

Supplemental figures for

The temporal dynamics of background selection in non-equilibrium populations

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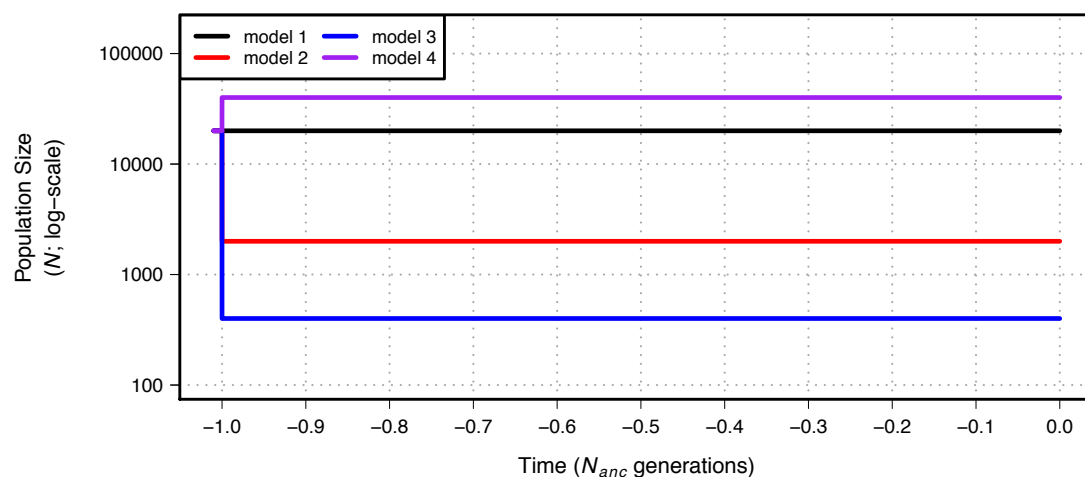


Figure S1 Demographic models 1-4 simulated in our study. Time proceeds forward from left to right and is scaled by the N of the population at the initial generation (N_{anc} ; 20,000 individuals). Demographic model 2 experiences a population contraction to 2000 individuals while demographic model 3 experiences a population contraction to 400 individuals. Demographic model 4 experiences a population expansion to 40,000 individuals. All population size changes are instantaneous for models 2-4. See Table 1 for additional model parameters.

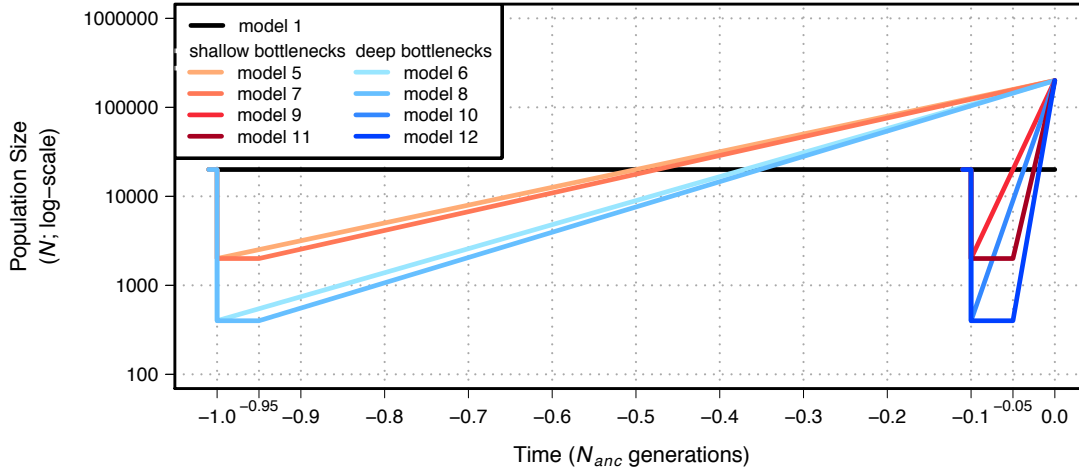


Figure S2 Demographic models 1 and 5-12 simulated in our study. Time proceeds forward from left to right and is scaled by the N of the population at the initial generation (N_{anc} ; 20,000 individuals). Demographic models with a shallow bottleneck (models 5, 7, 9, and 11) experience a population contraction to 2000 individuals while demographic models with a deep bottleneck (models 6, 8, 10, and 12) experience a population contraction to 400 individuals. After contraction, demographic models 5-12 undergo exponential growth to a final population size of 200,000 individuals. See Table 1 for additional model parameters.

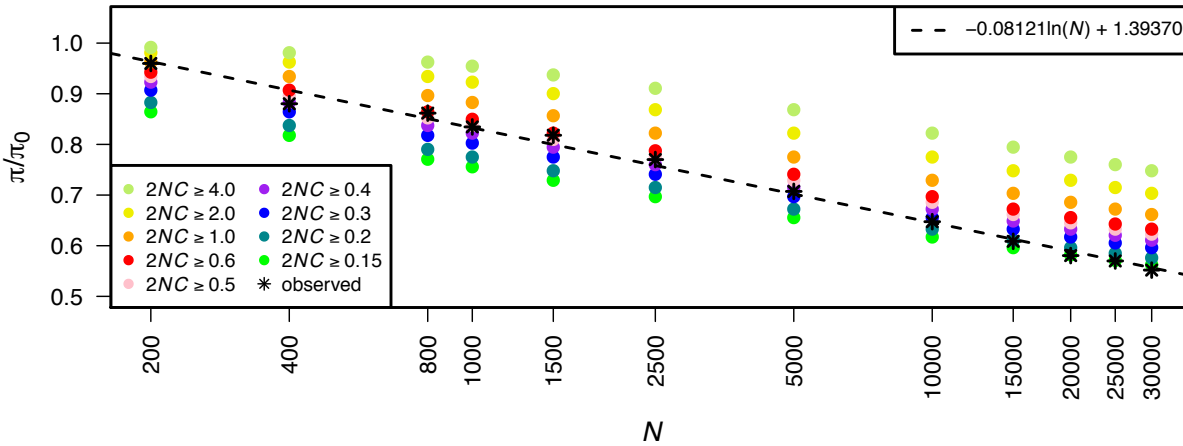


Figure S3 Estimate of π/π_0 from the classic model (Nordborg *et al.* 1996) across different population sizes and different truncation thresholds on selection. Different γ values used to truncate selection (C) for the classic model are shown in the legend ($2NC \geq \gamma$). Black stars represent the observed π/π_0 from running simulations of BGS. The dashed line shows a log-linear model of π/π_0 fit to the simulations of BGS ($\pi/\pi_0 = -0.08121 \ln(N) + 1.39370$).

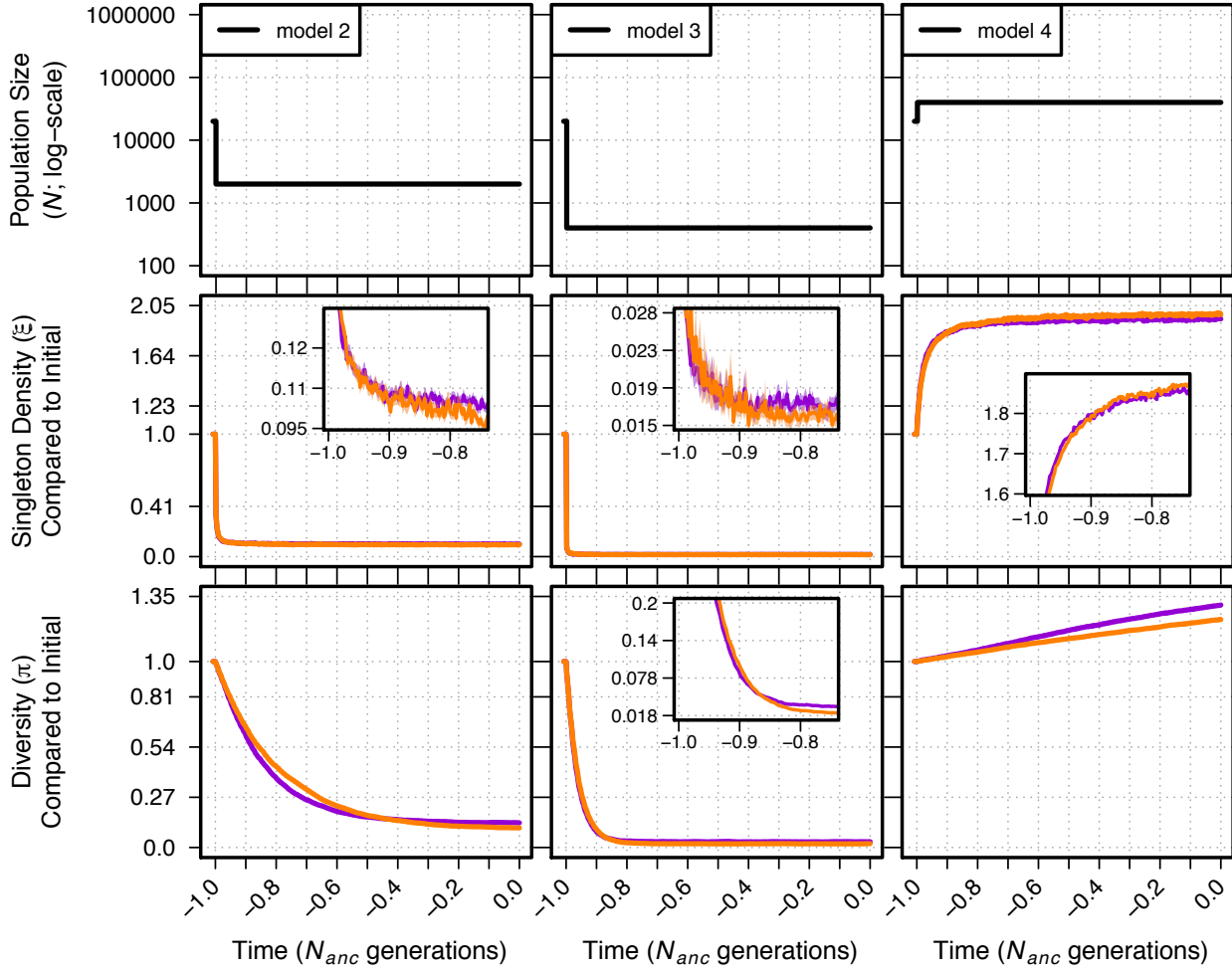


Figure S4 Singleton density (ξ) and diversity (π) for demographic models 2-4 under neutrality (orange lines) and BGS (violet lines) relative to their values in the initial generation prior to demographic change. The top panel shows each demographic model as in Figure 1. For greater detail, insets show data for generations over a smaller time scale and smaller y-axis (note: y-axes for insets are scaled linearly). Envelopes are 95% CIs calculated from 10,000 bootstraps of the original simulation data. The data used for this figure is identical to that of Figure 1.

