

<sup>1</sup> **File S1. Multi-allele Wright-Fisher model with selection and migration**

<sup>2</sup> Let  $\mathbf{X}^{(N)}(k) = (X_1^{(N)}(k), X_2^{(N)}(k), X_3^{(N)}(k), X_4^{(N)}(k))$  denote frequencies of the  $\mathcal{A}_1^i$ ,  $\mathcal{A}_2^i$ ,  $\mathcal{A}_1^c$   
<sup>3</sup> and  $\mathcal{A}_2^c$  alleles in  $N$  zygotes of generation  $k \in \mathbb{N}$  on the island. As discussed in Loog et al. (2017),  
<sup>4</sup> the population dynamics might not be influenced by natural selection and gene migration in  
<sup>5</sup> the early stage, thereby necessitating two additional population genetic quantities, the starting  
<sup>6</sup> times of natural selection and gene migration on the island, denoted by  $k_s$  and  $k_m$ , respectively.

<sup>7</sup> We then rewrite the selection coefficient and the migration rate as

$$s(k) = \begin{cases} 0, & \text{if } k < k_s \\ s, & \text{otherwise} \end{cases} \quad \text{and} \quad m(k) = \begin{cases} 0, & \text{if } k < k_m \\ m, & \text{otherwise,} \end{cases}$$

<sup>8</sup> where the selection coefficient  $s$  and the migration rate  $m$  are both fixed from the timing of the  
<sup>9</sup> onset of natural selection and gene migration up to present. **Conditional on the allele frequencies**  
<sup>10</sup> **of the population at generation  $k$ , we have**

$$\mathbf{X}^{(N)}(k+1) \mid \mathbf{X}^{(N)}(k) = \mathbf{x} \sim \frac{1}{2N} \text{Multinomial}(2N, \mathbf{p}),$$

<sup>11</sup> where

$$\begin{aligned} p_1 &= (1 - m(k))x_1 \frac{1 - hs(k)(x_2 + x_4)}{1 - 2hs(k)(x_1 + x_3)(x_2 + x_4) - s(k)(x_2 + x_4)^2} \\ p_2 &= (1 - m(k))x_2 \frac{1 - hs(k)(x_1 + x_3) - s(k)(x_2 + x_4)}{1 - 2hs(k)(x_1 + x_3)(x_2 + x_4) - s(k)(x_2 + x_4)^2} \\ p_3 &= (1 - m(k))x_3 \frac{1 - hs(k)(x_2 + x_4)}{1 - 2hs(k)(x_1 + x_3)(x_2 + x_4) - s(k)(x_2 + x_4)^2} + m(k)x_c \\ p_4 &= (1 - m(k))x_4 \frac{1 - hs(k)(x_1 + x_3) - s(k)(x_2 + x_4)}{1 - 2hs(k)(x_1 + x_3)(x_2 + x_4) - s(k)(x_2 + x_4)^2} + m(k)(1 - x_c) \end{aligned} \tag{1}$$

<sup>12</sup> are the allele frequencies of an effectively infinite population on the island after random mating,  
<sup>13</sup> natural selection and gene migration from generation  $k$  to  $k+1$ . In Eq. (1),  $x_c$  is the frequency  
<sup>14</sup> of the  $\mathcal{A}_1^c$  allele in the continent population, which is fixed over time.

<sup>15</sup> We define the multi-allele Wright-Fisher model with selection and migration to be the ran-  
<sup>16</sup> dom process  $\mathbf{X}^{(N)} = \{\mathbf{X}^{(N)}(k), k \in \mathbb{N}\}$  evolving in the state space

$$\Omega_{\mathbf{X}^{(N)}} = \left\{ \mathbf{x} \in \left\{ 0, \frac{1}{2N}, \dots, 1 \right\}^4 : \sum_{i=1}^4 x_i = 1 \right\}$$

<sup>17</sup> with multinomial sampling probabilities described in Eq. (1). The transition probabilities of  
<sup>18</sup> the allele frequencies from one generation to the next depend only on the current generation,  
<sup>19</sup> which implies that the Wright-Fisher model  $\mathbf{X}^{(N)}$  is a Markov process.

