MPDE 2017 ABSTRACTS

KEYNOTES

Mats Gyllenberg (University of Helsinki)

Evolution and optimisation

It is a wide spread misconception that evolution optimizes some quantity like fitness or reproductive success. In this talk I give a brief introduction to adaptive dynamics, which is a mathematical theory that explicitly takes into account the interaction between population dynamics (ecology) and evolution by natural selection. Using the well-known rock-scissors-paper-game as a metaphor, I give necessary and sufficient conditions for when there is a function which is optimized by natural selection. It turns out that evolutionary optimization is extremely rare and hardly can happen in nature.

Robert Holt (University of Florida)

On the interplay of demographic stochasticity, fitness, and the niche concept

The concepts of "fitness" and "niche": are arguably among the most central concepts of evolutionary biology and ecology. Both are often related to population measures such as intrinsic growth rates (e.g., Ronald Fishers' Malthusian parameter). My presentation will review the ways these two concepts are related, and explore some consequences of demographic and environmental stochasticity, and spatial dynamics. My talk will end with discussion of niche conservatism and evolution, pertinent to the issue of evolutionary rescue in our rapidly changing world.

Cang Hui (University of Stellenbosch)

Trait evolution within bipartite ecological networks

Bipartite ecological networks are formed by interactions between species which exploit each other for survival and are crucial components to sustain ecosystem function and services, foster biodiversity and affect community stability. Despite their diversity, bipartitle ecological interactions exhibit surprisingly well-organised structures. In particular, they are often found to be within a certain range of connectance, nestedness and modularity, as well as a right skewed degree distribution. Evidently, these multiple features of bipartite ecological networks are not independent of each other, suggesting that an integrated model is required to better capture the intrinsic dynamic features of species interactions. Here, we review a list of eco-evolutionary models for investigating the pattern emergence in bipartite ecological networks with trait-mediated interactions phylogenetic modelling, adaptive interaction switching and adaptive dynamics. First, using knowledge of the phylogenies of the interacting species, our model yielded a significantly better fit to a quarter of a set of mutualistic networks. This highlights the importance, in a substantial minority of cases, of inheritance of interaction patterns without excluding the potential role of ecological novelties in forming the current network architecture. Second, the model allowing interaction switches between partner species produced predictions which fit remarkably well with observations, and thus the interaction switch is likely a key ecological process that results in observed structures of real- world networks. Finally, trait-based adaptive dynamics models highlight the importance of assortative interactions and the balance of costs incurred by coevolving species as factors determining the eventual phenotypic outcome of co- evolutionary interactions. The interplay of ecological and evolutionary processes through trait-mediated interactions can explain these widely observed architectures in bipartite networks. Coevolutionary networks provide an ideal model for modelling complex adaptive systems, which can help to address challenges from global changes facing many complex social-ecological systems.

Horst Malchow (University of Osnabrck)

Noise-mediated coexistence of competitors

Stochastic reaction-diffusion equations are a popular modelling approach for studying interacting populations in a heterogeneous environment under the influence of environmental fluctuations. Although the theoretical basis of alternative models such as Fokker-Planck diffusion is not less convincing, movement of populations is most commonly modelled using the diffusion law due to Fick. An interesting feature of Fokker-Planck diffusion is the fact that for spatially varying diffusion coefficients the stationary solution is not a homogeneous distribution - in contrast to Fick's law of diffusion. Instead, concentration accumulates in regions of low diffusivity and tends to lower levels for areas of high diffusivity. Thus, the stationary distribution of the Fokker-Planck diffusion can be interpreted as a reflection of different levels of habitat quality. Moreover, the most common model for environmental fluctuations, linear multiplicative noise, is based on the assumption that individuals respond independently to stochastic environmental fluctuations. For large population densities the assumption of independence is debatable and the model further implies that noise intensities can increase to arbitrarily high levels. Therefore, instead of the commonly used linear multiplicative noise model, the environmental variability is implemented by an alternative nonlinear noise term which never exceeds a certain maximum noise intensity. With Fokker-Planck diffusion and the nonlinear noise model replacing the classical approaches a simple invasive system is investigated based on the Lotka-Volterra competition model. It is found that the heterogeneous stationary distribution generated by Fokker-Planck diffusion generally facilitates the formation of segregated habitats of resident and invader. However, this segregation can be broken by nonlinear noise leading to coexistence of resident and invader across the whole spatial domain, an effect that would not be possible in the non-spatial version of the competition model for the parameters considered here.

