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Mathematical analysis and simulation in ecology and evolution: A new model of isolation-by-distance that overcomes longstanding technical limitations

Abstract

In population genetics, models of isolation-by-distance (IBD) are crucial for understanding the role of evolutionary processes in the generation and maintenance of population genetic structure. However, despite the great importance and ubiquity of IBD in nature, a realistic mathematically tractable model is still missing due to the formidable technical difficulty of modelling nonlinear stochastic population dynamics. Instead, existing models of IBD use oversimplified and unrealistic approximations where spatial and/or temporal complexity is ignored, or only a limited number of evolutionary processes can be considered, e.g. selection and local density-dependent population regulation pose a long-standing problem. Here, we present a model of IBD which overcomes these technical limitations. The model takes into account explicit continuous spatial stochastic dynamics, selection, local density-dependent population regulation, limited spatial dispersal, genetic drift, mutation. We present approximate analytical solutions, asymptotically exact in a biologically relevant limit, for IBD patterns for neutral and non-neutral markers using arbitrary interaction kernels. Simulations show good agreement with our analytical predictions.