In this manuscript, the authors seek to understand how different population genetic and ecological parameters affect the geographic properties of the distribution of gene genealogies (i.e., patterns of isolation by distance) across the genome for a sample of individuals. Specifically, they are interested in how the mechanics of mating and dispersal affects the distribution of parent-offspring distances. They investigate this question using a simulation-based approach, and implement a maximum-likelihood (ML) estimator of the mean parent-offspring distance. They demonstrate (1) a correspondence between the shape of the dispersal kernel specified as well as the magnitude of the simulated dispersal and the resultant distribution of parent-offspring distances and (2) that competition-based density regulation, as well as mate-choice radius, both affect parent-offspring distances. They further demonstrate that their ML estimator of dispersal works pretty well and is impacted by the mating radius simulated.

This is a timely manuscript that contains lots of information that will be useful to many researchers who are interested in spatial population genetics (also landscape genetics, phylogeography, etc.). Overall, the paper is well-written and the details of the analyses are, for the most part, clear. However, I have some minor comments on the scholarship (I think some relevant work is overlooked) and a more major concern with the authors' interpretation and presentation of their results.

<u>Major Comments</u>:

In the Results, the authors present the lack of perfect correspondence between $\widehat{DD}$ (the empirical parent-offspring distance distribution) and DF (the specified dispersal function) as something unexpected, a framing that reappears in the discussion. For me, this framing was both confusing and a little bit misleading. Using genetic methods, it is only ever possible to learn about effective parameters (e.g., effective dispersal, effective density). Because the SLiM model includes a spatial mate choice component, the DF specified in SLiM will should not be the same as the $\widehat{DD}$. That is to say, in these simulations, effective dispersal differs from the specified DF not only because the DF describes the distribution of dispersal distances from in the census population, rather than just in nodes of the tree sequence with the sampled individuals as its tips, but also because the distribution of distances from offspring to parents (backward in time) will necessarily incorporate the spatial mechanics of mate choice. Focusing on the discrepancy between DF and $\widehat{DD}$ as a main result therefore seems like a confusing choice on the part of the authors, because it feels like a feature of their simulation (rather than an emergent property or a surprising result). Note also that this discrepancy has been discussed elsewhere in the spatial population genetic literature; see Smith et al 2023 ("Dispersal inference from population genetic variation using a convolutional neural network"), in which the authors derive the "mean squared directional displacement between a child and a randomly chosen parent" as a function of the mother-offspring and mother-father spatial mechanics. (Although note that their model, which simulated both dispersal and mate choice from truncated Gaussian distributions with the same variance, is somewhat different from the one implemented in this manuscript).

To be clear, I absolutely think that it's interesting to explore the effects of mating and dispersal forward-time parameters of effective dispersal observed in, or inferred from, the tree-sequence. I just think the manuscript would be more effective if it's framing of these points was clearer.

<u>Minor Comments</u>:

L96: This is nitpicky but I think it would help with the clarity of the introduction of the simulations if you specified here (rather than just in the detailed methods) that generations are non-overlapping.

L27-29: also lots of simulation-based studies and statistical inference. See Battey, Kern, & Ralph "Space is the Place: effects of continuous spatial structure on analysis of population genetic data" as well as Bradburd & Ralph "Spatial population genetics: it's about time," both of which contain many references that might be appropriate to cite here (especially work by Malecot and Rousset).

L38-39: see also: Smith & Weissman "Isolation by Distance in Populations with Long-Range Dispersal"

L138: Because "scattering" has specific connotations in the spatial population genetic literature (see, e.g., Wakeley 1999 "Non-equilibrium migration in human history", Wilkins 2004 "A Separation-of-Timescales Approach to the Coalescent in a Continuous Population"), it might avoid confusion to use a different term here.

Figure 4: I'm a little confused about the simulations and what's being shown in this Figure. Are the dots all the individuals present in the simulation over 10 generations, or simply following a single lineage? If the former, I think it might be a more generalizable spatial model to have competition induce stronger density-dependence so that individuals occupy a larger portion of the available range. If increasing the strength of competition (to induce a more spatially homogeneous density) leads to higher rates of simulation failure because of local Allee effects, you can avoid this by increasing the total population size.