



Quasi Equilibrium, Variance Effective Size and Fixation Index for Populations with Substructure

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Abstract

We present a general method for joint computation of the variance effective size N_{eV} , the fixation index F_{ST} and the coefficient of gene differentiation G_{ST} for a class of structured populations with very general migration and reproduction properties, where the size of each particular subpopulation is constant in time. Our approach is relevant when migration rates are of larger magnitude than mutation rates, so that new mutations can be ignored before quasi equilibrium between genetic drift and migration is obtained. The vector valued time series of subpopulation allele frequencies is divided into two parts; one corresponding to genetic drift of the whole population and one corresponding to the dynamics of fluctuations of allele frequencies between subpopulations. After a simple standardization, the latter is shown to be in equilibrium, conditional on that no allele is fixed in the population. This enables us to compute quasi equilibrium approximations of N_{eV} , F_{ST} and G_{ST} .

Our findings are illustrated for several reproduction and migration scenarios, including the island model, stepping stone models and a model where one subpopulation acts as a genetic reservoir. We also discuss overlapping generations and extensions to randomly varying subpopulation sizes.

Key words: Autoregressive time series, island model, quasi equilibrium, stepping stone models, spatial allele frequency fluctuations, structured populations, temporal allele frequency fluctuations.

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