

Figure S1: Runtimes for a “minimal” model with local mate choice and density-dependent Beverton–Holt feedback on mortality, plotted against **(A)** carrying capacity (K) and **(B)** interaction scale (σ_X , written SX). Runtimes are shown for models that do both mate choice and local density computations (solid lines) using (pairwise) interactions, and (dotted lines, all overlapping) using spatial maps, as described in Boxes 8 and 9. Also, **(C)** final population sizes after 100 time steps for the same combinations of K and σ_X shown in (A) and (B), for otherwise equivalent models that use either pairwise interactions (horizontal axis, “slow version”), or spatial map methods (vertical axis, “fast version”).

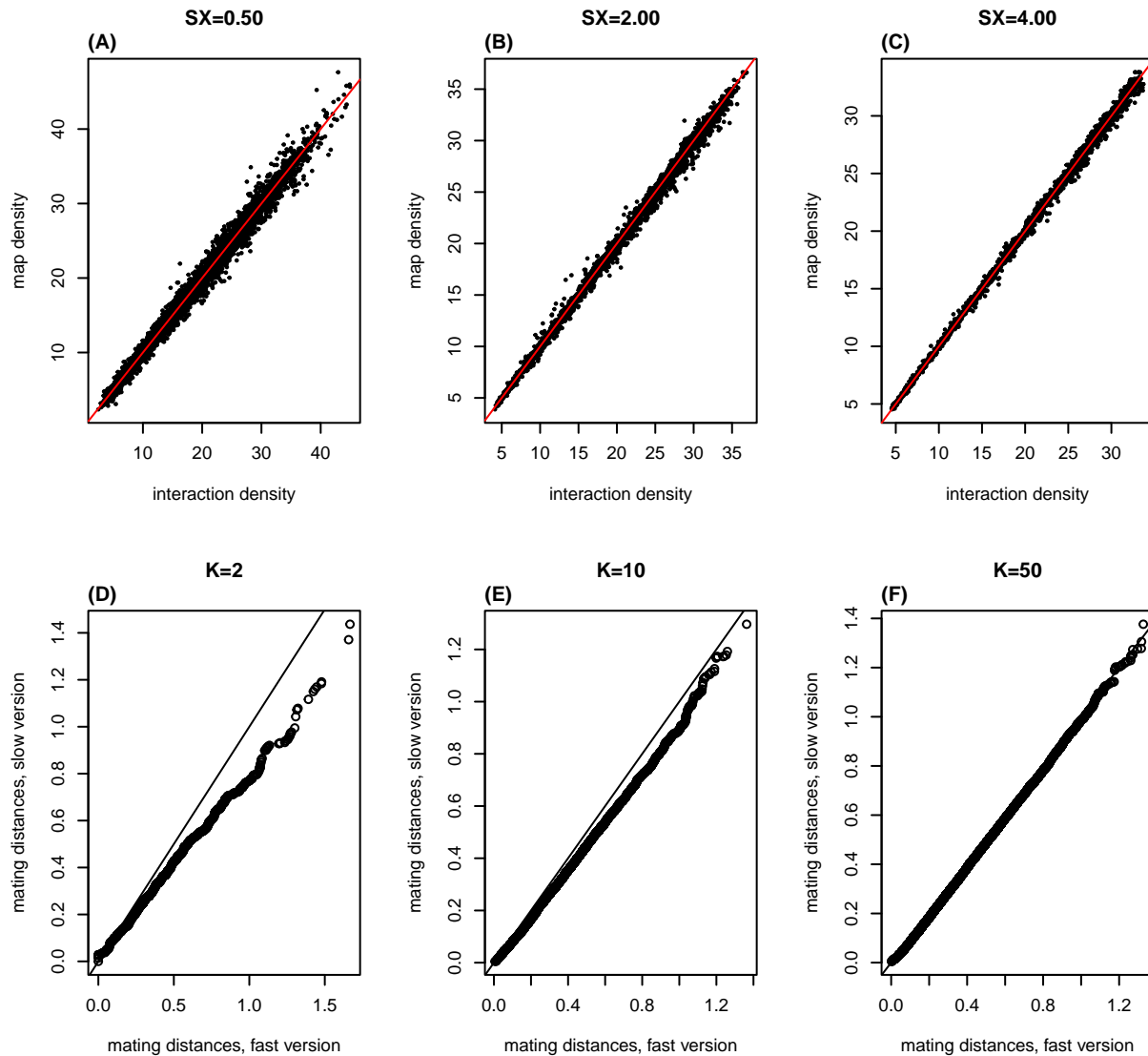


Figure S2: **(A-C)** Local density around each of 10^4 individuals, measured both using pairwise interactions (equation (1)) and interpolation on a spatial map (Box 8). Each panel shows 10^4 individuals randomly sampled from a separate simulation of the type described in Figure S1, but with K increasing