

Parallel Session

## Population Biology I

**THE CARRYING SIMPLEX IN NON-COMPETITIVE  
LOTKA-VOLTERRA SYSTEMS**

ATHEETA CHING

Atheeta.Ching.11@ucl.ac.uk

Department of Mathematics, University College London, Gower Street, WC1E 6BT, UK.

Joint work with Stephen Baigent (University College London).

*Keywords:* Carrying Simplex, Lotka-Volterra, Populations, Manifold, Competition.

For some competitive Kolmogorov systems, there is an invariant Lipschitz manifold called the carrying simplex which is an attractor in the positive orthant; in fact, all trajectories are asymptotic to one on this manifold [2]. Many other properties of the carrying simplex have been proven such as how its convexity affects the behaviour of the system [1, 3]. This carrying simplex exists in types of competitive Lotka-Volterra population models where it is the boundary of the basin of repulsion of the origin and contains all non-trivial limit sets. Our work explores non-competitive deterministic systems, investigating whether this manifold exists and which properties still hold. We also find an analytic formula for the carrying simplex in the two species case.

**References**

- [1] Baigent, S. (2013). *Geometry of carrying simplices of 3-species competitive Lotka-Volterra systems*. *Nonlinearity* **26** (4), 1001-1029.
- [2] Hirsch, M. W. (1988). *Systems of differential equations which are competitive or cooperative: III. Competing species*. *Nonlinearity* **1** (1), 51-71.
- [3] Zeeman, E. C., Zeeman, M. L. (2002). *An  $n$  dimensional Lotka-Volterra system is generically determined by the edges of its carrying simplex*. *Nonlinearity* **15** (6), 2019-2032.

Parallel Session

## Population Biology I

### **ANALYSIS OF A FUNCTIONAL RESPONSE WITH PREY-DENSITY DEPENDENT HANDLING TIME UNDER AN EVOLUTIONARY PERSPECTIVE**

CECILIA BERARDO

cecilia.berardo@helsinki.fi

Department of Mathematics and Statistics, University of Helsinki, Gustaf Hällströmin katu 2b, 00014,  
Helsinki, Finland

Joint work with Stefan Geritz (University of Helsinki) and Mats Gyllenberg (University of Helsinki).

*Keywords:* Adaptive dynamics, Predator-prey dynamics, Functional response, Prey-density dependent handling time, Prey-density dependent conversion coefficient.

We give a derivation, in terms of mechanisms at the individual level, of a functional response involving the ability for the handling predator to resume searching spontaneously or after the interaction with the living prey. This ecological setting results in a prey-density dependent handling time. Here the conversion coefficient of prey into predators is given as a function of the prey density. We consider the resulting two ordinary differential equations system and study the model at the population level, by the comparison with the dynamics of the well-known Gause model. Using the theory of adaptive dynamics, we analyse the Darwinian evolution of the functional response.

Parallel Session

## Population Biology I

### FORMATION OF POPULATION CLUSTERS IN DENSITY DEPENDENT RANDOM WALKS

JOHN R. ELLIS

jxe348@student.bham.ac.uk

School of Mathematics, University of Birmingham, Edgbaston, Birmingham, B15 2TT, UK

Joint work with Natalia Petrovskaya (School of Mathematics, University of Birmingham)

*Keywords:* Population dynamics, Spatial pattern, Random walk, Density dependent movement.

Increasing the understanding of how some populations group together can be useful in many areas, including the study of invasive species, conservation and pest monitoring and control. Using individual based modelling we have simulated the formation of clusters in a population of invertebrate species, clusters being defined as patches of the high population density, along a one-dimensional domain. We model the animal movement by a random walk, where the spatial step size at each time interval is generated from a selected probability density function. Also introduced to the model is a density dependent directional bias so that an individual is more likely to move in the direction of higher densities of its fellows.

We will present the results from the simulations when the normal distribution and a power law distribution have been used to generate animal movement. It will be discussed how the frequency and stability of the clusters are related to the choice of parameters in the model (e.g. the strength of density dependence). One important result emerging in the model is the feature of dynamic clusters where the number of clusters fluctuates as time progresses. It will be argued in the talk that the existence of dynamic clusters is entirely defined by the properties of the probability density function as the dynamic clustering behaviour disappears when a power law probability density function is changed to the normal distribution.

Parallel Session  
Population Biology I

## REACTION-DIFFUSION MODELS FOR POPULATIONS WITH KINESIS

NURDAN CABUKOGLU

nc243@le.ac.uk

University of Leicester

Joint work with Alexander N. GORBAN (University of Leicester)

*Keywords:* Kinesis, Diffusion, Population, Extinction, Allee effect.

