

## MINISYMPOSIUM

### TOPICS IN STRUCTURED POPULATION DYNAMICS

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**Minisymposium Keywords:** Population dynamics, continuous-time population models, evolution equations.

Simple population models can be made more capable of better capturing biologically meaningful issues by means of adding continuous and discrete structure to the population. Structured population dynamics, which is a very active area of research in mathematical biology, addresses ecological, evolutionary and epidemiological problems through evolution equations for the densities with respect to structuring variables such as age, genetic phenotype or physical space. In this minisymposium of the European Conference on Mathematical and Theoretical Biology (ECMTB) in Lisbon, young and senior researchers will present recent developments on structured population dynamics covering a broad spectrum of applications.

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*Minisymposium: Topics in structured population dynamics*

## FROM INDIVIDUALS TO POPULATIONS: DENSITIES VERSUS HISTORIES

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*Keyword:* Model formulation.

Population models can be built in a mechanistic way by describing the behaviour of its individuals, which can be thought to be affected only by two factors: the environment and the characteristics defining the individual. The environment captures the aspects of the external world that have an impact on the individuals (such as food concentration, predator pressure or the population distribution itself). The individuals are characterized by properties that can be either internal (such as size, energy reserves or foraging activity) or external (such as position or orientation).

In this talk we review the derivation of a dynamical system at the population level taking into account phenomenological ingredients at the individual level. We show that two different formulations can be given depending on the state variable used to describe the population: either the density of the population or the history of birth rates. The relations between them as well as some open questions are discussed.

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# A KINETIC MODELLING APPROACH FOR TUMOUR-MACROPHAGES INTERACTIONS IN HETEROGENEOUS CELL POPULATIONS

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*Keywords:* Heterogeneous macrophage, Tumour populations.

The heterogeneity of macrophage populations (with the M1 and M2 cells representing the two extremes of the phenotypes) has led to difficulties in understanding and controlling the innate immune responses to infections and cancer. For example, while it is known that the M1 cells have anti-tumour effects, while the M2 cells have pro-tumour effects, the heterogeneity of macrophage populations inside tumours (with both M1 and M2 phenotypes) makes it difficult to predict tumour evolution.

Here, we introduce a class of kinetic equations for the interactions between a population of immune cells (i.e., macrophages structured by their phenotype) and a population of tumour cells (structured by their mutation status). We then use this model to confirm numerically that tumour progression is associated with an M2-like immune phenotype, while tumour reduction occurs in the presence of M1-like cells. Finally, we discuss various approaches that can be taken to ensure long-term tumour control (and eventual elimination).

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# LIMIT PROCEDURE FOR THE COMPUTATION OF $R_0$ IN STRUCTURED POPULATION MODELS

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*Keywords:* Basic reproduction number, Next-generation operator, Limit process.

The computation of the basic reproduction number  $R_0$  for autonomous continuously structured population models strongly depends on whether the density of newborns per unit of time (birth rate) and the population density are considered in the same functional space or not.

When it is not possible to directly apply the standard theory for the basic reproduction number, we can elaborate a suitable limit process.

For the standard case, one readily gets the (positive, bounded) next-generation operator and the basic reproduction number  $R_0$  as its spectral radius, from the evolution equation of the population.

When the latter is not possible without enlarging the functional space, we can obtain the next-generation operator as the limit of a suitable sequence of next-generation operators.

Our approach is illustrated with two age-structured problems: a model of migration of individuals between age-structured local populations (age-structured metapopulation) and a model for a population with diffusive age (i.e. the biological age which differs from the time since birth). In addition, we have highlighted the possible advantages of computing  $R_0$  instead of the Malthusian parameter.

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# LANGUAGE COMPETITION: ANALYSIS AND QUALITATIVE SIMULATIONS OF A DETERMINISTIC AGE-STRUCTURED MATHEMATICAL MODEL

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*Keyword:* Language competition.

Language competition modelling consists in describing the language exchanges between speech communities in a region where different languages coexist. This work introduces a competition model between two monolingual and one bilingual populations. This model is based on both existing mean field theory models of language competition and demographic models from population dynamics. It also includes age structure. We prove the well-posedness and positivity-preserving properties of this model. Existence of asynchronous exponential growth solution is proved for general systems and sufficient condition is given for uniqueness of such a profile. Under some hypotheses, total population distribution is proved to tend to an asynchronous exponential growth system.

Qualitative numerical results of the system are also given to illustrate some of the behaviours of the model.

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