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, 1997

Now also available on WWW
`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
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De Boelelaan 1087
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Email: `kooi@bio.vu.nl`

Contents

Contributions to this newsletter were made by: Odo Diekmann, Hans Heesterbeek, Hans Metz, Stefan Geritz.

1 Editorial

There is now a home-page for the NLS Population Dynamics and Epidemiology project. The URL is: `http//:www.bio.vu.nl/thb/users/nls` It is possible to download the Newsletter in PostScript format from this home page. 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 calen dar is updated more frequently. Please do not hasitate to contact for updates, improvements, suggestions and so on.

I acknowledge the help from Matthijs Luger, Theoretical Biology, VU Amsterdam with preparing the home-page.

Address change

Since November 1st Peter de Ruiter has a new position at the University Utrecht for three days per week. The other two days he will stay at the AB-DLO. His two addresses are:
Prof.dr. P.C.de Ruiter,
Department of Environmental Studies, P.O. Box 80115, 3508 TC Utrecht. tel. 030-2532140, 030-2532359 (secr.) fax. 030-2532746 email:`p.deruiter@frw.ruu.nl`
and
DLO-Institute for Agrobiology and Soil Fertility (AB-DLO), P.O. Box 129, 9750 AC Haren. tel. 050-5337772 030-5337777 (secr.) fax. 050-5337291 email: `p.c.deruiter@ab.dlo.nl`

2 Reports

2.1 Report on the mini-symposium *Beyond Adaptive Dynamics* January 24, 1997, Leiden

The program explored the conceptual connections between economic theory and adaptive dynamics and evolutionary game theory as perceived by biologists, as well as some frontiers of the theory of adaptive dynamics as it is presently developing.

Peter Hammerstein

The opening talk by Peter Hammerstein (Berlin) discussed the problem of equilibrium selection in game theory. The classical Nash equilibrium concept has the problem that there are very many Nash equilibria, i.e. strategies such that if everybody plays that strategy it wouldn't pay a single individual to start playing an alternative strategy. Many of these are very counterintuitive. For instance, in a game which is played in a number of subsequent moves, there may exist Nash strategies of the overall game which are based on a threat. However, it may be that once the opponent has made the move that according to the threat is to be punished, their is no gain in effecting the threat. This would take away the threat. Strategies such that there reduction to a subgame are still Nash are called subgame-perfect. Removing the subgame-imperfect strategies reduces the set of allowed equilibrium strategies. Other idea's are the "trembling hand" in which only strategies are allowed which stay Nash when infrequent mistakes occur in the chosen action, or the idea that we should take into account the occurrence of mistakes in the perception of one's opponent moves. The problem is how all these ideas stand up against the context of the game. For instance effecting threats may actually be functional if a game is played repetitively or is observed by future opponents. Biology provides at least some context for the various possible assumptions. But we are a long way from a good overview yet.

Karl Sigmund

Karl Sigmund (Vienna) gave a survey of the ways in which state-space representations can be constructed and employed to represent strategies with different sorts of memories for repeated games and explained the nature of the results obtained so far for various families of games with the same two-letter alphabet of possible pure strategies available per player and round, where the simultaneous moves of the two players were characterized by different inequalities among the pay-offs for the various combinations of moves.

Richard Law

Richard Law (York) tackled the interrelation of the social sciences and evolutionary biology from still another angle in a novel analysis of the "tragedy of the commons". Apart from the further mathematical elaboration his analysis of the problem differed in three ways from previous analyses. First of all he considered a renewable resource, secondly he kept the number of exploiters of that common resource finite, and thirdly he considered a scheme in which the exploiters changed their behaviour on the basis of the pay-off in the previous round in a manner which led to equations of the same form as the "canonical equations of adaptive dynamics" which also formed one of the main subjects of Ulf Dieckmann's talk. The outcome was that under mild conditions a much smaller level of overexploitation of the resource occurs than the tragical amount commonly predicted. The last two talks concentrated on the central concepts of adaptive dynamics per se.

