

## 1 **Supplementary Appendix B: Testing Lande’s Diffusion Approximation and the Probability** 2 **Density Function**

3 In addition to implementing the simulation model, we used Lande’s diffusion  
4 approximation (Lande 1981, eq. (3)) in a simplified simulation to verify its accuracy. This  
5 verification is important because we need to know whether ignoring deviations from the line of  
6 equilibria (as in eq.(3)) underestimates divergence in trait means. We used the same 324  
7 parameter combinations as in the full simulations. For each of 500,000 replicate population pairs  
8 at each generation  $t$ , we drew values of  $\bar{z}$  and  $\bar{y}$  from a bivariate normal distribution with means  
9 of zero and variance-covariance matrix described by Lande’s dispersion matrix (eq. (3)). Once  $\bar{z}$   
10 and  $\bar{y}$  were determined for each population at 1,000 and 10,000 generations, we proceeded as in  
11 the full simulation model and calculated  $Jl$  for each replicate pair. We then compared the mean  
12 and variance of  $Jl$  and the proportion of pairs with  $Jl > 1.6$  to the results of the full simulation to  
13 determine the accuracy of the diffusion approximation.

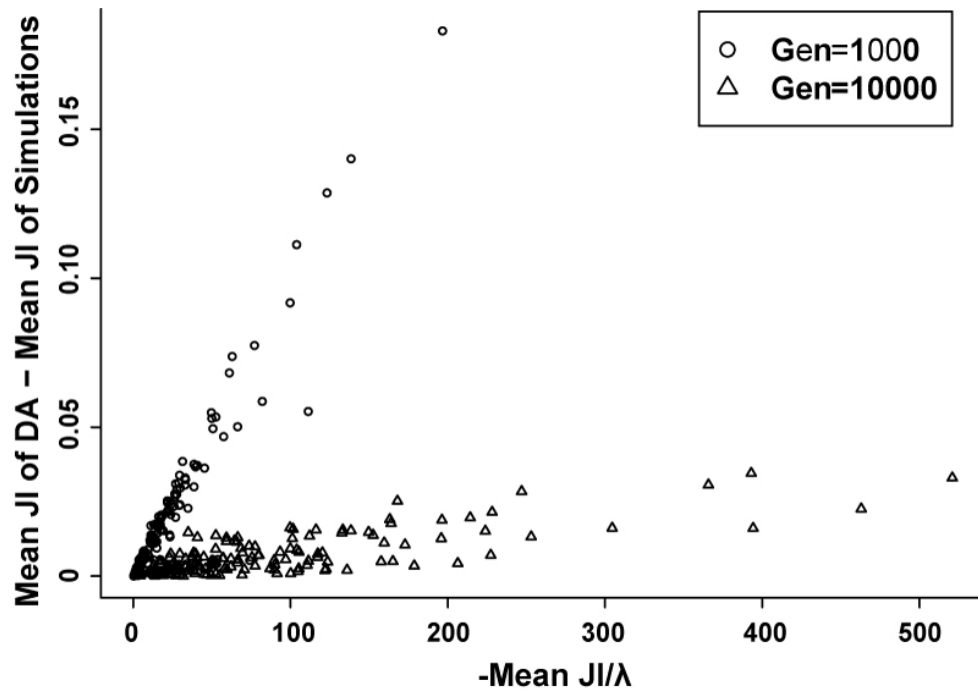
14 Additionally, for all 324 parameter combinations we performed numerical integration in  
15 R (R Core Development Team 2007) using the probability density function of  $\pi_{AB}$ , eq. (6), to  
16 determine the expected value of  $\pi_{AB}$ ,  $E[\pi_{AB}, t]$ , at generation  $t$ . From this value we  
17 approximated  $Jl$  as  $2(1 - E[\pi_{AB}, t])$ . In addition, we used numerical integration to calculate the  
18 probability of obtaining a value of  $\pi_{AB} < 0.2$ , which corresponds to the probability of obtaining a  
19 value of  $Jl > 1.6$ .

### 20 ***Results for Diffusion Approximation and Probability Density Function***

21 We compared the simulation results (table 1) to results using two other approaches (tables B1  
22 and B2, Online Appendix B). First, we sampled pairs of populations from Lande’s (1981)  
23 diffusion approximation (DA) described by equation (3) and calculated  $Jl$  for each pair. Mean  $Jl$

1 and proportion of pairs with  $JI > 1.6$  for each parameter combination in table 1 was estimated  
2 from 500,000 such replicate samples. Second, we applied a few additional assumptions to create  
3 a probability density function (PDF) for  $JI$  and used this function to calculate directly the mean  
4  $JI$  and proportion of population pairs with  $JI > 1.6$ .

