SUPPLEMENTAL MATERIAL: FILE S5
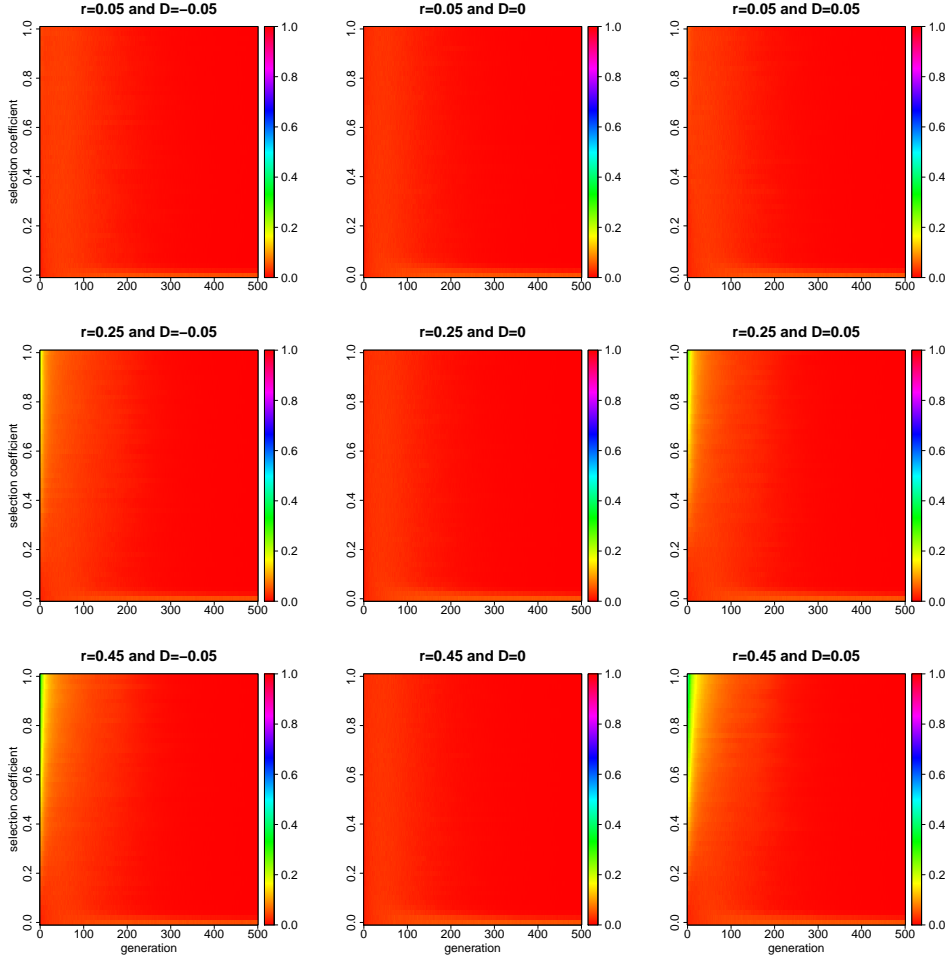
RESULTS WITH THE TOTAL VARIATION DISTANCE

FIGURE 1. Dynamics of the total variation distance $TV(\pi_1^{(v)}, \pi_1^{(f)})$ simulated with the varying selection coefficient $s_{\mathcal{A}}$ and recombination rate r over 500 generations under the two-locus Wright-Fisher model with selection for the population initially in different levels of linkage disequilibrium when gene action at locus $\mathcal{A}$ is completely additive. We generate $M = 10^5$ independent realizations in Monte Carlo simulation and adopt $N = 500$, $s_{\mathcal{B}} = 0.05$, $h_{\mathcal{A}} = 0.5$ and $h_{\mathcal{B}} = 0.5$.
