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Large scale behaviour of the spatial Lambda-Fleming-Viot process

N. Berestycki, A.M. Etheridge, A. Veber

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We consider the spatial Lambda-Fleming-Viot process model for frequencies of genetic types in a population living in R^d, in the special case in which there are just two types of individual, labelled 0 and 1. At time zero, everyone in the half-space consisting of points whose first coordinate is non-positive is type 1, whereas everyone in the complementary half-space is of type 0. We are concerned with patterns of frequencies of the two types at large space and time scales. We consider two cases, one in which the dynamics of the process are driven by purely `local' events and one incorporating large-scale extinction recolonisation events. We choose the frequency of these events in such a way that, under a suitable rescaling of space and time, the ancestry of a single individual in the population converges to a symmetric stable process of index alpha in (1,2] (with alpha=2 corresponding to Brownian motion). We consider the behaviour of the process of allele frequencies under the same space and time rescaling. For alpha=2 and d>1 it converges to a deterministic limit. In all other cases the limit is random and we identify it as the indicator function of a random set. In particular, there is no local coexistence of types in the limit. We characterise the set in terms of a dual process of coalescing symmetric stable processes, which is of interest in its own right. The complex geometry of the random set is illustrated through simulations.

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