20 **File S2. Additional results for the analysis of simulated data**

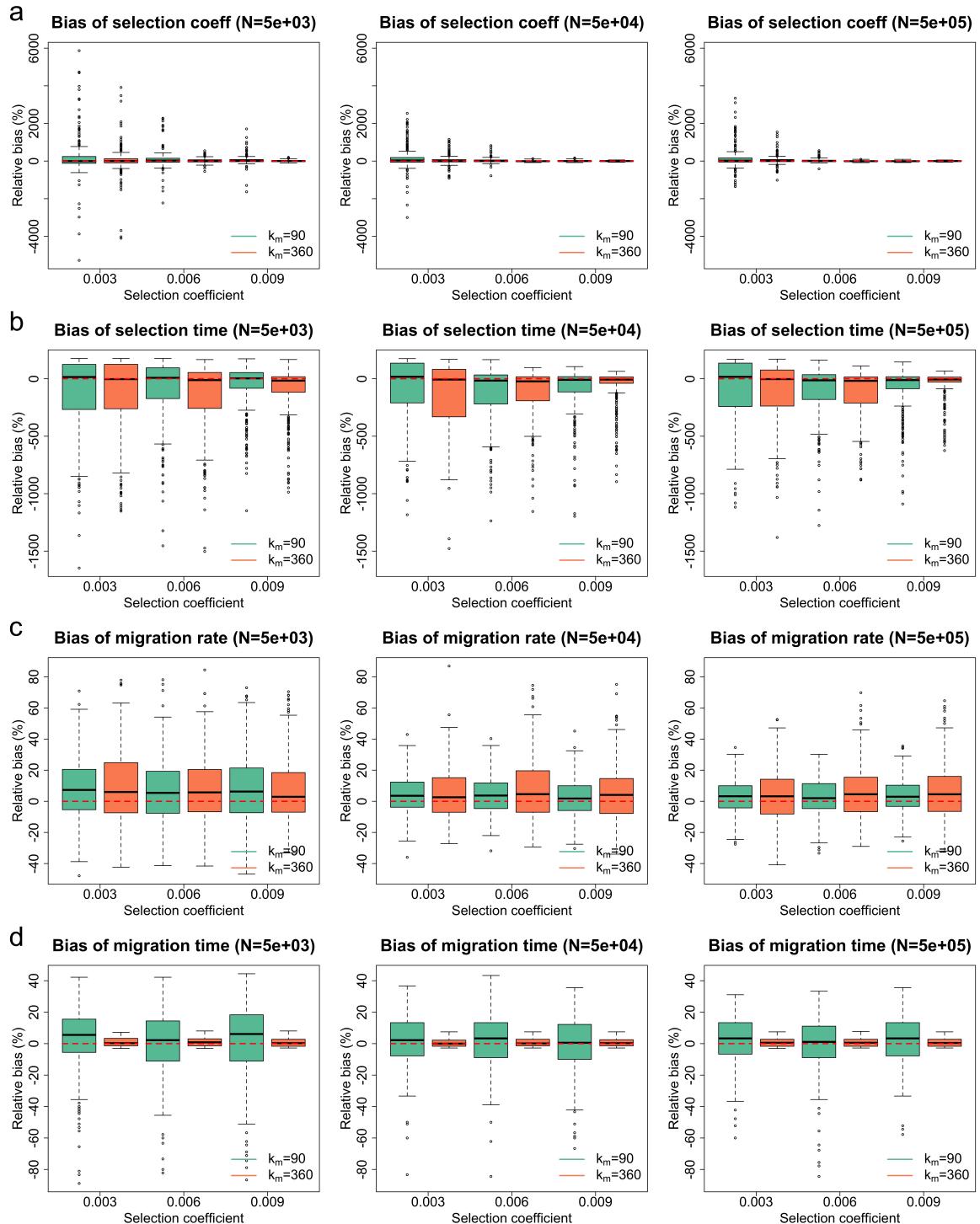


Figure S1: Empirical distributions of the estimates for 300 datasets simulated for the case of continent allele counts unavailable at the **first three sampling time points**. Aquamarine boxplots represent the estimates produced for the case of natural selection starting after gene migration, and coral boxplots represent the estimates produced for the case of natural selection starting before gene migration. Boxplots of the relative bias of (a) the selection coefficient estimates (b) the selection time estimates (c) the migration rate estimates and (d) the migration time estimates.

$N$	$k_m$	$s$	Bias	Rel. Bias	RMSE	Rel. RMSE
5000	90	0.003	0.00468	1.56050	0.02829	9.43106
5000	90	0.006	0.00502	0.83661	0.02561	4.26886
5000	90	0.009	0.00373	0.41479	0.02070	2.29946
5000	360	0.003	0.00093	0.31030	0.01953	6.51146
5000	360	0.006	0.00127	0.21204	0.00713	1.18760
5000	360	0.009	0.00045	0.05030	0.00491	0.54500
50000	90	0.003	0.00434	1.44527	0.01713	5.71086
50000	90	0.006	0.00157	0.26180	0.00805	1.34137
50000	90	0.009	0.00034	0.03819	0.00419	0.46556
50000	360	0.003	0.00100	0.33222	0.00682	2.27354
50000	360	0.006	0.00004	0.00686	0.00262	0.43607
50000	360	0.009	-0.00008	-0.00845	0.00260	0.28852
500000	90	0.003	0.00392	1.30796	0.01613	5.37626
500000	90	0.006	0.00099	0.16565	0.00540	0.89923
500000	90	0.009	-0.00014	-0.01584	0.00342	0.37963
500000	360	0.003	0.00156	0.52107	0.00700	2.33239
500000	360	0.006	-0.00025	-0.04204	0.00226	0.37589
500000	360	0.009	-0.00005	-0.00506	0.00225	0.24999

(a) Bias and RMSE of the selection coefficient estimates.

