2018-00572 - PhD Position / Individual-based models in adaptive dynamics and long time evolution under assumptions of rare advantageous mutations

Contract type : Public service fixed-term contract
Level of qualifications required : Graduate degree or equivalent
Function : PhD Position

Context

Team

TOSCA, INRIA Nancy Grand-Est,

Contacts

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This PhD project is proposed for Inria CORDI funding (https://www.inria.fr/recherches/jeunes-chercheurs/etre-doctorant/mode-d-emploi).

Assignment

The theory of “adaptive dynamics” is a branch of evolutionary biology, which studies the links between Ecology (interactions between individuals and their environment, including the other individuals of the population) and Evolution. Models of adaptive dynamics describe the population at the level of individuals, where individuals are characterized by their (phenol)types, and aim at studying the influence of the mechanisms of heredity (reproduction), mutation and selection (as a consequence of ecological interactions) on the long time evolution of the population. This theory has its origin in Metz et al. (1996), and the success of the theory comes from its ability to explain and predict the emergence and maintenance of diversity within a single species and without geographical separation. The basic mechanism of diversification is called “evolutionary branching” and corresponds to a transition from a population state where all the individuals have similar types to a population state where two subpopulations with different types coexist but continue to interact (for example they continue to compete for the similar resources). The theory of adaptive dynamics also provides a description of the long-term evolution of the dominant type in the population as solution of the so-called “canonical equation of adaptive dynamics” driven by a fitness gradient, where the fitness describes the possibility of mutant invasions and is constructed from ecological parameters.

The mathematical analysis of models of adaptive dynamics aims at understanding the canonical equation and the phenomenon of evolutionary branching. Two main approaches have been developed so far: an approach based on PDE’s (initiated in Diekmann et al., 2005), and an approach based on stochastic individual-based models (initiated in Champagnat, 2006). The probabilistic approach has given the more precise results so far (Champagnat and Méléard; 2011, Baar et al., 2017). The general idea is to consider a model where each birth, death and mutation is described, as well as a competition mechanism, and to consider a parameter scaling under which the population distribution over the type space concentrates to Dirac masses (i.e. to subpopulations in which all the individuals have the same type). The parameter scaling studied so far corresponds to a combination of large population, rare mutations and small mutations. The crucial assumption is the assumption of rare mutations, which give sufficient time to the selection process to eliminate disadvantaged traits. The canonical equation then corresponds to motion of Dirac masses and evolutionary branching to a transition from a single Dirac mass to two Dirac masses.

General Information

- Theme/Domain : Stochastic approaches
- Town/city : Nancy
- Inria Center : CRI Nancy - Grand Est
- Starting date : 2018-09-01
- Duration of contract : 3 years
- Deadline to apply : 2018-05-01

Contacts

- Inria Team : TOSCA
- Recruiter : Champagnat Nicolas / nicolas.champagnat@inria.fr

The keys to success

Application deadline

May 1st, 2018 (Midnight Paris time)

How to apply

In addition, send the following documents to in a single pdf or ZIP file: nicolas.champagnat@inria.fr

- CV.
- A cover/motivation letter describing your interest in this topic.

- Your degree certificates and transcripts for Bachelor and Master (or the last 5 years).
- Master thesis (or equivalent) if it is already completed, or a description of
Although successful, this approach is criticized by biologists (Waxman and Gavrilets, 2005), since it relies on an unrealistic assumption of very rare mutations. It would be much more realistic to assume that only advantageous mutations are rare (indeed, most of the mutations have deleterious effects and increase the mortality of individuals, or have nearly neutral effects).

Bibliography:

Main activities
The goal of this PhD thesis is to study mathematically the consequences of the assumptions of rare advantageous mutations on adaptive dynamics, and more specifically on the canonical equation and evolutionary branching.

A first task consists in constructing a realistic model accounting for this phenomenon. Two possibilities can be considered:

1. Adapt existing models by imposing that most of the mutations occur in a fixed direction of the type space, and choosing ecological parameters such that selection drives the population in the opposite direction. This approach requires to prescribe directions of positive fitness. Since fitness is a complex function of ecological parameters, this cannot be done so easily, but existing tools should apply easily to this case.

2. Include genetics to the model and genotype to phenotype map: for example, we can consider a sequence of genes on a chromosome with additive effects on phenotypes, with weights converging to 0. If we assume that most of the mutations affect genes with small effects on phenotype, then most of the mutations are neutral and “significant” mutations occur on a long time scale. Here, the study of adaptive dynamics is harder, but might give significant biological insights on the time scale of evolution and how diversity in a species is related to genetic parameters.

The study of the canonical equation in both cases is a first step, for which existing methods are expected to apply. The study of evolutionary branching is more complicated since it both involves modelling and methodological difficulties, so this problem will be addressed in a second step in the PhD.

This work is essentially probabilistic, but might also require a numerical work to implement and test various models. Regular contacts with biologists (specifically Régis Ferrière, from the Ecology and Evolution Laboratory of ENS Paris) will be organized to validate the models and help spread the results to the biological community.

Skills

Required qualifications
Master in applied mathematics and a strong background in Mathematics.
Specific knowledge on probability theory and stochastic processes are required.
A strong interest in biological applications is also important.

Language
French or English
Benefits package

- Subsidised catering service
- Partially-reimbursed public transport

Remuneration


Monthly salary after taxes: around 1596.05€ for 1st and 2nd year. 1678.99€ for 3rd year. (medical insurance included).