

The manuscript by Ianni-Ravn et al. provides a simulation study investigating the effect of spatial demographic parameters (dispersal distance of offspring from the gestating parent, competition distance, mate choice distance) on the distribution of observed dispersal distance. They also assess the accuracy of an estimator of dispersal distance from genetic data, showing potentially relevant insights for empirical studies.

The study provides a new framework for how to think about dispersal that is including mating distance. I enjoyed reading the manuscript, the results are clearly described and easy to follow.

I have a few comments that might lead to better correspondence with real biological systems.

Main comments:

- I would appreciate a more detailed description of the simulation setup. In particular, it seems that the simulation is conditional on a constant population size of 50 individuals. I assume parents are selected at random, but weighted by their fitness? How exactly is fitness down-scaled as a function of the number of competing individuals (i.e. provide the formula)? How is it guaranteed that mating individuals are within the mating distance? E.g. if an individual is too far away from any potential mate, does it effectively have zero fitness? Would fitness increase with increasing number of potential mating partners? These details should be added to section 5.1 (Spatial simulations).

- This type of relative fitness approach where the population size stays constant might not be very realistic (in reality population size fluctuates due to local competition and resources, there is no globally regulated population size). I wonder if it would be feasible to explore simulations that don't have this constraint (i.e. nonWF models in SLiM)?

- This also relates to the occurrence of clusters in the simulations with small mating distances - is there any intuition on why these clusters appear?

- One assumption that is made is that the offspring's initial position is at the gestating parent's position. In reality, parents at some point move to the same location for mating and potentially for raising offspring together. I.e. it could be that the male moves to the female, the female moves to the male, or the offspring is raised somewhere between the original male and female parent location. I don't think this invalidates the simulations or any of the conclusions, but I think it would help if it is discussed more explicitly how these situations relate to the simulations or any of the results.

Minor comments:

- Commonly used terms should be used if possible. E.g. Coalescent tree instead of "simplified tree" or phylogeny. It was not clear to me if the "unsimplified tree" is the pedigree or if it just

includes genetic ancestors at a locus. Also, it should be stated more explicitly that a single locus is investigated, i.e. there is no recombination.

- Please provide the derivation of the formula for the maximum likelihood estimate of sigma, or provide a citation.

- Figure 9: The labels (a, b, c) are missing. In the caption for (c) it says that "each panel shows a slice of 250 generations" -- I don't see what this refers to, there is just a single panel.