

Prestige bias in cultural evolutionary dynamics

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Abstract

If the traits of more successful individuals are more likely to be adopted, the resulting cultural transmission is described as being success-biased. Prestige may be used as a proxy for success. Here, we model prestige bias as a combination of indirect success bias and influence bias, the latter meaning that the choice of a role-model depends on the number of individuals that have already copied that role-model. The effect of prestige on cultural evolutionary dynamics is analyzed using mathematical analysis and stochastic simulations. Analytic approximations to the stochastic role-model choice process facilitate the mathematical analysis and reduce the computational complexity of simulations. Approximations are given to the fixation probability and the fixation time of an invading cultural trait in different environments. We show that indirect success bias effectively plays the role of natural selection, whereas influence bias effectively plays the role of genetic drift. Influence bias, which may be strong in communities where social media are prevalent, also accelerates the evolutionary dynamics, as can be expected in a rich-get-richer process.

Introduction

22 Cultural transmission of attitudes, preferences, beliefs, norms, and behaviors may combine vertical
transmission, in which parents transmit to their offspring; oblique transmission, in which adults
24 (teachers, leaders, and even strangers) transmit to unrelated offspring; and horizontal transmission, in
which individuals from the same age cohort transmit to one another [4]. It has been demonstrated that
26 non-vertical cultural transmission can maintain maladaptive traits, which can be beneficial in changing
environments [21, 55].

28 Transmission biases may cause a cultural trait to have a higher rate of transmission than its frequency in
the population. *Success bias* occurs when individuals prefer to copy from role models that demonstrate
30 success in some activity, such as fishing, growing yams, using medicinal plants [24], or hunting [54],
and it can increase the probability of learning a trait that is present in those successful individuals [53].
32 Indeed, in a tournament between learning strategies [7], most winning strategies included a mixture
of success-biased social learning and individual learning, implying that success-biased learning is a
34 good strategy, but that by itself it is not enough to best other strategies, even when success is measured
accurately.

36 Boyd and Richerson [5, Ch. 5] suggested that the assessment of success can be divided to three
categories: *direct bias*, *indirect bias* and *frequency-dependent bias*. Direct bias occurs when one
38 phenotype is more attractive than other phenotypes, and is evaluated by *directly* testing the trait. For
example, an individual observing a ping-pong match can try the observed paddle grips to determine
40 which grip is better. Frequency-dependent bias occurs when the probability of copying a phenotype
is higher or lower than the frequency of the phenotype among demonstrators. For example, suppose
42 the common paddle grip is used by 60% of the demonstrators; if the this grip is adopted by 80% of
copiers, then transmission is under positive frequency bias, also called *conformity*; if it is adopted
44 by 40% of copiers, then transmission is under negative frequency bias, or *anti-conformity* [15]. The
effects of conformity and anti-conformity on cultural evolution have been studied with both models
46 [36, 37, 52] and experiments [3]. Indirect bias occurs when an individual uses one phenotype to
determine the attractiveness of another phenotype. For example, an observer may copy the paddle
48 grip of the ping-pong player who scored more points in the match, thus indirectly evaluating the grip
by the points scored. However, this may cause mismatches between the copied trait and the rest of
50 the cultural or genetic repertoire of the individual [51]. Furthermore, Boyd and Richerson [5, Ch. 8]
suggest that maladaptive traits may spread widely in a population if indirect bias is strong enough,
52 e.g., by a runaway process caused by a cultural equivalent of sexual selection [8]. Indeed, helping
behaviors can evolve due to horizontal transmission bias even without any benefit to the recipient, or
54 when the benefit is much larger than the cost [35].

Heinrich and Broesch [24] studied such indirect success biases, which they call cross-domain success
56 bias or *prestige bias* (e.g., great fishermen may be chosen as role-models for growing yams). They
suggested that such biases, over generations, can lead to cultural adaptations, and that although prestige
58 can lead to maladaptive traits spreading in the population, it can also accelerate the spread of adaptive

traits [5, Ch. 8]. Prestige bias may be more common in humans than success bias [6], and prestige is
60 often mentioned in the cultural evolution literature, although there are few models of it.

