

Supplementary Figures for Prestige bias in cultural evolutionary dynamics

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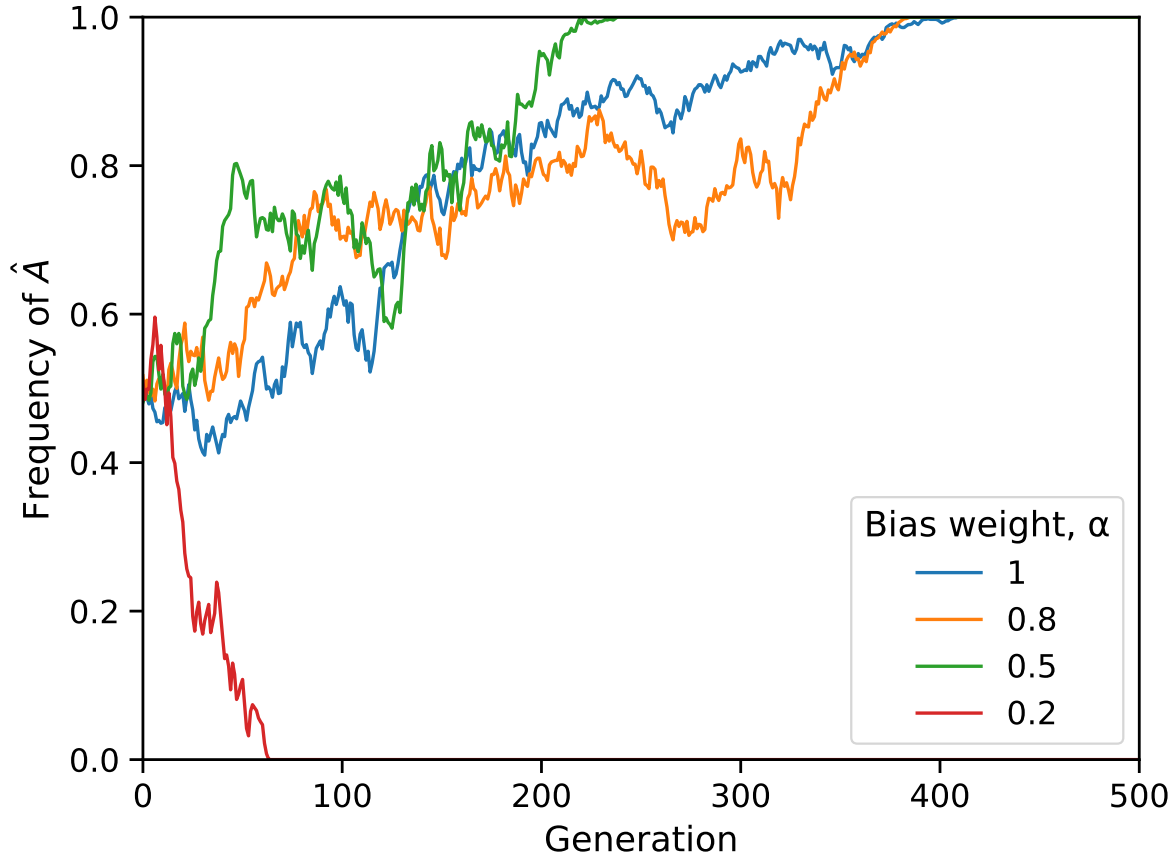


Figure S1: Example dynamics of the dichotomous model with varying bias weight. The dichotomous model is defined in eq. 11. Shown are full dynamics without DM or GBD approximations. Here, population size, $N = 1,000$; ideal phenotype value, $\hat{A} = 1$; success bias value, $\beta(A) = 0.99$; initial phenotype frequencies are 50%-50%.

