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Acceleration of Evolutionary Spread by Long-Range Dispersal

OSKAR HALLATSCHEK, University of California, Berkeley

The spreading of evolutionary novelties across populations is the central element of adaptation. Unless population are well-mixed (like bacteria in a shaken test tube), the spreading dynamics not only depends on fitness differences but also on the dispersal behavior of the species. Spreading at a constant speed is generally predicted when dispersal is sufficiently short-ranged. However, the case of long-range dispersal is unresolved: While it is clear that even rare long-range jumps can lead to a drastic speedup, it has been difficult to analyze the ensuing stochastic growth process. We present a simple self-consistent argument supported by simulations that accurately predicts evolutionary spread for broad distributions of long distance dispersal. In contrast to the exponential laws predicted by deterministic “mean-field” models, spread is either according to a super-linear power-law or a stretched exponential law, depending on the tails of the dispersal kernel. Fluctuations and the relation to supercritical long-range percolation are discussed. Due to the simplicity of our model, which lacks any complex interactions between individuals, we expect our results to be applicable to a wide range of spreading processes. Our results may be used, in particular, to estimate the spread of modern human epidemics, which are greatly accelerated by the human aviation. Based on joint work with Daniel S. Fisher, Stanford.