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Quantitative Biology > Populations and Evolution

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Evolutionary branching is analysed in a stochastic, individual-based population model under mutation and selection. In such models, the common assumption is that individual reproduction and life career are characterised by values of a trait, and also by population sizes, and that mutations lead to small changes in trait value. Then, traditionally, the evolutionary dynamics is studied in the limit of vanishing mutational step sizes. In the present approach, small but non-negligible mutational steps are considered. By means of theoretical analysis in the limit of infinitely large populations, as well as computer simulations, we demonstrate how discrete mutational steps affect the patterns of evolutionary branching. We also argue that the average time to the first branching depends in a sensitive way on both mutational step size and population size.

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Evolutionary branching in a stochastic

population model with discrete mutational

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