Bob Scholes (University of the Witwatersrand)

The Global Carbon cycle and where it intersects with population processes

Katriona Shea (Pennsylvania State University)

Using multiple models to address uncertainty, value of information, and optimal control of disease outbreaks

Major disease outbreaks often generate multiple modeling efforts to assist with forecasting and management. Uncertainty about appropriate parameters, model structure and management intervention implementation can generate significant disagreements, which in turns hampers policy-making for animal and public health. Using examples from human and livestock diseases, I outline approaches to address uncertainty and learning to help improve epidemiological management.

Sheetal Silal (University of Cape Town)

Supporting Malaria Elimination in the Asia-Pacific through Mathematical Modelling

Countries in the Asia-Pacific region have made significant progress in combatting malaria, reducing deaths from the disease by more than 25% since 2000 and several countries are now working towards elimination with a regional goal for a malaria-free Asia-Pacific by 2030 endorsed at the highest levels. A mathematical model was developed to project rates of decline to elimination by 2030 and determine the costs for elimination in the Asia-Pacific region. The mathematical model is characterized as a dynamic economic-epidemiological multi-species model that will estimate the impact of interventions against the transmission of Plasmodium falciparum and Plasmodium vivax malaria. This talk will highlight results of the modelling project through an open source application aimed at making mathematical models more accessible to policy-makers and other key stakeholders.

TALKS

Danish Ahmed (Prince Mohammad Bin Fahd University)

Reproducing trap count patterns for random walks using a modified diffusion equation.

Many empirical and theoretical studies support the conclusion that Brownian random walks and diffusion models as their mean field counterpart, form appropriate modelling techniques for animal movement. However, this traditional approach has been challenged and conflicting evidence also suggests that under some conditions an alternative movement pattern such as Lvy walks can provide a better description. Lvy walks differ from Brownian walks since they allow for a higher frequency of large steps, resulting in a faster movement. Identification of the correct movement model which most accurately fits the underlying behaviour is somewhat problematic and in this case has stemmed into a highly controversial issue. Since trap counts are affected by the type of movement pattern, in principle it seems that the main challenge is to identify the exact mechanisms which govern the movement. The theme of this talk is to demonstrate that this is probably not the case, at least in the context of pest trapping; especially when almost identical trap counts are reproduced for inherently different movement models with distinct characteristics. This brings into question the relative importance of identifying the movement mechanisms, where emphasis should be on the ecological context in integrated pest monitoring programmes.

Yixuan He (Dartmouth College)

A Simple Mathematical Model for Vascular Tumor Growth

Mathematics can provide huge contributions to experimental cancer investigation as it is a powerful tool to test hypotheses and confirm experiments, allowing researchers to gain a better understanding of cancer growth dynamics and to design better treatment strategies. In this study, we present a simple mathematical model of vasculature tumor growth with and without drug treatments that is complex enough to replicate experimental data on a range of tumor properties in vivo and provide quantitative insight into tumor vasculature, while restraining the number of parameters in the system of differential equations to the number of measured quantities. Our results improve current understanding of tumor development in vivo as well as drug pharmacodynamics in order to facilitate the design of optimal treatment strategies.

Cang Hui (Stellenbosch University)

Multi-site Zeta Diversity as a unified framework for biodiversity partitioning

One central biodiversity measure is beta diversity, or turnover, which captures the essence of variation in diversity in space and time. However, beta diversity metrics have been shown to be unduly influenced by the rare species in an assemblage. Zeta-diversity, which provides the average number of shared elements across n systems, was recently proposed as an alternative for measuring compositional turnover in plants and animal assemblages. It is also valuable for application to any system that can be characterised by an RxQ matrix. It provides a significant advance over previous pairwise approaches by capturing the contribution of the full suite of narrow, intermediate and wide-range elements to turnover. In so doing it provides additional insights on the role of common species in driving patterns of biodiversity.