A broader definition of prestige is the “widespread respect and admiration felt for someone or something
62 on the basis of a perception of their achievements or quality” (New Oxford American Dictionary).
Indeed, Chudek et al. [31] have defined prestige bias as “a tendency to learn from individuals to whom
64 others have preferentially attended, learned or deferred”, and demonstrated its occurrence in in 3-4
year old children. Henrich and Gil-White [26] gave a similar definition of prestige as “freely conferred
66 deference”, in contrast to *dominance*, and provided examples from the anthropological literature.

To distinguish this form of indirect bias from other definitions of prestige, we call it *influence bias*. This
68 is an important distinction, as influence is a context-dependent bias, rather than a content-dependent
bias: it does not depend on the phenotype itself but rather on the number of copiers that have already
70 copied each role-model, which may be easier and more accurate to estimate than success. Influence
bias also differs from conformity, which depend on the frequency of a trait in the population or in a
72 sample of role-models, rather than the social dynamics of copying.

In contemporary human society, social media make it especially easy to estimate the social and cultural
74 influence individuals have over others, which can have an effect on decision making. Online social
networks such as *Facebook* and *Instagram* are known to affect the influence of individuals [39, 40, 41],
76 and specific marketing practices have been invented to capitalize on this effect [38].

In the following, we develop a stochastic model of cultural transmission with prestige bias that combines
78 both cross-domain indirect success bias and influence bias. We develop analytic approximations for this
model and analyze its dynamics. We also find approximations for the probability and time to fixation
80 of a ‘successful’ phenotype (i.e., that is subject to success bias). Comparing these approximations to
Kimura’s approximations for the fixation of a favorable allele [19, 45], we demonstrate that success
82 and influence bias play the role of natural selection and genetic drift, respectively.

Models

84 We begin with a continuous trait model with indirect bias suggested by Boyd and Richerson [5], propose
an extension with influence bias, and then develop a model with a dichotomous trait. We implement our
86 stochastic models and approximations, perform statistical analyses, and produce figures using Python
[42] with NumPy [43] and Matplotlib [44]. Source code is available at [https://github.com/yoavram-](https://github.com/yoavram-lab/PrestigeBias)
88 [lab/PrestigeBias](https://github.com/yoavram-lab/PrestigeBias).

Continuous trait

90 We follow the Boyd and Richerson model [5], assuming only oblique transmission of the trait and
omitting the indirect trait in order to reduce model complexity. Consider a population of N individuals,
92 described by a single trait that takes continuous values. Each generation, N naive individuals, or
copiers, choose an individual from the previous generation, or role-models, from which they will copy

94 their trait. Similar to a Wright-Fisher model, generations are non-overlapping, and the entire population
 is replaced in each generation. The population at time t can be described by $\mathbf{A}(t) = (A_1(t), \dots, A_N(t))$
 96 where $A_i(t)$ is trait value of individual i at time t , and the initial population is drawn from a standard
 normal distribution, $\mathbf{A}(0) \sim N(0, 1)$. Cultural transmission is modeled by a function F such that

$$98 \quad A_i(t + 1) = F_i(\mathbf{A}(t)) . \quad (1)$$

Success bias. Boyd and Richerson [5, Ch. 8, p. 247-249] describe a transmission algorithm by defining
 100 F , a weighted average of the traits of all role-models, as

$$F_i(\mathbf{A}) = \sum_{j=1}^N G_{i,j} \cdot A_{i,j} , \quad (2)$$

102 where $G_{i,j}$ is the success bias of role-model j in the eyes of copier i ,

$$G_{i,j} = \frac{\beta(A_{i,j})}{\sum_{k=1}^N \beta(A_{i,k})} , \quad (3)$$

104 $A_{i,j}$ is the absolute trait value that copier i estimates for role-model j with some error $e_i \sim N(0, \eta^2)$,

$$A_{i,j} = A_j + e_i, \quad (4)$$

106 and $\beta(\cdot)$ is the bias function that quantifies the success bias of a role-model [5, eq. 5.11],

$$\beta(A_{i,j}) = b \cdot \exp \left(- \frac{(A_{i,j} - \hat{A})^2}{2J} \right) , \quad (5)$$

108 with \hat{A} as the arbitrary optimal trait value, and J and b as parameters that control the bias strength.
 Therefore, $G_{i,j}$ is a relative success score that copier i assigns to role-model j .

