SUPPLEMENTAL MATERIAL: FILE S4

Results with different population sizes
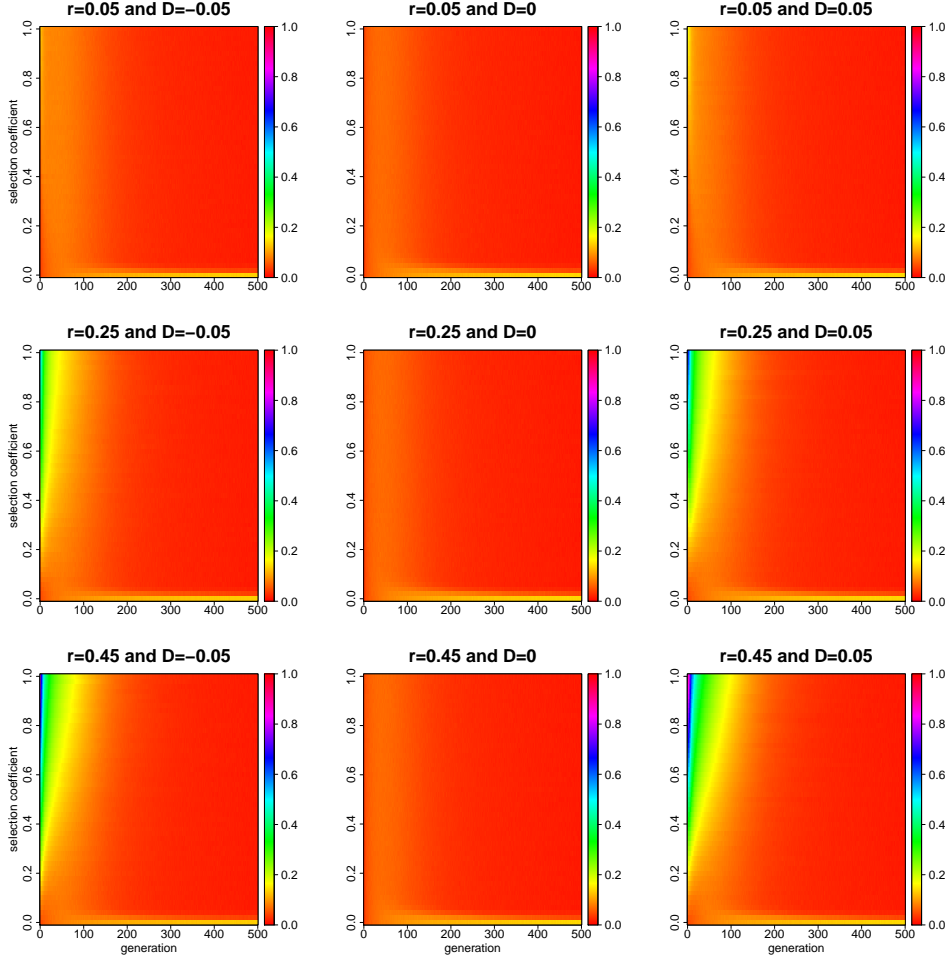

FIGURE 1. Dynamics of the Hellinger distance $H(\pi_1^{(v)}, \pi_1^{(f)})$ simulated with the varying selection coefficient $s_{\mathcal{A}}$ and recombination rate r over 500 generations under the two-locus Wright-Fisher model with selection for the population initially in different levels of linkage disequilibrium when gene action at locus $\mathcal{A}$ is completely additive. We generate $M = 10^5$ independent realizations in Monte Carlo simulation and adopt $N = 5000$, $s_{\mathcal{B}} = 0.05$, $h_{\mathcal{A}} = 0.5$ and $h_{\mathcal{B}} = 0.5$.
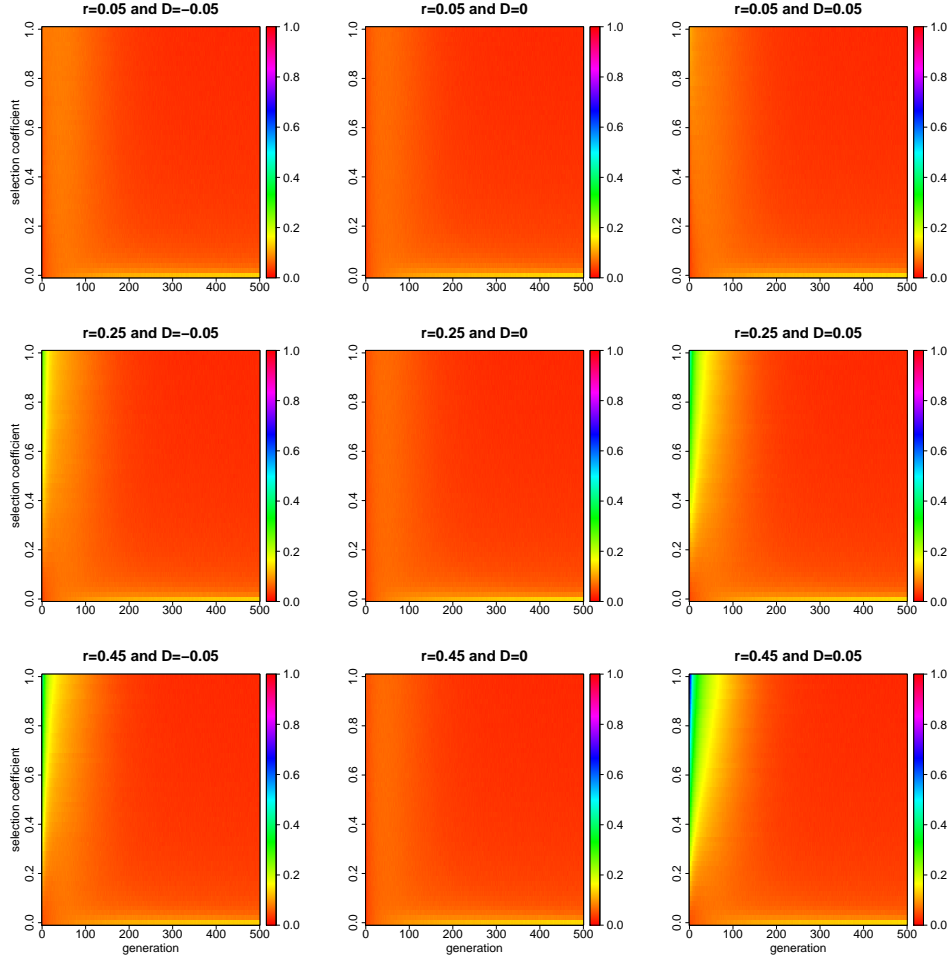
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FIGURE 2. Dynamics of the Hellinger distance $H(\pi_1^{(v)}, \pi_1^{(f)})$ simulated with the varying selection coefficient $s_\mathcal{A}$ and recombination rate r over 500 generations under the two-locus Wright-Fisher model with selection for the 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 $N = 5000$, $s_\mathcal{B} = 0.05$, $h_\mathcal{A} = 0$ and $h_\mathcal{B} = 0.5$.