Pietro Landi Stellenbosch University

Adaptive dynamics and evolutionary branching: Theory and applications

Adaptive Dynamics is a mathematical framework for the study of phenotypic evolution driven by selection in the ecological context. Its main innovative feature is the formalization of evolutionary branching, that is, the sympatric divergence of two morphs under disruptive selection from a single phenotype. Subsequent evolutionary branching events are thus responsible for the increase of polymorphism in the community and, possibly, sympatric speciation.

The mathematical conditions for evolutionary branching were introduced in the late 1990s, but the formalization of critical branching events has only recently been developed. Moreover, such critical condition triggering evolutionary branching has been systematically used to study the evolution of polymorphism in prey-predator communities, in bio-economic models of fisheries, and in life-history strategies, along ecological and environmental gradients.

Gilbert Langat (University of Stellenbosch)

Adaptive interaction switching improves the stability of multispecies competitive communities.

Species interactions in nature form large complex networks suggested being unstable [1] contrary to naturally observed communities that can maintain a high number of diversity through species coexistence. Adaptive switching of interaction partners has been postulated as one of the factors shaping community structure and stability [2, 3]. However, existing studies on interaction switching behaviour have focussed on one form of interaction switching with little attention to the comparison between different switching procedures. Using Robert May's ideology of using random matrices [1], we attempt to understand the effect of community complexity on community stability in the presence of various adaptive interaction switching behaviours in a competitive ecosystem. Here, we use a modified Lotka-Volterra model in which species adaptively switch their interacting partner either by elimination of highly competitive partners or by optimization by choosing less competitive partners. We showed that adaptive switching improves community stability in terms of its productivity, evenness, resilience, and nestedness. Moreover, the level of stability is decreasing with the level of connectance. Specifically, the optimization procedure of switching performs better in enhancing community stability for highly connected communities. We argue that adaptive interaction switching is an essential element for understanding the maintenance of diversity in complex competitive communities.

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Guillaume Latombe (Stellenbosch University)

How dispersal, abiotic selection and biotic competition interact to shape plant communities: lessons from the Community Assembly Phase Space

Plant traits influence a range of biotic processes, including species dispersal ability, performance under particular abiotic conditions, and inter- and intra-specific interactions. Regardless of the type of niche, communities were generally thought to lie along a neutral-niche continuum, bounded by pure neutral and pure niche processes. Recent work showed that when neutral dispersal and abiotic niche selection processes interact, they reinforce each other and lead to communities with characteristics that lie outside of the expected continuum. The Community Assembly Phase Space (CAPS) was proposed to overcome the limited representation of the continuum. Here we apply CAPS to examine how neutral dispersal, abiotic niche selection, and biotic competition interact to shape communities, using a spatially explicit individual-based model. As for dispersal-abiotic niche selection interactions, dispersal and biotic competition processes can reinforce each other through feedbacks, generating communities with patterns that lie beyond the neutral-niche continuum. By contrast, the interactions between abiotic niche selection and biotic competition, based on different feedbacks, mostly generated communities lying between those produced by each process separately. Understanding the effects of feedbacks in colonization processes is therefore necessary to understand and explain the structure of communities.

Henri Laurie (University of Cape Town)

Do we have a theory of biology?

Clearly, we have lots of biological theory, but each of them concern a relatively small part of biology as a whole. I note first that a patchwork of theories that differ in assumptions, concepts and techniques may be coherent enough to combine into a theory.

I then present an optimistic interpretation of what may be called the undergraduate theory of biology: as we move from the tree of life to individual species, populations, individuals and metabolism, we have connections that combine these very different theories into a coherent whole, indeed “a theory of biology”. Moreover, this theory is vibrant, new details and connections are arriving at breathtaking pace.

Alternatively, one can offer a pessimistic version, in which the connections are not what they seem and indeed it appears as if the components of the patchwork do not, properly speaking, connect well enough to be considered coherent.

I am not sure which of these two versions I find more persuasive.