Geza Meszena

Geza Meszena (Budapest) considered some extensions of the ideas of MacArthur and Tilman on resource based competition to an evolutionary context. In those cases where the environment can be characterized by a finite number of variables which monotonically influence fitness and which are monotonically influenced by the sizes of various evolving populations there is a duality between adaptive dynamics as a random walk in trait space and as a random walk in environment space. In environment space a new set of geometrical arguments come to the fore that can be exploited to derive new insights about the geometry of adaptive trait substitutions, thus forging a closer link between the ecological interpretation and the more abstracted viewpoint of adaptive dynamics. The final talk by Ulf Dieckmann (Laxenburg) concentrated on the derivation through formal limit arguments of adaptive dynamics as a continuous motion in trait space from individual-based models for the underlying population dynamics. This derivation went in two steps.

1. The starting point is a population dynamics formalized as a number of coupled birth and death processes. Individuals in each population reproduce and die with birth and death rates which depend on the overall community composition. The individuals in each process are characterized by a trait that is inherited and that determines their role in the community interaction. These traits are inherited almost faithfully: most of the time a daughter is of the same type as her mother, but sometimes the trait value of the daughter is a little displaced.

2. The assumptions of large population sizes plus mutation limitation give the population dynamics the possibility to deterministically equilibrate in between the arrivals of new mutants. Mutants then arrive as single individuals and therefore have to pass through a stochastic boundary layer where demographic noise sets the scene. This stochastic process results in either extinction or an entering of the deterministic realm. The extinction probability can be calculated from a branching process approximation. If we look on a large time scale we see a sequence of instantaneous mutant substitutions, inducing small jumps in the (equilibrium) population density.

3. If the mutational steps are small the resulting random walk in trait space can be approximated by a differential equation known as "the canonical equation of adaptive dynamics". The resulting chain of models, related to each other through limit arguments, provides a nice connection between various previously disconnected approaches to phenotypic evolutionary change.

One further point that may be worth noting is that the meeting also led to a number of somewhat heated discussions, in particular about the scenarios underlying adaptive branching. The adaptive dynamics community has a number of rather specific opinions about this topic which at times give rise to considerable disagreement. As it happens there also are a number of groups that work on these issues from a more empirical perspective at the host institution, the Leiden EEW. In the wake of the mini-symposium a series of discussions have been, and

are still, going on at the EEW. Through this link the mini-symposium by now has contributed to at least one paper:
F. Galis & J.A.J. Metz (1998) *Why are there so many cichlid species? On the interplay of speciation and adaptive radiation.* TREE 13: 1-2.

2.2 Visit report of prof. Marek Kimmel (Rice University, Houston, USA), December 8, 1997, Utrecht

Marek Kimmel was in Paris en route to Pau and this provided a good opportunity to suggest a small detour to the Netherlands for a visit to Odo Diekmann, Utrecht and Hans Heesterbeek, Centre for Biometry Wageningen. His area current interest is to extract information on historical changes in the size of populations from data on present-day DNA polymorphism in that population (e.g. looking at DNA repeat sequences such as microsatelite data). The theory is based on branching processes.

In the renewed spirit of our NLS-programme in its final phase, we tried to broaden the group of biologists that could benefit from the activities of the programme. On Monday morning we could arrange a meeting between Marek Kimmel and Pim van Hooft (Department of Terrestrial Ecology and Nature Management of the Agricultural University Wageningen), who represents a group that is interested in problems very similar to Marek's. The group studies microsatelites in African buffalo, to elucidate population changes during a major epidemic of rinderpest in the nineteenth century. Both Marek and Pim judged this discussion as valuable and illuminating for both parties.

In the afternoon there was a programme of four well-attended lectures: Marek Kimmel, Johannes Mueller, Sido Mylius and Hans Heesterbeek. The audience for Marek's lecture consisted of 25 people, of whom 15 were still left at the end of the afternoon. We had the feeling that the lectures were much appreciated. In summary, this extremely short visit was very worthwhile.

