Mean time to extinction for metapopulation

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Mean extinction time for stochastic processes have been calculated and applied to several ecological data. As in the review [1], these stochastic models can be categorized into three classes; discrete-time Markov chain, continuous-time Markov chain, stochastic differential equation. Especially, in the single population model for continuous-time birth and death processes, we can obtain the explicit form as the solution of recursive equation (e.g. [7]). However, most of them analyze the case of a single population without any kinds of spatial structures, except a few literatures ([2, 3, 6]).

On the other hand, it is well-known that the metapopulation can persist longer in comparison to the single population even for the equal size of total population, because the asynchronous dynamics between local populations have the rescue effect on each local population and the recolonization from others escape the whole metapopulation extnction even once a local extinction occurs (e.g. [4, 5]). In our presentation, we show the numerical results of the mean time to extinction for several metapopulation models, and trace the reason for the longer persistence of metapopulation.

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