Yoram Louzoun (Bar Ilan University)

Fluctuations-induced coexistence in public goods dynamics

Cooperative interactions between individuals in a population and their stability properties are central to population dynamics and evolution. We introduce a generic class of nonlinear dynamical systems describing such interactions between producers and non-producers of a rapidly equilibrating common resource extracted from a finite environment. In the deterministic mean field approximation, fast-growing non-producers drive the entire population to extinction.

However, the presence of arbitrarily small perturbations destabilizes this fixed point into a stochastic attractor where both phenotypes can survive. Phase space arguments and moment closure are used to characterize the attractor and show that its properties are not determined by the noise amplitude, but rather it is stabilized by the stochastic nonlinear dynamics. Spatial Monte Carlo simulations with demographic fluctuations and diffusion illustrate a similar effect, establishing the validity of the two dimensional stochastic differential equation as an approximation.

The functional distribution of the noise emerges as the main factor determining the dynamical outcome. Noise resulting from diffusion between different regions, or additive noise, induce coexistence while multiplicative or local demographic noise do not alter the outcome of deterministic dynamics. The results are discussed in a general context of the effect of noise on phase space structure.

Yoram Louzoun (Bar Ilan University)

Commensal pathogens as a source of a coexistence mechanism

Most known organisms carry commensal viruses or bacteria. These parasites are often treated as an inevitable nuisance. We here show that they may be essential for the survival of the host specie, and may actually be the force driving speciation.

Viruses that do not hurt their natural host but are deadly for other species have been argued to facilitate invasion. We show using a generic SIR model that the opposite may be the general case. Such viruses may be the force sustaining multiple distinct populations through spatial segregation, in the absence of physical barriers. This segregation protects the hosts against invasion by neighboring, possibly more fit, populations. The virus induced segregation can eventually lead to allopatric speciation, with no animal dispersal, geographical changes or human activities.

We further propose a mechanism, where the introduction of a new virus to a population with a heterogeneous response (based for example on the MHC polymorphism) can lead to the segregation of distinct sub-populations reacting to different strains of the virus. The existence of such a mechanism may require further experimental validation.

Henintsoa Onivola Minoarivelo (Stellenbosch University)

Evolutionary diversification in mutualistic networks

Ecological and evolutionary changes observed in mutualistic communities are shaped by several mechanisms such as intra-trophic competition and co-evolutionary mutualistic selection. We explore how those mechanisms affect community assembly processes such as adaptive diversification and the emergence of biodiversity. To capture both ecological and evolutionary processes simultaneously, we followed the theory of adaptive dynamics. Using the Lotka-Volterra framework, we built an eco-evolutionary model and simulated the ecological dynamics of populations as well as the evolutionary dynamics of involved phenotypic traits. Depending on the initial trait values, two possible evolutionary regimes emerged, portraying that the system is prioritized for whether capturing environmental resources or mutualistic benefits. Diversification and overall biodiversity are mostly driven by frequency-dependent competition, while mutualism plays an important role in proliferating evolutionary stability. Because different setups of initial traits in a community can lead to alternative evolutionary regimes, it becomes essential to clarify the past evolutionary dynamics so as to draw conclusions on key community assembly processes.

Peter Mpasho Mwantobe (University of Malawi)

Mathematical analysis of a lymphatic filariasis model with quarantine and treatment

Background

Lymphatic filariasis is a globally neglected tropical parasitic disease which affects individuals of all ages and leads to an altered lymphatic system and abnormal enlargement of body parts.

Methods

A mathematical model of lymphatic filariaris with intervention strategies is developed and analyzed. Control of infections is analyzed within the model through medical treatment of infected-acute individuals and quarantine of infected-chronic individuals.

Results

We derive the effective reproduction number, R_0, and its interpretation/investigation suggests that treatment contributes to a reduction in lymphatic filariasis cases faster than quarantine. However, this reduction is greater when the two intervention approaches are applied concurrently.

Conclusions

Numerical simulations are carried out to monitor the dynamics of the filariasis model sub-populations for various parameter values of the associated reproduction threshold. Lastly, sensitivity analysis on key parameters that drive the disease dynamics is performed in order to identify their relative importance on the disease transmission.