Kinesis is the non-directional movement as a response to the changing conditions. We suggested a model of purposeful kinesis with the diffusion coefficient directly dependent on the reproduction coefficient. This model is a straightforward formalisation of the rule: “Let well enough alone”. The well-being is measured by local and instant values of the reproduction coefficient. The kinesis strategy depends on well-being: Animals stay longer in good conditions and leave quicker bad conditions. If the well-being is measured by the instant and local reproduction coefficient then the minimal model of kinesis can be written as follows:

$$\partial_t u_i(x, t) = D_{0i} \nabla \left( e^{-\alpha_i r_i(u_1, \dots, u_k, s)} \nabla u_i \right) + r_i(u_1, \dots, u_k, s) u_i, \quad (1)$$

where:  $u_i$  is the population density of  $i$ th species,  $s$  represents the abiotic characteristics of the living conditions (can be multidimensional),  $r_i$  is the reproduction coefficient, which depends on all  $u_i$  and on  $s$ ,  $D_{0i} > 0$  is the equilibrium diffusion coefficient (defined for  $r_i = 0$ ), the coefficient  $\alpha_i > 0$  characterises dependence of the diffusion coefficient on the reproduction coefficient. Equations (1) describe dynamics of the population densities for arbitrary dynamics of  $s$ . For the complete model the equations for environment  $s$  should be added. The space distribution strategy is summarised in the diffusion coefficient  $D_i = D_{0i} e^{-\alpha_i r_i}$ , which depends only on the local in space and time value of the reproduction coefficient. Diffusion depends on well-being measured by this coefficient. This is the kinesis constant  $a_i$ . It can be defined as

$$a_i = - \frac{1}{D_{0i}} \left. \frac{dD_i(r_i)}{dr_i} \right|_{r_i=0}.$$

In the first approximation,  $D_i = D_{0i}(1 - a_i r_i)$ . This model (1) can be considered as the *minimal model of purposeful kinesis*. We have used the instant and local reproduction coefficient  $r$  for defining of purposeful kinesis. The analysis of several benchmark situations demonstrates that, indeed, sometimes this formalisation works well. If the food exists in low-level uniform background concentration and in rare (both in space and time) sporadic patches then purposeful kinesis defined by the instant and local reproduction coefficient (1)

is evolutionarily beneficial and allows animals to utilise the food patches more intensively. If there are periodic (or almost periodic) fluctuations in space and time of the food density  $s$  then purposeful kinesis defined by the instant and local reproduction coefficient (1) is evolutionarily beneficial and allows animals to utilize these fluctuations more efficiently. If the reproduction coefficient  $r(u, s)$  is not a monotonically decreasing function of  $u$  for every given  $s$  (the Allee effect) then the “Let well enough alone” strategy may delay the spreading of population. This strategy can lead to the failure in the evolutionary game when the colonization of new territories is an important part of evolutionary success. At the same time, the “Let well enough alone” strategy can prevent the effects of extinction caused by too fast diffusion and, thus, decrease the effect of harmful diffusion [1]. Moreover, we are studying on impact of the purposeful kinesis on running waves. The population with Allee effect also has the travelling wave behaviour with kinesis. We analyze the travelling distance in time and how the velocity changes with  $\alpha$ .

## References

- [1] A.N. Gorban and N. Cabukoglu. (2018). *Basic Model of Purposeful Kinesis*, Ecological Complexity, 33, pp.75-83.

Parallel Session  
Population Biology I

## HOW MIGHT A POPULATION HAVE STARTED?

PETER JAGERS

jagers@chalmers.se

Mathematical Sciences, Chalmers and University of Gothenburg, 412 96 Gothenburg, Sweden  
Joint work with P. Chigansky (Hebrew University) and F. C. Klebaner (Monash University).

*Keyword:* Population size dependent branching processes.

Many populations, e.g. of cells, bacteria, viruses, or replicating DNA molecules, but also of species invading a habitat, or physical systems of elements generating new elements, will be observable only when their number is large, say a proportion of the environmental carrying capacity  $K$  or some corresponding regulating or system scale unit. If start is from a small (as compared to  $K$ ) number  $Z_0$  of individuals, not hampering each other while few, the population will, initially, grow in a branching process like, roughly exponential fashion,  $Z_t \sim m^t W$ , where  $Z_t$  is the size at discrete time  $t$ ,  $m$  is the offspring mean per individual (during the initial stage), and  $W$  a sum of  $Z_0$  i.i.d. random variables. It will, thus, become detectable (i.e. of the same order as  $K$ ) only after around  $\log K$  generations, when its density  $X_t := Z_t/K$  will tend to be of the order of a strictly positive random variable, dependent upon the starting number  $Z_0$ , but typically not in a one-to-one fashion.

In this work, we make these arguments precise, studying general population-size and also system-size dependent processes in discrete time, as  $K \rightarrow \infty$ , where population size is normed by  $K$ , which may also be the time unit. The fundamental idea is coupling the initial system to a branching process.

Due to early fluctuations before population size comes anywhere close to carrying capacity, the first feasible population size observations, thus, may or may not allow precise determination of the initial number  $Z_0$ . This can be viewed as a very general phenomenon, the randomness of a system being relegated to its start, as it were, when the system becomes large and its scale as well as the time scale are properly adjusted. The early variability expresses itself as a veil of uncertainty concealing the process initiation.

The important concrete special case of finding the copy number at start of quantitative PCR under Michaelis-Menten kinetics was pursued in [1]. After mentioning the corresponding case of binary splitting, as a simple showcase model for tumour growth or bacterial populations in situations where the population size and carrying capacity influence reproduction, we go on to general, discrete time, Markov, population (or number of elements) and carrying-capacity dependent branching processes.

## References

- [1] P. Chigansky, P. Jagers, and F. C. Klebaner (2017) *What can be observed in real time PCR and when does it show?* J. Math. Biol. 76(3), 679-695. doi.org/10.1007/s00285-017-1154-1(2017)