linearly over 20 time steps, and different values of σ_X (labeled SX). **(D-F)** Q-Q plots comparing realized distributions of mating distances between simulations as above but either using individual-based mate choice (horizontal axis, “slow version”) or using map-based mate choice as in Box 9 (vertical axis, “fast version”), at three values of density (K). Shown are the quantiles of the distances to the most recent mate for roughly 30,000 individuals in each simulation; at lower densities, the “fast version” tends to have slightly longer mating distances.

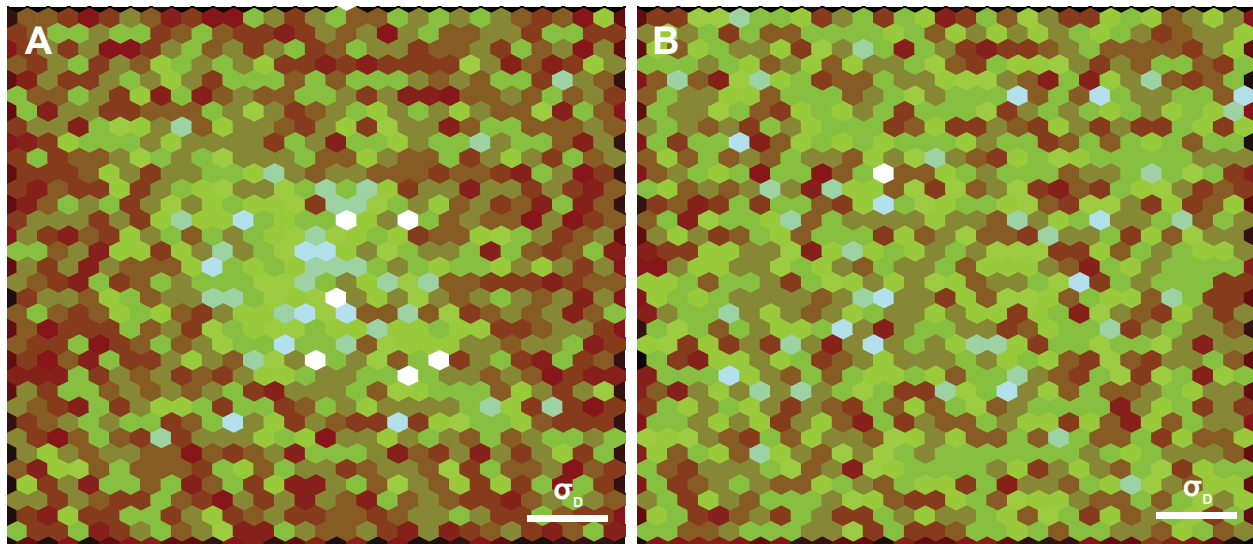


Figure S3: Fatter-tailed dispersal reduces clumping. Fry plots illustrate the distance between each pair of individuals at a given tick. The dense region of points near the origin in the Gaussian panel indicates many pairs of individuals are separated by small distances. Points shown are pairwise distances ≤ 1 from an arbitrary time step from one replicate. Here, $\sigma_D = 0.3$. **(A)** Gaussian dispersal kernel. **(B)** Student's t dispersal kernel.

