AN INDIVIDUAL-BASED MODEL OF COEXISTENCE AND COMPETITION BETWEEN CRYPTIC NEMATODE SPECIES

AISLING J. DALY
aisling.daly@ugent.be

KERMIT Research Unit, Department of Mathematical Modelling, Statistics and Bioinformatics, Ghent University

Joint work with Nele De Meester**, Jan M. Baetens*, Tom Moens**, and Bernard De Baets*
* KERMIT Research Unit, Ghent University
** Marine Biology Research Group, Ghent University

Keywords: Individual-based model, Spatially explicit model, Cryptic species, Competition, Coexistence.

Several possible mechanisms have been suggested to underpin the coexistence of cryptic species, including differences in resource use or in tolerances to environmental conditions [1]. Recent experimental work has uncovered such coexistence in a community of four cryptic *Litoditis marina* species, a bacterivorous marine nematode inhabiting the littoral zone [2]. Important differences in functionality and stress tolerance were found to exist between the cryptic species, which the authors hypothesize to play a role in mediating their coexistence despite high levels of interspecific competition. To untangle the mechanisms governing the dynamics of this system, mathematical modelling can be a powerful tool. For example, it can be employed for scenario analyses that test the *in silico* community’s response to changing environmental conditions.

We use an individual-based modelling approach to simulate this system of four interacting species, due to its high levels of inter- and intra-specific variability. This approach allows for the representation of the individual variability of the system as well as its spatial heterogeneities, both of which are hypothesized to support the coexistence of competing species [3]. For these reasons, individual-based models have recently been highlighted as one of the preferred *in silico* approaches for assessing the effects of climate change on marine organisms [4].

Our model simulates the key demographic processes (reproduction, dispersal and competition) explicitly at the individual level. The changing characteristics of each individual — including age, size, physiological energetics, and location — are tracked through time as individuals interact with each other and their environment. As a result of this multitude of interactions at the individual level, patterns emerge naturally at the population level. The model is parameterized with data characterizing the four cryptic species in terms of their
growth rates, dispersal ability and competitive interactions, as well as their responses to changing environmental conditions.

We conduct simulation studies and scenario analyses to investigate the effects of changing abiotic and biotic conditions on the structure, stability and functionality of the in silico community. Differences in the species’ tolerance to abiotic changes play an important role in the dynamics of the system, while biotic changes affect the persistence of the underlying competition structure and threaten coexistence. Our results permit insight into the fundamental mechanisms supporting the coexistence of these cryptic species, as well as furthering the understanding of the dynamics and functioning of communities threatened by climate-related environmental changes. Our work therefore represents a first step towards the development of an integrated model of interactions between key marine species.

References


ON MATHEMATICAL MODEL FOR FISSION-FUSION BATS POPULATION

Anna Poskrobko  
a.poskrobko@pb.edu.pl

Faculty of Computer Science, Bialystok University of Technology, ul. Wiejska 45A, Bialystok, Poland  
Joint work with Antoni Leon Dawidowicz (Faculty of Mathematics and Computer Science,  
Jagiellonian University, ul. Lojasiewicza 6, 30-348 Kraków, Poland).

Keywords: Differential equations, Population model, Bats.

We present the construction of mathematical model describing the growth of bats’ population. The model is based on the system of ordinary differential equations. We consider some natural bats’ abilities and a location of natural roosts in the area, what determine searching and populating tree cavities. Bats’ roost searching strategy determines the development of subpopulations and fission-fusion societies. We present some properties of the model. Presented results are illustrated by computer simulations.

Acknowledgements: This work is supported by Bialystok University of Technology (Grant No. S/WI/1/2016) and founded by the resources for research by Ministry of Science and Higher Education.
ANALYSING THE IMPACT OF TRAP GEOMETRY ON PITFALL TRAP COUNTS

DANISH ALI AHMED
dahmed1@pmu.edu.sa
Department of Mathematics and Natural Sciences, Prince Mohammad Bin Fahd University (PMU),
Al Khobar, KSA
Joint work with Sergei Petrovskii (Department of Mathematics, University of Leicester, University road, Leicester, LE1 7RH, UK)

Keywords: Pest monitoring, Trap counts, Random Walk, Diffusion, Individual based modelling.