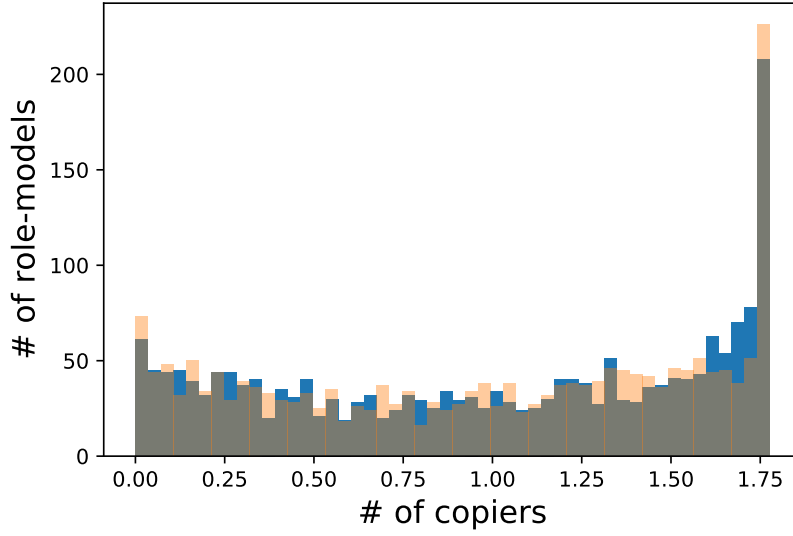


Figure S2: Numerical validation of the GB approximation. The approximation (orange) fits simulation results (blue) well when using 1,000 simulations. Here, population size, $N = 2,000$; bias weight, $\alpha = 0.1$; ideal phenotype value, $\hat{A} = 1$; role-model traits $\mathbf{A} \sim N(0, 1)$; success bias value, $\beta(A) = 0.956$.

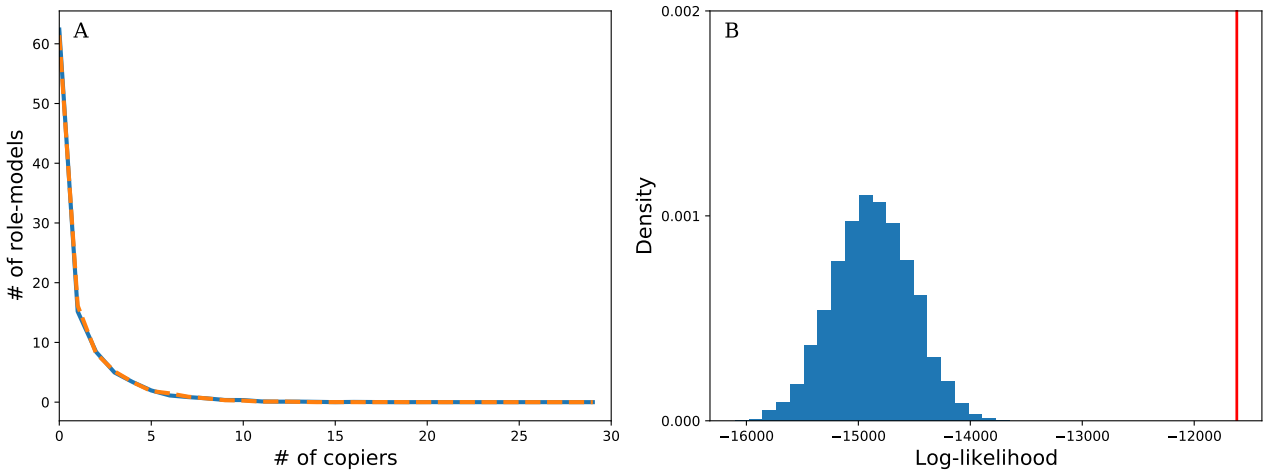


Figure S3: Numerical validation of the DM approximation. We performed computational simulations of the role-model choice process (eq. 10) and compared the distribution of the number of copiers to simulations when using the DMD approximation (corollary 2). **(A)** The difference between the DM distribution (orange) and the empirical distribution of the simulations (blue) is very small. **(B)** The log-likelihood of the DMD for results of the simulations (red vertical line) is much higher than the log-likelihood of permutations of simulations (blue histogram). Here, population size, $N = 100$; number of simulations, $m = 100$; phenotype values, $\hat{A} = 1$, $A \sim N(0, 1)$; success-bias weight, $\alpha = 0.5$. No estimation error or bias is applied, and traits are estimated and copied perfectly.