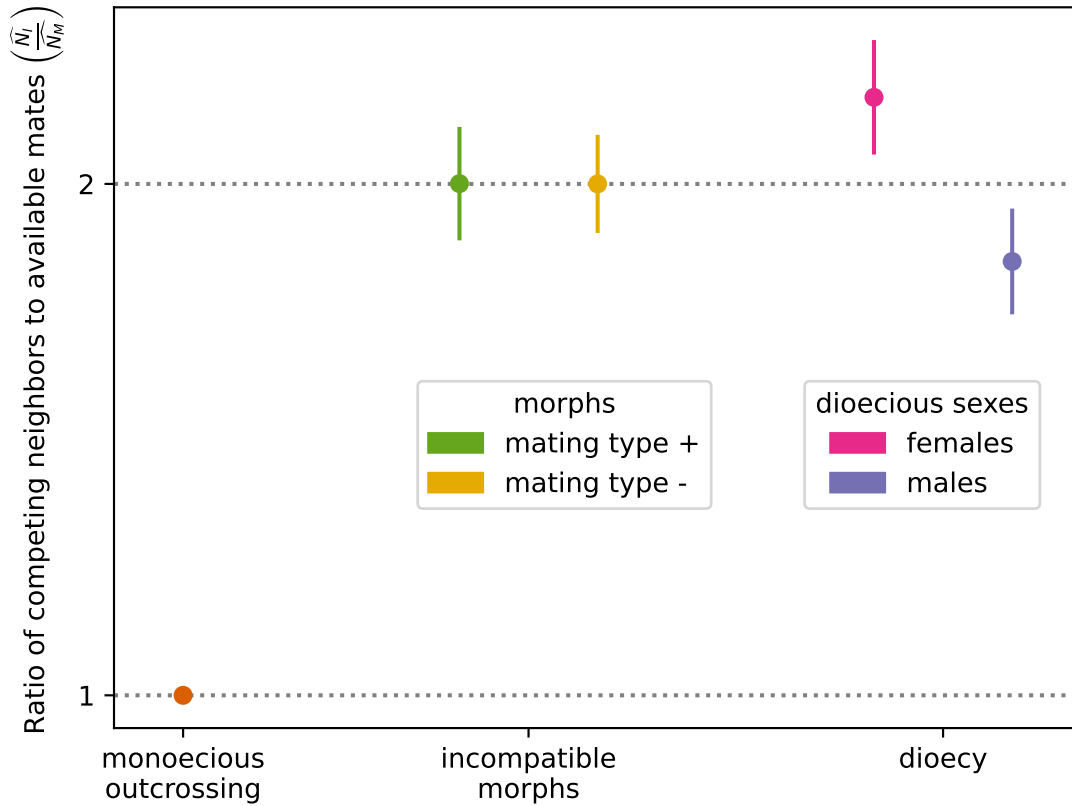


Figure S4: Ratio of competitive interactors to potential mating interactors differs within and among sexual mating systems. We calculate the mean number of competitors (within $3\sigma_X$) experienced by each individual, and divide by the mean number of potential mates (within $3\sigma_M$). Error bars show standard deviation of means across 50 independent time steps. Dashed lines show expected ratios of 1:1 for outcrossing among monoecious individuals, and 2:1 for two distinct mating types (\pm for mutually incompatible morphs, or female/male for dioecy).

