

File S1

Interference effects of deleterious and
beneficial mutations in large asexual
populations

Supporting Information

Kavita Jain

S1 Stochastic simulations

To test the theory developed in the main text, I simulated a population of N haploid asexuals in which an individual carrying k_d deleterious and k_b beneficial mutations was chosen to replicate with a probability proportional to its fitness $(1 - s_d)^{k_d}(1 + s_b)^{k_b}$, $0 < s_b, s_d < 1$. The beneficial fitness effect s_b was chosen from a truncated exponential distribution with mean \bar{s}_b and maximum beneficial effect equal to 0.1. Deleterious and beneficial mutations chosen from Poisson distribution with mean u_d and u_b , respectively, were then introduced; in case of mutators, the respective mutation rates were U_d and U_b . Back mutations were ignored so that the number of beneficial and deleterious mutations increase with time. These steps were performed starting from a resident population at mutation-selection equilibrium with zero beneficial mutations, and each simulation was run until the time T_{MR} when the Muller's ratchet clicked for the first time. For the background population to stay in equilibrium, one requires the Muller's ratchet to click slowly and therefore the population size $N \gg s_d^{-1}e^{u_d/s_d}$ is required. Thus for weakly deleterious mutations, very large populations need to be simulated (e.g., for $s_d = 2 \times 10^{-3}$, $u_d = 5s_d$, a population of size $> 10^5$ is needed). With the available computational resources, I have been able to simulate population sizes of the order 10^5 .

The fixation probability of a single beneficial mutant with fixed effect was measured by counting the number of runs in which more than 90% of the

population carried the beneficial mutation in 10^3 replicates for $s_d = 10^{-2}$ (2000 for $s_d = 2 \times 10^{-3}$). To find the substitution rate and selection coefficient fixed during the adaptation process, in each simulation run, the number of beneficial mutations \mathcal{K}_b carried by maximum number of individuals in the population and the selection coefficient \mathcal{S}_b averaged over the population were recorded (WILKE, 2004). The average substitution rate $E[k_b]$ and the average selection coefficient $E[s_b]$ were then found by averaging \mathcal{K}_b/T_{MR} and \mathcal{S}_b , respectively, over 10^3 independent runs of the model described above. I also calculated these quantities using (12) and (17) where the fixation probabilities were found numerically by solving the recursion equation (5) and also using the analytical result (9).

Figures S1 and S2 show the simulation results for fixation probability of a single beneficial mutant, and also those obtained by numerically solving the full recursion equation (1) and the quadratic approximation (5). Overall, the results from (1) and simulation results agree well, but (5) overestimates these since, as already mentioned in the main text, the quadratic approximation is valid when the selection coefficients and mutation rates are small. I also note that for smaller $s_d = 0.002$, there is a large discrepancy between the simulation and theoretical results when s_b equals u_d in Fig. S1 and U_d in Fig. S2, possibly, because the fixation probability is predicted to drop sharply for these parameters and may be subject to large fluctuations. Figure S3 shows results for the average substitution rate and average selection coefficient fixed using the three methods described above. I find that the

results from stochastic simulations are consistently lower than the theoretical results as also observed in previous work (ORR, 2000; BACHTROG and GORDO, 2004; WILKE, 2004; PARK *et al.*, 2010).

