

A general framework for modeling effective sizes and gene differentiation of structured populations

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A general class of models is introduced for structured populations. These can be divided into a number of subpopulations, for instance geographic sites or age classes. The local subpopulation (census and effective) sizes are possibly time varying, including subpopulation extinction and recolonization, bottlenecks, cyclic changes or exponential growth.

In order to quantify short term genetic variation in the population, we consider a neutral model with migration. Exact matrix analytic recursion formulas are derived for gene identities, gene diversities, coalescence probabilities and genetic drift variables. These recursions provide a general framework for computing different types of effective sizes N_e of the population, such as the inbreeding, variance, nucleotide diversity and eigenvalue effective size. We also compute predictions of how much the subpopulations differ genetically, as quantified by Nei's G_{ST} .

It is argued that in order to adequately summarize the most important properties of the population, single values of N_e and G_{ST} are not enough, even if the subpopulation sizes are constant. Instead, it is suggested that their dynamic behaviour are reported as curves, as a function of time. We then discuss how these N_e and G_{ST} curves are affected by the way in which subpopulations are weighted, This includes for instance the case when some subpopulations are unknown, and only the known subpopulations are assigned positive weights. In this case, we speak of a functional effective size. Other schemes include weighting subpopulations proportionally to sizes or reproductive values.

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