5 All three methods yielded very similar results in both measures of sexual isolation. The  
6 largest discrepancies between mean  $JI$  values, observed for the parameter values that we  
7 examined, occurred between the simulation results on the one hand and the DA and PDF results  
8 on the other. The key parameter affecting deviations between methods was the leading  
9 eigenvalue ( $\lambda$ ) of the matrix describing evolutionary movement (eq. (11b) in Lande 1981). This  
10 rate parameter determines how rapidly populations evolve towards the line of equilibrium. Both  
11 the DA and the PDF are based on the dispersion matrix, eq. (3), which assumes that  $-1 < \lambda < 0$   
12 and  $t \gg -1/\lambda$  (Lande 1981). As  $\lambda$  approaches 0, selection is weak and drift away from the line of  
13 equilibrium causes the stochastic simulations to predict less reproductive isolation than the DA  
14 and PDF models, in which all evolution occurs along a single axis (the line of equilibrium). This  
15 discrepancy erodes, however, as  $t$  increases, and the difference was only substantial in our results  
16 for the few parameter sets in which  $\lambda \approx 0$  and in which  $JI$  was substantial after only 1,000  
17 generations (fig. B1, tables B1 and B2). The PDF method performs as well as the DA on small to  
18 intermediate time scales, but consistently underpredicts  $JI$ , especially at longer timescales. This  
19 difference might be expected given that the simplifying assumption that within population trait  
20 means were equal was used to derive the PDF results. Nevertheless, the disparity is relatively  
21 minor and qualitative predictions from all three models are identical. While the simulation  
22 method carries the fewest assumptions, both the DA and the PDF simplify computations by  
23 orders of magnitude at a small cost in accuracy.



1  
2 **Figure B1.** Difference in mean  $J_I$  between the diffusion approximation (DA) and the full  
3 simulation model for all 324 parameter combinations. The key parameter determining the  
4 difference between the DA and simulation methods is the leading eigenvalue ( $\lambda$ ) of the matrix  
5 describing evolutionary movement, scaled by the expected value of  $J_I$ . As the value of  $\lambda$   
6 approaches 0, the strength of selection back towards the line of equilibrium weakens, resulting in  
7 more drift off the line of equilibrium and more discordance between the full simulation model  
8 and the DA (which assumes evolutionary motion only along the line of equilibrium). Thus, when  
9 the mean  $J_I$  is predicted to be high and  $\lambda$  is small, the discrepancy between the two methods  
10 increases. However, this effect erodes with time and reaches substantial levels for relatively few  
11 parameter combinations.

**Table B1:** The percentage of replicate population pairs evolving substantial isolation by drift as a function of population size, inheritance, and selection simulated using the diffusion approximation.

$\gamma$	$\omega^2$	$v^2$	$\alpha$	After 1,000 generations						After 10,000 generations					
				$G=H=0.2$			$G=H=0.6$			$G=H=0.2$			$G=H=0.6$		
				$N_e$			$N_e$			$N_e$			$N_e$		
				5000	1000	500	5000	1000	500	5000	1000	500	5000	1000	500
0.6	25	20	0.8	0	0	0	0	0	0	0	0	0	0	0	0
0.6	50	20	0.4	0	0	0	0	0	0	0	0.01	0.61	0	2.35	9.59
0.6	25	10	0.4	0	0	0	0	0	0.02	0	0.41	3.91	0.02	8.48	16.9
0.6	100	20	0.2	0	0	0	0	0	0.01	0	0.33	3.65	0.01	8.66	22.1
0.6	50	10	0.2	0	0	0	0	0.01	0.51	0	2.91	12	0.49	20.3	35.5
0.6	25	5	0.2	0	0	0.02	0	0.25	3.19	0.02	9.46	23	3.15	32.2	45.1
0.6	100	10	0.1	0	0	0	0	0.07	1.61	0	6.22	18.7	1.58	27.9	44.1
0.6	50	5	0.1	0	0	0.15	0	0.92	6.55	0.14	15.3	31.1	6.59	40.6	55.1
0.6	100	5	0.05	0	0	0.34	0	1.71	9.25	0.35	19.1	35.5	9.14	44.9	59.2
0.7	25	20	0.8	0	0	0	0	0	0	0	0	0	0	0	0
0.7	50	20	0.4	0	0	0	0	0	0	0	0.02	0.71	0	2.63	10.1
0.7	25	10	0.4	0	0	0	0	0	0.03	0	0.48	4.28	0.03	9.06	17.3
0.7	100	20	0.2	0	0	0	0	0	0.04	0	0.6	5.09	0.04	10.9	25.1
0.7	50	10	0.2	0	0	0	0	0.02	0.9	0	4.17	14.7	0.89	23.2	38.4
0.7	25	5	0.2	0	0	0.05	0	0.47	4.47	0.06	11.8	26.1	4.48	35.1	46.5
0.7	100	10	0.1	0	0	0.02	0	0.23	3.09	0.02	9.42	23.5	3.13	33.2	48.8
0.7	50	5	0.1	0	0.01	0.42	0	2.02	9.83	0.42	20.1	36.2	9.98	45.4	59.1
0.7	100	5	0.05	0	0.03	1.1	0	3.78	14.1	1.1	25.5	41.9	14.3	51	64
0.9	25	20	0.8	0	0	0	0	0	0	0	0	0	0	0	0
0.9	50	20	0.4	0	0	0	0	0	0	0	0	0.16	0	0.97	6.13
0.9	25	10	0.4	0	0	0	0	0	0	0	0.11	1.88	0	5.21	14.1
0.9	100	20	0.2	0	0	0	0	0	0.05	0	0.71	5.57	0.05	11.5	25.9
0.9	50	10	0.2	0	0	0	0	0.03	0.99	0	4.5	15.3	0.99	23.9	38.9
0.9	25	5	0.2	0	0	0.07	0	0.54	4.76	0.07	12.4	26.9	4.82	35.9	46.9
0.9	100	10	0.1	0	0	0.23	0	1.24	7.71	0.23	17	33	7.66	42.4	56.6
0.9	50	5	0.1	0	0.1	1.97	0	5.54	17.6	1.95	29.4	45.4	17.6	53.7	65.2
0.9	100	5	0.05	0	1.16	7.43	0.12	14.5	30.2	7.38	42.4	56.9	30.3	64.2	73.9