110 Boyd and Richerson [5] note that the deterministic blended transmission algorithm they use has
 alternatives. We can develop a similar stochastic model with transmission from a single random
 112 role-model where instead of eq. (2), we define the transmission function F as a random variable with
 its distribution given by

$$114 \quad \Pr(F_i(\mathbf{A}) = A_j) = G_{i,j} ; \quad (6)$$

here $G_{i,j}$ is the probability that copier i chooses to copy the trait of role-model j .

116 **Influence bias.** Here we introduce a new element to the model by assuming that in each generation,
 copiers choose their role-models one by one. Denote by $K_{i,j}$ the number of copiers that choose role-
 118 model j after copier i chose a role-model. Thus, i out of N copiers had already chosen a role-model,
 $\sum_{j=1}^N K_{i,j} = i$, and there are $N - i$ copiers that have yet to choose a role-model. The stochastic process
 120 of role-model choice,

$$\{\mathbf{K}_i = (K_{i,1}, \dots, K_{i,N})\}_{i=1}^N , \quad (7)$$

122 is described by the recurrence equation

$$K_{i,j} = K_{i-1,j} + S_{i,j}, \quad i, j = 1, 2, \dots, N, \quad (8)$$

124 where $S_{i,j} = 1$ if the i -th copier chose role-model j and 0 otherwise, and the initial state is $K_{0,j} = 0$.

126 Following eq. (6), the probability that the i -th copier chose role-model j is given by the prestige of role-model j in the eyes of copier i ,

$$128 \quad Pr(S_{i,j} = 1 \mid S_{1,j}, S_{2,j}, \dots, S_{i-1,j}) = G_{i,j}. \quad (9)$$

The prestige $G_{i,j}$ of role-model j in the eyes of copier i is determined by success—the estimated biased trait value $\beta(A_{i,j})$ —and influence—the number of copiers that chose role-model j before copier i , $K_{i-1,j}$, replacing eq. (3) with

$$132 \quad G_{i,j} = \frac{\alpha_{ij} \cdot \beta(A_{i,j}) + (1 - \alpha_{ij}) \cdot K_{i-1,j}}{W_i}. \quad (10)$$

Here, the bias weight α_{ij} determines the relative weighting of success and influence bias. It is a characteristic of the interaction of role-model j with copier i that determines the relative significance of direct success vs. influence in the role-model's overall prestige in the eyes of the copier.

136 Different individuals may evaluate the importance of success and influence differently. Additionally, we assume each role-model displays its influence and success individually. For example, individuals with more followers but lacking skill may emphasize the number of their followers rather than their skill.

140 The trait of role-model j estimated by copier i , $A_{i,j}$, remains as in eq. (4), and W_i is a normalizing factor that sums the numerator over all role-models ($1 \leq j \leq N$) to ensure $\sum_{j=1}^N G_{i,j} = 1$.

142 **Dichotomous trait**

We introduce a simplified version where the trait has only two phenotypes: an optimal phenotype \hat{A} and a sub-optimal phenotype A . All role-models with the same phenotype will contribute to the probability that that phenotype is transmitted, and thus influence is determined by the number of copiers that have already chosen a role-model with either phenotype. In addition, for simplicity and for easier mathematical analysis, we assume α is homogeneous, which entails exchangeability between role-models. Therefore, the probability that the i -th copier copies phenotype A is

$$G_{i,A} = \frac{(N - X)\alpha'\beta(A) + K_{i,A}}{i - 1 + (N - X)\alpha'\beta(A) + \alpha'X}, \quad (11)$$

150 where X is the number of role-models with trait \hat{A} ; $K_{i,A}$ is the number of copiers that already chose A when copier i chooses a role-model; assuming (without loss of generality) that $\beta(\hat{A}) = 1$; and defining

152 $\alpha' = \frac{\alpha}{1-\alpha}$ as the odds ratio of the bias weight. Complementing this, the probability of the i -th copier to copy phenotype \hat{A} is $G_{i,\hat{A}} = 1 - G_{i,A}$. The rest of the details follow the continuous trait model.