Chinenye Assumpa Nnakenyi (Stellenbosch University)

Structural emergence in pollination networks via adaptive interaction switching on Galápagos islands

Network structures such as nestedness and modularity are reported to be evident from pollination networks and potentially influence the stability of the system. But mechanisms underlying the emergence of such structures are poorly understood. From ten island networks of the Galpagos archipelago, we explore the emergence and explain the observed structure of the pollination networks using models based on adaptive rewiring, plus geographic factors such as island size and isolation, and sampling effort. In the models, we used a modified Lotka-Volterra model of mutualism that implements resource competition, functional response of pollination, and adaptive interaction switching (AIS) to predict the level of weighted nestedness and modularity in observed pollination networks. Thereafter, we assessed the effect of geographic and sampling factors on network structures, together with predictions from the AIS models, using regression and variance partitioning. We found that pollination networks in 8 out of 10 islands were nested, but not compartmentalized. The AIS models explained about 50% variation in observed levels of nestedness, but failed to predict the level of modularity better than by chance. Furthermore, the AIS models, together with island size, island isolation and sampling effort, accounted for more than 85% variation of observed nestedness, but only provided moderate supports (60%) to observed modularity. In addition, sampling effort and island size were the two main factors explaining the level of nestedness, while network modularity was primarily driven by island isolation. Therefore, the AIS models can predict an appreciable level of network structures in observed pollination networks. However, with the inclusion of geographical and sampling factors, the emergence of network structure can be much better explained. Sampling sufficiency proves to be essential for the detection of cross-island nestedness pattern in quantitative interactions while large islands could allow more diverse assemblages and foster nested structures. More isolated islands could be prone to convergent evolution that enhances compartmentalized network structures.

Sansao Pedro (Universidade Eduardo Mondlane)

Predicting Rift Valley Fever Inter-epidemic Activities and Outbreak Patterns: Insights from a Stochastic Host-Vector Model

Rift Valley fever (RVF) outbreaks are recurrent, occurring at irregular intervals of up to 15 years at least in East Africa. Between outbreaks disease inter-epidemic activities exist and occur at low levels and are maintained by female Aedes mcintoshi mosquitoes which transmit the virus to their eggs leading to disease persistence during unfavourable seasons. Here we formulate and analyse a full stochastic host-vector model with two routes of transmission: vertical and horizontal. By applying branching process theory we establish novel relationships between the basic reproduction number, R0, vertical transmission and the invasion and extinction probabilities. Optimum climatic conditions and presence of mosquitoes have not fully explained the irregular oscillatory behaviour of RVF outbreaks. Using our model without seasonality and applying van Kampen system-size expansion techniques, we provide an analytical expression for the spectrum of stochastic fluctuations, revealing how outbreaks multi-year periodicity varies with the vertical transmission. Our theory predicts complex fluctuations with a dominant period of 1 to 10 years which essentially depends on the efficiency of vertical transmission. Our predictions are then compared to temporal patterns of disease outbreaks in Tanzania, Kenya and South Africa. Our analyses show that interaction between nonlinearity, stochasticity and vertical transmission provides a simple but plausible explanation for the irregular oscillatory nature of RVF outbreaks. Therefore, we argue that while rainfall might be the major determinant for the onset and switch-off of an outbreak, the occurrence of a particular outbreak is also a result of a build up phenomena that is correlated to vertical transmission efficiency.

Prashant Kumar Srivastava (Indian Institute of Technology Patna)

