

Abstract Submitted
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Coalescence of genetic lineages in range expansions with obstacles and superdiffusive sector boundaries DANIEL BELLER, DAVID NELSON, Harvard University — In models of biological range expansions with simple diffusive wandering of both lineages and genetic boundaries in homogeneous space, it is straightforward to calculate the time since common ancestry for pairs of individuals at the front. However, model microbial systems such as *E. coli* show superdiffusive lateral wandering of genetic sector boundaries, due to roughening of the front with time, and this behavior drastically changes the coalescence of genetic lineages. Using stepping-stone simulations, we compute the distribution of backwards times to coalescence in range expansions with front roughening in the KPZ universality class. Genetic lineages are in this case superdiffusive as well, resulting in an exceptionally high concentration of coalescence events in the recent past. We then introduce heterogeneities in the form of obstacles (viewed spatially) or catastrophes of finite extent (viewed spatiotemporally). We discuss the scar-like signatures left by these obstacles/catastrophes in the distribution of coalescence times for individuals at the front, and associated measurable genetic properties of the population.

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