The summaries of these talk are:

Marek Kimmel:
Population Dynamics coded in the DNA: History of growth and migrations of modern humans

Department of Statistics Rice University Houston, TX, USA
Credits: Michael Bamshad, Ranajit Chakraborty, Leslea J.Davison, Ranjan Deka, Lynn B.Jorde, J.Patrick King, Andrzej Polanski, W.Scott Watkins

It has been proposed that modern humans evolved from a small ancestral population, which appeared several hundred thousand years ago in Africa. Descendants of the founder group migrated to Europe and then to Asia, not mixing with the pre-existing local populations (e.g. the Neanderthal men in Europe), but replacing them. Two demographic elements are present in this "out of Africa" hypothesis: numerical growth of the modern humans and their migration into Eurasia.

Did these processes leave an imprint in our DNA? To address this question, we use the classical Fisher-Wright-Moran model of population genetics, assuming variable population size and two models of mutation: the infinite-sites model and the stepwise-mutation model. We use the coalescence theory, which amounts to tracing the common ancestors of contemporary genes. We obtain mathematical formulae expressing the distribution of alleles given the time changes of population size $N(t)$ (some of them analogous to the Lyapunov's equation known from the control theory).

In the framework of the infinite-sites model, estimation of $N(t)$ requires using the reverse Laplace transform known to be unstable. Nevertheless, simulations indicate that the pattern of past population size change leaves its signature on the pattern of DNA polymorphism. Application of the theory to the published mitochondrial DNA sequences indicates that the current mitochondrial DNA sequence variation is not inconsistent with the logistic growth of the modern human population.

In the framework of the stepwise-mutation model, we demonstrate that population bottleneck followed by growth in size causes an imbalance between allele-size variance and heterozygosity. We analyze a set of data on tetranucleotide repeats which reveals the existence of this imbalance. The pattern of imbalance is consistent with the bottleneck being most ancient in Africans, most recent in Asians and intermediate in Europeans.

These findings can be interpreted as consistent with the "out of Africa" hypothesis, although by no means do they constitute its proof.

Sido Mylius (UvA): *The resident strikes back*

We investigate the interplay of population- and adaptive dynamics in the context of the timing of reproduction of Pacific Salmon. Coexistence of different population-dynamical attractors and resonance of life-span relative to population dynamical fluctuations can have a profound effect on invasibility and the resulting evolutionarily stable life-history. Different local attractors of the resident population dynamics can have different invasion properties. Successful invasion in one attractor can be followed by extinction of the former invader, ultimately leading the resident to the same attractor, but phase-shifted, or to another attractor. So a strategy can be "invasible, yet unbeatable".

Hans Heesterbeek (Centre for Biometry Wageningen), Mick Roberts: *A simple parasite model with complicated dynamics*

We show that a simple model for parasitic infection of farm animals, incorporating an environmental stage in the life-cycle of the parasite, acquired immunity and management practice can show complicated dynamics. The model incorporates the above aspects in a rudimentary but non-trivial way. The analysis shows that one has to be careful when using models to gauge effects of control measures for systems where these aspects play a major role.

3 Summaries of PhD-theses

Summary of the PhD-thesis by **Stefan Geritz**, EEW Leiden University,
Email: `geritz@zool.umd.edu`

The evolutionary significance of variation in seed size

Variation in seed size between and within individual plants of the same species is common and widespread. The central question of this thesis is how this variation can be explained as a consequence of natural selection under specific circumstances.