154 Results

Our models are defined by two nested stochastic processes. Change over multiple generations is described by the dynamics of the phenotype distribution at each generation, $\{\mathbf{A}(t)\}_t$, see eq. (1). The transition from one generation to the next is described by the number of copiers each role-model has after i copiers have chosen a role-model, $\{\mathbf{K}_i\}_{i=1}^N$, see eq. (7). We emphasize that the models are nested: $\mathbf{A}(t+1)$ can be computed from $\mathbf{A}(t)$ by evaluating \mathbf{K}_N , where $K_{N,j}$ is the number of copiers that chose role-model j after all copiers chose a role model. However, the former requires iterating over eqs. (8) and (9). Thus, we sought to find an equivalent stochastic process that has the same joint distribution as \mathbf{K}_N . We found two approximations for the distribution of \mathbf{K}_N , summarized here and explained in detail below. In both we assume that the bias weight is completely homogeneous, $\alpha_{i,j} = \alpha$ (it is also enough to assume that α_j is a bias of role-model j only, that is, it does not vary between copiers). Note that these approximations apply for both the and the continuous trait (eq. (10)) and the dichotomous trait (eq. (11)) models.

Generalized binomial approximation. The number of copiers of a specific role-model at each step, $K_{i,j}$, follows the *generalized binomial distribution* [16] and therefore,

(i) the expected number of copiers of role-model j equals its prestige in the eyes of the first copier, multiplied by the total number of copiers, that is, $E[K_{N,j}] = N \cdot G_{1,j}$ if trait estimation error is uniform for all copiers ($e = e_i$ for $i = 1, \dots, N$); and (ii) the expected number of copiers of each role-model equals its relative biased trait value, similar to the role of relative fitness in population-genetic models, that is, $E[K_{N,j}] = \beta(A_j + e)/\bar{\beta}$ if the bias weight is uniform for all role-models ($\alpha = \alpha_j$ for $j = 1, \dots, N$), where $\bar{\beta} = 1/N \sum_{j=1}^N \beta(A_j + e)$ is the population mean estimated trait value.

Dirichlet-Multinomial approximation. The role-model choice process, $\{\mathbf{K}_i\}_{i=1}^N$, is equivalent to a *Pólya urn* model if trait estimation error is uniform for all copiers ($e = e_i$ for all $i = 1, \dots, N$), meaning that the order of copiers does not matter.

178 Generalized binomial distribution

The generalized binomial distribution (GBD) emerges from a series of dependent Bernoulli trials (in contrast to the standard binomial distribution in which trials are independent) and is denoted by $GBD(n, p, \theta)$ where n is the number of trials, p is the probability of success of the first trial, and θ is the correlation between trials ($\theta = 0$ gives the standard binomial distribution).

184 **Result 1** (Generalized binomial approximation). *The number of copiers of role-model j after i copiers*
have chosen a role-model follows the GBD, $K_{i,j} \sim \text{GBD}(i, \alpha_j \cdot \beta(A_j + e))$ if $e_i = e$ for all role-models
186 *$i = 1, \dots, N$.*

Proof. Let $Q_j(k, i) = P(K_{i,j} = k \mid K_{i-1,j})$ be the probability that exactly k out of i copiers choose
188 role-model j given $K_{i-1,j}$ out of $i - 1$ copiers chose role-model j . Using conditional probability and
eq. (8),

$$190 \quad Q_j(k, i) = P_j(S_{i,j} = 1 \mid k - 1, i - 1) \cdot Q_j(k - 1, i - 1) + P_j(S_{i,j} = 0 \mid k, i - 1) \cdot Q_j(k, i - 1), \quad (12)$$

where $S_{i,j} = 1$ when the i -th copier chooses role-model j . Equation (12) is equivalent to eq. (2.1) by
192 [16], which completes the proof.

This result gives the following two corollaries on the expected number of followers of a given role-
194 model j by the end of the role-model choice process, $K_{N,j}$. The proof of Corollary 2 is in Appendix A.