$N$	$k_m$	$s$	Bias	Rel. Bias	RMSE	Rel. RMSE
5000	90	0.003	-210.90333	-1.17169	621.71914	3.45400
5000	90	0.006	-156.32667	-0.86848	521.88065	2.89934
5000	90	0.009	-109.42000	-0.60789	387.34442	2.15191
5000	360	0.003	-211.54333	-1.17524	597.03986	3.31689
5000	360	0.006	-232.78333	-1.29324	580.80568	3.22670
5000	360	0.009	-181.31667	-1.00731	430.67649	2.39265
50000	90	0.003	-159.88000	-0.88822	534.32684	2.96848
50000	90	0.006	-204.42000	-1.13567	478.61504	2.65897
50000	90	0.009	-151.97333	-0.84430	386.40670	2.14670
50000	360	0.003	-221.46333	-1.23035	555.05374	3.08363
50000	360	0.006	-201.02000	-1.11678	419.21672	2.32898
50000	360	0.009	-114.76333	-0.63757	308.31382	1.71285
500000	90	0.003	-149.65667	-0.83143	512.18792	2.84549
500000	90	0.006	-178.32333	-0.99069	429.41112	2.38562
500000	90	0.009	-151.04333	-0.83913	368.73452	2.04853
500000	360	0.003	-189.66667	-1.05370	509.13465	2.82853
500000	360	0.006	-199.08333	-1.10602	403.27948	2.24044
500000	360	0.009	-80.06333	-0.44480	240.24256	1.33468

(b) Bias and RMSE of the selection time estimates.

Table S1: Bias and RMSE of the estimates for the selection-related parameters from 300 datasets simulated for the case of continent allele counts unavailable at the first three sampling time points.

$N$	$k_m$	$s$	Bias	Rel. Bias	RMSE	Rel. RMSE
5000	90	0.003	0.00040	0.07937	0.00105	0.21004
5000	90	0.006	0.00029	0.05825	0.00106	0.21144
5000	90	0.009	0.00036	0.07207	0.00115	0.22989
5000	360	0.003	0.00046	0.09101	0.00121	0.24261
5000	360	0.006	0.00041	0.08229	0.00114	0.22836
5000	360	0.009	0.00036	0.07261	0.00110	0.21985
50000	90	0.003	0.00020	0.03988	0.00062	0.12413
50000	90	0.006	0.00018	0.03647	0.00061	0.12148
50000	90	0.009	0.00012	0.02493	0.00061	0.12123
50000	360	0.003	0.00024	0.04795	0.00089	0.17748
50000	360	0.006	0.00036	0.07178	0.00101	0.20215
50000	360	0.009	0.00025	0.04997	0.00093	0.18545
500000	90	0.003	0.00015	0.03082	0.00056	0.11246
500000	90	0.006	0.00013	0.02547	0.00059	0.11724
500000	90	0.009	0.00019	0.03719	0.00057	0.11341
500000	360	0.003	0.00022	0.04329	0.00087	0.17372
500000	360	0.006	0.00030	0.05903	0.00088	0.17657
500000	360	0.009	0.00031	0.06182	0.00094	0.18709

(a) Bias and RMSE of the migration rate estimates.

$N$	$k_m$	$s$	Bias	Rel. Bias	RMSE	Rel. RMSE
5000	90	0.003	2.41667	0.02685	19.15472	0.21283
5000	90	0.006	0.21333	0.00237	18.50171	0.20557
5000	90	0.009	1.71667	0.01907	21.02277	0.23359
5000	360	0.003	3.65333	0.01015	10.44956	0.02903
5000	360	0.006	3.70667	0.01030	10.05916	0.02794
5000	360	0.009	2.82333	0.00784	10.03278	0.02787
50000	90	0.003	1.77667	0.01974	14.92012	0.16578
50000	90	0.006	1.65333	0.01837	14.90011	0.16556
50000	90	0.009	0.14000	0.00156	15.82761	0.17586
50000	360	0.003	1.95667	0.00544	9.22551	0.02563
50000	360	0.006	2.50667	0.00696	9.32774	0.02591
50000	360	0.009	2.12667	0.00591	8.97552	0.02493
500000	90	0.003	1.62333	0.01804	14.32701	0.15919
500000	90	0.006	-0.50333	-0.00559	16.19311	0.17992
500000	90	0.009	2.09667	0.02330	13.71726	0.15241
500000	360	0.003	2.80333	0.00779	9.71820	0.02699
500000	360	0.006	2.71333	0.00754	9.71734	0.02699
500000	360	0.009	2.83333	0.00787	10.02630	0.02785

(b) Bias and RMSE of the migration time estimates.

Table S2: Bias and RMSE of the estimates for the migration-related parameters from 300 datasets simulated for the case of continent allele counts unavailable at the first three sampling time points.