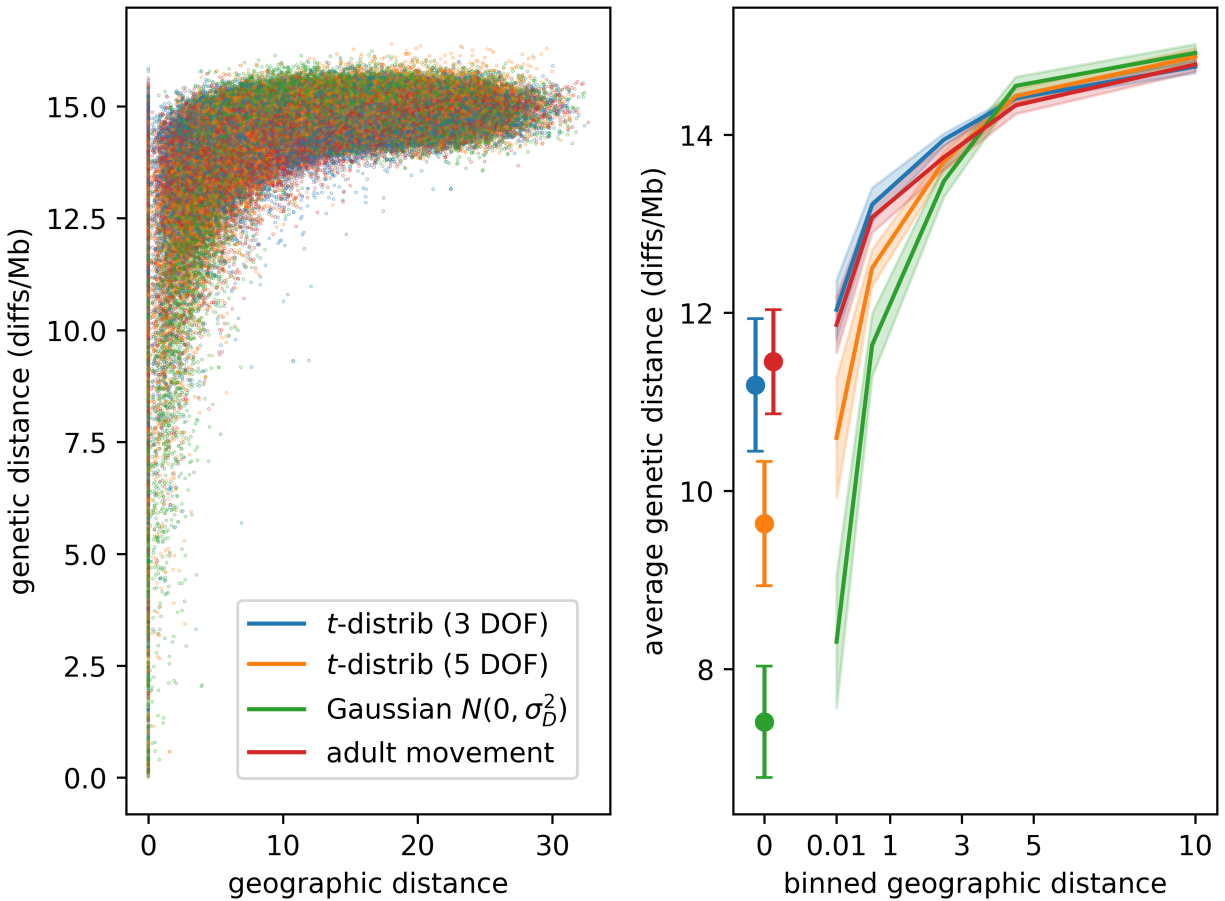


Figure S5: Fat-tailed dispersal and adult movement flatten genetic isolation-by-distance. Plots show genetic distance between pairs of individuals at increasing geographic distance. Points (A) and average curves (B) shown are from ten independent replicates. Error bars in (B) for pairs at < 0.01 units show one standard deviation. The scale of *t*-distributions is equal to the standard deviation of the normal distribution ($\sigma_D = 0.3$). Adult movement scenario uses Gaussian dispersal for movement at each time step.

