

SFB 680

MOLECULAR BASIS OF EVOLUTIONARY INNOVATIONS

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Predicting evolutionary change using statistical physics

The spreading of discrete entities occurs in many complex systems, and controls for instance the speed of chemical reactions, species invasions, epidemic outbreaks or biological adaptation. Unless population are well-mixed (like bacteria in a shaken test tube), the spreading dynamics not only depends on reaction rates but also on the dispersal behavior of the species. Spreading at a constant speed is generally predicted when dispersal is sufficiently short-ranged. I present a recent exactly solvable model for this wave-like spread and the associated genealogical trees, which are generated by a coalescent process with frequent multiple mergers. Spreading in the presence of rare long-range dispersal (e.g. triggered by aviation) has been unresolved so far: While it is clear that even rare long-range jumps can lead to a drastic speedup, it has been difficult to quantify the ensuing stochastic growth process. I present a simple self-consistent argument supported by simulations that accurately predicts the asymptotic spreading dynamics for fat-tailed jump distributions. I discuss our results in the light of population genetics, and show how they can be used to predict evolutionary change in simple microbial experiments.

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Institute for Theoretical Physics, Zùlpicher Str. 77, Seminar Room

Host: Joachim Krug and Michael Lässig

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