DELAY INDUCED OSCILLATIONS IN A DYNAMICAL MODEL FOR INFECTIOUS DISEASES

A delay differential equation model for the dynamics of infectious diseases is proposed and analyzed which accounts for the effect of information on susceptible. As the information generation is dependent of the prevalence of disease, the delay in reporting the prevalence may be an important factor. Keeping this in mind the the dynamics of information with delay effect is modeled by a separate rate equation. Moreover, the time lag in waning immunity related with protective measures (such as vaccination, self protection, responsive behaviour etc.) is also accounted. Model analysis is carried out and it is found that the disease free equilibrium exists unconditionally whereas unique infected equilibrium is obtained when the basic reproduction number (R_0) is greater than unity. It is observed that the disease free equilibrium is locally stable irrespective of the effect of delays when $R_0 < 1$. When $R_0 > 1$, the model dynamics exhibits rich and complex dynamics in presence of time delays. Due to delay effect, model analysis accentuates the occurrence of oscillatory behaviour of the population around the infected equilibrium via Hopf bifurcation, for both in single delay as well as two delay case. Numerical experiments are performed to analyze and support the obtained results. We also obtained the value of critical delay for a set of parameters such that infected equilibrium loses stability and oscillations are observed in populations indicating the complex behaviour in presence of delays. Thus it is very important to reduce the time lag in reporting of infected. Also we find a region of stability in the space of both delays so that infected equilibrium is stable and the count of infective can be brought down using some other alternate control interventions.

Tithnara Anthony Sun (University of Osnabrck)

A social-ecological model of lake pollution dynamics: coupling bistable systems

Freshwater lake systems can undergo rapid transitions between alternative stable states: a clear one with low levels of phosphorus and a turbid one with high levels of phosphorus. This has been well described in a model by Carpenter et al. (1999)*.

The phosphorus loading, in turn, is influenced by human collective behaviour, which can also be subject to such critical transitions. The resulting coupled social-ecological model has been studied by Suzuki and Iwasa (2009)**.

Here, we consider a simplified version of the model that allows for a systematic analysis of the parameters' influence on the system's dynamics. To this end, we consider the existence, position, basins of attraction and resilience of possible equilibria.

There can be up to nine equilibria, of which up to four may be stable.

This is joint work with Frank Hilker.

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Ezio Venturino (Università di Torino)

EFFECTS OF HERD SHAPE IN ECOLOGICAL PREDATOR-PREY INTERACTIONS

Following earlier ideas, [1, 6, 4, 5, 2], we illustrate a few models for two-populations interactions, assuming that one of the populations has a social behavior, gathering together in herds.

The basic feature consists in assuming the populations interaction to occur mainly through the perimeter or the surface of the herd, depending on the spatial setting of the ecosystem. Here we relax the assumption on the shape of the herd, allowing also complicated forms, [3]. Mathematically, the functional response is modeled via a generic power function, rather than a square root term. A novelty of the outcomes of these models is the rather peculiar phenomenon of extinction in finite time, [6, 5, 2].

The population equilibrium levels are sensitive to the herd shape and thus also to the dimensionality of the underlying environment, but sensitivity analysis shows that these changes are very similar.

In the cases of obligated mutualism for the individualistic population and of competition, the coexistence equilibrium value is independent of the shape of the herd.

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James Wilsenach (University of Edinburgh)

The Applicability of Field Theories in The Population Sciences

One of the properties that make ecological systems so unique is the range of complex behavioural patterns that can be exhibited by even the simplest communities with only a few species. Much of this complexity is commonly attributed to stochastic factors that have very high-degrees of freedom. Orthodox study of the evolution of these simple networks has generally been limited in its ability to explain complexity, since it restricts evolutionary adaptation to an inertia-free process with few degrees of freedom in which only gradual, moderately complex behaviours are possible. An attractive approach used in other disciplines such as sociology to explain this complexity is to treat population trends as arising from a combination of stochastic as well as intrinsic and extrinsic field forces. We proposed a model inspired by particle-mediated field phenomena in classical physics in combination with fundamental concepts in adaptation, which suggests that small but high-dimensional chaotic dynamics near to the adaptive trait optimum could help explain complex properties shared by most ecological datasets, such as aperiodicity and pink, fractal noise spectra. This type of complexity could contribute to apparent stochasticity and long-term unpredictability, especially when spurred on or amplified by stochastic factors that share variational and spectral properties with the underlying dynamics.

POSTERS

Irina Bashkirtseva (Ural Federal University)

How to prevent the extinction in stochastic ecological systems by feedback regulators

We discuss a problem of the analysis and prevention of catastrophic shifts in ecosystems with environmental noise. To solve this problem, we suggest a new control approach based on the synthesis of the required probabilistic distributions of the stochastic persistence regimes. We discuss constructive abilities of different types of feedback regulators in the solution of this control problem. Our approach is applied to the stochastically forced population models with Allee effect. We analyze a phenomenon of the noise-induced extinction via method of confidence domains. Controlling these domains we provide a persistence of the ecological system.