A major challenge in ecological field studies is to reliably estimate the population abundance of a species. In the case of insect pest monitoring, pitfall traps are usually installed to obtain trap counts. Translating these counts accurately to obtain direct population estimates can be a difficult task, since it is unclear which factors impact trap catch patterns, and to what extent. Examples of such factors include changes in; environmental conditions, habitat landscape, population size, movement behaviour, individual traits, trap shape, design and setting etc. The result thereof is a system of substantial ecological complexity, and thus it is near enough impossible to untangle information on factor impact. The issue becomes more problematic if experiments are to be replicated - under supposedly controlled conditions. In this talk, our focus is on trap geometry and the subsequent effect on trap count dynamics, a current open question - to date poorly understood. We propose a theoretical approach, by simulating movement in a homogenous environment within a confined domain, in the presence of a trap of alternating shapes. We consider two different movement models commonly used for insect movement, namely, stochastic Brownian motion and the Correlated Random Walk (CRW). The CRW allows for directional persistence, resulting in a more realistic movement description if movement tracks are recorded on a shorter time scale. By analysing trap count patterns for these distinct movement processes within these different geometries, we present a novel study with theoretical arguments, which reveal the impact of pitfall trap geometry on the efficiency of catches.
AVERAGING THE POPULATION PROJECTION MATRICES OVERESTIMATES THE STOCHASTIC GROWTH RATE

DMITRII O. LOGOFET
diniLaL@postman.ru

Laboratory of Mathematical Ecology, Institute of Atmospheric Physics, Russian Academy of Sciences, Moscow, Russian Federation

Keywords: Matrix population models, Pattern-geometric average.

When calibrated with field data, each population projection matrix (PPM) indirectly characterizes the environment that has realized in the interval between two consecutive censuses (e.g., years) and generates a number of explicit quantitative characteristics the local population has revealed for that interval. A time series of different PPMs generates the series of differing characteristics, hence respectively different predictions of the population fate. Two concepts are proposed in the literature to summarize the outcome of the whole observation period – a recent original one (Logofet, 2018) called the pattern-geometric average and an earlier one by Tuljapurkar (1990) called stochastic growth in the random environment. The outcome of the former one is the dominant eigenvalue, $\lambda_1$, of the pattern-geometric average matrix $G$, while the earlier concept leads to an estimate of the stochastic growth rate $\lambda_S$ as the discrete analogue to the first Lyapunov exponent. Recent case studies of two alpine herbaceous species under 9 years of observation have revealed that $\lambda_1(G)$ is markedly greater than the $\lambda_S$ obtained in several series of Monte Carlo experiments. The hypothesis that this is always true has to be verified in future case studies on matrix population modelling, and it should also have a fundamental reason in the mathematical properties of infinite products among nonnegative matrices.

References


TOXIN-MEDIATED COMPETITION IN BACTERIAL COMMUNITIES

ANDREW DEAN
andrew.dean@liverpool.ac.uk
University of Liverpool

Joint work with Mal Horsburgh and Bakhti Vasiev (University of Liverpool).

Keywords: Bacterial Ecology, Antimicrobial Resistance, Competition, Invasion.

The rise of antimicrobial resistance is one of the greatest challenges facing the global community in the twenty-first century. One possible solution is the exploitation of natural competition between microbial species in order to combat pathogens. For example, the human skin microbiome invariably contains the commensal bacteria *Staphylococcus epidermidis* and *S. hominis*, whose presence may aid in preventing colonisation by the potentially pathogenic *S. aureus*. However, the dynamics involved in such interactions are complex and difficult to study in sufficient detail in the laboratory. We have therefore developed an ODE model of a simple bacterial ecosystem incorporating both passive competition for resources and active inhibition via toxin production. We analyse this model under various ecological scenarios in conjunction with existing empirical data. We are thus able to elucidate the interplay between passive and active competition and its effect on the populations under consideration, paying particular attention to a species’ ability to defend against invasions from a competitor and the role of resistance in such interactions.