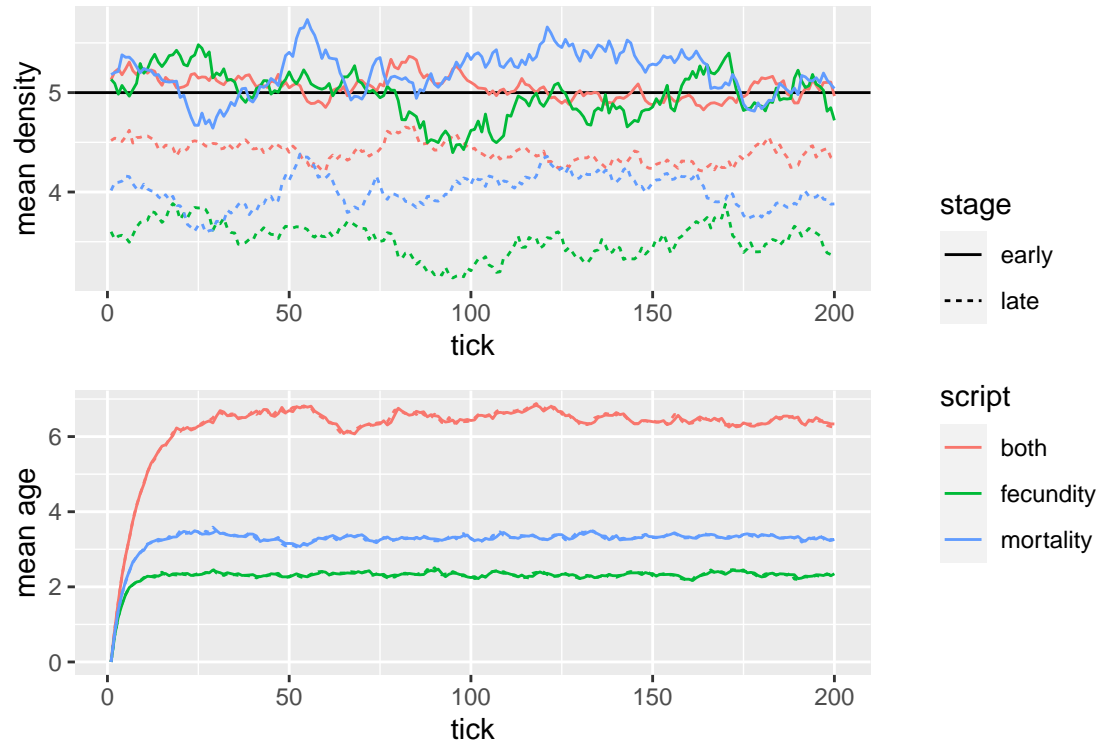


Figure S6: Traces from spatial simulations of the three “Beverton–Holt” models shown in Figure 1. **(Top)** Average local density for all individuals, measured both between birth and death (“early”) and between death and birth (“late”), and **(bottom)** mean ages across 200 time steps. Horizontal line shows the value of $K = 5$; local population density determines population regulation between birth and death for all models. Other parameters: $\sigma_D = \sigma_X = 1.2$, and range was a 25×25 square area.