- In Chapter 1 I review some of the empirical data on how seed size affects plant fitness, and I summarize a number of models for the evolution of seeds size variation each of which emphasizes a different aspect of a plant's life-history or its environment.
- In Chapter 2 I show that small-scale spatial variation in seed density due to random seed dispersal may favor the evolution of variation in seed size both within and between individual plants if competition among seedlings is sufficiently asymmetric in favor of larger seeds.
- In Chapter 3 I show that coevolution with a seed predator may favor the evolution of variation in seed size both between and within individual plants if there is a trade-off in the predator's attack rate for different seed sizes.
- In Chapter 4 I develop a general framework and a mathematical toolbox for modeling the dynamics of mutation-limited evolution. Special emphasis is put on the generation of phenotypic variation by branching of the evolutionary tree during which a given lineage already present in a population divides into two distinct and subsequently diverging daughter lineages.
- In Chapter 5 I apply the above mentioned modeling framework to show that strong competitive asymmetry and high resource levels favor evolutionary branching and co-existence of plants with different seed sizes when large seeds have a substantial precompetitive advantage over smaller seeds. If precompetitive seed and seedling survival is high for small and large seeds alike, evolutionary branching may be followed by extinction of one or more lineages (including mass-extinction). Various results presented in this chapter are model-independent and point the way to a more general evolutionary bifurcation theory describing how the number and stability properties of evolutionary equilibria changes as a consequence of changing model parameters.

4 Master Class Spatio-Temporal patterns

What follows is the **final** schedule for the spring semester of the Master Class Spatio-Temporal patterns. June 2–6 1998 a final Summer School "Spatio-Temporal Patterns" Twente University, the Netherlands with five speakers. See **Calendar** for more details.

x means two times 45 minutes, □ means a full day.
Morning classes are from 11.00-13.00; afternoon classes are from 14.00-16.00, except in week 11-16 on thursdays and fridays: On those days the schedule is 12.00-13.00 and 14.00-17.00
U = Utrecht, G = Groningen, A = Amsterdam,
1 = Monday, 2 = Tuesday, 3 = Wednesday, 4 = Thursday, 5 = Friday.

week	5	6	7	8	9	10	11	12	13	14	17	18	23
numerical mathematics: model-properties-solutions	□U4	□U4	□U4	□U4	□U4	□U4							s
(non)linear statistical analyses of processes in space and time							□U5	□U5	□U4	□U4	□U5	□U5	u
seminar in preparation of the final summer school (a)	xU3	xU3	xU3	xU3	xU3	xU3	xU3	xU3	xU3	xU3	xU3	xU3	m
ergodic theory (m)	xU1	xU1	xU1										m
empirical orthogonal functions (a)					xG1	xG1							e
visualization (m)					xG1	xG1	□G1		xG1				r
experimental analyses dynamical systems (a)		□G2	□G2										s
variational methods (m)								xU3	xU3	xU3			c
meteorology & chaos (m)	xU3	xU3	xU3	xU3	xU3	xU3							h
morphology											□A1	□A1	o
ecology (a)				□U2									o
heartfibrilation (a)	xU1	xU1									xU3	xU3	l

5 Calendar

January 6, 1998

Mini-symposium on Adaptive Dynamics on the occasion of Stefan Geritz' PhD organized by the Section Theoretical Evolutionary Biology of the Institute of Evolutionary and Ecological Sciences, EEW, RUL, in collaboration with the project Population Dynamics of the NWO priority program Non-Linear Systems.

Address: Van der Klaauw Laboratory
'grote collegezaal' (in the blue building)
Kaiserstraat 63, Leiden

10:00 - 11:00 Hans Metz (EEW, RUL). *From Population Dynamics to Adaptive Dynamics, and introduction for the uninitiated*

11:00 - 12:00 Éva Kisdi (Department of Genetics, Eötvös University). *Evolutionary Loitering and Branching in a Model for Asymmetric Competition*

13:00 - 14:00 Mats Gyllenberg (Department of Mathematics, University of Turku). *Adaptive Dynamics under Predation*

14:00 - 15:00 Stefan Geritz (Department of Zoology, University of Maryland). *The Adaptive Dynamics of Seed Size Evolution*

Addendum: Between 16:15 and 17:00 Stefan Geritz will defend his PhD entitled 'The Evolutionary Significance of Variation in Seed Size' in the old Senate office, Rapenburg 73, Leiden.

