), The Netherlands)

J.A.P. Heesterbeek (Centre for Biometry Wageningen (DLO), The Netherlands)

Invited speakers:

R.M. Anderson (University of Oxford, United Kingdom)

K. Dietz (Tuebingen University, Germany)

Abstract:

This session focuses on the mathematical modelling of the spread of infectious diseases in human and animal populations. In particular, we invite talks dealing with the effects of contact patterns, stochastic phenomena, multiple hosts and evolutionary aspects of infectious diseases.

3. Sequencing, Folding and Molecular Structure

Organisers:

J.J.M. Riethoven (European Bioinformatics Institute, United Kingdom) F.H.D. van Batenburg (Leiden University, the Netherlands)

Invited speakers:

M.S. Waterman (University of Southern California, USA)

P.G. Higgs (University of Manchester, United Kingdom)

Abstract:

Focusing on the more theoretical and mathematical issues and advances in this exciting field of bioinformatics, this one-day session will include topics on DNA fragment assembly, sequence/protein comparison, sequence analysis, secondary and tertiary structure (prediction) of macro- molecules such as RNA, DNA and proteins, sequence analysis, and gene prediction.

4. Evolution, Game Theory and Adaptive Dynamics

Organisers:

F.J.Weissing (Groningen University, The Netherlands)

C.G.F. de Kovel (Utrecht University, The Netherlands)

Invited speakers:

J.A.J. Metz (Leiden University, the Netherlands)

(To Be Confirmed) S.C. Stearns (University of Basel, Switzerland)

Abstract:

The last three decades have revolutionized the way we think about evolution at various levels of organisation. New theoretical ideas on topics as molecular evolution, genetic conflicts, frequency- and density-dependent selection, sexual selection, spatial interactions, or non-equilibrium dynamics have played a major role in this process. Still there are major challenges as, for example, the integration of genetic and phenotypic approaches to natural selection, or the incorporation of developmental genetics into evolutionary theory. Several of these topics will be addressed in this session. We will also consider the empirical relevance of present-day models and discuss whether new modelling approaches are required to improve the testability of evolutionary theories.

5. Computational Neuroscience

Organisers:
J. van Pelt (Netherlands Institute for Brain Research, The Netherlands)
A. van Ooyen (Netherlands Institute for Brain Research, The Netherlands)
Invited speakers:
D. Willshaw (University of Edinburgh, United Kingdom)
(To Be Confirmed) T. Sejnowski (The Salk Institute for Biological Studies,USA)
Abstract:
Understanding the brain in health and disease is perhaps the greatest challenge for science in the next century. Because the brain is an extremely complex and organised system from the molecular up to the behavioural level, this goal can not be achieved without modelling and computational approaches. This Session aims at emphasizing this role of Mathematical Modelling and Computer Simulation in Neuroscience. Participants are invited to present progress in understanding the structure, function and development the brain.

6. Immunology and Within-Host Dynamics of Pathogens

Organisers:
R. Mehr (Princeton University, USA)
R.J. de Boer (University of Utrecht,The Netherlands)
Invited speakers:
L.A. Segel (The Weizmann Institute of Science, Israel)
T.B. Kepler (North Carolina State University, USA)
Abstract: The immune system is a typical example of a complex system having many feedback interactions. Our intuition for understanding the functioning of the immune system is therefore be markedly sharpened by studying mathematical models. These models involve regulatory networks, competition, and evolution. Recent mathematical work on the within-host dynamics of viruses like HIV, HBV, and HCV have had great impact on our understanding of such infections.

Afternoon Sessions

1. Individual-Based Population Dynamics

Organiser:
S.A.L.M. Kooijman (Free University, The Netherlands)
Abstract:
We like to welcome contributions that highlight

- problems that relate individual dynamics to population performance
- mass and energy conservation at the population level
- relationships between structured and unstructured population dynamics (effects of aggregation, simplification)
- analyze structured population dynamics in terms of bifurcation analysis and transient behaviour
- interactions between (structured) populations (food chains, food webs)

2. Gene Networks

Organisers:
D. Thieffry (University of Brussels, Belgium)
L. Glass (McGill University, Canada)
Abstract:

Structure and Dynamics of Gene Networks: As molecular data about specific regulatory mechanisms of gene expression are rapidly accumulating, there is an increasing need for integrative and formal tools. This session aims to review the different theoretical approaches dealing with the dynamical analysis of gene networks. It will cover the analysis of specific functional modules, as well as methodologies addressing gene networks at the level of whole organisms. It will encompass some of the tools to derive the dynamical behaviour resulting from specific network structures, but also attempts to infer regulatory architectures from temporal and/or spatial data of gene expression.

3. Pattern Formation and Morphogenesis

Organiser:

P.K. Maini (University of Oxford, United Kingdom) Abstract:

Recently, many advances have been made in understanding pattern formation in certain chemical and biological systems, and in the derivation of macroscopic models from observations at the microscopic level. This session will focus on the modelling and analysis of pattern formation in these areas.

