First set of Beverton-Holt simulations for testing sparse modeling code, generated via the “Linear response of lambda to environment” section in the included R code file.

* All these data are with 10 species and 50 plots (independent runs) for simulations 1 and 2, and 200 plots for simulations 3 and 4
* Alphas are set at the beginning of each simulation and consistent for all plots  
  + - Intraspecific alphas are always 0.01.
    - Generic competitors alphas are drawn from a normal distribution with a mean 0.001 and sd of 0.0003.
    - Non-generic competitors are chosen by a single draw from a poisson distribution with lambda of 2 to determine how many species should be non-generic, and then randomly selecting which ones those should be. For each of these species, a single draw from an exponential distribution with a rate of 0.5 determines what that non-generic competition term should be, this is multiplied with the generic draw (mean 0.001 sd 0.0003) for each pair of competitor-responders.
* Starting populations are drawn from a normal distribution with mean of 80 and sd of 100. Populations less than 0 are set to 0. Starting populations are drawn independently for each species and each plot.
* Lambdas are determined in different ways for each of the included files:  
  + - 1. no variation: Mean lambda drawn from uniform distribution from 0 to 1.5, which is then exponentiated in the function resulting a range from 1 to 4.5. Lambda consistent for all 50 plots.
    - 2. demographic heterogeneity only: Mean (pre-transformed) lambda drawn from uniform distribution from 0 to 1.5. A demographic stochasticity parameter is drawn for each species in each plot from a normal distribution with mean 0 and sd 0.2 and added to the mean, which is then exponentiated in the function.
    - 3. monotonic environmental response only: Mean lambda drawn from uniform distribution from 0 to 1.5, environmental response drawn from a normal distribution with a mean of 0 and sd of 0.5 -- these are then added together before being exponentiated. For each plot, lambda for each species is calculated as the mean lambda plus the interaction between the environmental response of that species and the environmental condition of that plot.
    - 4. monotonic environmental response + demographic heterogeneity: Mean lambda drawn from uniform distribution from 0 to 1.5, environmental response drawn from a normal distribution with a mean of 0 and sd of 0.5, demographic heterogeneity drawn for each species for each plot from a normal distribution with a mean of 0 and sd of 0.1 -- these are then all three added together before being exponentiated.
    - 5. optimum environmental response: Environmental response is from Eqn 3 in Thompson et al 2020 Ecology Letters. Density-independent growth lambda is based on max density-independent growth lambda.max, the environmental condition in the plot run.env, the environmental optimum of the species z.env[i], and the abiotic niche breadth sigma.env[i]. When sigma.env[i] is small, the abiotic niche is narrow. We lambda.max instead of lambda.mean, which is outside of the exponentiation in the function above, so I've set this as a uniform draw between 1 and 5 for now. Instead of lambda.env we have two parameters: z.env (environmental optimum for each species) and sigma.env (niche breadth). z.env is drawn from a normal distribution with the same sd as the plot condition for the runs. sigma.env is drawn from an exponential distribution with a rate of 0.2, whicH means roughly 1/2 will be < 2 and 1/3 will be < 1.

Species with interaction alpha draws from the non-generic distribution

3a - 8, 10

3b - 2, 4, 9

4a - 1, 3, 4

4b - 3

5a - 5, 6

5b - 8, 9

5c - 1, 4, 7