

Quasi equilibrium methods in population genetics

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Abstract

We consider time evolution of a population with some kind (geographical, social, ethnic, ...) of substructure. It is assumed that a limited amount of migration takes place between the subpopulations. Two classical questions in population genetics are to quantify the degree of spatial heterogeneity between the subpopulations (fixation index) and the degree of inbreeding (effective population size).

In this talk we introduce a general framework for answering these (and other) questions. The idea is to model the spatio-temporal variation at a number of genetic markers as vector valued autoregressive processes and consider their quasistationary behaviour, conditional on that no variant (allele) at each marker of interest has taken over the whole population.

Part of this work is joint with Nils Ryman and Per Erik Jorde.