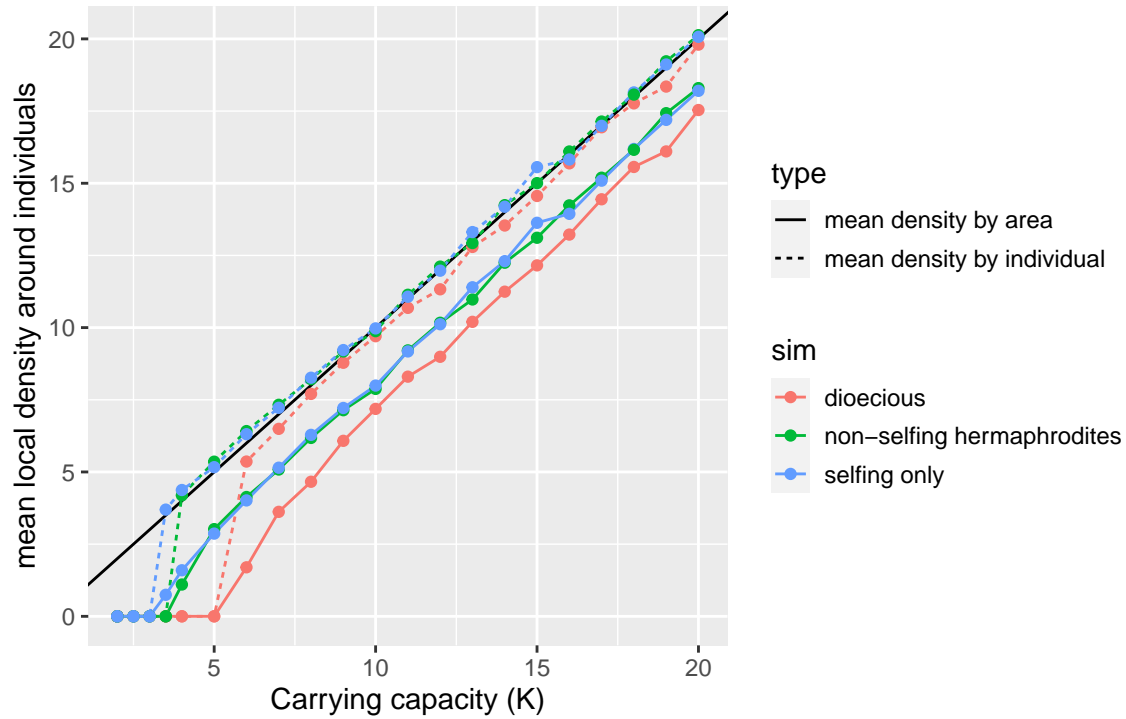


Figure S7: Average realized population density at equilibrium of three different models, plotted against the “carrying capacity” parameter, K . Each model uses Beverton–Holt regulation of mortality with the same parameters ($\sigma_D = \sigma_I = \sigma_M = 0.3$), and differ only in that “*dioecious*” individuals are one of two sexes: only females reproduce and only if they mate with a male; “*non-selfing hermaphrodites*” also must mate with another individual, but all individuals can reproduce; and “*selfing*” individuals can all reproduce and have no need for mating. Furthermore, mean fecundity is $f = 0.5$ for the dioecious simulations and $f = 0.25$ for the others. Dotted lines show mean local density experienced by individuals; solid lines show total population size divided by total area. All simulations die out at low density, but those requiring mating die out at higher K : in each case, when N_M is around 0.4.

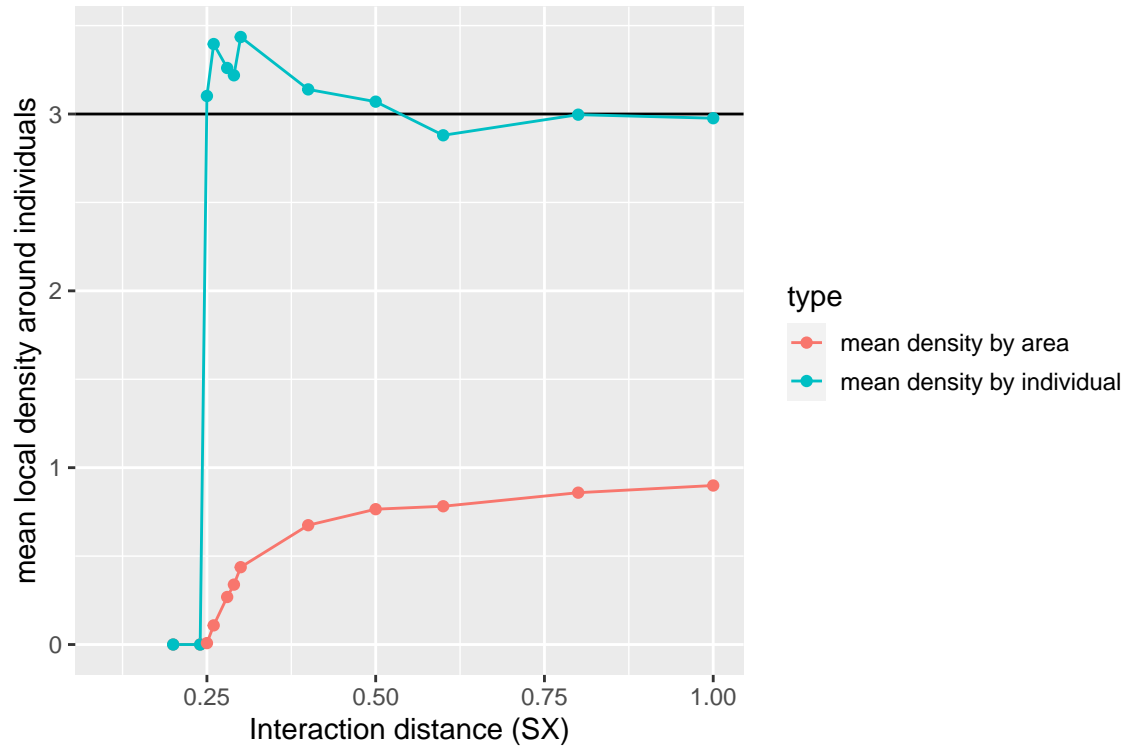


Figure S8: Mean density at equilibrium in simulations with different values of σ_X (SX in the figure). The blue line shows mean density around individuals (*i.e.*, the average of local density calculated with equation (1) for all individuals), the red line shows total population size divided by area (a 25×25 box), and the horizontal line is at $K = 3$. The simulation uses Beverton–Holt control of mortality with $\sigma_D = 0.5$, reproduction entirely through selfing, and no adult movement. The population dies out if σ_X is below 0.25, while for $0.25 \leq \sigma_X \leq 0.5$, total density (*i.e.*, density averaged by area) increases, while mean density experienced by individuals is larger than K and decreases.