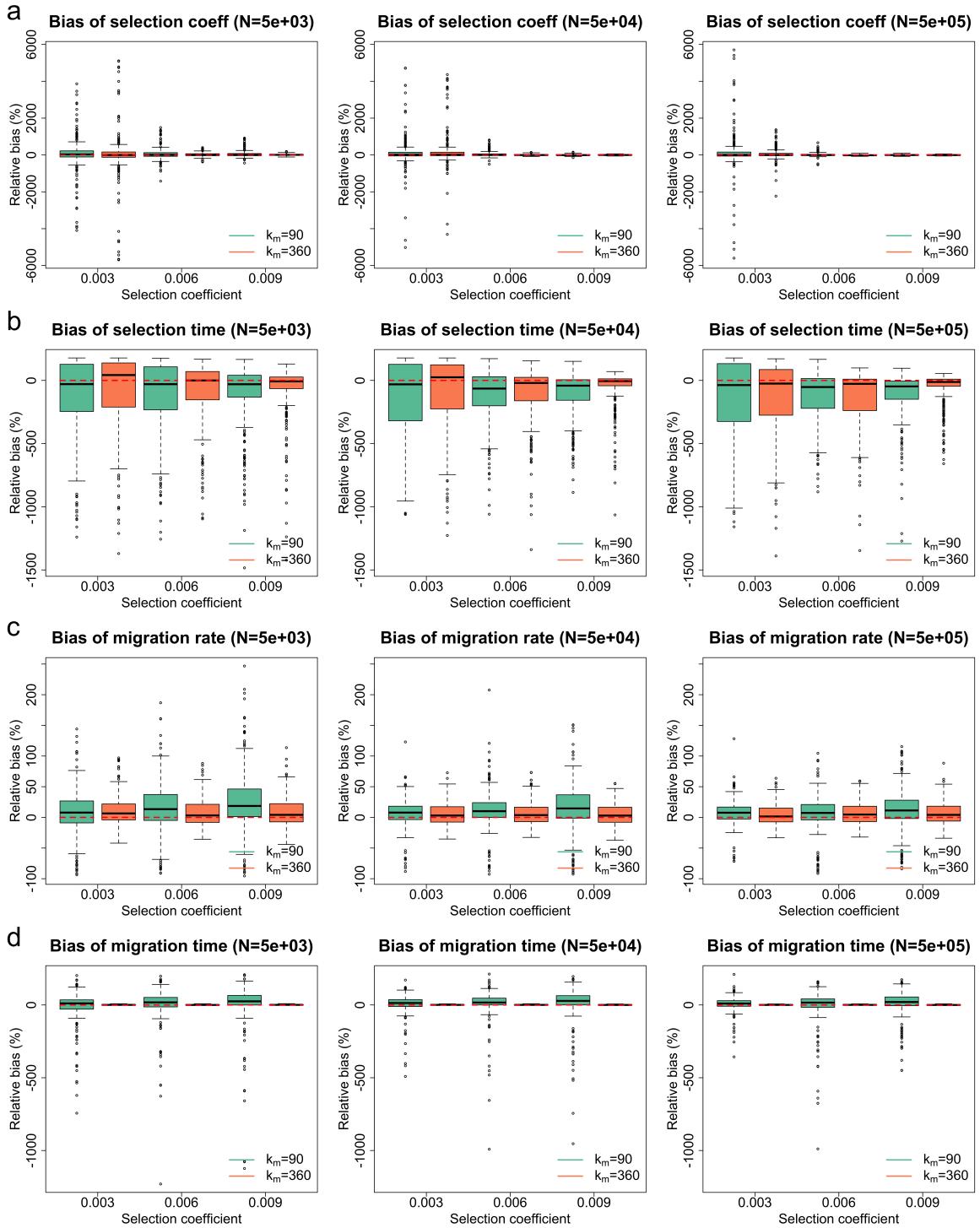


Figure S2: Empirical distributions of the estimates for 300 datasets simulated for the case of continent allele counts unavailable at [the first seven sampling time points](#). Aquamarine boxplots represent the estimates produced for the case of natural selection starting after gene migration, and coral boxplots represent the estimates produced for the case of natural selection starting before gene migration. Boxplots of the relative bias of (a) the selection coefficient estimates (b) the selection time estimates (c) the migration rate estimates and (d) the migration time estimates.

$N$	$k_m$	$s$	Bias	Rel. Bias	RMSE	Rel. RMSE
5000	90	0.003	0.00110	0.36598	0.02556	8.52108
5000	90	0.006	0.00347	0.57809	0.01812	3.02069
5000	90	0.009	0.00400	0.44399	0.01475	1.63932
5000	360	0.003	0.00046	0.15463	0.03540	11.80007
5000	360	0.006	0.00083	0.13876	0.00635	1.05828
5000	360	0.009	0.00093	0.10374	0.00472	0.52497
50000	90	0.003	0.00291	0.97150	0.02415	8.04869
50000	90	0.006	0.00171	0.28420	0.00768	1.27929
50000	90	0.009	0.00012	0.01355	0.00383	0.42527
50000	360	0.003	0.00524	1.74530	0.02562	8.54085
50000	360	0.006	0.00020	0.03408	0.00275	0.45771
50000	360	0.009	-0.00009	-0.01039	0.00250	0.27750
500000	90	0.003	0.00322	1.07406	0.03035	10.11574
500000	90	0.006	0.00088	0.14618	0.00622	1.03736
500000	90	0.009	-0.00024	-0.02651	0.00321	0.35614
500000	360	0.003	0.00144	0.48093	0.00901	3.00300
500000	360	0.006	-0.00040	-0.06742	0.00224	0.37318
500000	360	0.009	-0.00049	-0.05478	0.00237	0.26347

(a) Bias and RMSE of the selection coefficient estimates.