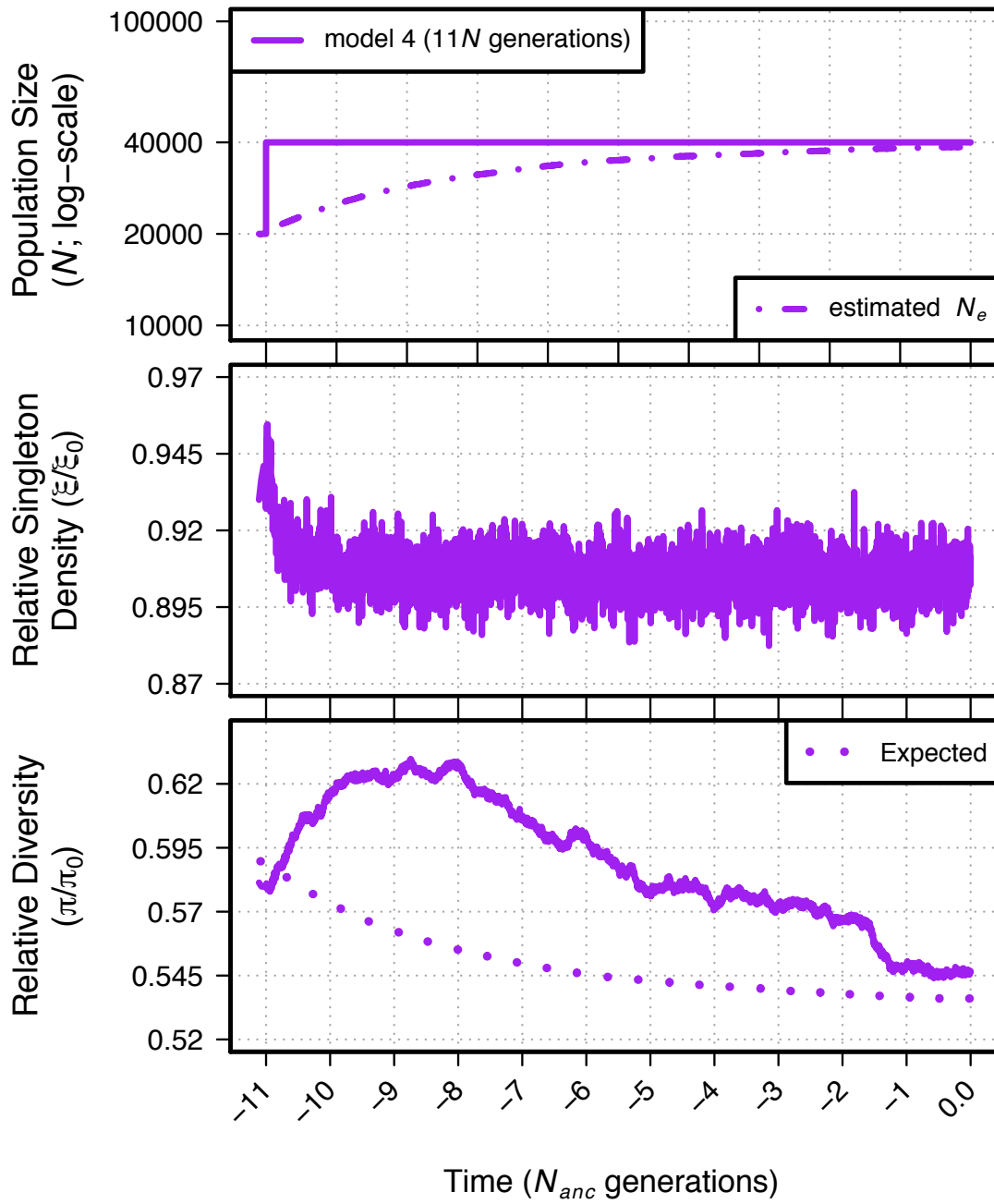


Figure S5 Relative singleton density (ξ/ξ_0) and relative diversity (π/π_0) across 11 N_{anc} generations for demographic model 4. The top panel shows the demographic model; time proceeds forward from left to right and is scaled by the N of the population at the initial generation (N_{anc} ; 20,000 individuals). Dot-dashed lines in the top panels show the estimated N_e from observed π_0 . Dotted lines in the bottom panel show the equilibrium expectation of π/π_0 from a log-linear model of simulated BGS with the specific selection parameters and the estimated N_e at each time point (see Figure S3).

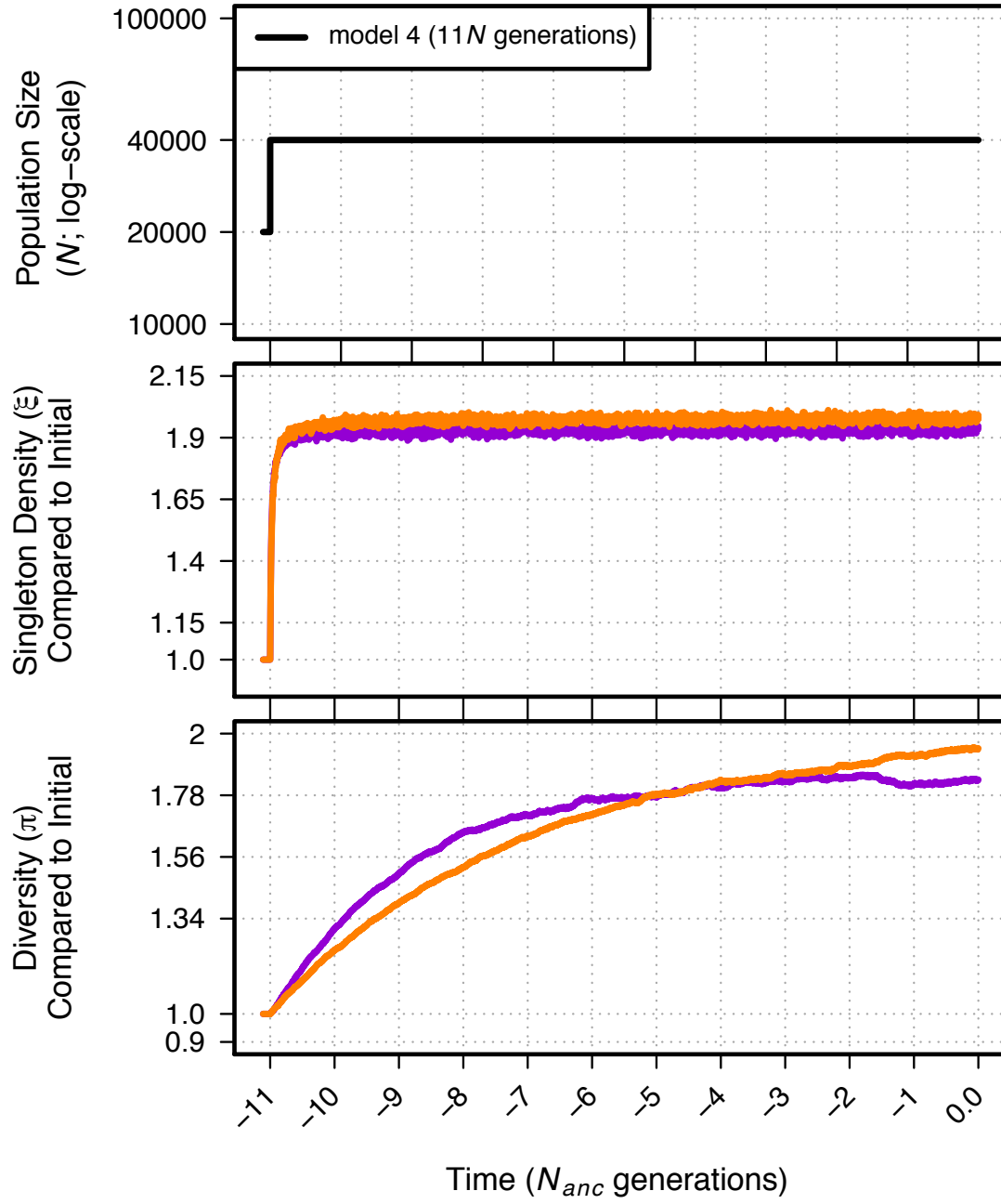


Figure S6 Singleton density (ξ) and diversity (π) relative to the initial generation for neutral (orange) and BGS (violet) simulations of demographic model 4 over 11 N_{anc} generations. The top panel shows the demographic model.

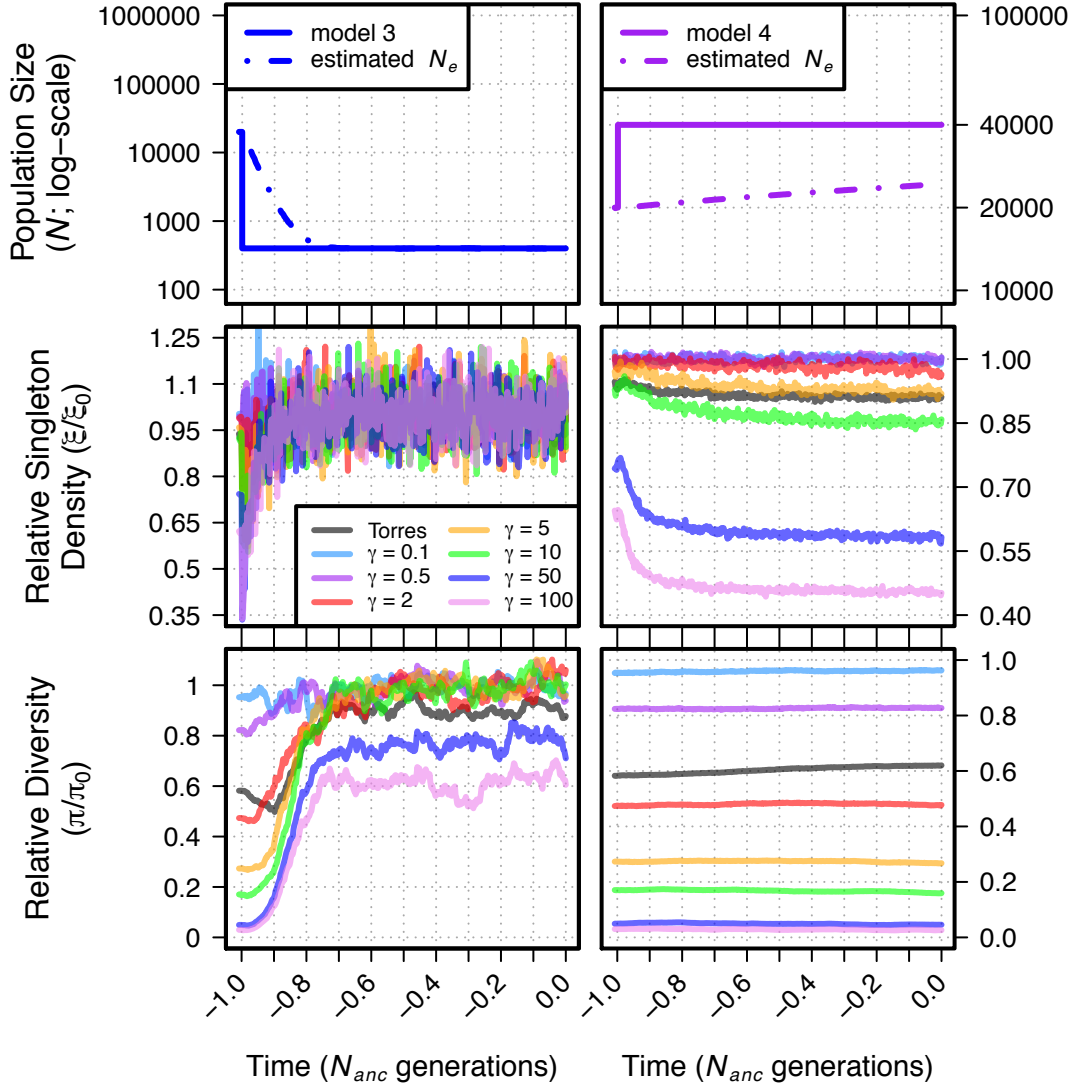


Figure S7 Relative singleton density (ξ/ξ_0) and relative diversity (π/π_0) across time for demographic models 3 and 4 for varying values of γ (where $\gamma = 2N_{anc}$). γ was drawn from a single value for these simulations such that mean and median γ were the same. For comparison, we also include the results of our simulated two DFE model (indicated as "Torres" in the legend; mean $\gamma \approx 424$, median $\gamma \approx 0.056$). The top panel shows the demographic model; time proceeds forward from left to right and is scaled by the N of the population at the initial generation (N_{anc} ; 20,000 individuals). Dot-dashed lines in the top panels show the estimated N_e from observed π_0 . Lines for π/π_0 and ξ/ξ_0 are transparent to show greater detail.

