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Spatial Autocorrelation for Subdivided Populations with Invariant Migration Schemes

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Abstract

For populations with geographic substructure and selectively neutral genetic data, the short term dynamics is a balance between migration and genetic drift. Before fixation of any allele, the system enters into a quasi equilibrium (QE) state. Hössjer and Ryman (2012) developed a general QE methodology for computing approximations of spatial autocorrelations between subpopulations, subpopulation differentiation (fixation indexes) and variance effective population sizes. In this paper we treat a class of models with translationally invariant migration and use Fourier transforms for computing these quantities. We show how the QE approach is related to other methods based on conditional kinship coefficients between subpopulations under mutation-migration-drift equilibrium. We also verify that QE autocorrelations are closely related to the expected value of Moran's autocorrelation function and treat limits of continuous spatial location (isolation by distance) and infinite gitters of subpopulations. The theory is illustrated with several examples including island models, circular and torus stepping stone models, von Mises models, hierarchical island models and Gaussian models. It is well known that the fixation index contains information about the effective number of migrants. The spatial autocorrelations is complementary and typically reveal the type of migration (local or global).

Key words: Fixation index, Fourier transforms, kinship coefficients, quasi equilibrium, spatial autocorrelations, translationally invariant migration.

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