$N$	$k_m$	$s$	Bias	Rel. Bias	RMSE	Rel. RMSE
5000	90	0.003	-218.83000	-1.21572	613.45370	3.40808
5000	90	0.006	-197.30000	-1.09611	546.14176	3.03412
5000	90	0.009	-179.02667	-0.99459	483.29569	2.68498
5000	360	0.003	-161.02000	-0.89456	575.71969	3.19844
5000	360	0.006	-147.86333	-0.82146	459.69421	2.55386
5000	360	0.009	-124.24000	-0.69022	390.64411	2.17025
50000	90	0.003	-235.89667	-1.31054	586.78393	3.25991
50000	90	0.006	-210.80000	-1.17111	434.06003	2.41144
50000	90	0.009	-188.10667	-1.04504	366.53007	2.03628
50000	360	0.003	-162.66333	-0.90369	552.28193	3.06823
50000	360	0.006	-182.22667	-1.01237	419.28852	2.32938
50000	360	0.009	-98.90000	-0.54944	284.07125	1.57817
500000	90	0.003	-230.90000	-1.28278	581.75415	3.23197
500000	90	0.006	-218.24667	-1.21248	420.77265	2.33763
500000	90	0.009	-193.38333	-1.07435	378.31113	2.10173
500000	360	0.003	-214.52667	-1.19181	533.35112	2.96306
500000	360	0.006	-237.16333	-1.31757	459.57492	2.55319
500000	360	0.009	-108.98667	-0.60548	256.16190	1.42312

(b) Bias and RMSE of the selection time estimates.

Table S3: Bias and RMSE of the estimates for the selection-related parameters from 300 datasets simulated for the case of continent allele counts unavailable at the first seven sampling time points.

$N$	$k_m$	$s$	Bias	Rel. Bias	RMSE	Rel. RMSE
5000	90	0.003	0.00046	0.09142	0.00182	0.36452
5000	90	0.006	0.00083	0.16636	0.00216	0.43224
5000	90	0.009	0.00132	0.26459	0.00275	0.54990
5000	360	0.003	0.00052	0.10371	0.00133	0.26544
5000	360	0.006	0.00038	0.07693	0.00116	0.23158
5000	360	0.009	0.00044	0.08795	0.00123	0.24646
50000	90	0.003	0.00035	0.06965	0.00118	0.23574
50000	90	0.006	0.00060	0.11954	0.00160	0.32043
50000	90	0.009	0.00084	0.16716	0.00203	0.40665
50000	360	0.003	0.00027	0.05318	0.00091	0.18284
50000	360	0.006	0.00032	0.06317	0.00098	0.19592
50000	360	0.009	0.00026	0.05257	0.00090	0.17914
500000	90	0.003	0.00035	0.07016	0.00107	0.21309
500000	90	0.006	0.00028	0.05678	0.00147	0.29372
500000	90	0.009	0.00064	0.12884	0.00177	0.35351
500000	360	0.003	0.00025	0.05038	0.00087	0.17486
500000	360	0.006	0.00033	0.06518	0.00095	0.18910
500000	360	0.009	0.00036	0.07105	0.00100	0.20017

(a) Bias and RMSE of the migration rate estimates.

$N$	$k_m$	$s$	Bias	Rel. Bias	RMSE	Rel. RMSE
5000	90	0.003	-6.86667	-0.07630	96.89169	1.07657
5000	90	0.006	4.27667	0.04752	108.71174	1.20791
5000	90	0.009	7.58000	0.08422	136.62328	1.51804
5000	360	0.003	4.09667	0.01138	10.95491	0.03043
5000	360	0.006	2.77667	0.00771	9.73156	0.02703
5000	360	0.009	3.60333	0.01001	10.45227	0.02903
50000	90	0.003	4.36667	0.04852	60.81349	0.67571
50000	90	0.006	9.32333	0.10359	90.97170	1.01080
50000	90	0.009	11.73333	0.13037	108.29035	1.20323
50000	360	0.003	3.25667	0.00905	9.98916	0.02775
50000	360	0.006	3.64333	0.01012	10.28381	0.02857
50000	360	0.009	2.28333	0.00634	9.20344	0.02557
500000	90	0.003	6.21000	0.06900	45.52241	0.50580
500000	90	0.006	-6.70333	-0.07448	108.67571	1.20751
500000	90	0.009	13.19333	0.14659	78.06728	0.86741
500000	360	0.003	2.68333	0.00745	9.70550	0.02696
500000	360	0.006	3.45333	0.00959	10.37272	0.02881
500000	360	0.009	2.43333	0.00676	9.84412	0.02734

(b) Bias and RMSE of the migration time estimates.

Table S4: Bias and RMSE of the estimates for the migration-related parameters from 300 datasets simulated for the case of continent allele counts unavailable at the first seven sampling time points.

