

Cornell University Library

arXiv.org > q-bio > arXiv:1204.3075

Search or Article-id

All papers 🚽 Go!

(Help | Advanced search)

Download:

- PDF
- Other formats

Current browse context: q-bio.PE

< prev | next >

new | recent | 1204

Change to browse by:

cond-mat cond-mat.stat-mech q-bio

References & CitationsNASA ADS



Quantitative Biology > Populations and Evolution

Stochastic delocalization of finite populations

Lukas Geyrhofer, Oskar Hallatschek

(Submitted on 13 Apr 2012 (v1), last revised 17 Dec 2012 (this version, v2))

Heterogeneities in environmental conditions often induce corresponding heterogeneities in the distribution of species. In the extreme case of a localized patch of increased growth rates, reproducing populations can become strongly concentrated at the patch despite the entropic tendency for population to distribute evenly. Several deterministic mathematical models have been used to characterize the conditions under which localized states can form, and how they break down due to convective driving forces. Here, we study the delocalization of a finite population in the presence of number fluctuations. We find that any finite population delocalizes on sufficiently long time scales. Depending on parameters, however, populations may remain localized for a very long time. The typical waiting time to delocalization increases exponentially with both population size and distance to the critical wind speed of the deterministic approximation. We augment these simulation results by a mathematical analysis that treats the reproduction and migration of individuals as branching random walks subject to global constraints. For a particular constraint, different from a fixed population size constraint, this model yields a solvable first moment equation. We find that this solvable model approximates very well the fixed population size model for large populations, but starts to deviate as population sizes are small. The analytical approach allows us to map out a phase diagram of the order parameter as a function of the two driving parameters, inverse population size and wind speed. Our results may be used to extend the analysis of delocalization transitions to different settings, such as the viral quasi-species scenario.

Subjects:Populations and Evolution (q-bio.PE); Statistical Mechanics
(cond-mat.stat-mech)Cite as:arXiv:1204.3075 [q-bio.PE]
(or arXiv:1204.3075v2 [q-bio.PE] for this version)

Submission history

From: Lukas Geyrhofer [view email] [v1] Fri, 13 Apr 2012 18:52:29 GMT (938kb,D) [v2] Mon, 17 Dec 2012 13:09:09 GMT (1015kb,D)

Which authors of this paper are endorsers?

Link back to: arXiv, form interface, contact.