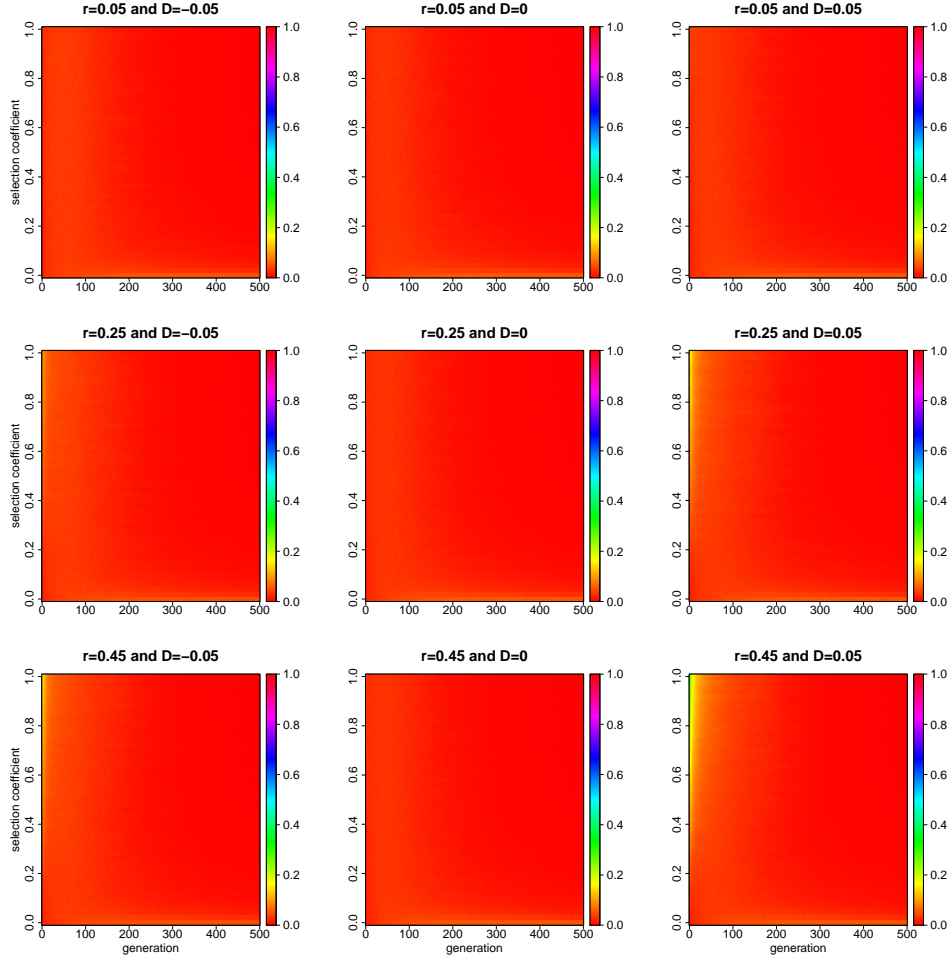
FIGURE 2. Dynamics of the total variation distance $TV(\pi_1^{(v)}, \pi_1^{(f)})$ simulated with the varying selection coefficient $s_{\mathcal{A}}$ and recombination rate r over 500 generations under the two-locus Wright-Fisher model with selection for the population initially in different levels of linkage disequilibrium when gene action at locus $\mathcal{A}$ is completely dominant. We generate $M = 10^5$ independent realizations in Monte Carlo simulation and adopt $N = 500$, $s_{\mathcal{B}} = 0.05$, $h_{\mathcal{A}} = 0$ and $h_{\mathcal{B}} = 0.5$.