21 **File S3. Additional results for the analysis of real data**

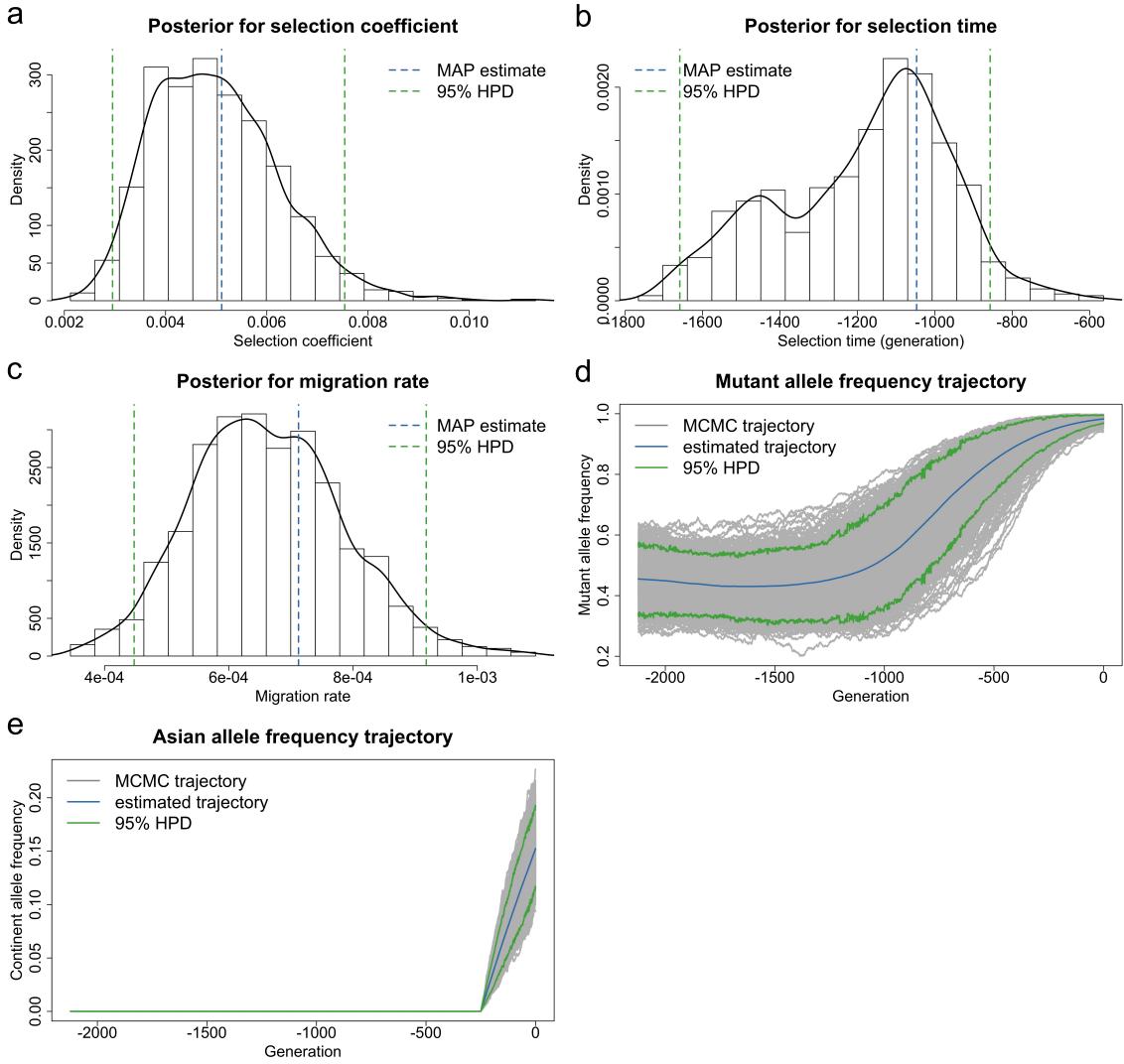


Figure S3: Bayesian estimates for aDNA data of European chicken genotyped at the *TSHR* locus from Loog et al. (2017) for the case of the population size  $N = 26000$ . Posteriors for (a) the selection coefficient (b) the selection time and (c) the migration rate. Estimated underlying trajectories of (d) the mutant allele frequency and (e) the Asian allele frequency in the European chicken population. The MAP estimate is for the joint posterior, and may not correspond to the mode of the marginals.