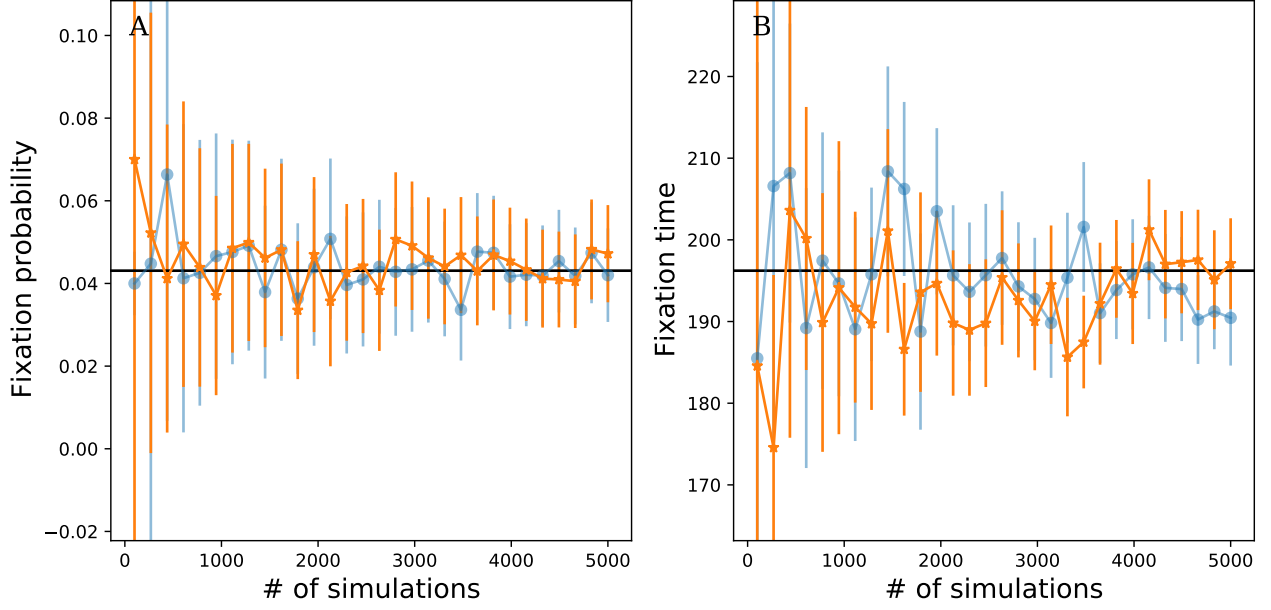


Figure S4: DMD approximation precision as function of number of simulations. Our DMD approximation (orange) agrees with stochastic simulation results (blue) when using 1,000 or more simulations. Both fluctuate around the analytic fixation probability approximation (black; eq. 19). Markers are averages across simulations, error bars are 95% confidence intervals. Here, population size, $N = 1000$; success-bias weight, $\alpha = 0.5$; phenotype values, $\hat{A} = 1, A = 0.7$; success-bias value, $\beta(A) = 0.956$.