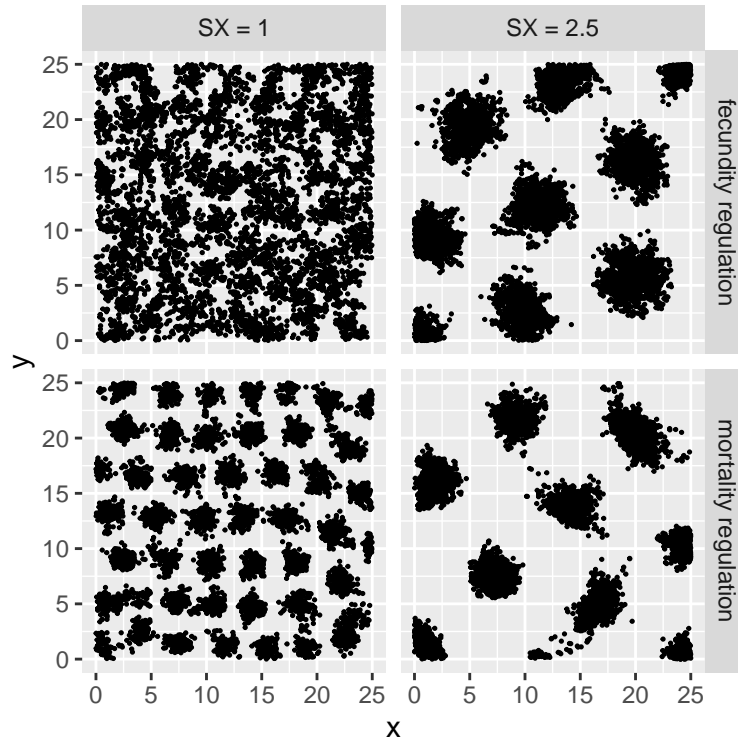


Figure S9: Examples of simulations exhibiting clumping, using $\sigma_D = 0.2$, two different values of σ_X (labeled SX), and two different types of density-dependent feedback (either mortality or fecundity regulation, as in Figure S6).