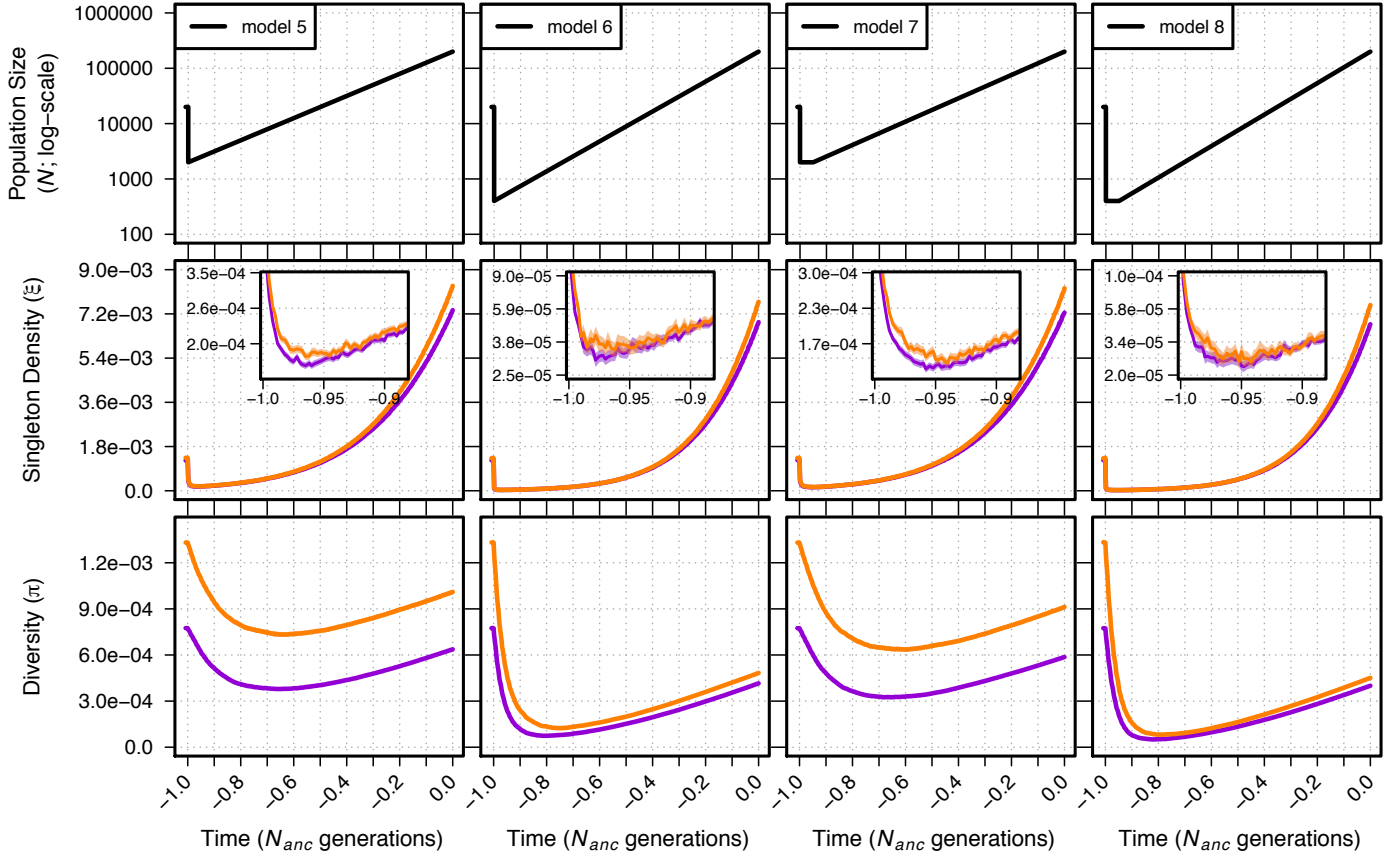


Figure S8 Singleton density (ξ per site) and diversity (π per site) for models 5-8. The top panel shows each demographic model; time proceeds forward from left to right and is scaled by the N of the population at the initial generation (N_{anc} ; 20,000 individuals). Diversity statistics are shown for neutral simulations (orange lines) and simulations with BGS (violet lines). Insets show diversity using a log scale for improved detail. Envelopes are 95% CIs calculated from 10,000 bootstraps of the original simulation data.

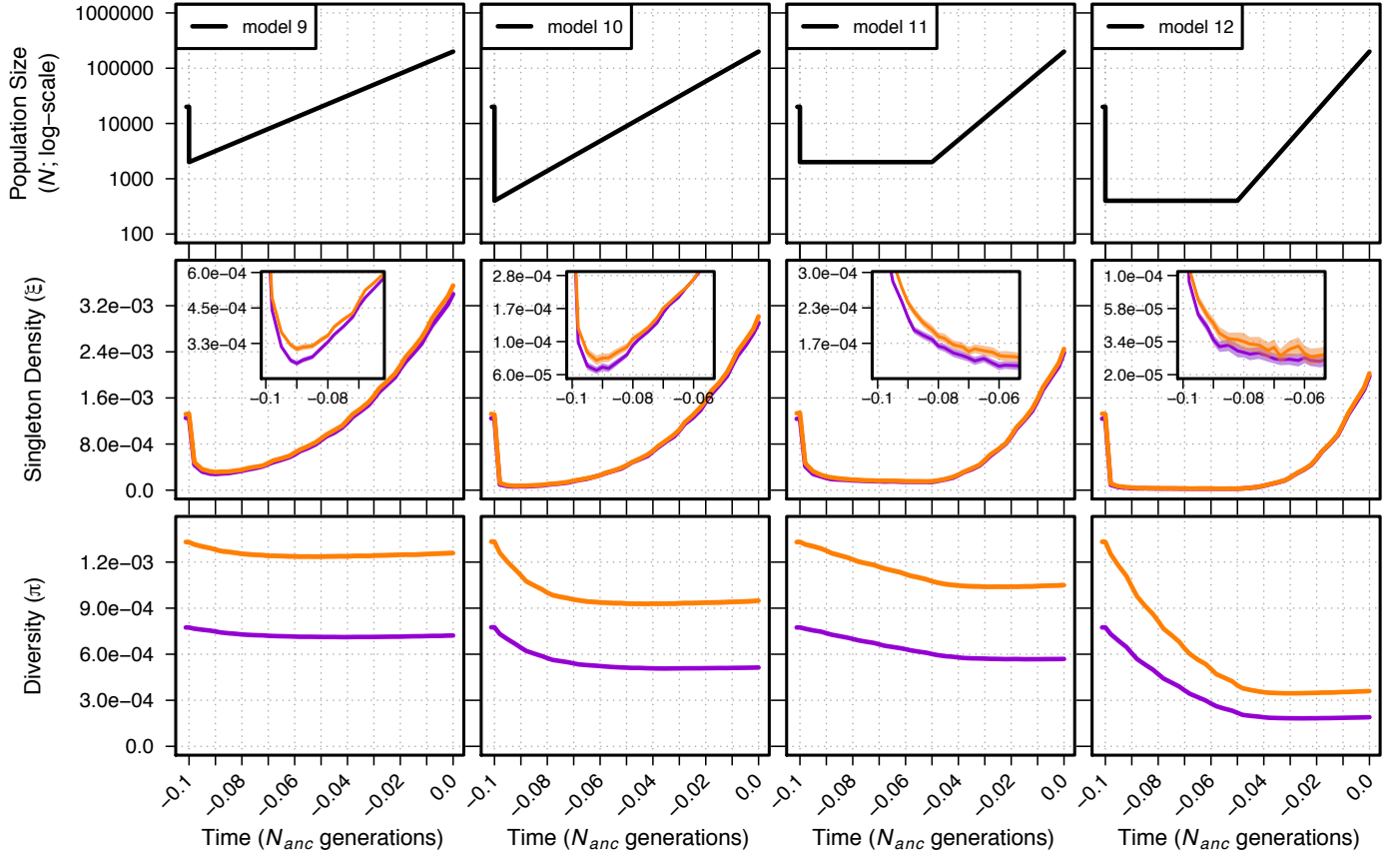


Figure S9 Singleton density (ξ per site) and diversity (π per site) for models 9-12. The top panel shows each demographic model; time proceeds forward from left to right and is scaled by the N of the population at the initial generation (N_{anc} ; 20,000 individuals). Diversity statistics are shown for neutral simulations (orange lines) and simulations with BGS (violet lines). Insets show diversity using a log scale for improved detail. Envelopes are 95% CIs calculated from 10,000 bootstraps of the original simulation data.

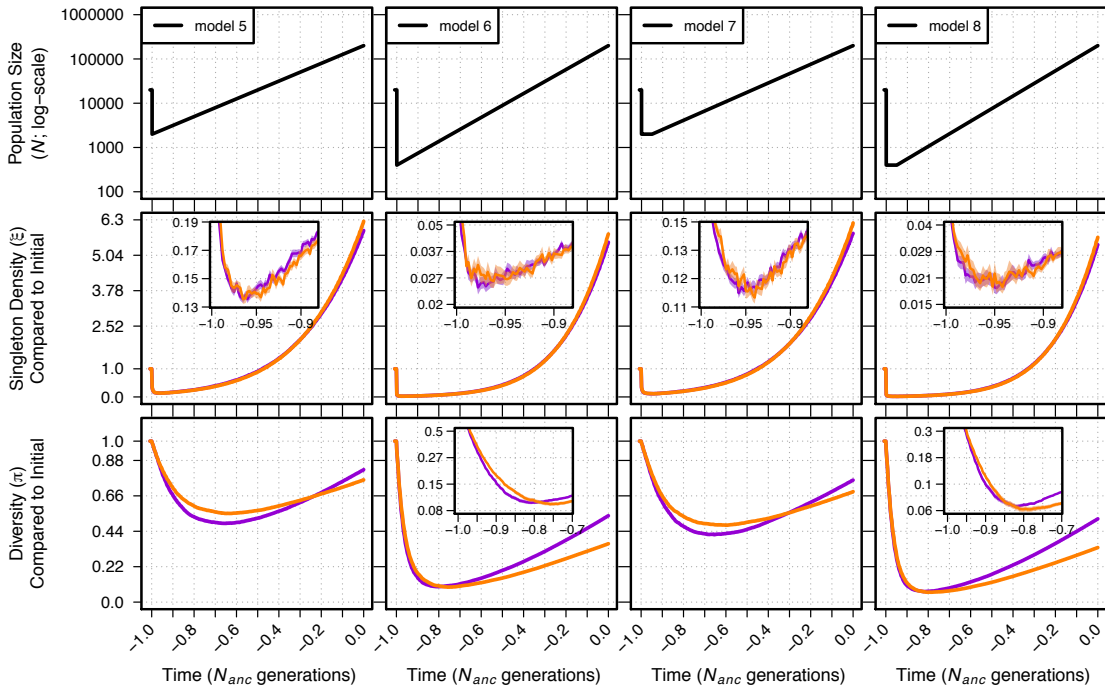


Figure S10 Singleton density (ξ) and diversity (π) relative to the initial generation for neutral (orange) and BGS (violet) simulations of demographic models 5-8. The top panel shows each demographic model as in Supplemental Figure S8. Insets show diversity over a shorter timescale and use a log scale for diversity for improved detail. Envelopes are 95% CIs calculated from 10,000 bootstraps of the original simulation data. The data used for this figure is identical to that of Supplemental Figure S8.

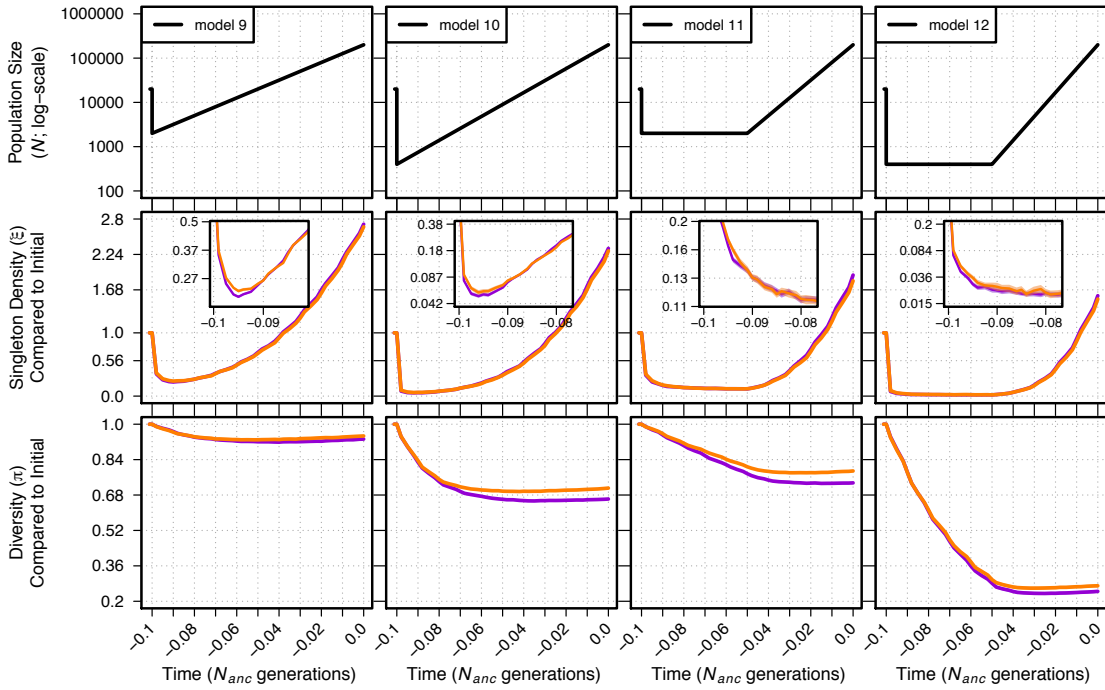


Figure S11 Singleton density (ξ) and diversity (π) relative to the initial generation for neutral (orange) and BGS (violet) simulations of demographic models 9-12. The top panel shows each demographic model as in Supplemental Figure S9. Insets show diversity over a shorter timescale and use a log scale for diversity for improved detail. Envelopes are 95% CIs calculated from 10,000 bootstraps of the original simulation data. The data used for this figure is identical to that of Supplemental Figure S9.