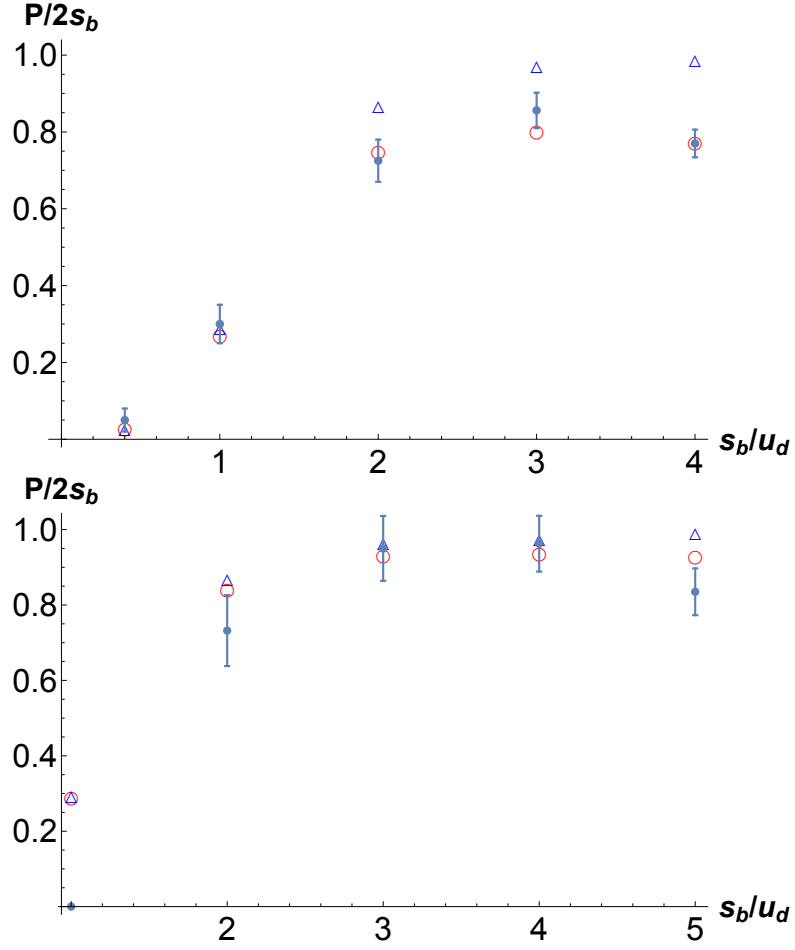


Figure S1: Fixation probability for $N = 6 \times 10^5$ when the beneficial effect s_b is varied. The other parameters are $s_d = 0.01$ (top) and 0.002 (bottom) with $u_d = 5s_d, U_d = u_d$. The data from stochastic simulations (\bullet) with errorbars representing the standard deviation, and by numerically calculating (1) (\circ) and (5) (\triangle) are shown.