Jeremy Bingham (University of Stellenbosch)

Diversity in intra- and inter-group cooperation on fragmented landscapes

The problem of cooperation has been studied in many contexts, and additions to the standard problem which allow for the fixation of cooperation abound. Many of these extensions assume (beyond differences in strategies) homogeneity in the population. We explore the potential for the fixation of diversity in cooperation levels, within and between two population groups using repeated 2-player games. In addition, we examine the effects of eco-evolutionary feedback and landscape fragmentation on the diversity and levels of cooperation which occur.

Karimatou Djenabou (University of Stellenbosch)

An Adaptive Optimal Diet Model

Improved realism in the description of resource-consumer interaction include the consideration of physiological constraints (e.g., consumer functional response) or behavioural mechanisms, such as resource choice maximising the energy intake or switching behaviour when resources become rare. From the former idea, optimal foraging theory (OFT) has emerged as the premise for optimal diet models (ODM).

While OFT and typical ODM are based on the so-called bang-bang (zero-one) rule, i.e., a resource is always taken or ignored upon an encounter, diet models considering switching behaviour are mainly characterized by a disproportionate increase (respectively, decrease) in the number of attacks upon a resource type, when the abundance of the latter increases (respectively, decreases). Though both mechanisms have been proved to promote permanence and stability of resource-consumer dynamics, only ODM considers optimization of predator's food intake.

We propose an adaptive optimal diet model (AODM) which considers both the switching behavior (allowing for partial preference) and the global maximization of energy intake, under different levels of consumers specialization and a generalized Holling type II functional response. The AODM displays larger permanence region and stronger stabilizing effect than ODM. Although allowing partial preference, the AODM predicts nearly the same energy intake rate as ODM . When consumer specialization is large, maximum energy intake of AODM equals that predicted by ODM.

Vitalis Lagat (University of Stellenbosch)

Incorporating spatial auto-correlation in the statistical null model test of co-occurrence

To avoid conflicts and optimally exploit environmental resources, species will partition available habitats, forming co-occurrence patterns. Such datasets are often described as a species-by-site matrix. Null models based on permutations with constraints on row or column sums have been used in this regard, with the Chessboard score (C-score) a common metric for detecting significant signals of association or dissociation, from which the type of biotic interactions can be inferred. However, such a permutation test often ignore the spatial auto-correlation of species distributions which could lead to counter-intuitive results in the null model test. Consequently, tests should account for the spatial auto-correlation of each species. This poster thus presents a permutation null model test that can progressively include the spatial auto-correlation of species. The newly designed null model depicted inter-specific competition as a factor structuring ecological communities.

Luthando Mayekiso (University of Stellenbosch)

Fitting a stock synthesis model to the South African anchovy stock

Fishery stock assessment models are fish demographic analyses that can be used by fisheries managers to determine the consequences of alternative fishing policies. The availability of this information in a form that fisheries managers can use makes for better decisions that benefit the stock, other environmental populations and the communities that depend on the stock. Stock synthesis is an implementation of integrated analysis (IA) which is a more inclusive approach to fish stock assessment modelling that allows for the use of a greater variety of available data. The objective of the study is to formulate an optimal characterisation of the stock synthesis model for the South African anchovy (Engraulis capensis) stock that makes use of all available data and can also scale to new forms of data. The problem involves formulating an optimal stock synthesis model specification for the South African anchovy stock that assimilates all available data and can scale to new data. The specified model will be used to generate stock estimates and other population biological reference parameters that can be used for optimal fish stock management. The sample design is stratified random sampling (based on gear, landing site, boat and other variables) of the study area for anchovy, plankton and environmental variables for the period 1997 to 2016. The collection methods are fishery-independent bi-annual anchovy stock hydro-acoustic surveys, fishery-dependent seasonal anchovy commercial catch surveys, plankton catch surveys and continuous environmental sensor data. The available data on the stock (and its environment) will be formulated within the modelling framework of the 2005 Stock Synthesis II program to generate spatially disaggregated time series estimates and other stock management biological reference parameters for the period 1997 to 2016.The sample is composed of seasonal commercial catch data from landings of the anchovy stock, bi-annual anchovy acoustic data, plankton catch data and ocean sensor data (underwater environmental data) in the South African anchovy habitat between Port Nolloth and Port Elizabeth. The fitted stock synthesis model will provide a method for generating spatially disaggregated stock estimates that make use of available data and can scale to new data. The model will also provide other stock management information that can be used to optimally manage the South African anchovy stock.