January 7–11, 1998

NLS winterschool on Population Dynamics, Woudschoten, January 7–11 1998 Registration form at the end of the announcement. Please feel free to pass this message on to anyone you think would be interested in modelling population dynamics.

The school will be organised along the same lines as the 1996 Winterschool. Five speakers will each give five lectures on their field of expertise. In addition to these lectures all participants will give a short presentation of their own work and interest (two minutes, one transparancy). During the school some papers will be studied in small groups culmunating in a short plenary presentation of the findings.

The five speakers are:

Ulf Dieckmann (Vienna)	stochastic theory and adaptive dynamics
Josef Hofbauer (Vienna)	deterministic dynamical systems in population dynamics and population genetics
Mous Sabelis (Amsterdam)	population ecology
Mats Gyllenberg(Finland)	metapopulation dynamics
Olof Leimar (Sweden)	behaviour and evolutionary dynamics

The aim of this winterschool is to give (beginning) PhD students in population biology a better understanding of the way mathematics can be applied to appoach biological problems. Participants will be given a background in many relevant deterministic and stochastic mathematical and numerical modelling apoaches. There are now 55 participants from all over the world!

June 2–6, 1998

Summer School "Spatio-Temporal Patterns" will be held at Twente University, the Netherlands.

This course is intended for young researchers with a strong mathematical interest, and should provide them with a good overview of various approaches to understand patterns displayed by the space-time characteristics of physical, chemical, biological, ... phenomena. There will be five main lecturers, and each of them will lecture 6 hours. Their names, the title of their lectures and a short abstract are listed below.

Right at the beginning of the course, participants will be asked to present themselves, their background and scientific interests, in a "3 minutes/1 overhead transparency" presentation. We expect 30-40 participants.

Participants and lecturers will be lodged in hotel "de Logica". Prices are Dfl. 50,- per day for a double room and Dfl. 65,- per day for a single room. As the number of rooms is limited, we ask people to share a room as much as possible. The organisers cannot provide any financial support (neither for travel, bed and breakfast, nor for subsistence). We therefore have kept the admission fee as low as possible: Dfl. 100,–.

Applications (The application form is attached below) can be send to: `M.Plekenpol@math.utwente.nl` Admission is on the basis of arrival of the application.

The course is sponsored by MRI, the SWON-NWO program "Dynamical Systems and Pattern Formation", ... and is organised by Odo Diekmann, Arjen Doelman, Stephan van Gils and Ronald Meester.

The lecturers are:

Rick Durrett (Cornell)	Stochastic and Spatial Models
Jean-Pierre Eckman (Geneva)	Some topics in the study of partial differential equations on the infinite line
Nick Ercolani (Tucson)	tba
Satya Majumbar (Bombay)	Self-organised Criticality
Yasumasa Nishiura (Sapporro)	Asymptotic and transient dynamics in pattern formation of nonlinear dissipative systems

June 21–26, 1998

Fifth International Conference 'Mathematical Population Dynamics Zakopane, Poland, June 21–26, 1998. This conference will be an interdisciplinary forum where applied mathematicians, statisticians, engineers, computer scientists, biologists, epidemiologists, biomedical scientists and ecologists can share their experiences.

Web site: `http://www.cyf-kr.edu.pl/zakopane/index.html`
Information: Mr. Jaroslaw Smieja, Department of Automatic Control, Silesian Technical University, Akademicka 16, 44–101 Gliwice, Poland.
E-mail: `JSMIEJA@peach.ia.polsl.gliwice.pl`

September 4–8, 1998

Alcala First International Conference on Mathematical Ecology, Alcala de Henares (Madrid) Spain.

Plenary Lectures: **P.Auger** (University Claude Bernard Lyon 1, France), **H.Caswell** (Woods Hole Oceanograplic Institution, USA), **J.Cushing**, **T.G.Hallam** (University of Tennessee, USA), **J.Horwood** (CEFAS Lowestoft, UK), **S.A.L.M.Kooijman** (Free University Amsterdam), **S.Levin**, **F.Milner**, **D.Rand**, **S.Rinaldi** (Politecnico di Milano, Italy).