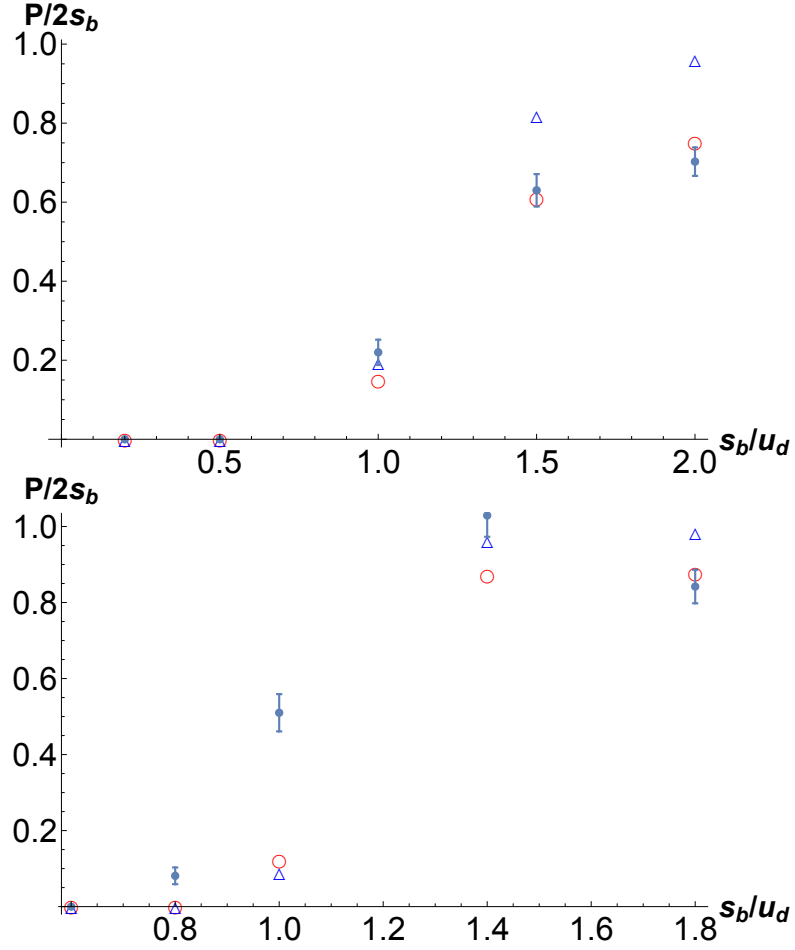


Figure S2: Fixation probability for $N = 6 \times 10^5$ when the beneficial effect s_b is varied. The other parameters are $s_d = 0.01, u_d = 5s_d, U_d = 2u_d$ (top) and $s_d = 0.002, u_d = 5s_d, U_d = 5u_d$ (bottom). The data from stochastic simulations (\bullet) with errorbars representing the standard deviation, and by numerically calculating (1) (\circ) and (5) (\triangle) are shown.

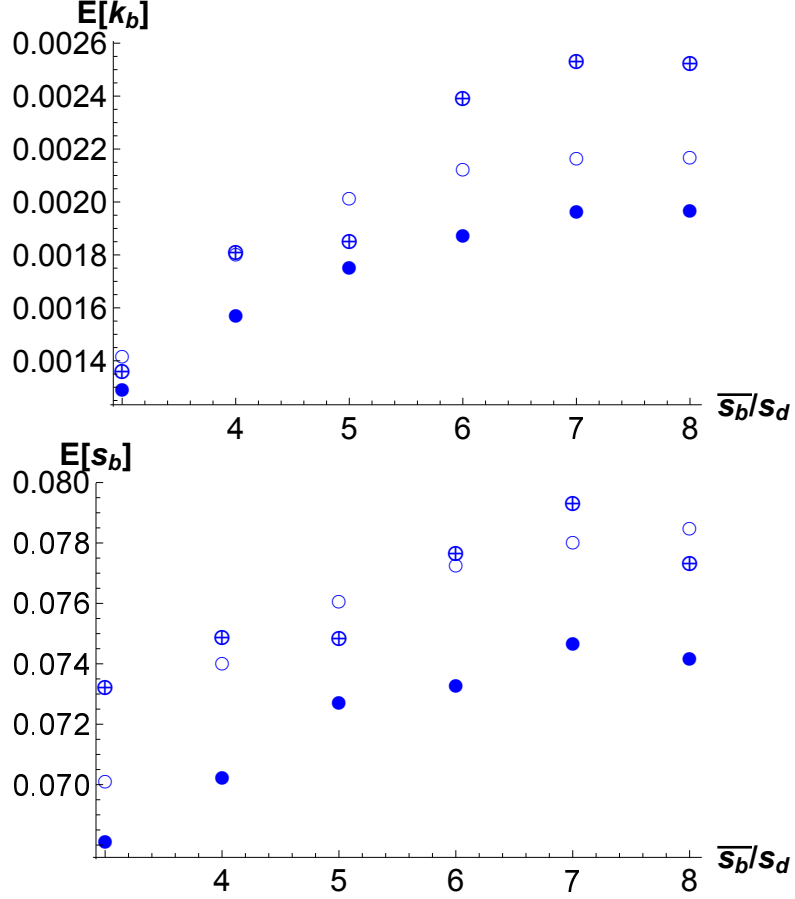


Figure S3: Expected substitution rate $E[k_b]$ and average fixed selection coefficient $E[s_b]$ for $N = 2 \times 10^5$ when the average beneficial effect \bar{s}_b is varied. The other parameters are $s_d = 0.01$, $u_d = 5s_d$, $u_b = 5 \times 10^{-7}$. The data from numerical simulations (\bullet) and numerical integration of (12) and (17) using quadratic approximation (5) (\oplus) and analytical expression (9) (\circ) are shown.

References

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- ORR, H. A., 2000 The rate of adaptation in asexuals. *Genetics* **155**: 961–968.
- PARK, S.-C., D. SIMON, and J. KRUG, 2010 The speed of evolution in large asexual populations. *J. Stat. Phys.* **138**: 381–410.
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