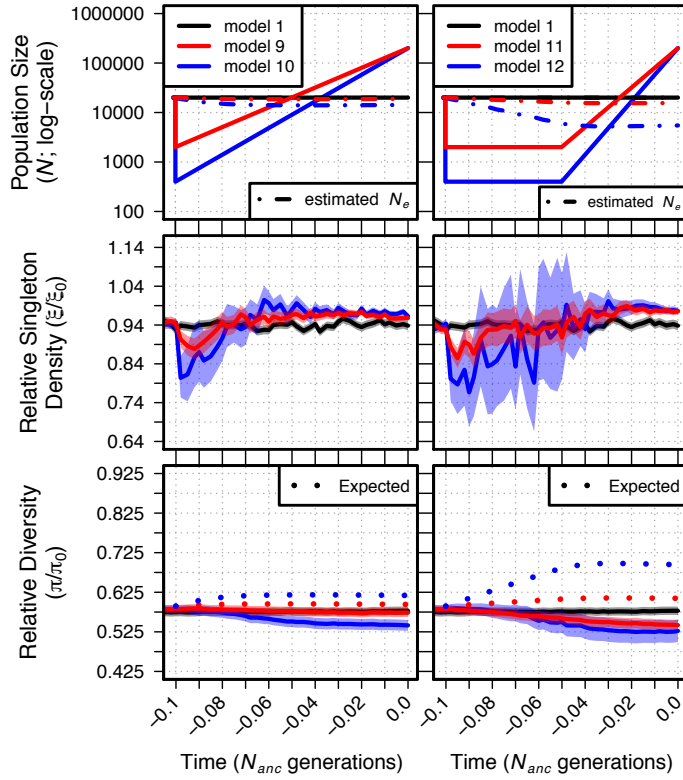
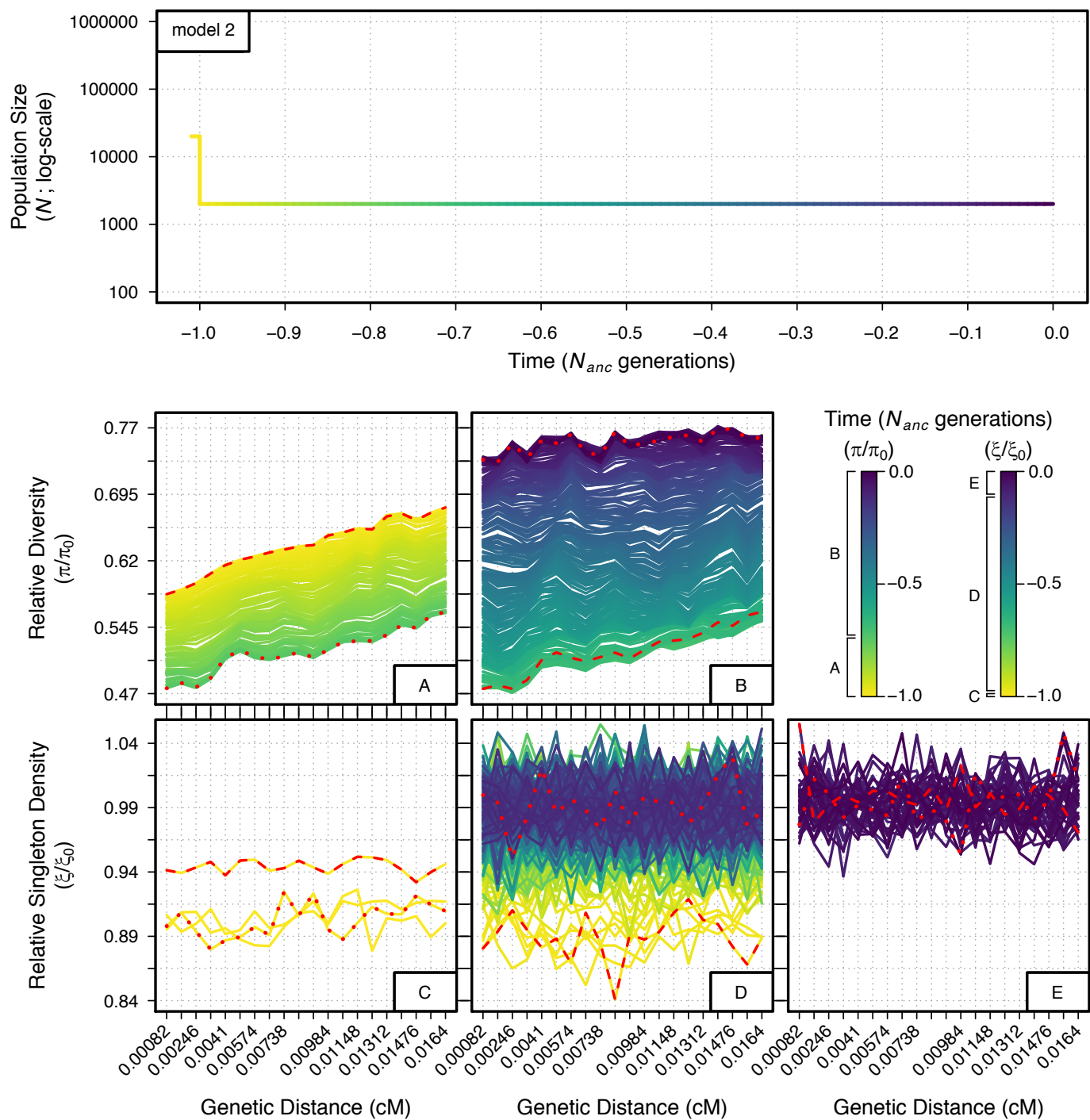
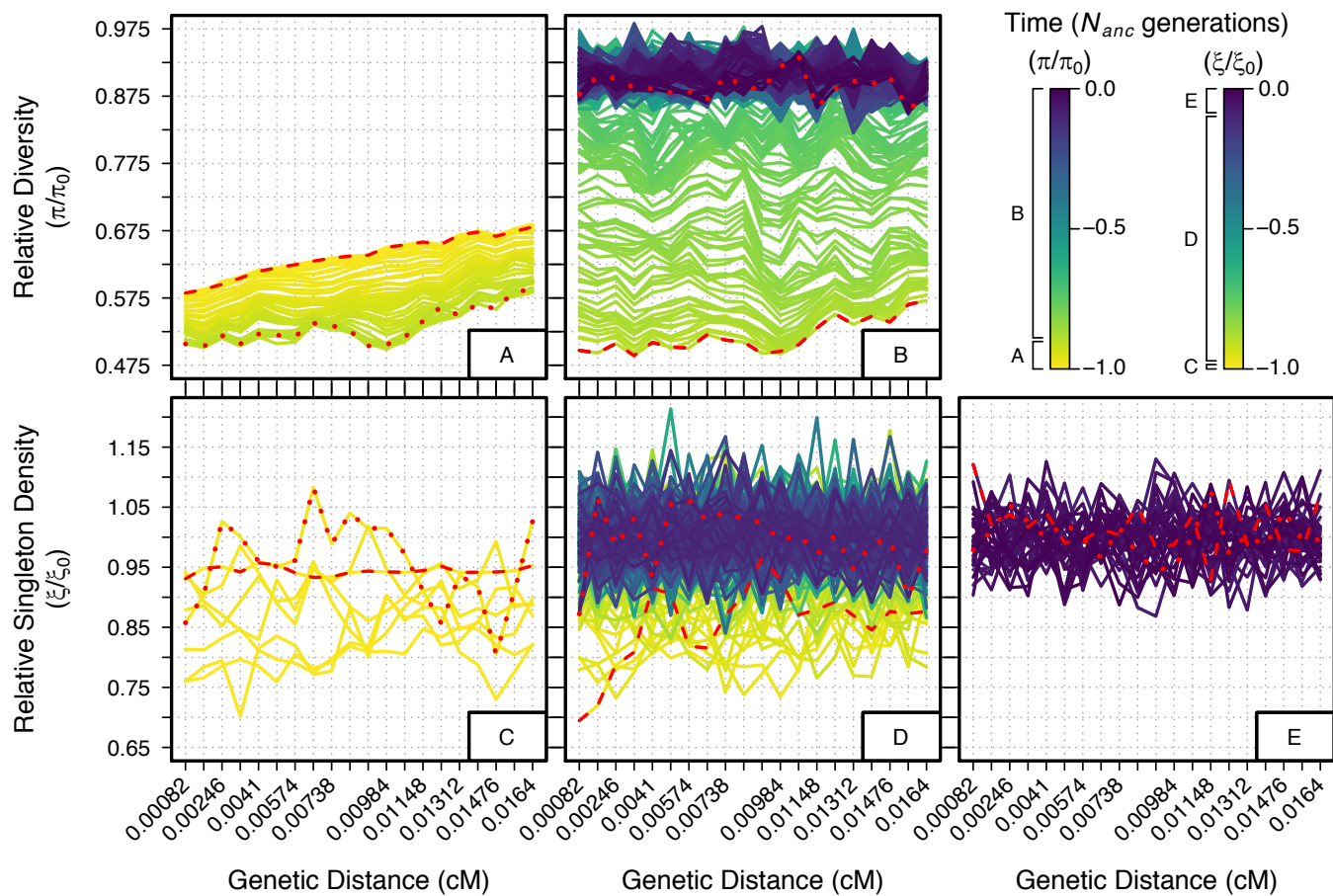
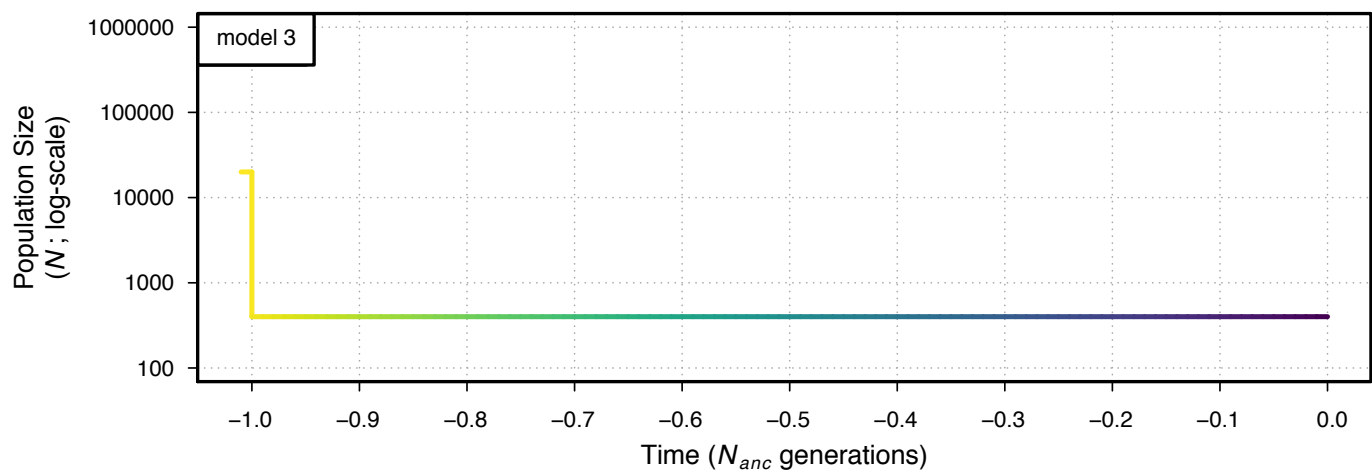
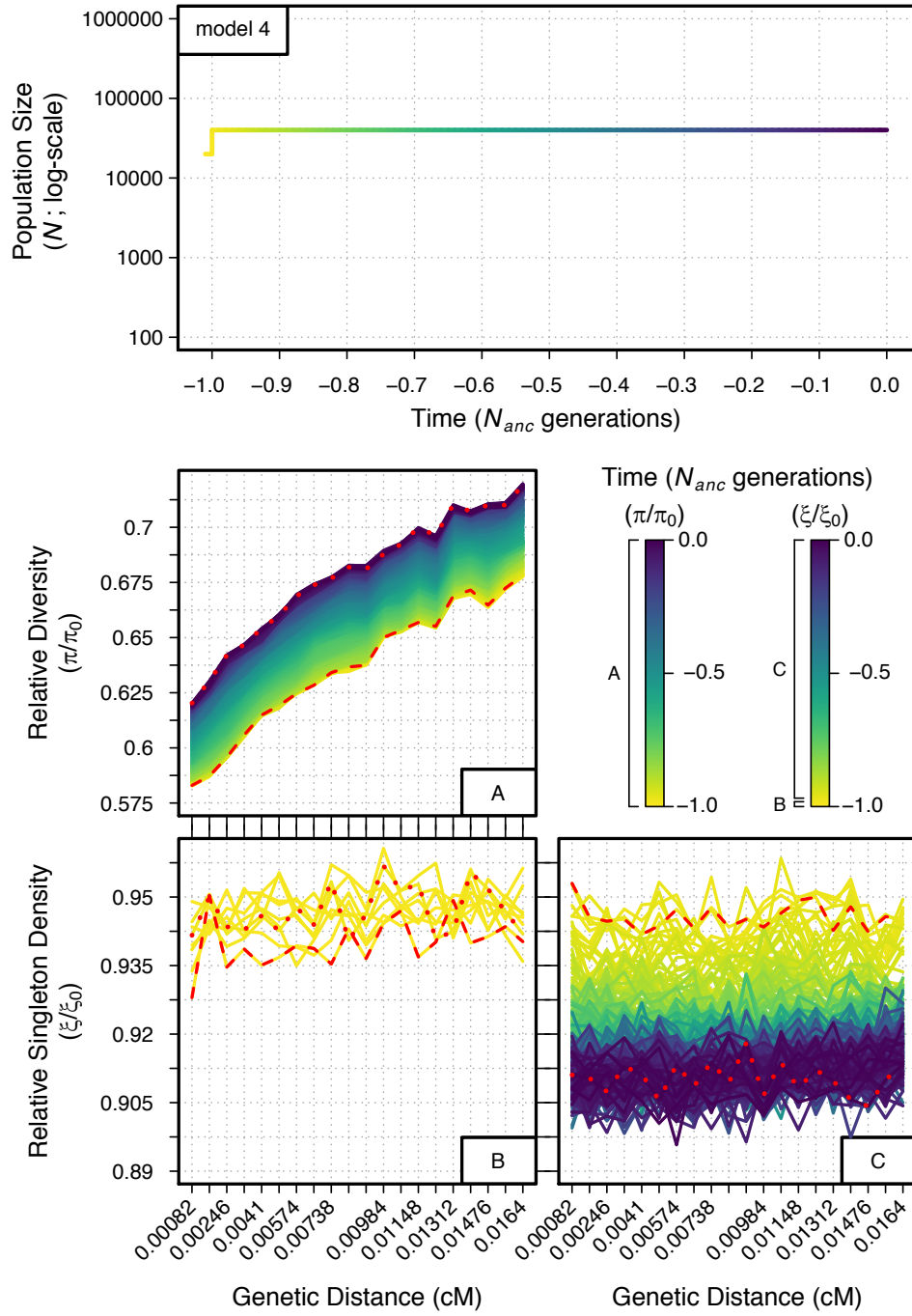
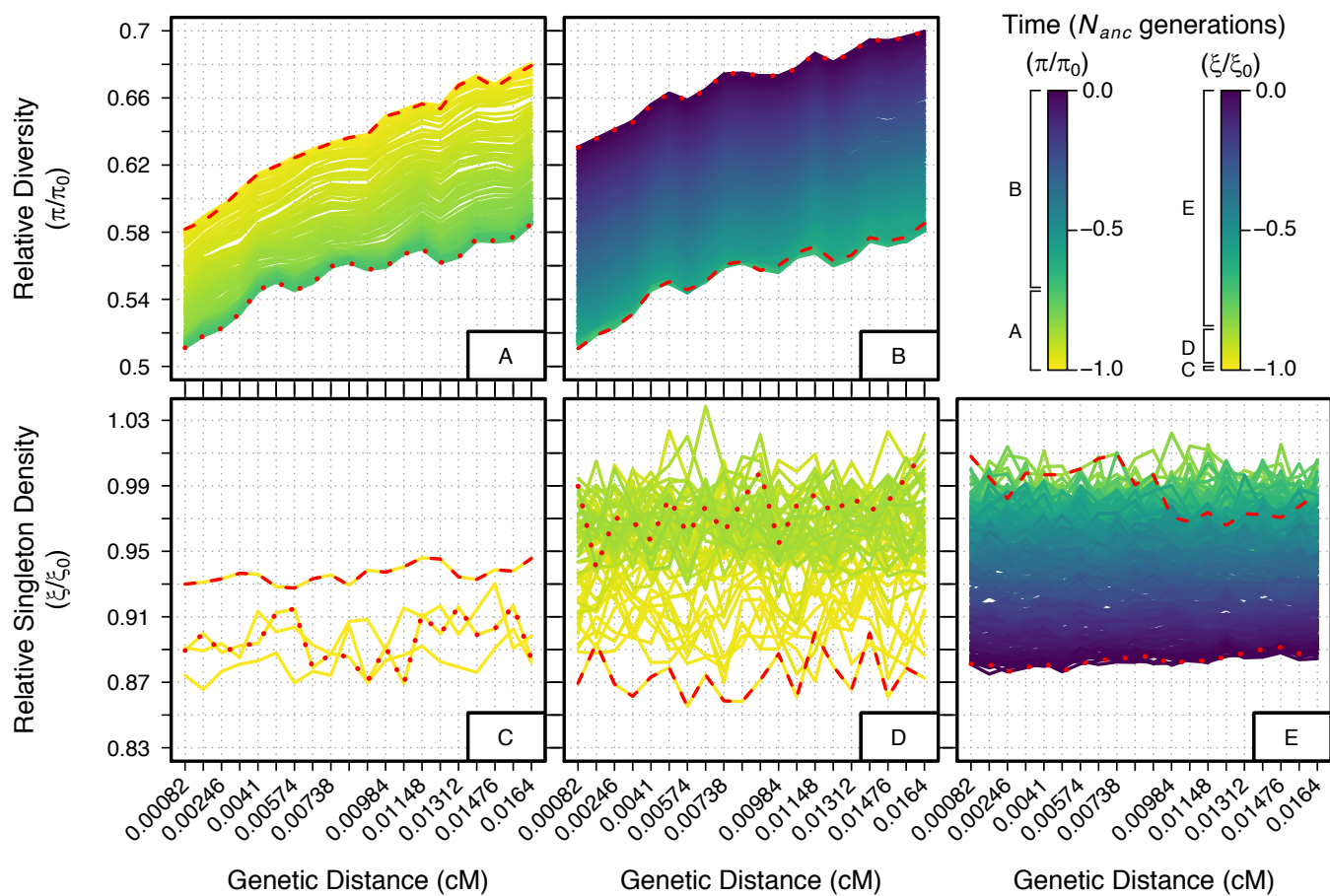
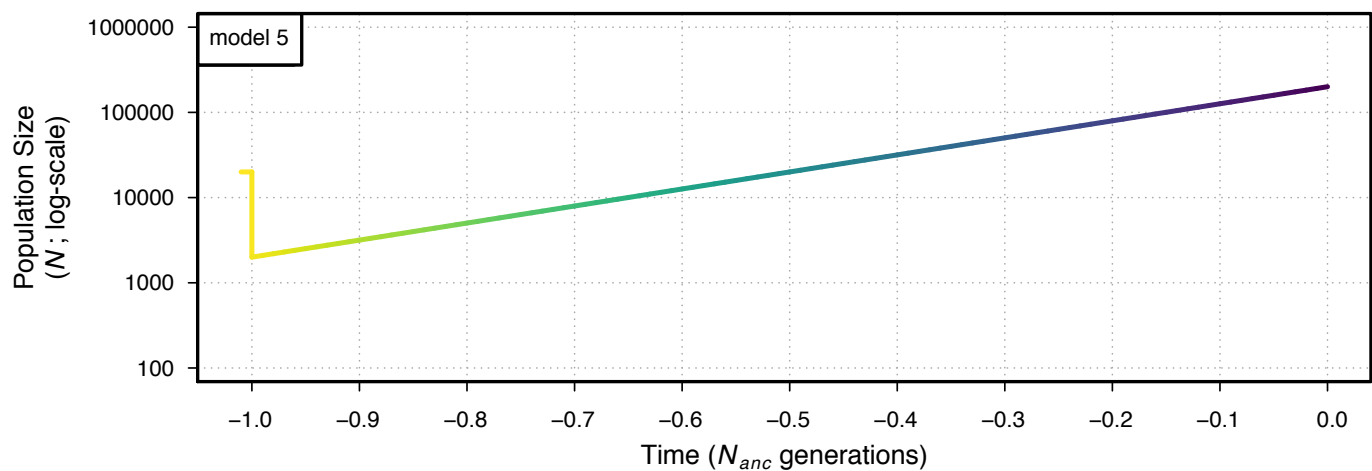