196 **Corollary 1.** *The expected number of copiers of role-model j after all copiers have chosen a role-*
model is $E[K_{N,j}] = N \cdot G_{1,j}$, where $G_{1,j}$ is the probability of the first copier to copy role-model
198 *j .*

Proof. Drezner and Farnum [16, eq. (2.3)] show that $E[k] = N \cdot Q_j(1, 1)$ (modified from their
200 notation). $Q_j(1, 1)$ is the initial probability to choose role-model j , before any role-model choices are
made. $Q_j(1, 1) = G_{1,j}$ by definition, which completes the proof.

202 **Corollary 2.** $E[K_{N,j}] = \alpha_j \cdot \beta(A_j + e) / \overline{\alpha \cdot \beta(A + e)}$, where the averaging in the denominator is over
the role-models index, j .

204 The special case where the bias weight is uniform for all role-models ($\alpha = \alpha_j$ for $j = 1, \dots, N$) is
interesting, because we can evaluate the expected number of copiers using a linear equation

$$206 \quad E[K_{Nj}] = N \cdot \frac{\alpha \cdot \beta(A_j + e)}{\sum_{m=1}^N \alpha \cdot \beta(A_m + e)} = \beta(A_j + e) \left/ \overline{\beta(A + e)} \right., \quad (13)$$

where the only variable is $A_j + e$, because $\overline{\beta(A + e)}$ is the mean of the distribution of the trait values,
208 modified by some constant parameters of β . We can then write $L = 1 / \overline{\beta(A + e)}$ and

$$E[K_{Nj}] = L \cdot \beta(A_j + e). \quad (14)$$

210 **Numerical validation.** To validate our results we ran 1,000 simulations of the full model, and
compared the results with Corollary 2. We compare the distribution of number of copiers by plotting
212 the histograms of both our simulations results and the expected values based on Corollary 2. We used
the average of the 1,000 simulations to eliminate drift errors, as can be seen in Figure S1.

214 Although basic, Figure S1 shows good fit of the GB approximation. This validation is initial, and we
do more extensive validations on the Dirichlet-Multinomial approximation, because that is what we
216 will use in our analysis.

Dirichlet-Multinomial distribution approximation

218 **Pólya urn model.** This stochastic process consists of N draws from an urn with an initial number of
colored balls of M colors. When a ball is drawn, it is then placed back in the urn together with an
220 additional new ball of the same color. Let $\mathbf{U}_i = \{u_{i,1}, u_{i,2}, \dots, u_{i,M}\}$ where $u_{i,j}$ is the number of balls of
the j -th color in the urn after i draws. Let $S_{i,j} = 1$ when drawing a j -colored ball on the i -th draw, and
222 0 otherwise. The probability that $S_{i,j} = 1$ given \mathbf{U}_{i-1} is

$$P(S_{i,j} = 1 \mid \mathbf{U}_{i-1}) = \frac{u_{i-1,j}}{\sum_{m=1}^M u_{i-1,m}} = \frac{o_j + w_{i-1,j}}{\sum_{m=1}^M o_m + w_{i-1,m}} = \frac{o_j + w_{i-1,j}}{i - 1 + \sum_{m=1}^M o_m}, \quad (15)$$

224 where o_j is the initial number of balls of color j in the urn, and $w_{i,j}$ is the cumulative number of new
balls that were added to the urn after i draws of color j .

226

Result 2 (Pólya urn model). *The role-model choice process, $\{\mathbf{K}_i\}_{i=1}^N$, is equivalent to a Pólya urn
228 model if both trait estimation error and bias weight are uniform in the population, $e = e_j$ and $\alpha = \alpha_j$
for all $j = 1, \dots, N$.*

230 *Proof.* Write $\alpha' = \frac{\alpha}{1-\alpha}$ as the bias weight ratio, and $A'_j = A_j + e$. From eq. (10) and because
 $\sum_{j=1}^N K_{i,j} = i$, we have

$$G_{i,j} = \frac{\alpha' \beta(A'_j) + K_{i-1,j}}{\sum_{m=1}^N [\alpha' \beta(A'_m) + K_{i-1,m}]} = \frac{\alpha' \beta(A'_j) + K_{i-1,j}}{i - 1 + \sum_{m=1}^N \alpha' \beta(A'_m)}. \quad (16)$$

Substituting $M = N$, $o_j = \alpha' \beta(A'_j)$, and $w_{i,j} = K_{i,j}$ in eq. (15) gives eq. (16), thus completing the
234 proof.