We simulate the dynamics of the Hellinger distance $H(\pi_1^{(v)}, \pi_1^{(f)})$ 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 5000 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. These illustrations confirm the
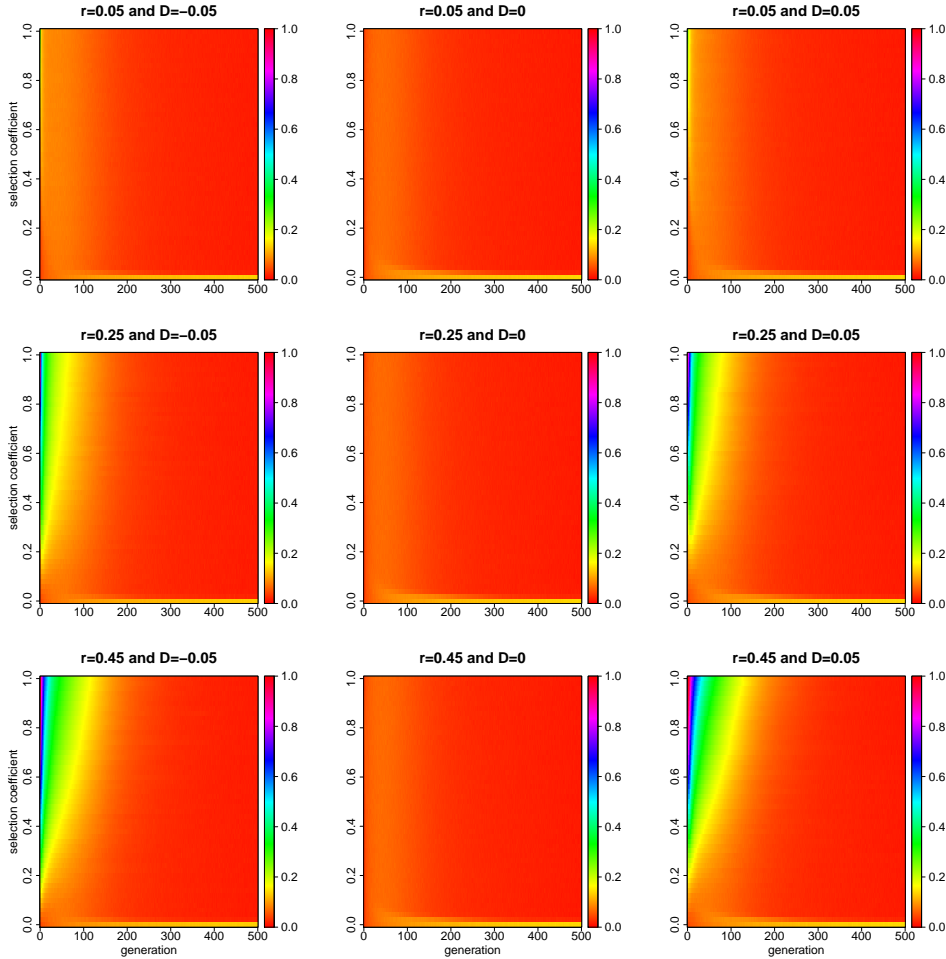
FIGURE 3. Dynamics of the Hellinger distance $H(\pi_1^{(v)}, \pi_1^{(f)})$ simulated with the varying selection coefficient $s_{\mathcal{A}}$ and recombination rate r over 500 generations under the two-locus Wright-Fisher model with selection for the population initially in different levels of linkage disequilibrium when gene action at locus $\mathcal{A}$ is completely recessive. We generate $M = 10^5$ independent realizations in Monte Carlo simulation and adopt $N = 5000$, $s_{\mathcal{B}} = 0.05$, $h_{\mathcal{A}} = 1$ and $h_{\mathcal{B}} = 0.5$.

conclusions we have achieved in our work and also show that the difference in the behaviour of the two-locus Wright-Fisher model between viability and fecundity selection becomes more significant with the population size increasing (*i.e.*, the effect of genetic drift on the evolving population decreasing). Intuitively, this is due to the fact that the performance of natural selection and genetic recombination affecting the population dynamics becomes relatively more significant as the effect of genetic drift on the evolving population decreases (see Hamilton, 2011).

REFERENCES

Hamilton, M. (2011). *Population Genetics*. Wiley-Blackwell, Chichester.