FORWARD-TIME, INDIVIDUAL-BASED SIMULATIONS AND THEIR USE IN PRIMATE LANDSCAPE GENETICS

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A number of analytical methods and software frameworks have been developed for analyzing patterns of genetic variation within a taxon taking a spatially-explicit landscape perspective (e.g., Geneland, CircuitScape, Alleles In Space, Marlin). None of these approaches, however, use a bottom-up, agent-based approach to explore how landscape-level patterns might emerge from the behavior of heterogeneous sets of individuals (e.g., animals of different sex, age, or rank) as they interact with social and physical environments that are likewise heterogeneous in space. Here, I describe the preliminary development of an individual-based simulation model that has promise for exploring the emergence of population genetic structure from individual behavior within a spatially-explicit framework. The model incorporates multiple aspects of primate social systems that are seldom accommodated in traditional population genetic simulations (e.g., dominance based mating, sex-biased and parallel dispersal, age-specific vital rates, overlapping generations). At the same time, it is spatially-explicit: model agents, each characterized by a position in space as well as a multilocus genotype, inhabit a geographically-heterogeneous environment in which location can influence an agent's behavioral decisions as well as the nature of the social environment experienced at that location. Users can simulate genetic data for model runs with great flexibility, or the model can be run using empirical genetic and/or landscape data. For landscape geneticists, the model may prove useful as it allows users to flexibly explore the effects of changing landscape parameters, or assumptions about how individual animals interact with their environment, on the patterning of genetic variation across the landscape.