We simulate the dynamics of the total variation distance $TV(\pi_1^{(v)}, \pi_1^{(f)})$ simulated with the varying selection coefficient $s_{\mathcal{A}}$ and recombination rate r over 500 generations under the two-locus Wright-Fisher model with selection for the population of 500 individuals initially in different levels of linkage disequilibrium in the following three particular scenarios according to the types of gene action at locus $\mathcal{A}$: completely additive ($h = 0.5$) in Figure 1, completely dominant ($h = 0$) in Figure 2 and completely recessive ($h = 1$) in Figure 3, respectively, where according to Rachev
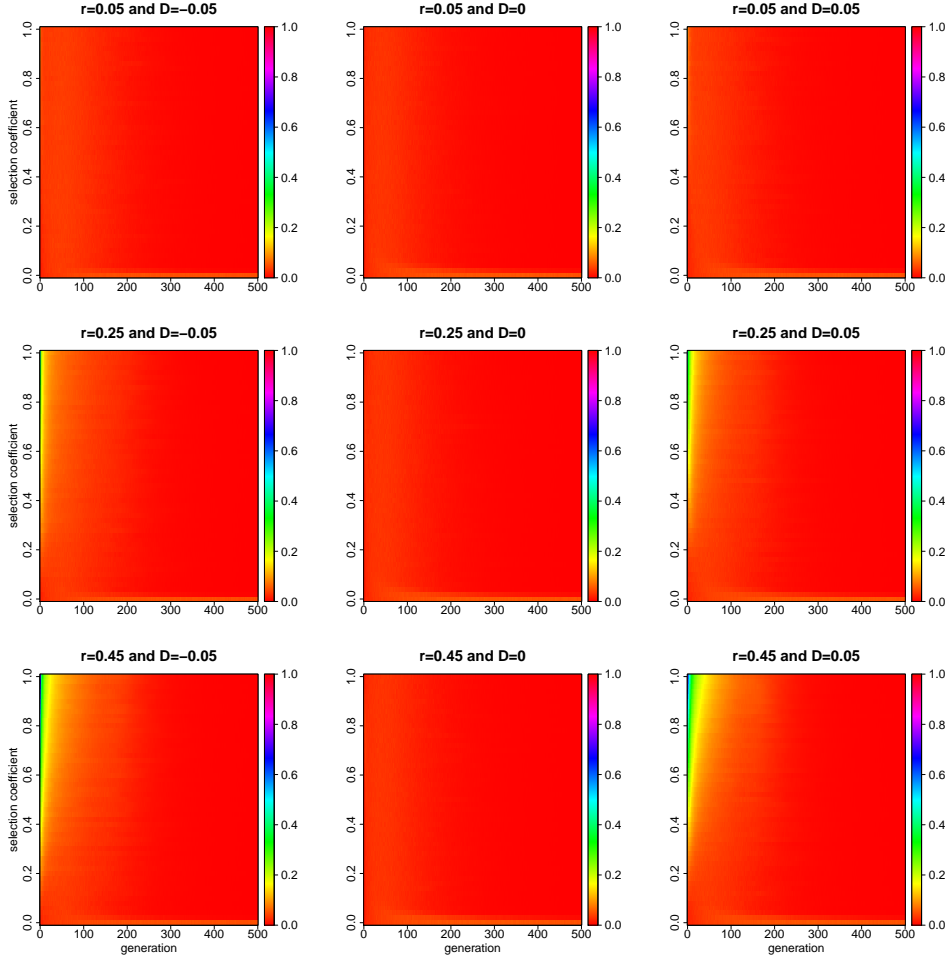
FIGURE 3. Dynamics of the total variation distance $TV(\pi_1^{(v)}, \pi_1^{(f)})$ simulated with the varying selection coefficient $s_{\mathcal{A}}$ and recombination rate r over 500 generations under the two-locus Wright-Fisher model with selection for the population initially in different levels of linkage disequilibrium when gene action at locus $\mathcal{A}$ is completely recessive. We generate $M = 10^5$ independent realizations in Monte Carlo simulation and adopt $N = 500$, $s_{\mathcal{B}} = 0.05$, $h_{\mathcal{A}} = 1$ and $h_{\mathcal{B}} = 0.5$.

et al. (2013), the total variation distance is defined as

$$TV(\pi^{(v)}, \pi^{(f)})(\boldsymbol{x}_0, k) = \frac{1}{2} \sum_{\boldsymbol{x}_k} \left| \pi^{(v)}(\boldsymbol{x}_0, \boldsymbol{x}_k) - \pi^{(f)}(\boldsymbol{x}_0, \boldsymbol{x}_k) \right|. \tag{1}$$

These illustrations confirm the conclusions we have achieved in our work.

References

Rachev, S. T., Klebanov, L., Stoyanov, S. V., and Fabozzi, F. (2013). *The methods of distances in the theory of probability and statistics.* Springer-Verlag, New York.