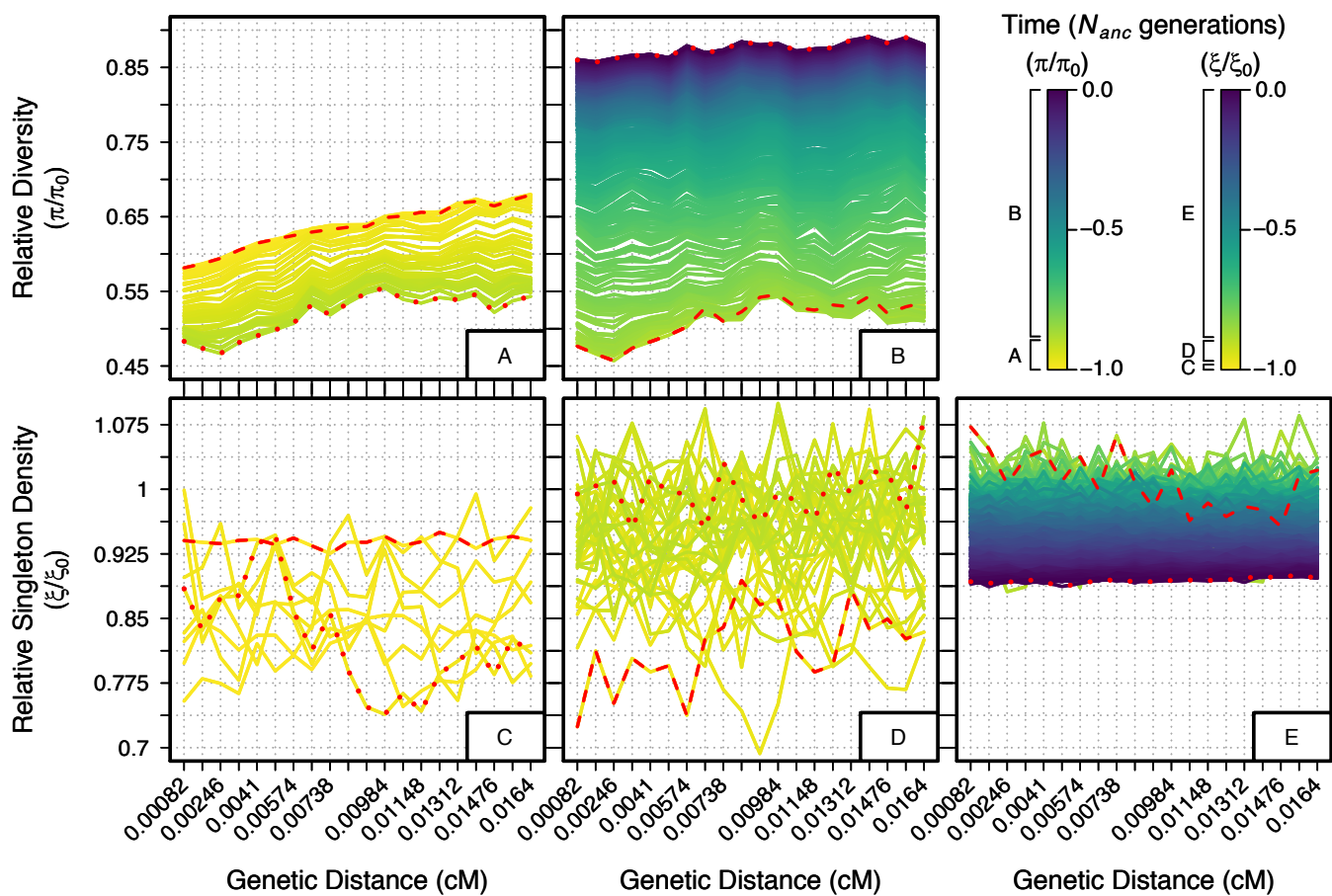
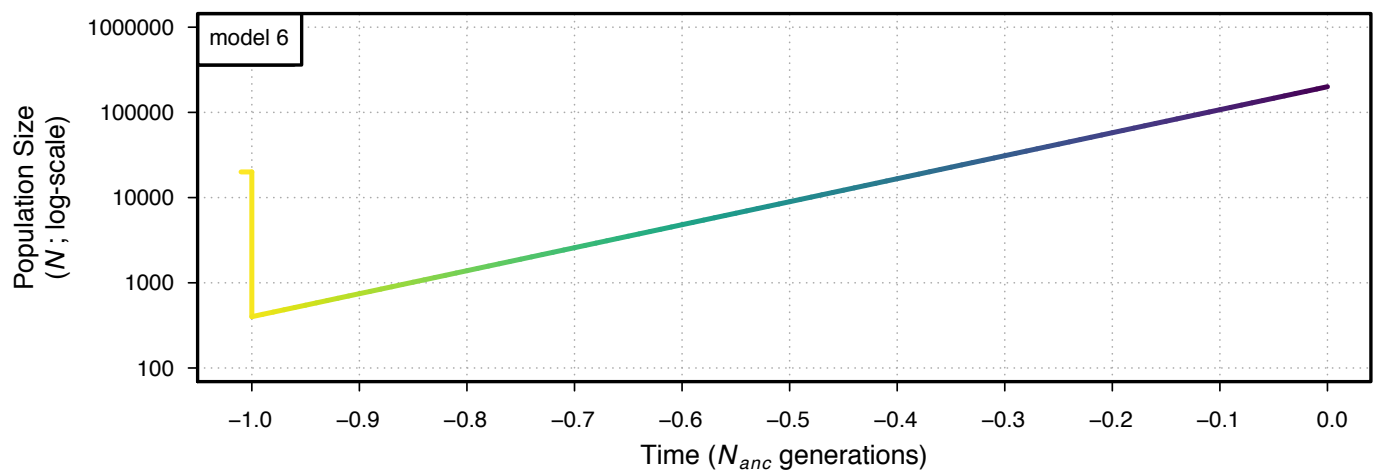
Figure S12 Relative singleton density (ξ/ξ_0) and relative diversity (π/π_0) across time for demographic models 1 and 9-12. The top panel shows each demographic model; time proceeds forward from left to right and is scaled by the N of the population at the initial generation (N_{anc} ; 20,000 individuals). Dot-dashed lines in the top panels show the estimated N_e from observed π_0 . Dotted lines in the bottom panel show the equilibrium expectation of π/π_0 from a log-linear model of simulated BGS with the specific selection parameters and the estimated N_e at each time point (see Figure S3). Envelopes are 95% CIs calculated from 10,000 bootstraps of the original simulation data.