Note: The proportion of replicate pairs of populations with substantial isolation ( $JI > 1.6$ ) shown in each cell represent the summary of 500, 000 pairs of replicate populations after 1,000 or 10,000 generations of evolution

**Table B2:** The percentage of replicate population pairs evolving substantial isolation by drift as a function of population size, inheritance, and selection estimated using the probability density function.

$\gamma$	$\omega^2$	$v^2$	$\alpha$	After 1,000 generations						After 10,000 generations					
				$G=H=0.2$			$G=H=0.6$			$G=H=0.2$			$G=H=0.6$		
				$N_e$			$N_e$			$N_e$			$N_e$		
				5000	1000	500	5000	1000	500	5000	1000	500	5000	1000	500
0.6	25	20	0.8	0	0	0	0	0	0	0	0	0	0	0.03	1
0.6	50	20	0.4	0	0	0	0	0	0	0	0	0.29	0	1.51	8.58
0.6	25	10	0.4	0	0	0	0	0	0.01	0	0.19	2.8	0.01	7.28	20.5
0.6	100	20	0.2	0	0	0	0	0	0	0	0.16	2.57	0	6.85	19.8
0.6	50	10	0.2	0	0	0	0	0	0.26	0	1.98	9.94	0.26	17.8	34.1
0.6	25	5	0.2	0	0	0.01	0	0.12	2.16	0.01	7.51	20.8	2.16	30.4	46.7
0.6	100	10	0.1	0	0	0	0	0.04	1.22	0	5.21	17	1.22	26.2	42.8
0.6	50	5	0.1	0	0	0.09	0	0.68	5.55	0.09	13.8	29.4	5.55	39.2	54.5
0.6	100	5	0.05	0	0	0.28	0	1.48	8.48	0.28	18.2	34.5	8.48	44.1	58.6
0.7	25	20	0.8	0	0	0	0	0	0	0	0	0	0	0.02	0.81
0.7	50	20	0.4	0	0	0	0	0	0	0	0	0.35	0	1.73	9.22
0.7	25	10	0.4	0	0	0	0	0	0.01	0	0.23	3.13	0.01	7.86	21.4
0.7	100	20	0.2	0	0	0	0	0	0.01	0	0.32	3.72	0.01	8.9	22.9
0.7	50	10	0.2	0	0	0	0	0.01	0.5	0	2.96	12.4	0.5	20.9	37.4
0.7	25	5	0.2	0	0	0.02	0	0.24	3.19	0.02	9.66	24	3.19	33.7	49.8
0.7	100	10	0.1	0	0	0.01	0	0.15	2.46	0.01	8.18	21.8	2.46	31.5	47.7
0.7	50	5	0.1	0	0	0.3	0	1.52	8.61	0.3	18.4	34.7	8.61	44.3	58.7
0.7	100	5	0.05	0	0.02	0.93	0	3.37	13.3	0.93	24.5	41.1	13.3	50.2	63.4
0.9	25	20	0.8	0	0	0	0	0	0	0	0	0	0	0	0.04
0.9	50	20	0.4	0	0	0	0	0	0	0	0	0.06	0	0.53	4.88
0.9	25	10	0.4	0	0	0	0	0	0	0	0.04	1.17	0	3.96	14.6
0.9	100	20	0.2	0	0	0	0	0	0.02	0	0.38	4.06	0.02	9.45	23.7
0.9	50	10	0.2	0	0	0	0	0.01	0.58	0	3.25	13	0.58	21.7	38.3
0.9	25	5	0.2	0	0	0.03	0	0.29	3.5	0.03	10.2	24.8	3.5	34.6	50.5
0.9	100	10	0.1	0	0	0.14	0	0.92	6.57	0.14	15.4	31.3	6.57	41	56
0.9	50	5	0.1	0	0.06	1.49	0	4.68	16	1.49	27.6	44.1	16	53	65.7
0.9	100	5	0.05	0	0.98	6.78	0.09	13.6	29.2	6.78	41.4	56.4	29.2	63.7	73.9

Note: The proportion of replicate pairs of populations with substantial isolation ( $JI > 1.6$ ) shown in each cell expected value of  $JI$  solved by numerical integration of the probability density function (eq. (6)).