

# Continuum approximation of invasion probabilities for stochastic population models

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## Abstract

When an individual with a novel trait is introduced in a new environment, we would like to understand what drives the likelihood that its lineage will persist. In deterministic population models, whether the invasive population “succeeds often depends on whether the parameters of the system fall in a super- or sub-critical regime. In stochastic population models, the parameters must be super-critical for there to be a substantial probability of invasion, but even in the super-critical regime, chance alone allows for many invasive lineages to quickly go extinct.

In this talk, we compare popular continuum approximations for the invasion probability to its exact solution. In particular, methods known as “Diffusion (or Stochastic Differential Equation) Approximation” and “Exponential Approximation” are derived. We find analytical expressions for these approximations in the large population limit and then use numerical methods to evaluate the performance of the approximation methods for finite populations. Interestingly we find that the diffusion approximation fails to obtain the correct large population limit, but can perform well for small populations that experience near critical dynamics. The exponential approximation obtains the right large population limit in the supercritical regime, but fails to capture nonmonotonic characteristics of the invasion probability for small to intermediate sized populations.