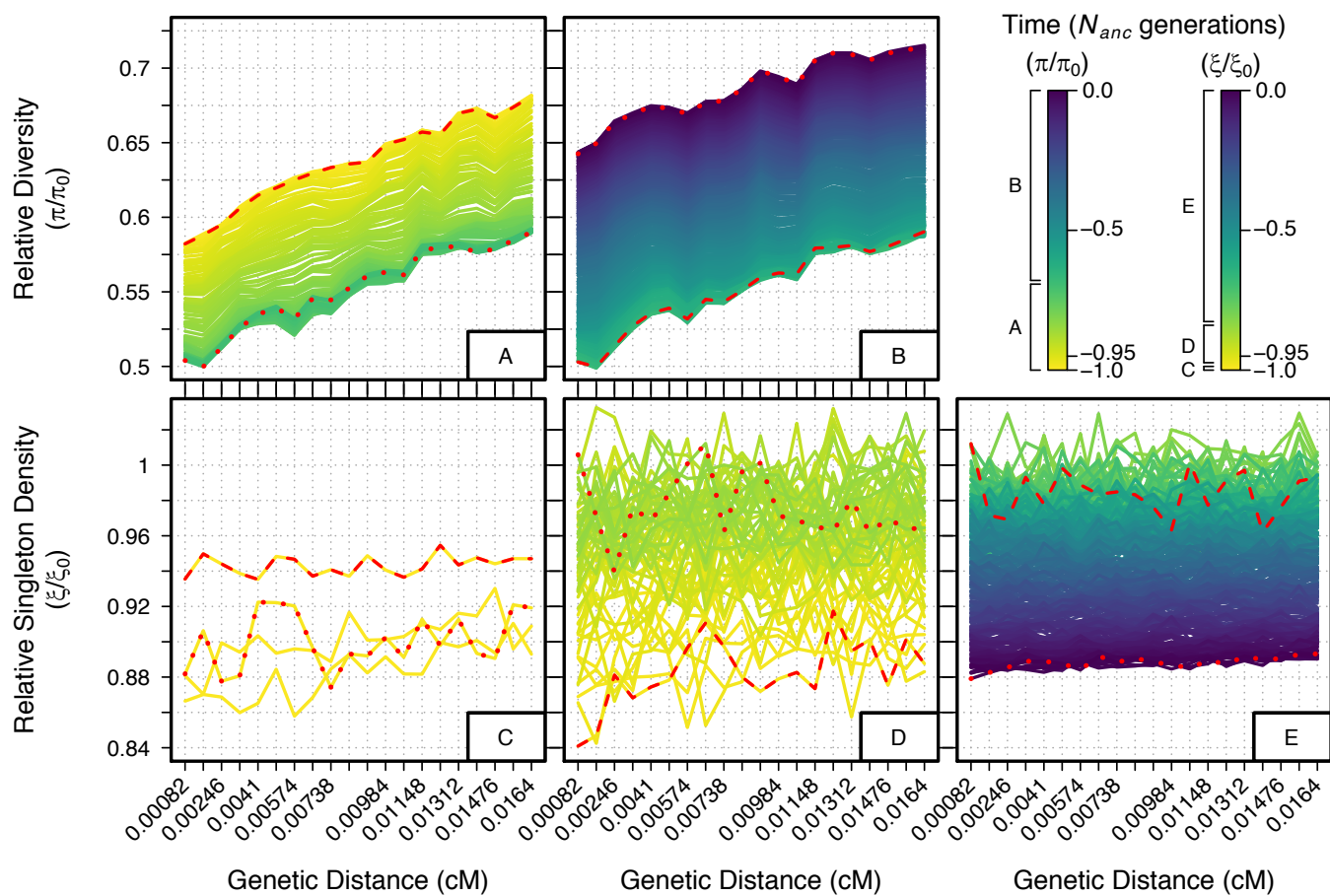
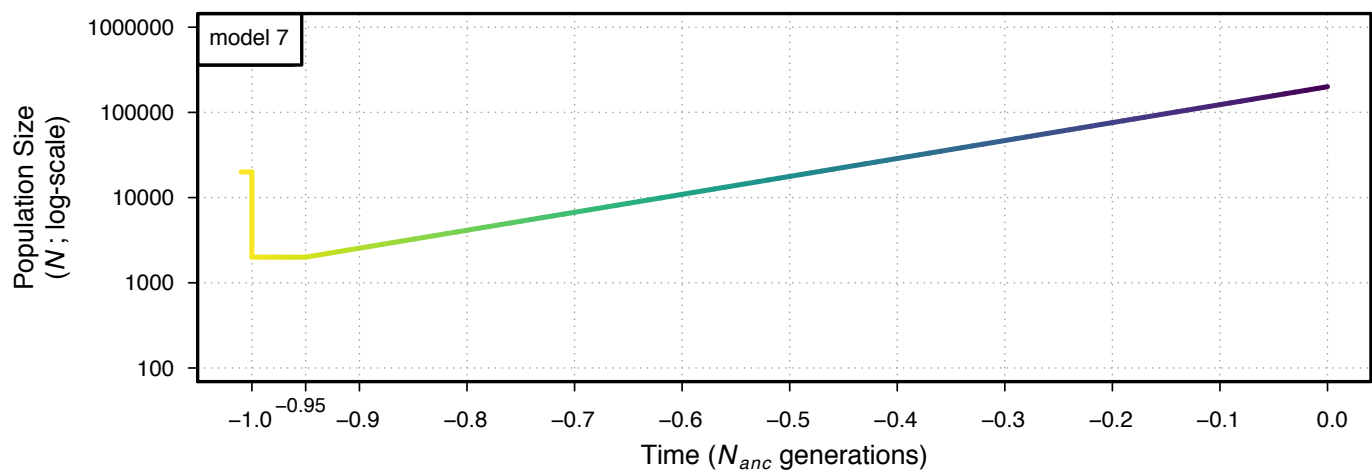