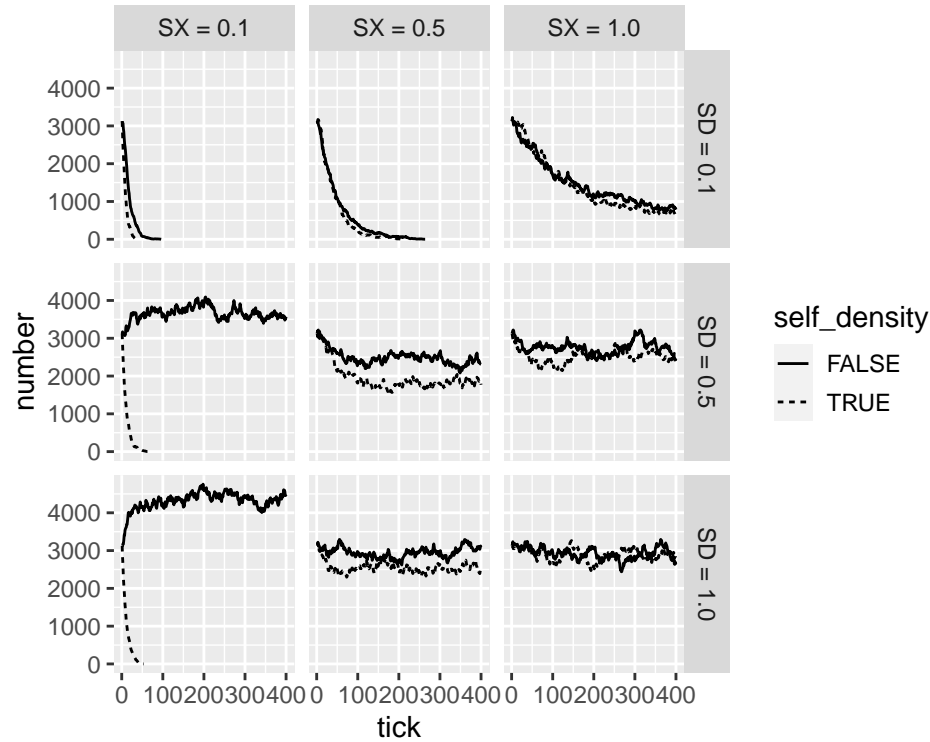


Figure S10: Population sizes through time for simulations with various values of dispersal scale (σ_D , here SD) and interaction scale (σ_X , here SX), with or without inclusion of the focal individual in local density calculations. Each simulation had Beverton–Holt density-dependent feedback on mortality (as in Figure S6), and was run with $K = 5$ on a 25×25 square area, and were started with $5 \times 25 = 3125$ individuals (so, lines that are roughly flat are fluctuating around a total density of $K = 5$). Solid lines compute “local density” for control of mortality of each individual using equation 1, while dotted lines do the same except excluding the focal individual.

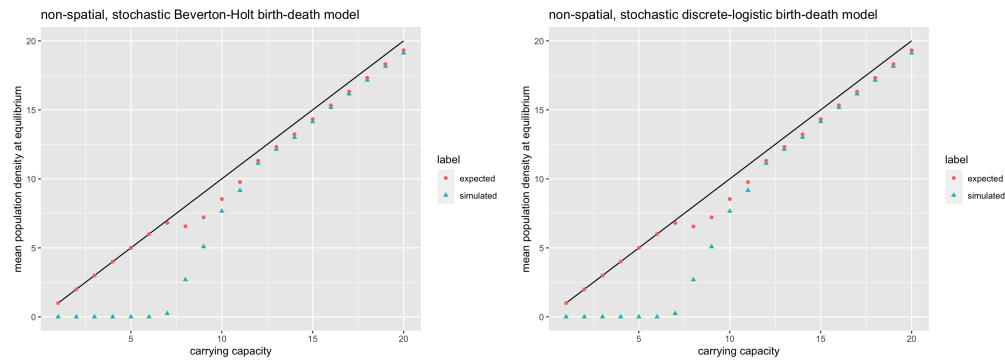


Figure S11: Expected population density obtained using equation (11) and actual average population density in non-spatial models with (left) Beverton–Holt regulation of mortality for which “expected” is $K - \frac{Var[U]}{(f+1)K}$, and (right) discrete logistic regulation of mortality, for which “expected” is $K - \frac{Var[Y]}{K}$. Non-spatial simulations were run in R. Solid line is where density is equal to carrying capacity, which is true for deterministic model.

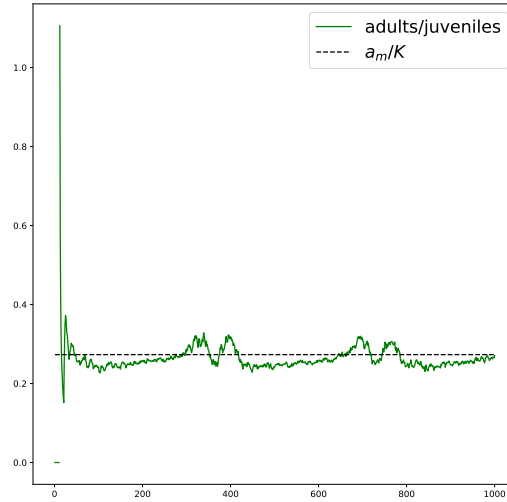


Figure S12: Ratio between adult and juvenile mosquito counts.

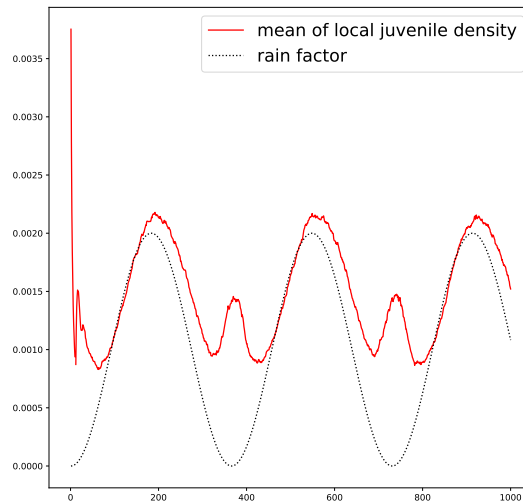


Figure S13: Local population density of juvenile mosquitoes plotted against rain factor, which is minimum carrying capacity at each time point.