Summary of the talk of Bas Kooijman `bas@bio.vu.nl`:*The Dynamic Energy Budget model for structuring populations on the basis of physiological processes*

The Dynamic Energy Budget (DEB) model consists of a set of simple, mechanistically inspired, rules for the uptake and use of substrates (food) by an individual organism. It specifies the key processes of feeding, assimilation, development, maintenance, growth, reproduction (or division) and ageing quantitatively, and is meant to apply to all organisms on earth. These processes can by specified realistically for animals, feeding on other animals, with only one internal reserve and structural body mass as state variables, while cumulated damage is required as third state variable to specify the aging process. Organisms, such as algae, which can be limited in their growth by several types of nutrients (and/or light), require more types of reserves. Organisms, such as plants, which use different organs for the uptake of different nutrients and light, also require more types of structural biomass. These extensions with respect to the simpler model for animals, follow naturally from the set of simple rules, and specify all energy and mass fluxes simultaneously, on the basis of the principle of homeostasis. These fluxes include dissipating heat, water, oxygen and carbon dioxide (among others). The theory, therefore, provides a fundamental basis for the coupling between energy and mass fluxes in organisms.

Since the DEB model relates substrate uptake to surface area and maintenance to volume of structural biomass, changes in shape are important in the specification of the key processes. The DEB model reduces to a very simple structure for 1D-isomorphs: organisms for which surface area is proportional to volume. It can be shown that organisms that divide into two parts at a fixed investment into maturation, such as microorganisms, behave approximately as 1D-isomorphs, irrespective of their actual changes in shape during growth. Several popular models for the growth of microorganisms turn out to be special cases of the DEB-model. The distinction between the individual and population level disappears for 1D-isomorphs, and physiologically structured population models reduce to unstructured ones, which can be represented as a simple set of ode's. This does not hold for organisms with big ratios between adult and neonate size.

The set of rules that specify the DEB-model imply the existence of a maximum body size for each species of organism, and classifies all its parameters into two categories: intensive parameters that do not depend on maximum body size, and extensive parameters that can be shown to be proportional to volumetric length. The rules, therefore, imply trends in parameter values, when species with different maximum body sizes are compared. These trends turn out to be realistic for many physiological and life history quantities that can be written as functions of parameter values, such as respiration rate, life span, maximum reproduction rate, etc. This property is of great help to reduce the number of parameters in the application of the DEB-model to specify the dynamics of food webs, for instance.

The DEB-model is simple enough to obtain some analytical results for populations in steady state, while some popular software packages can be used successfully to analyse the population dynamics in simple environments, such as the chemostat. It appears to be possible to obtain at least some of the rules on which the DEB-model is based from more detailed models on molecular kinetics. The DEB-model seems, therefore, usefull in linking physiological processes to population dynamics.

Keywords: Mass and Energy balances, homeostasis, body size scaling relationships, multiple nutrient limitations.
References: Kooijman, S.A.L.M. (1993) Dynamic Energy Budgets in Biological Systems, Theory and application in ecotoxicology. Cambridge University Press.

Special Sessions

P.Auger, Lyon. Aggregation methods and perturbations in population dynamics,
B.W.Kooi, Amsterdam. Bioenergic modelling of ecosystems,
J.L.Gouzé, Nice. Control theory applied to ecological problems,
S.Tuljapurkar, Los Altos. Do variable environments affect life history trade-offs?
J.Michalski, Laussane. Food webs,
Jia Li, Alabama. Mathematical modeling in infectious diseases,
M.A. Zavala, Princeton. Perspectives in modeling vegetation dynamics,
H. Heesterbeek, Wageningen. Population ecological effects of parasites,
V.Kaitala, Helsinki. Spatial population dynamics: models and empirical testing,
H.Malchow, Osnabtück, **J.Brindley**, Leeds, and **A.B.Medvinsky**, Pushchino. Spatial, temporal and spatio-temporal structures in oceanic plankton populations,
M.Popescu, Bucharest. Stability and analysis in the dynamics of systems,
E.Sánchez, Madrid, and **O.Arino**, Pau. Structured Population Dynamics: Comparison of individual and global models,
T.Kostova, Sofia. Structured population models: Behavior of solutions: Analytical and numerical approaches.