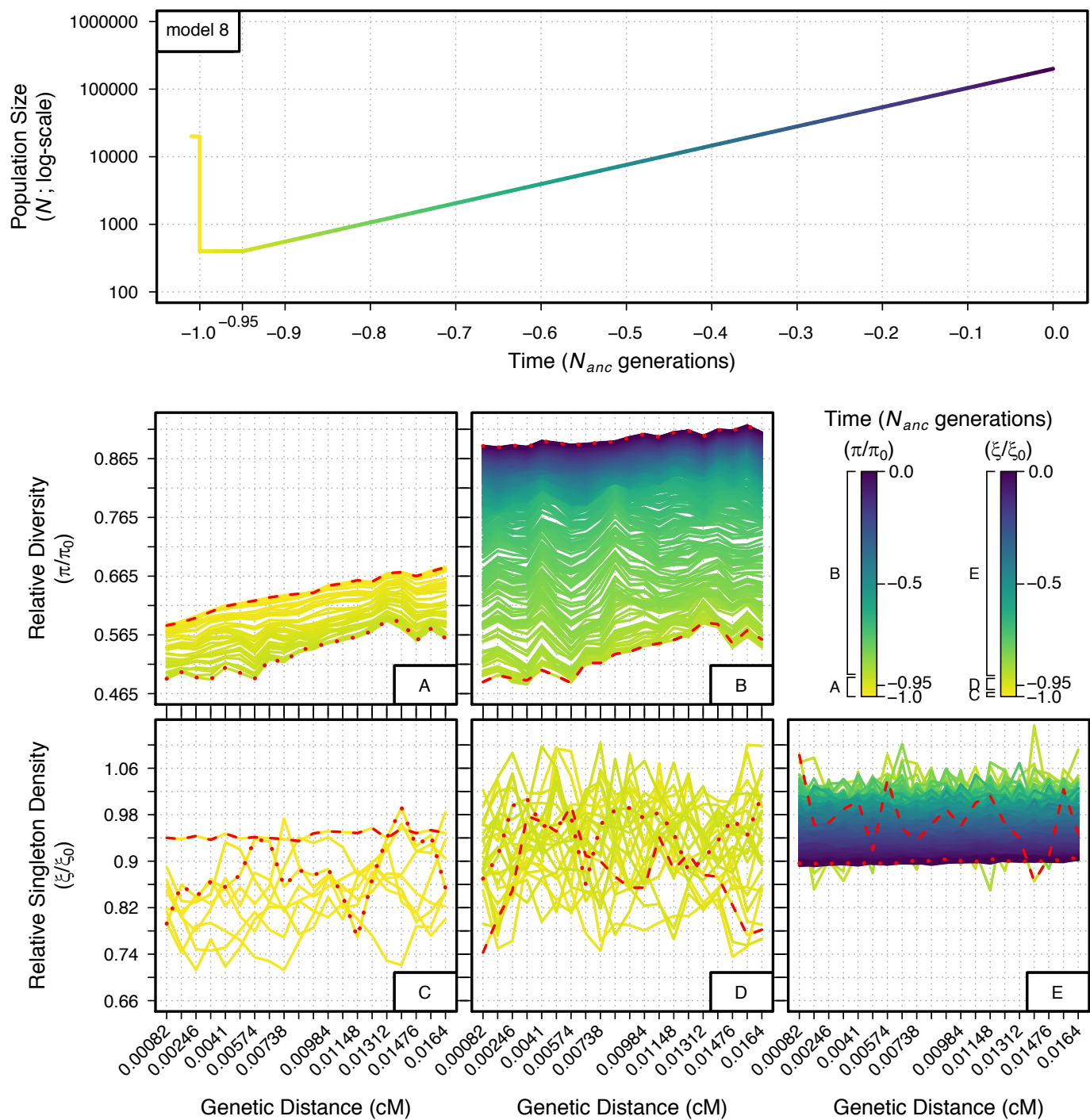


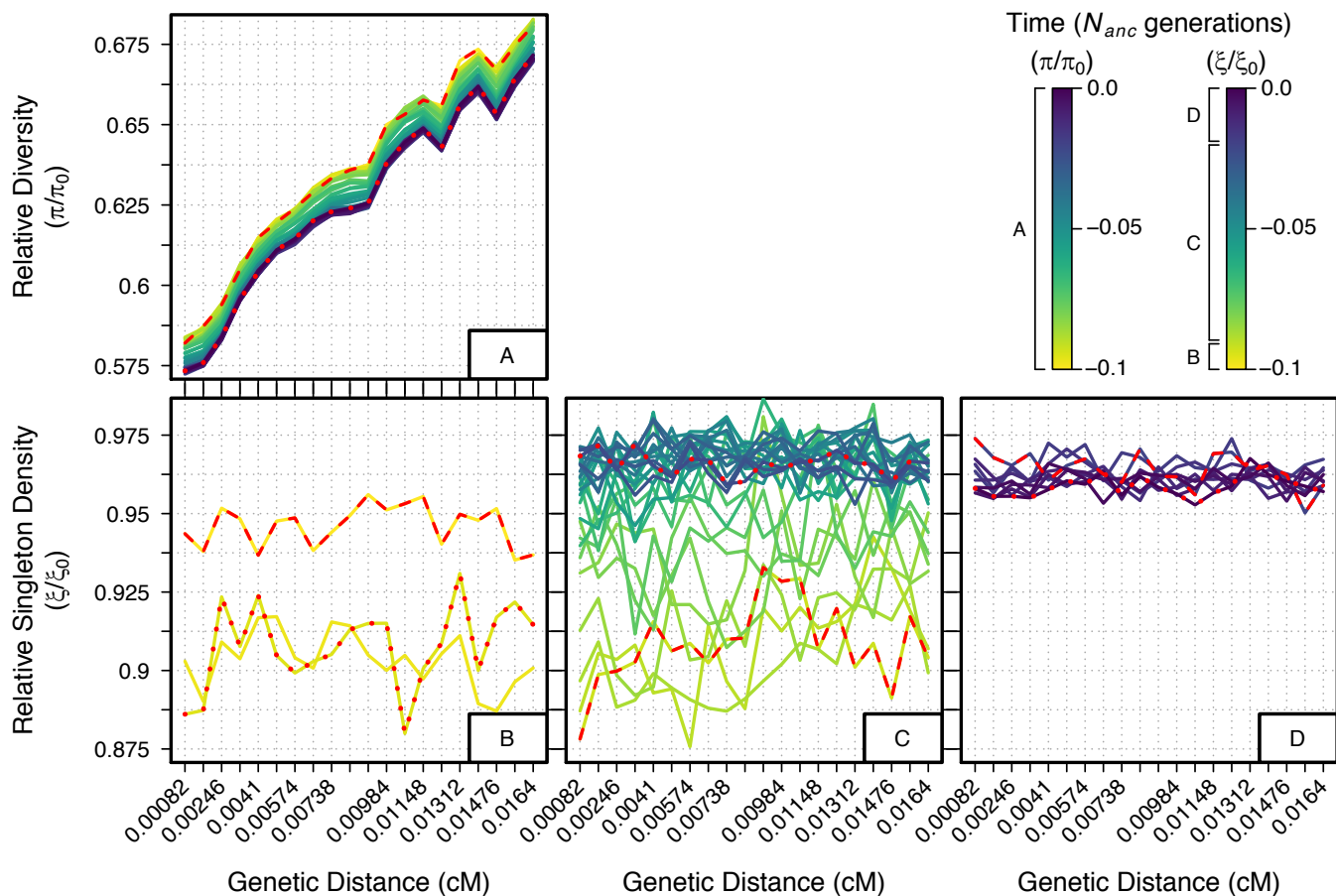
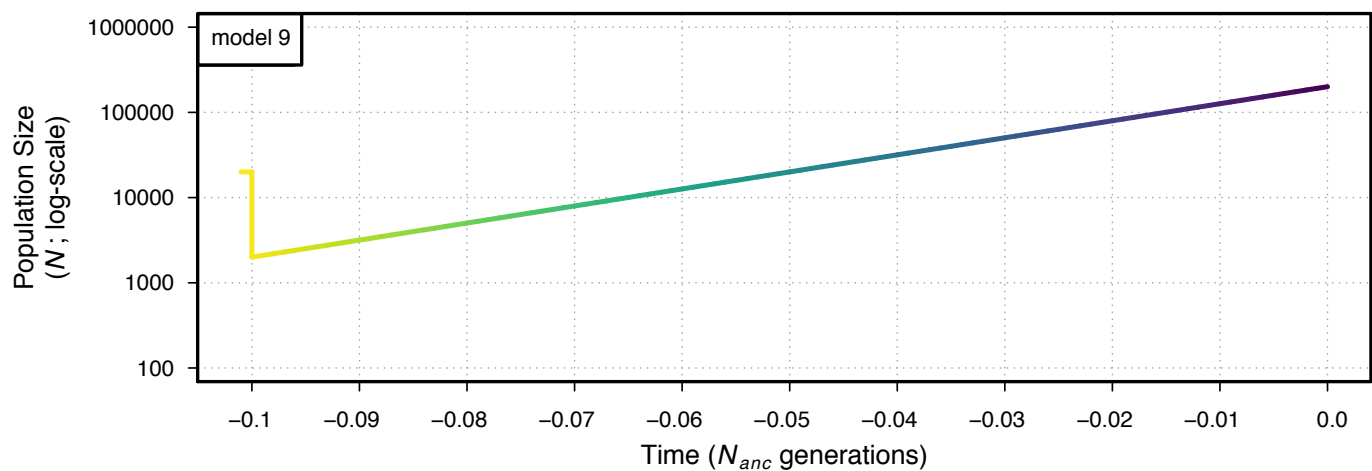


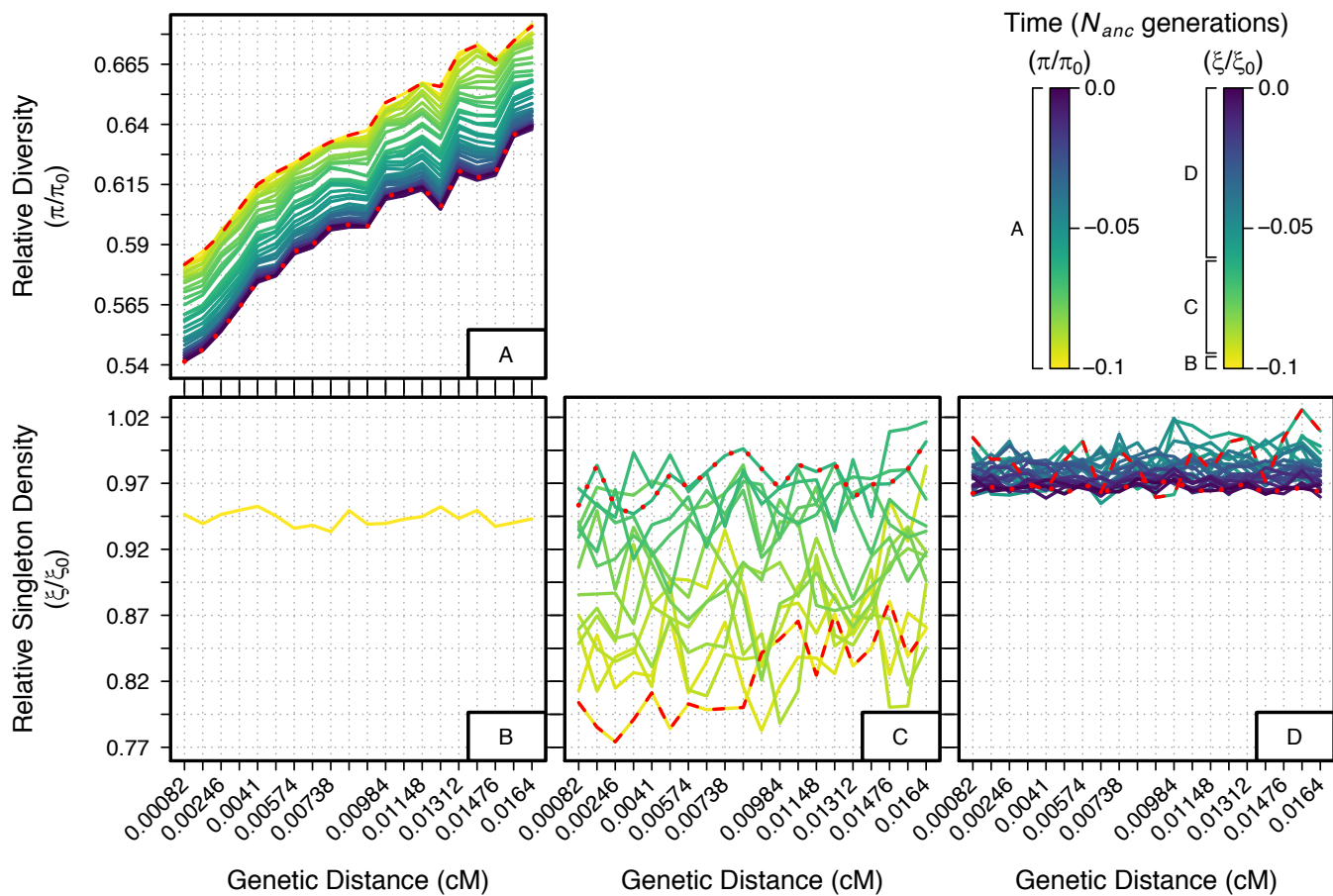
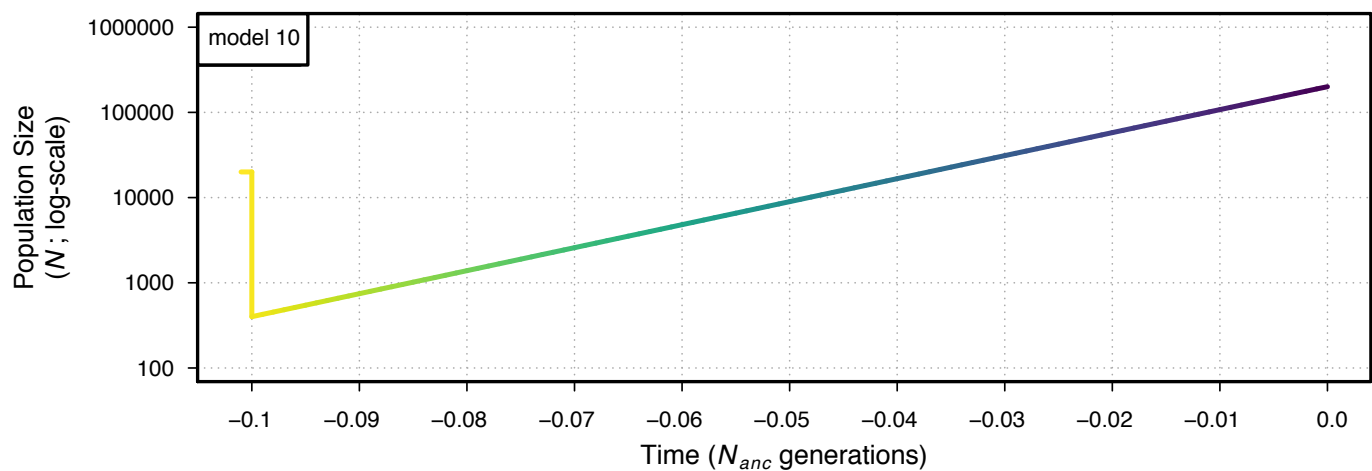


