Project description

In population dynamics mathematical models are used to predict the evolution of species in their habitat. Implementation of these models in computer codes permits the prediction of the time course of the population size by simulation. This is done in fisheries and agricultural sciences, for water quality management where plankton dynamics is investigated to understand algal blooms, for landscape design and management, bio-conservation and global change for the study how change in climates influences the dynamics of the species and visa versa.

A wide range of different mathematical models at different levels of sophistication have been proposed in the literature. In the Lotka-Volterra model the population is described by the number of the identical individuals which make up the population. Modelling of growth and death as well as the interaction between prey and predator yields the wellknown predator-prey model.

This classical Lotka-Volterra model has been altered in many ways to model food webs more realistically. The inclusion of more populations is one of them and this yields mathematical models for so-called food webs. The dynamics of the food 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, see for instance [1]. 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. This is one of the main subjects of research of the Lyon Group headed by P. Auger in Lyon, France. The second technique is worked out in [2] by the VU Group headed by S.A.L.M. Kooijman in Amsterdam, the Netherlands.

These reduced 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).

The collaboration between the two groups started in the framework of the research project "Population dynamics and epidemiology" sponsored by the NWO Priority Program Nonlinear Systems (NLS). This cooperation led to a joint article [3] in a special issue of the journal *Mathematical and Computer Modelling* on 'Aggregation and Emergence in Population Dynamics'. A second paper [4] is submitted for publication to the journal

Mathematical Biosciences.

In this proposal asks for financial support for visits of members of both groups. We will apply the same aggregation method to more realistic models for food webs. In that case there exist several populations at each trophic level. Then the reduced model predicts more complex dynamics, for instance, predators at a trophic level can either coexist or exclude each other. It is clear that the applicability of that model for ecological systems, is much broader.

In nature, ecological communities are sometimes composed of groups of species with strong interactions in the same group and weak interactions between different groups corresponding to hierarchically organized communities [5, 6, 7]. Numerical simulations of Lotka-Volterra communities involving many species have also shown that after a transient phase during which several populations get extinct, the final structure of the community is hierarchical. In future studies, we intend to use aggregation techniques to simplify hierarchical community graphs. This will be done by aggregating populations of each group into a single compartment described by its total biomass being the aggregated variable. For each isolated cluster, mass conservation laws will be observed.

Aim of the project

Most of the mathematical models of food webs are simplified, i.e. with a single population at each trophic level. The aim of this project is to use aggregation methods to take into account several populations at each level, for example two predators. We shall study hierarchically organized food webs. The aggregation method will allow us to obtain a simplified model governing the time variations of slow global variables, for example the total biomass of each trophic level. The dynamics of the reduced model will be performed by use of classical methods (phase portrait, bifurcation diagrams ...).

Calendar

First year: Bibliography. Obtention of the dynamical system describing the food web.
Study of aggregation and averaging methods for community structure models. We shall start with a Lotka-Volterra model with several trophic levels and several species at each level. The intra-level interactions will be strong in comparison to inter level interactions.
Second year: Use of aggregation methods to derive the reduced model. Study of the couplings between the intra and inter levels dynamics.

- Third year: Bifurcation analysis of the reduced models. This gives a good insight into the consequences of different population dynamic models on the dynamic behaviour of the food web under various environmental conditions.

Complementarity between the two groups

The project has an important component relating to mathematical methods for the study of complex communities. Both groups have competences in complementary areas: - Aggregation methods, reduction of the dimension, theory of perturbations (P. Auger and J.C. Poggiale).

- Use of methods for bifurcation analysis. (B.W. Kooi and S.A.L.M. Kooijman).

The Dutch team has also a great experience in the use of mathematical models of communities in batch or chemostat conditions and its confrontations to real data.

References

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