Summary of the session organized by Hans Heesterbeek `J.A.P.HEESTERBEEK@cpro.dlo.nl` : *Population ecological effects of parasites*

It has been well-studied, both theoretically and by observation, that parasites and infectious agents can be important determinants of community structure and that they can regulate host population growth. Recently, there is renewed interest for ecosystem effects of infections in a number of important areas that all deserve more attention from mathematical modellers. Concrete examples are: 1. diseases in metapopulations (improved connectedness of sub-populations leads to increased spread of infections; implications both for nature management and for understanding dynamics of human infections such as measles); 2. the role of parasites in structuring foodwebs; 3. the role of infections in structuring spatial phenomena observed in stochastic spatial models; 4. the role of parasites in driving spatial genetic host diversity.

Summary of the session organized by Bob Kooi `kooi@bio.vu.nl` : *Bioenergic modelling of ecosystems*

The classical Lotka-Volterra model has been altered in many ways to model food webs more realistically. The dynamics of the web is mathematically described as a set of coupled nonlinear ordinary differential equations. This makes application of the theory of nonlinear dynamics systems possible. Commonly used models for food chains have been studied intensively using bifurcation analysis. Various types of dynamic behaviours were described in the literature: point attractors, limit cycles and chaos. The chaotic behaviour includes boundary crises and global homoclinic and heteroclinic bifurcations. Nowadays computer packages are available to perform these bifurcation analyses. Application to a entire food web is, however, still cumbersome. Modelling a whole food web, including all sorts of complex ecological phenomena such as competition, omnivory would require a large number of parameters. Furthermore the obtained bifurcation diagrams may be difficult to interpret and there is always a danger to miss important bifurcation points. This hampers direct application of the theory of nonlinear dynamic systems.

To reduce the number of parameters, different methods can be applied. One might consider the use of aggregation techniques and body size scaling relationships across species. When time-scales differ greatly, singular perturbation techniques can be used. On the other hand, bifurcation theory could be used to classify the calculated bifurcations, in order to detect the intrinsic characteristics of food web dynamics.

In this session researchers are invited to contribute their views on the issue of modelling communities. These models allow the quantitative investigation of a number of hypotheses which have been put forward to explain dynamic phenomena of ecosystems in nature (for instance: the shortness of food chains). Also welcome are contributions with application of these mathematical approaches to real-life problems in e.g. conservation biology or ecotoxicology.

Web site: `http://www.ciencias.alcala.es/depmat/aicme.htm`
Information: Rafael Bravo de la Parra Departamento de Matematicas Universidad de Alcala 28871 Alcala de Henares (Madrid) Spain,
E-mail: `aicme@mat.alcala.es`

29 June–3 July, 1999

International Conference on Theory and Mathematics in Biology and Medicine Joint meeting of the European Society for Mathematical and Theoretical Biology (ESMTB) and the American Society for Mathematical Biology (SMB). Place: Amsterdam. Organising body: Dutch Society for Theoretical Biology (NvTB).

Application form Summer School "Spatio-Temporal Patterns" will be held at Twente University, the Netherlands.

Last Name :

First Name :

Title :

Institute :

Postal address:

Country :

Email address :

Arrival : (date & time)

Departure : (date & time)

* please indicate your preferences to the following

Single room	yes	no	(Dfl 65,– p.p. p.n. incl. breakfast)
Double room	yes	no	(Dfl 50,– p.p. p.n. incl. breakfast)
Lunch	regular	vegetarian	(Dfl 15,– per lunch)
Diner	regular	vegetarian	(Dfl 35,– per diner)