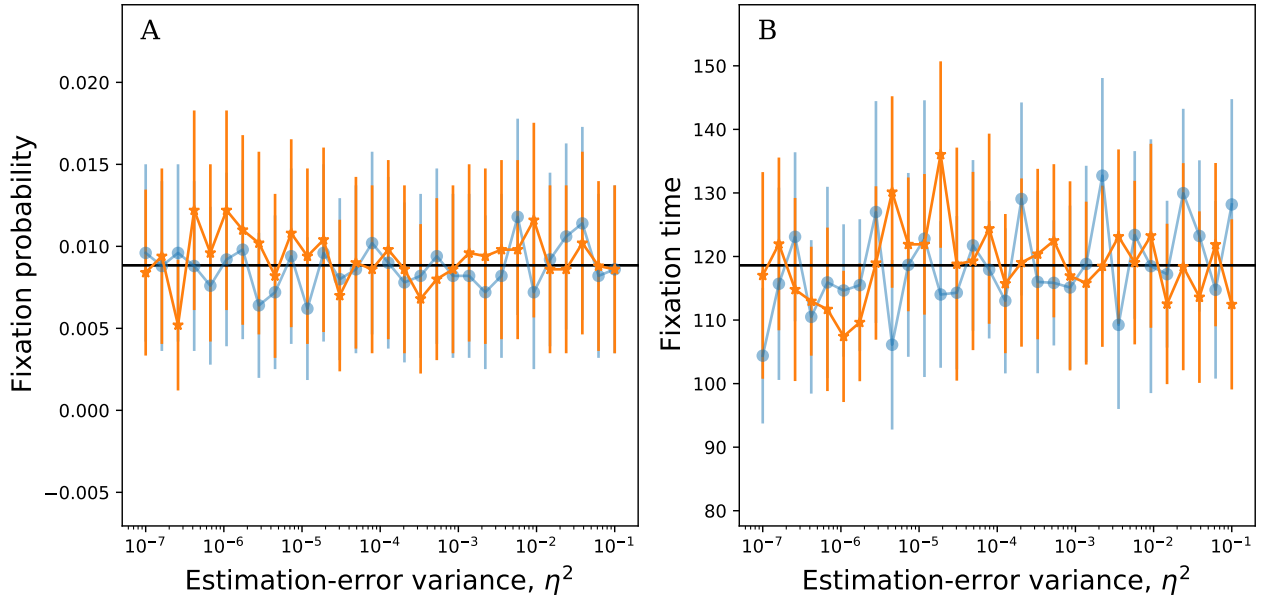


Figure S5: Robustness of DMD approximations to success estimation error. Both the DMD approximation (orange) and our approximation (black) agree with the stochastic simulations (blue), even with a high estimation error. Markers are averages across simulations, error bars are 95% confidence intervals. 5,000 simulations per data point; population size, $N = 1000$; success-bias weight, $\alpha = 0.1$; phenotype values, $\hat{A} = 1, A = 0.7$; bias strength parameter $J \sim N(1, \eta^2)$ where η^2 is on the x-axis.