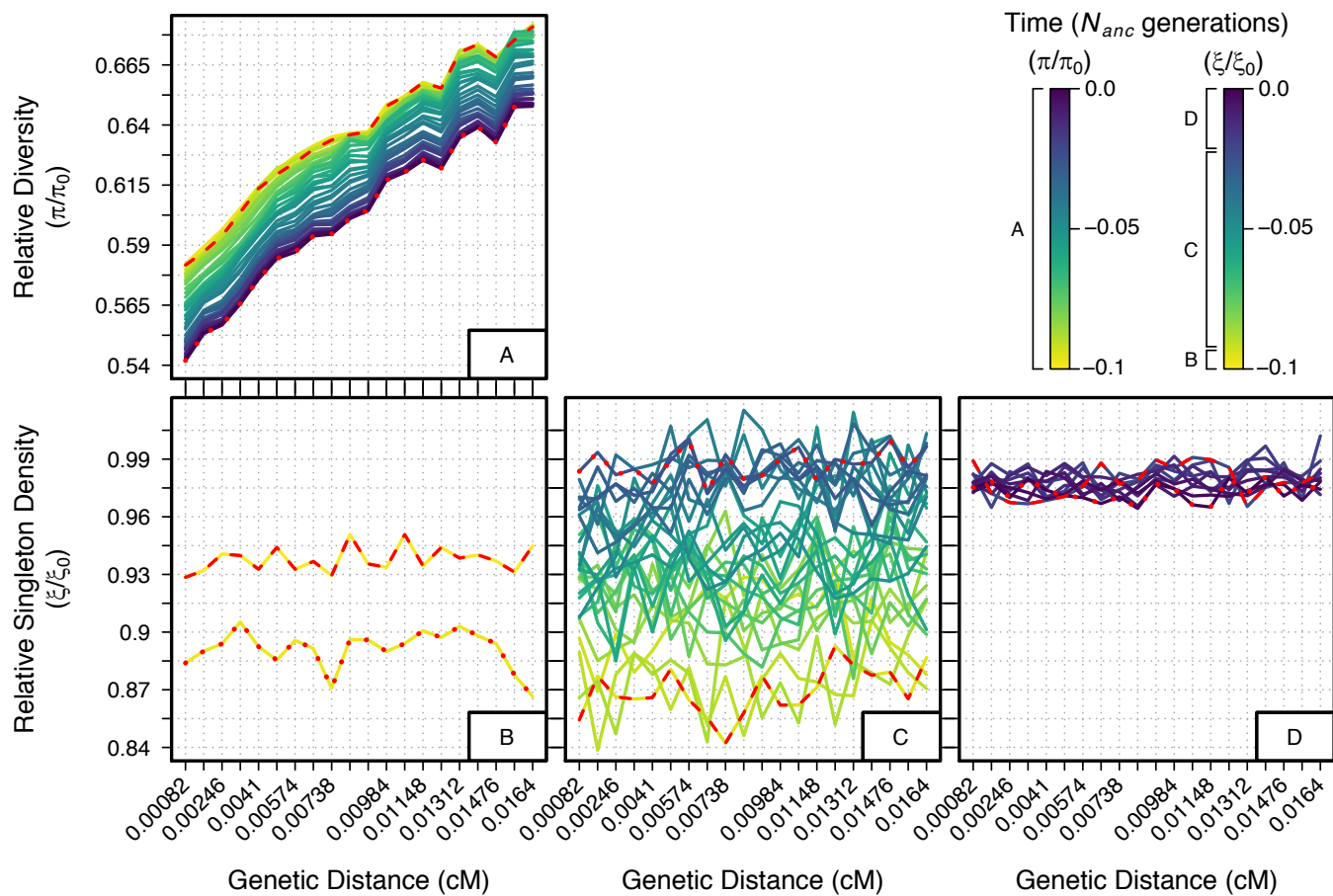
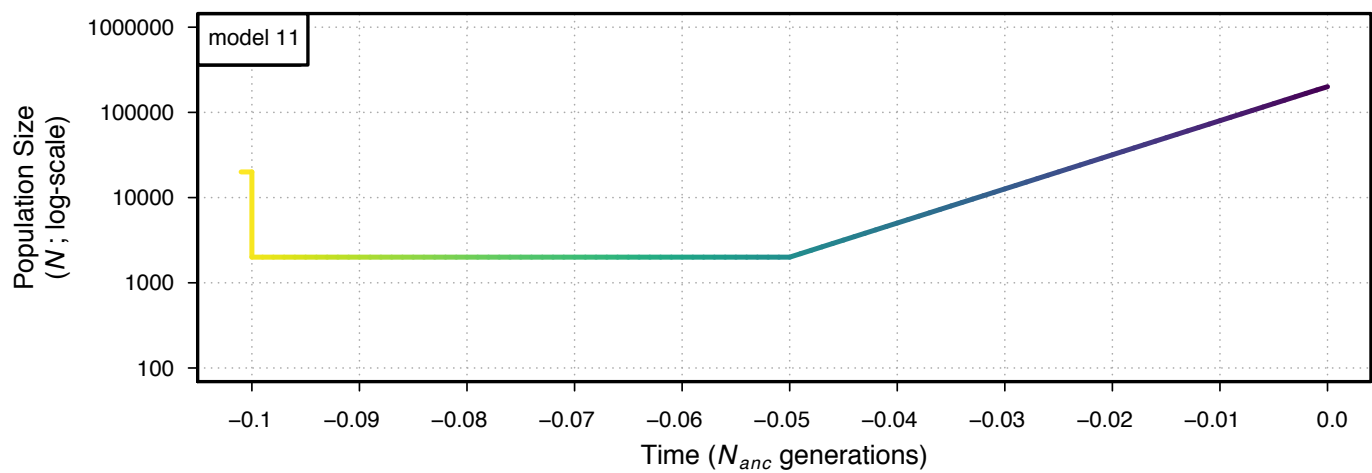












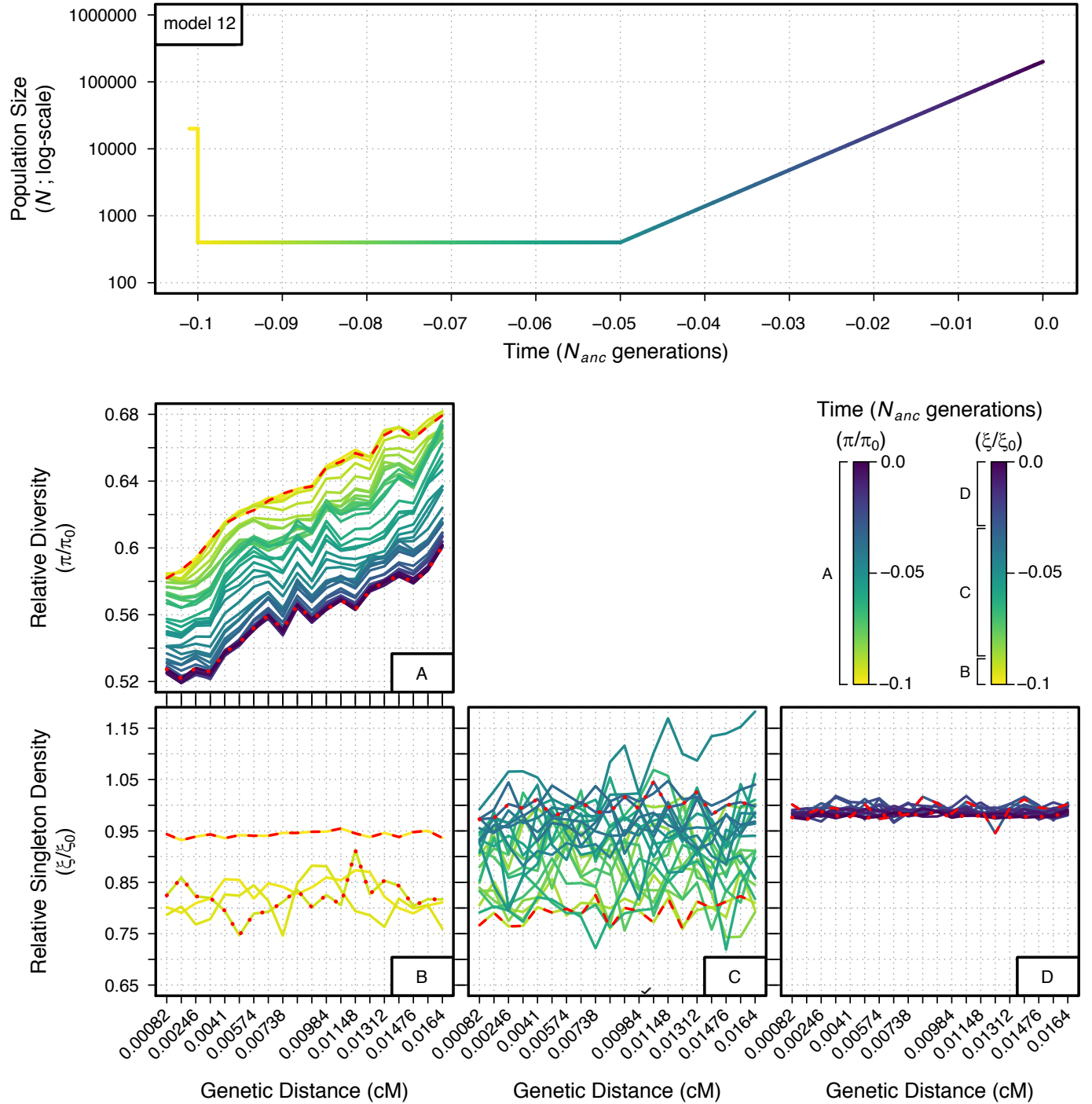


Figure S13 Relative diversity (π/π_0) and singleton density (ξ/ξ_0) through time for demographic models 2-12 measured across a neutral 200 kb region under the effects of BGS. The genetic distance of each 10 kb bin from the selected locus is indicated on the x-axes of the bottom two panels, with genetic distance increasing from left to right. Each line measuring π/π_0 and ξ/ξ_0 across the 200 kb neutral region represents a specific generation of the demographic model (401 discrete generations for demographic models 2-8, 41 discrete generations for demographic models 9-12). Specific generations are indicated by the color of the demographic model at the top of each figure (time is scaled in units of N_{anc} generations [20,000 individuals]) and in the figure legend. When necessary, multiple plots are given for π/π_0 and ξ/ξ_0 in order to prevent overlap of the measurements between generations (see legend for specific generations covered in each plot). Red dashed lines and red dotted lines indicate the first generation and last generation measured, respectively, for each specific plot.