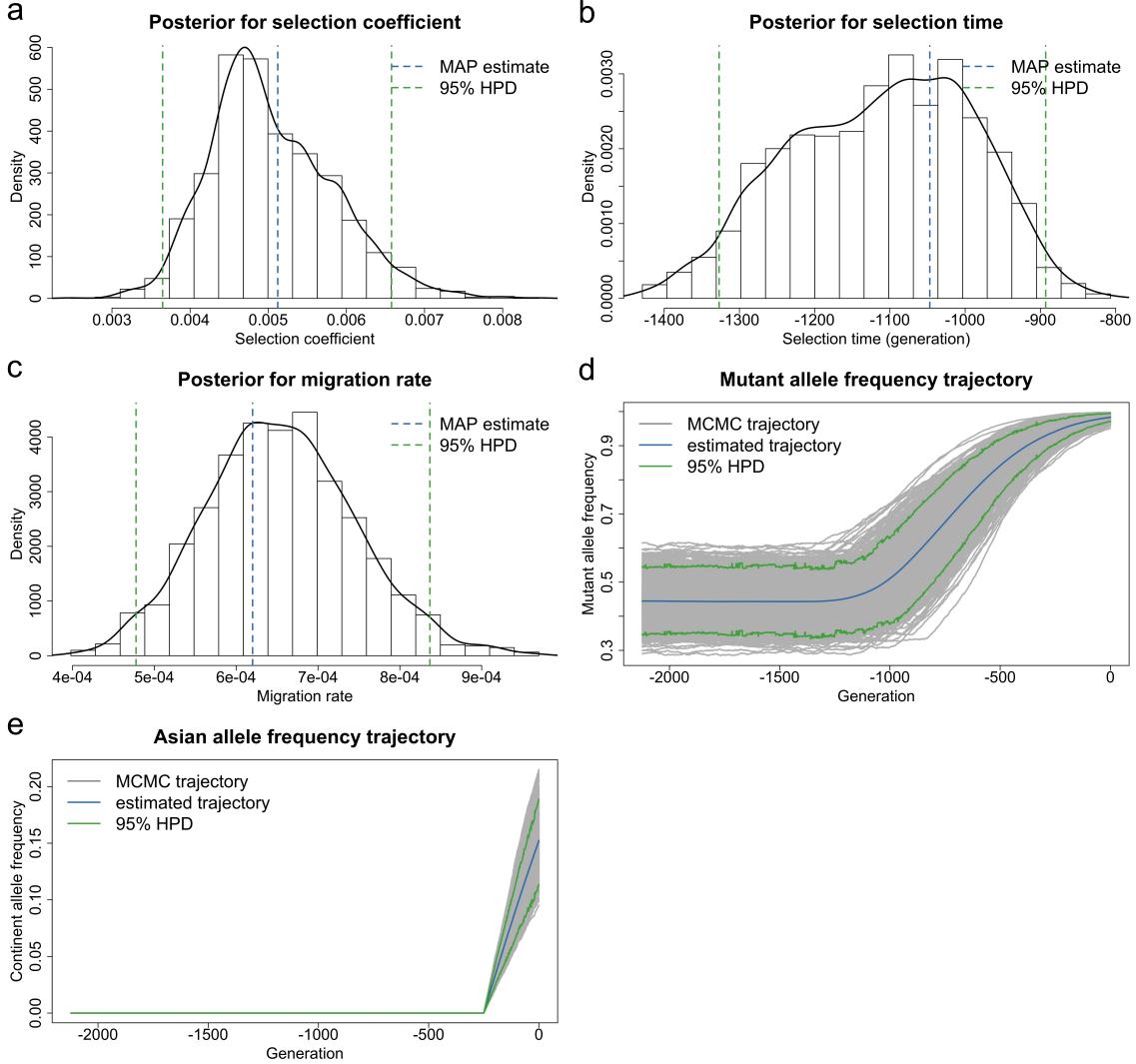


Figure S4: Bayesian estimates for aDNA data of European chicken genotyped at the *TSHR* locus from Loog et al. (2017) for the case of the population size  $N = 460000$ . Posteriors for (a) the selection coefficient (b) the selection time and (c) the migration rate. Estimated underlying trajectories of (d) the mutant allele frequency and (e) the Asian allele frequency in the European chicken population. The MAP estimate is for the joint posterior, and may not correspond to the mode of the marginals.

