Appendix B from A. B. Duthie and J. M. Reid, "Evolution of Inbreeding Avoidance and Inbreeding Preference through Mate Choice among Interacting Relatives" (Am. Nat., vol. 188, no. 6, p. 000)

Exploratory Simulation Results



Figure B1: Examples of the dynamics of population size (*A*), inbreeding-avoidance allele (S^4 ; *B*) and neutral allele (N^- ; *C*) frequencies, and the distribution of pairwise kinship values and mean deleterious recessive allele frequencies (*D*) over 3,000 generations. Gray lines in *A*–*C* show nine replicate simulations with *s* = 0.016 and *c* = 0.005; black lines show one highlighted replicate. In *A*, population size is shown for females (solid line) and males (dashed line), including two simulations where populations went extinct. In *D*, the white line illustrates the mean frequency of *L*⁻ alleles across 1,000 loci. Shading indicates the distribution of kinship between all pairwise combinations of individuals, where increasingly lighter shades encompass a higher proportion of kinships. Black, dark gray, mid gray, and light gray encompass 75%, 90%, 99%, and 100% of all kinships, respectively. Dynamics of *L*⁻ frequencies and kinship distributions did not vary greatly among replicate simulations. Arrows indicate end population sizes (*A*), *S*⁴ frequency (*B*), *N*⁻ frequency (*C*), mean *L*⁻ frequency (*D*, top arrow), and mean kinship value (*D*, bottom arrow) after 3,000 generations.