Spatial population models

Alison Etheridge

University of Oxford

Abstract:

For over a century, mathematical models have played a fundamental role in theoretical population genetics. Indeed, genetics provided some of the earliest applications of the Ito calculus. In turn, population genetics provides a wealth of mathematical challenges.

In these lectures, we shall focus on the models which arise when we try to model the interplay between the forces of evolution (mutation, selection, random genetic drift etc) acting on a population and the spatial structure of that population. The challenge is to provide consistent forwards in time models for the way in which the frequencies of different genetic types evolve in the population, and backwards in time models for the ways in which individuals sampled from the population are related to one another.

We shall begin with the classical Kimura stepping stone model, which can be applied to subdivided populations. We then turn to the attempts of Malecot and Wright to model populations distributed across spatial continua, and the inconsistencies in their assumptions, consideration of which resulted in Felsenstein's famous 'pain in the torus'. We then present the spatial Lambda-Fleming-Viot model, which is one way in which one can overcome the pain in the torus, and use it to explore the interactions between patterns of genetic diversity and spatial structure. Under appropriate scalings we recover (stochastic) partial differential equations.

As time permits, we shall consider a broader range of models, capturing, for example, the patterns left behind when a population invades new territory, or when the local population density has a more complex influence on an individual's reproductive success, and present at least some heuristic arguments for the differences in patterns of relatedness between individuals sampled from the population that result.