Padma Murali (BITS Pilani)

MATHEMATICAL MODELING OF CORONARY ARTERY DISEASE (CAD): ANALYSIS REVEALS HBA1C AND TOTAL CHOLESTEROL TO BE SIGNIFICANT RISK PREDICTORS

The increasing prevalence of CAD (Coronary Artery Disease) calls for early detection of risk factors and effective clinical management. The predictive potential of commonly estimated clinical variables on CAD incidence was assessed using mathematical modeling and analysis. A random sample of 50 patients with CAD and a control group of 50 subjects without CAD were drawn from a cardiac specialty hospital in Chennai, India during 2011-2012 (mean age = 50.2 years, SD = 11.2 years). Medical data included age, gender, height, weight, body mass index, presence/absence of hypertension, systolic blood pressure, diastolic blood pressure, presence/absence of diabetes mellitus, fasting blood sugar, post-prandial blood sugar, HbA1c, total cholesterol, family history of CAD. Mathematical modeling using discriminant analysis was performed to understand significant contributors leading to CAD. The discriminant analysis resulted in a mathematical model using parameters, HbA1c and cholesterol. The model was found to be statistically significant and this was demonstrated by computing the F value. HbA1c and total cholesterol were found to be significant in predicting the occurrence of CAD.

Lev Ryashko (Ural Federal University)

Stochastic sensitivity analysis of noise-induced shifts in ecological models

Environmental noise is an inevitable attribute of dynamics of any population and ecosystem. Even small stochastic disturbances can cause abrupt catastrophic shifts in such systems. From mathematical point of view, such shifts can be explained by the noise-induced transitions between coexisting attractors in multistable systems, or by the specific non-uniformity of phase portraits in monostable systems. An analysis of the interplay between nonlinearity, multistability and stochasticity is an attractive problem of the modern theoretical ecology. In the analysis of noise-induced phenomena, a time-consuming direct numerical simulation is a basic tool. For the parametric analysis and solution of the control problems in ecosystems, this method is inapplicable.

In this talk, we give an overview of new analytical approach based on the stochastic sensitivity function technique and confidence domains method. Along with the brief mathematical background, we show how this approach can be successfully applied to the solution of the following problems. First is a parametric analysis of the stochastically forced regular (equilibria, cycles) and chaotic regimes of population models. The second problem is connected with the analysis of the probabilistic mechanisms of the noise-induced transitions, stochastic excitement and transitions to chaos, stochastic crossing of the dangerous borders and extinction. We demonstrate how our theoretical results can be constructively applied for the solution of these problems in some conceptual dynamic population models.

Josephine Naa Ayeley Tetteh (Stellenbosch University)

Bird flight performance and energy consumption: effect of body mass and wing traits

Bird flight has since ever fascinated men, making them wonder the techniques behind this ability. People have sought to discover the mechanisms used by birds to fly. Through experiments and theoretical research, driving factors of such fascinating phenomenon have been uncovered and wings have been recognised as the flight organs. From an aerodynamic point of view, the wing can be seen as an aerofoil which accelerates into the air to receive and transmit energy to the body of the bird to enable its lift. Flight performance is perceived to be dependent on certain wing traits and vast research have been carried out to investigate how such traits (e.g., area, length and shape) affect flight performance. In this project, we consider the aerodynamics of bird flight by categorising flight into linear flight and turning flight. Using aerodynamic equations, we formulated a model for bird flight which is being implemented in R statistical package. Knowing the wing traits of some bird species, we are also investigating the effect of their characteristic traits on the energy consumption associated with flight. Our findings suggest that a greater wing loading allows higher flight performance