4. Education in Mathematical Biology

Organiser:

J.R. Jungck (Beloit College, USA)

Abstract:

Not available

5. Parasites and Diseases in Wildlife

Organiser:

A. Pugliese (University of Trento, Italy)

Abstract:

This session aims at developing a common thread through different biological systems (micro- and macro-parasites; single or multi-host) and different modelling approaches. Topics will range from parasite interactions within hosts, through classical host-parasite systems, up to parasites' effect on communities.

6. Metabolic Control Networks

Organiser:

H. Westerhoff (Free University & University of Amsterdam, The Netherlands)

Abstract:

The living cell is one of the most complex objects studied by the natural sciences and mathematics. To a great extent this complexity derives the great many processes that occur in parallel, in a highly coordinated manner. Most of these processes lead to steady states, but others give rise to stationary oscillations, or even more complex patterns in space and time. The networks that are responsible for these dynamic processes, are structurally adaptable, as in a neural network. Intracellular 'compartments' are crowded with macromolecules. As a consequence of all this, functional processes of living cells are not controlled by a single 'rate-limiting' step in the corresponding metabolic pathway. Rather, control tends to be distributed over various levels of intracellular organisation, including metabolism, signal transduction, gene expression, and time, reflecting adaptation of the cell to earlier challenges. Only intensive mathematical modelling in conjunction with experiments entering the living cell, can make the living cell, and therewith the essence of life, understood. It will be the challenge of the next century to intensify the application of mathematics to cellular biochemistry. In this symposium, the most recent developments in theory and biomathematics concerning the living cell as a complex object, will be highlighted.

7. Whole Heart Modelling
Organiser:
S.A. Panfilov (University of Utrecht, the Netherlands)
Abstract:
This section will be devoted to major problems of mathematical modelling in cardiac electrophysiology. We are planing to discuss questions related to development of anatomically accurate models of the heart and human torso and questions on the best models for cardiac tissue. We also encourage participation of researchers interested in mechanisms of cardiac arrhythmias and in development of new methods for fighting these diseases.

8. Metapopulation Dynamics
Organiser:
J. Verboom (Institute for Forestry and Nature Research (IBN-DLO), The Netherlands)
Abstract:
Metapopulation models have been derived and analyzed for gaining insight into the dynamics of fragmented populations. The issue is still of interest, because of the ongoing destruction and fragmentation of habitat, and the hypothetical extinction vortex that may lead to extinction of many plant and animal species worldwide (also referred to as the extinction debt).

9. Toxicology
Organisers:
J.I. Freijer (National Institute of Public Health and the Environment (RIVM), The Netherlands)
M.J. Zeilmaker (National Institute of Public Health and the Environment (RIVM), The Netherlands)
Abstract:
This session on Toxicology focuses on the development of models of the toxicworking mechanism of chemicals and radiation. The main emphasis is on the translation of model concepts into mathematical/computer models and the parameterisation and application of the latter.

10. Particle Based Modelling
Organiser:
J. Kaandorp (University of Amsterdam, the Netherlands)
A.M. de Roos (University of Amsterdam, The Netherlands)
Abstract:
Particle based techniques (for example cellular automata,lattice gases, lattice Boltzmann method) are being applied in biological models at the molecular, complex, cel, individual, population and ecosystem level. This session will focus on the application and analysis of models that use any of these methods.

11. Networks, Cellular Signalling and Biological Rhythms
Organiser:
R. Heinrich (Humboldt-University Berlin, Germany)
Abstract:
This session focuses on the theoretical elucidation of the regulatory and dynamical properties of metabolic networks and of pathways of extracellular and intracellular signalling, as based on their stoichiometric and kinetic properties. Mathematical models concerning the whole variety of cellular mechanisms for energy transfer, phosphoryl transfer etc., for the action of different messengers, and for signalling via cell surface receptors or gap junctions are invited for presentation. Different modes of dynamic behaviour, such as amplification, oscillations, synchronization, transitions and multistationarity will be of interest. Attention is payed to

the confrontation with experimental data. Besides the results of simulating specific systems new methods for the modelling of these types of nonlinear dynamic systems may be presented.

12. Classification Methodology

Organiser:

(To be confirmed) T. Koski (Royal Institute of Technology, Stockholm, Sweden)

Abstract:

Important classification problems in biology and medicine include taxonomy and clinical diagnostics. The recent availability of DNA sequence data has had a great impact on the mathematical research in taxonomy and this is a field in rapid progress. This session will focus on recent developments and new approaches.

13. Miscellaneous

Abstract:

There will certainly be scientists willing to present interesting work at the conference that do not fit into one of the above sessions. The organising committee will evaluate the abstract submitted in this category separately and if possible organise a suitable way to include the presentations in the conference program.

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. A PARTICIPANT CAN ONLY SUBMIT 1 ABSTRACT AS FIRST AUTHOR. If a participant sends in more than a single abstract we will only take the first one submitted into consideration. 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.

Hotel Accommodation Preliminary reservations of rooms have been made in a range of hotels within the city of Amsterdam. Hotels in different categories are available for booking. Hotel reservations will be handled by the Conference Service of the Vrije Universiteit Amsterdam.

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		

Reservations could also be sent directly to:

Carlson Wagonlit Travel	Phone :	+31-(0)20-6241361
Dam 19	Fax :	+31-(0)20-4445825
NL 1012 JS Amsterdam	Email :	`agm@keytours.nl`
The Netherlands		

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`