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Predation effects on mean time to extinction under demographic stochasticity

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Abstract

Methods for predicting the probability and timing of a species' extinction are typically based on single species population dynamics. Assessments of extinction risk often lack effects of interspecific interactions. We study a birth and death process in which the death rate includes an effect of predation. Predation is included via a general nonlinear expression for the functional response of predation to prey density. We investigate the effects of the foraging parameters (e.g. attack rate and handling time) on the mean time to extinction. Mean time to extinction varies by orders of magnitude when we alter the foraging parameters, even when we exclude the effects of these parameters on the equilibrium population size. Conclusions are robust to assumptions about initial conditions and variable predator abundance. These findings clearly show that accounting for the nature of interspecific interactions is likely to be critically important when estimating extinction risk.

Keywords:

Trophic Interaction, Predator-Prey Model, Birth and Death Process, Quasistationary Distribution

1. Introduction

Population ecologists have long sought to understand how exogenous factors (such as environmental variability) interact with endogenous factors (such as body size, life history, trophic position) to determine the probability that a population will go extinct (Lande and Steinar, 2004). Such insights promise improvements in our understanding of species population dynamics in time and space (Bascompte et al., 1995), in the determinants of ecosystem stability and complexity (McCann, 2000; Allesina et al., 2012), and practical advances in our ability to conserve or eradicate populations (Witting et al., 2000; Liebhold et al., 2003).

Populations can take different routes to extinction. Extinction can occur either through progressive declines in population size, such as due to habitat deterioration, or through sudden crashes in abundance, such as through random catastrophes (Lande et al., 1993). Demographic stochasticity is caused by random variation among individuals in survival and reproduction. Environmental stochasticity is, on the other hand, random variation in the environment, which can lead to changes in the rates of processes influencing population dynamics (such as survival and reproduction rates; Lande and Steinar (2004)). While environmental stochasticity can be important for populations of any size, demographic stochasticity becomes particularly important at low population sizes.

Classical population theory shows that if demographic

stochasticity is the only stochastic process influencing the dynamics of a population then the mean time to extinction increases exponentially with equilibrium population size. In contrast, environmental stochasticity alone can lead to a power law relationship between the mean time to extinction and equilibrium population size (Lande et al., 1993; Foley, 1994). A major body of research to date has sought to understand how the characteristics of individual species influence their probability of extinction. For example, slow life histories and small geographical range sizes are associated with a high extinction risk (Purvis et al., 2000). One outcome of this large body of research is population viability analysis (PVA; Brook et al. (2000)). PVA combines the effects of these different factors to estimate the overall probability that a population will go extinct (Beissinger, 2002; Mace et al., 2008). However the single species models used for assessing population viability often lack the explicit incorporation of direct trophic interactions (Sabo, 2007; Sabo et al., 2008).

Interspecific trophic interactions have been widely studied, theoretically and experimentally, in the fields of population and community ecology. In his pioneering work Holling (Holling, 1959) proposed a simple non-linear relationship between prey density and predator feeding rate, known as the *predator functional response*, that is still widely used today. Since then, various modifications to Holling's original formulation have been made to represent different foraging mechanisms (Real, 1977; Abrams et al., 2000; Jeschke et al., 2002). A general expression for

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