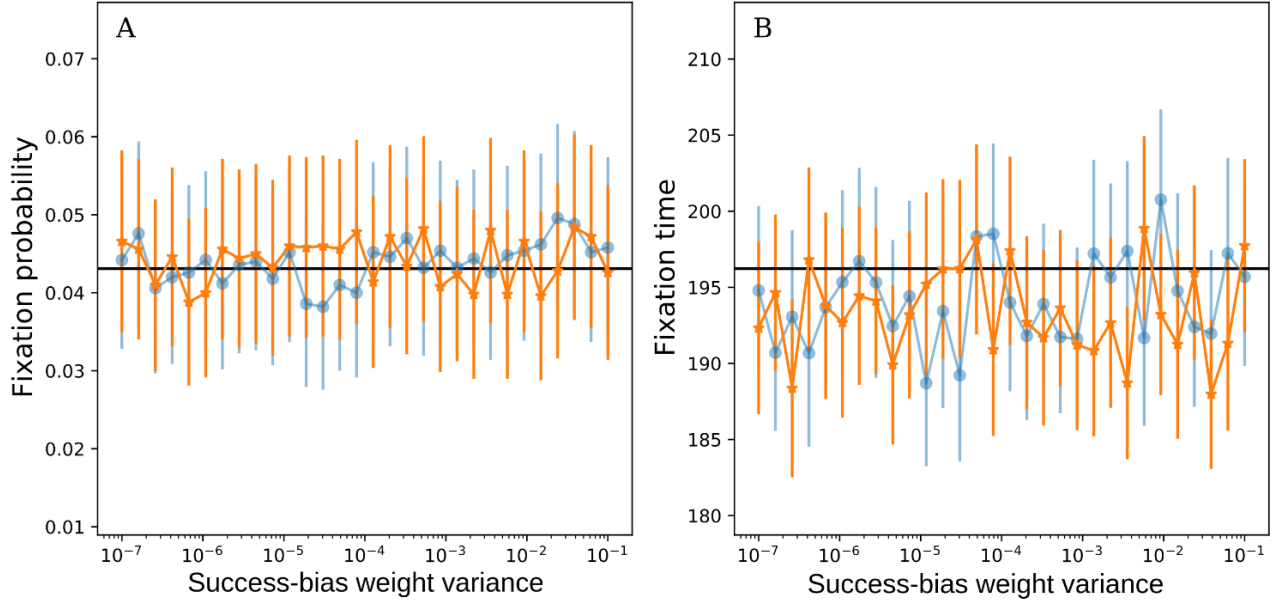


Figure S6: Robustness of DM approximations to variation in the bias weight α . Fixation probability does not seem to be affected by variation in success bias weight between role-models. Thus, both the DM approximation (orange) and Kimura's equation (black line) have a good fit to results of stochastic simulations (blue). Markers for average across 5,000 simulations, error bars are 95% confidence intervals. Here, population size, $N = 1000$; success bias weight is normally distributed, $\alpha_j \sim N(0.5, \epsilon^2)$ where $10^{-7} \leq \epsilon^2 \leq 10^{-1}$; phenotype values, $\hat{A} = 1, A = 0.7$; success bias value, $\beta(A) = 0.956$.

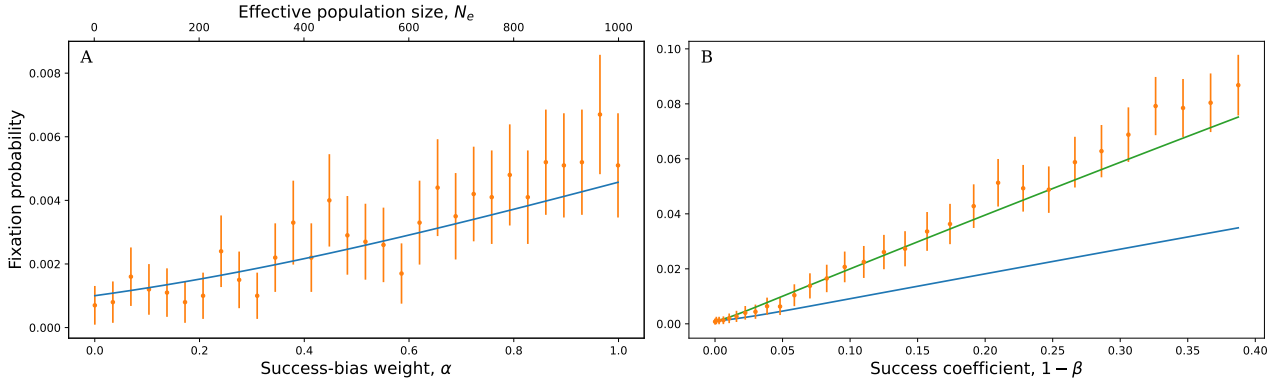


Figure S7: Fixation probability in a changing environment, $k > l$. (A) Fixation probability decreases with the success-bias weight (bottom x-axis) and effective population size (top x-axis). The approximation (blue; ??) agrees with simulation results (orange). (B) Fixation probability increases with the success coefficient, β . When success bias is large ($1 - \beta > 0.1$), simulation results (orange) are underestimated by the changing environment approximation (blue; eq. 23). With even larger success bias ($1 - \beta > 0.35$), even the constant environment approximation (green; eq. 19) slightly underestimates simulation results, likely because the diffusion equation approximation assumes weak 'selection'. Markers show average of 10,000 simulations, error bars show 75% (panel A) and 95% (panel B) confidence intervals. Here, population size is $N = 1,000$; In panel A, $A = 0.9$, $\hat{A} = 1$ ($1 - \beta = s = 0.005$), $k = 80$, and $l = 20$; In panel B, $0.01 < A < 0.99$, and $\hat{A} = 1$, which determines $1 - \beta$ via $\beta = \beta(A)/\beta(\hat{A})$ and eq. 5, $k = 80$, and $l = 20$, $\alpha = 0.1$;