

NextGen PVAs: Incorporating Eco-Evolutionary Processes into Population Viability Models

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ABSTRACT

We examine how the integration of evolutionary and ecological processes in population dynamics – an emerging framework in ecology – could be incorporated into population viability analysis (PVA). Driven by parallel, complementary advances in population genomics and computational methods, this review synthesizes how these advances can be combined into a NextGen PVA to offer powerful, new approaches to understand the influence of evolutionary processes on population persistence. The genomics revolution will improve parameter estimation for PVA models by providing genotypic information at large numbers of loci for both neutral and functional regions of the genome. We develop the conceptual basis of a NextGen PVA using individual-based models (IBMs) with individual level genotype tracking and dynamic genotype-phenotype mapping to explore emergent population level effects, such as local adaptation or purging of genetic load. Finally, we provide a conceptual example of a NextGen PVA that considers the relative effects of competing evolutionary processes, inbreeding depression and outbreeding depression, on an endangered Australian bird. As climate and other environmental changes increase in rate and scale, NextGen eco-evo PVAs will become essential research tools to evaluate the roles of adaptive potential and locally adapted traits on a population's probability of persistence.

KEY WORDS

Population Viability Analysis, Individually-Based Model, Climate Change, HexSim