

Probability and Statistics

Markov processes on two time-scales and population genetics

Ola Hössjer

Stockholm University, Sweden

The task of population genetics is to describe how the genetic composition of a population changes over time. This is of interest for instance in conservation biology, where loss of genetic variants and increased inbreeding is a threat to many species. Markov processes are very well suited to model how random drift, mutations, selection, recombinations and various demographic parameters affect the future fate of a population, with lost variants corresponding to absorbing states. For large populations, diffusion approximations are typically used in order to obtain a more tractable diffusion solution by means of Kolmogorov's equations.

In this talk I will present a general class of Markov processes that work on two time scales, with a continuous time diffusion solution describing the long term dynamics of the whole population, whereas a discrete time multivariate autoregressive process captures the more rapid fluctuations around a quasi equilibrium. These local fluctuations occur in a number of different contexts. They may be used, for instance, to describe genetic interchange between partially isolated geographic subpopulations, departures from random mating, genetic associations between nearby positions on the same chromosome, or maintenance of genetic variability under so called balancing selection. From the size of these local fluctuations we get a general recipe for finding the genetically effective size of a population, a parameter of great interest in conservation biology.