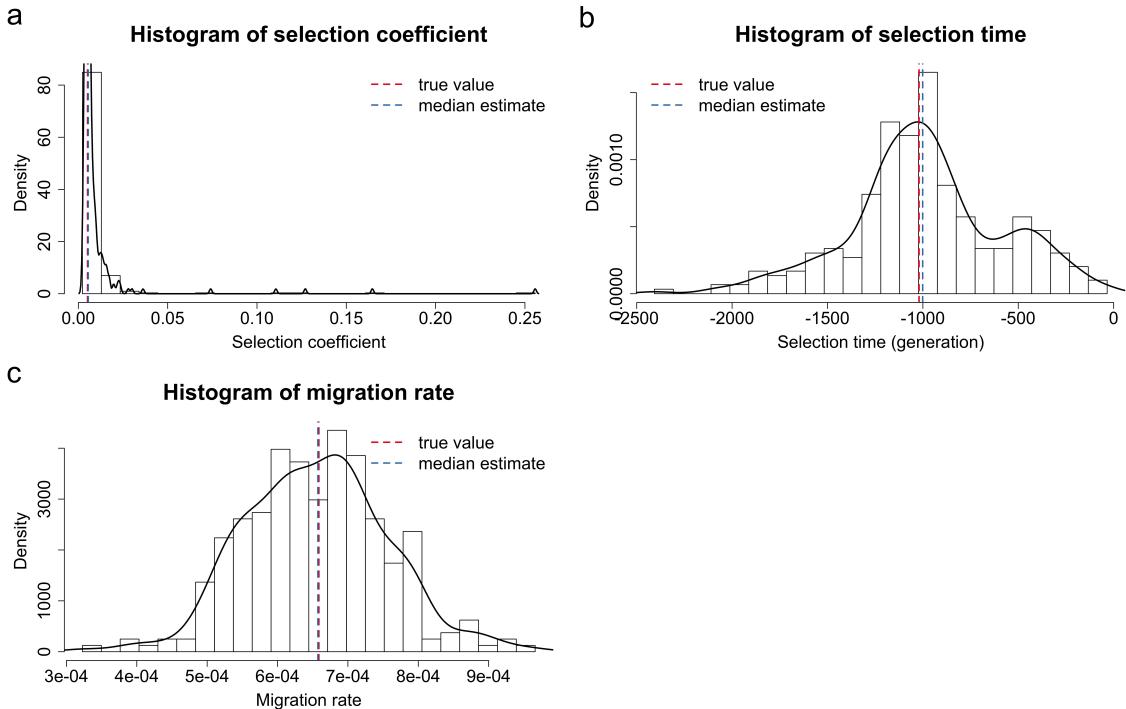


Figure S5: Empirical distributions of the estimates for 300 datasets simulated for *TSHR* based on the aDNA data shown in Table 2. We simulate the underlying population dynamics with the timing and strength of natural selection and gene migration estimated with the population size  $N = 180000$  shown in Table 3. Histograms of (a) the selection coefficient estimates (b) the selection time estimates and (c) the migration rate estimates.

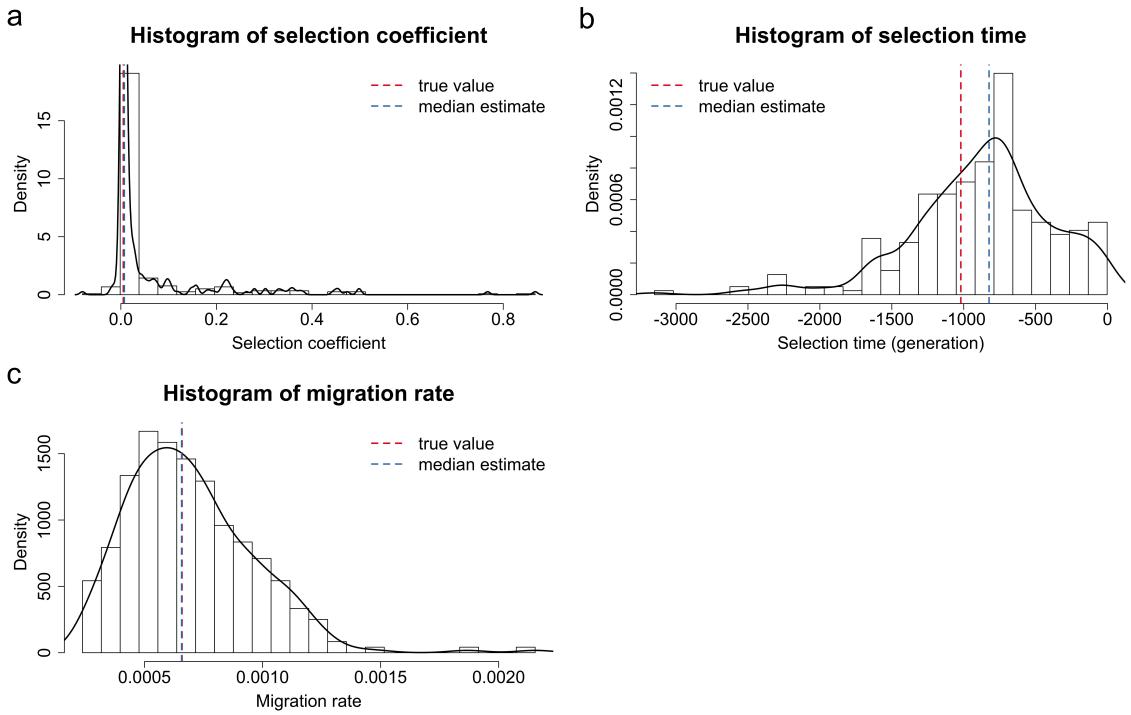


Figure S6: Empirical distributions of the estimates for 300 datasets simulated for *TSHR* based on the aDNA data shown in Table 2. We take the timing and strength of natural selection and gene migration to be those estimated with the population size  $N = 180000$  shown in Table 3, but the true population size in the simulation is taken to be  $N = 4500$ . Histograms of (a) the selection coefficient estimates (b) the selection time estimates and (c) the migration rate estimates. To aid visual comparison, we have picked the  $x$  axis in (a) not to cover all 300 estimates.

<sup>22</sup> **References**

<sup>23</sup> Loog, L., Thomas, M. G., Barnett, R., Allen, R., Sykes, N. et al. (2017). Inferring allele  
<sup>24</sup> frequency trajectories from ancient DNA indicates that selection on a chicken gene coincided  
<sup>25</sup> with changes in medieval husbandry practices. *Molecular Biology and Evolution*, 34, 1981–  
<sup>26</sup> 1990.