Frigyik et al. [17, section 2] prove that the proportion of different colored balls in a *Pólya urn model*
236 converges to the Dirichlet distribution as the number of draws approaches infinity, based on the *Mar-
tingale Convergence Theorem* [18]. We therefore have an approximation for the relative prestige each
238 role-model has when evaluated by copiers. Thus, choosing the role-models for all copiers is equivalent
to drawing from a multinomial distribution where the parameters are the modified weights from a
240 Dirichlet distribution and we have the following corollary.

242 **Corollary 3.** *The number of copiers of each role-model approximates a Dirichlet-Multinomial distri-
bution, $\mathbf{K}_i \sim \text{DM}(N, \mathbf{G}_1)$, under the conditions of Result 2.*

244 **Numerical validation.** To validate our analytical result (Corollary 3) and test its sensitivity to the
assumptions ($e_i = e$ and $\alpha_i = \alpha$ for $i = 1, \dots, N$) we compare it to results of stochastic simulations of
246 the full model. First, we compute an observed distribution of the number of copiers from the average
empirical distribution of multiple simulations. We then compare this observed distribution with the
248 expected theoretical DM distribution (Figure S2A). The difference in distributions was not perceived
when plotting both distributions on the same figure, so we used the difference instead. The maximum
250 difference is 0.5 role-models, which indicates a very good fit. In addition, we tested the likelihood
of the observed data to be drawn from the DM distribution, against a shuffle of the parameters vector
252 of the DM distribution itself (Figure S2B). We see that the negative log likelihood of the observed
data is much higher than any other shuffled version of the parameters vector, strongly supporting our
254 approximation.

Next, we examined the fixation probability and fixation time of a favored phenotype \hat{A} when invading
256 a population of phenotype A and compared results from the full model and the DM approximation.
Thus, we assume the population has a single individual with phenotype \hat{A} and $N - 1$ individuals
258 with phenotype A . That the number of simulations needed to sufficiently approximate our model
with the DM approximation is roughly 1,000 (Figure S3). We examined the robustness of the DM
260 approximation to relaxing the approximation assumptions. First, we relaxed our assumption of no
estimation error e . Estimation error in the original model was drawn from a normal distribution, and
262 added to the trait value before evaluation of the bias ($A_{ij} = A_j + e_i$). When estimation error is applied,
we sample J_i for each copier i from a normal distribution with varying scale (variance). Even when the
264 standard deviation is 0.1, the fixation probability and time are similar (Figure S4). We also relaxed our
assumption of a uniform bias weight α (i.e., $\alpha_i = \alpha$). We allowed α to vary in the population, drawing
266 α_j for each role-model j from a normal distribution such that $\alpha_j \sim N(0.5, q)$ where $q \in [10^{-7}, 10^{-1}]$.
We found again that results of the DM approximation are similar to those from stochastic simulations
268 of the full model (Figure S5).

Fixation probability and time

270 After finding that the DM distribution is a good approximation of the (within-generation) role-model
choice process, we turn our attention to the (between-generation) evolutionary dynamics. We focus on
272 the fixation probability and conditional fixation time (conditioned on the population reaching fixation)
of a favored phenotype, using a diffusion-equation approximation approach, similar to analyses of
274 population-genetic models [19, 45, 46]. We are mainly interested in the effect of the bias weight, α ,
which determines the relative effect of success and influence on prestige bias, given by eq. (10). For
276 simplicity, we do not include role-model estimation error in this analysis, i.e $e_i = 0$ for every copier
 i . As shown above, transmission in our model is approximately DM distributed (Corollary 3 and
278 eq. (16)).

We start by finding the expectation and variance of the change in frequency from one generation to the
280 next, which are the drift and diffusion terms of the diffusion equation. The proof is in Appendix B.

282 **Result 3** (Drift and diffusion terms in a constant environment). *Let x and x' be the frequency of type \hat{A}*
in a population with N individuals in the current and next generation, and β be the success coefficient
 284 *of phenotype A , $\beta = \beta(A) < \beta(\hat{A}) = 1$. Then,*

$$E[x' - x] \approx x(1 - x)(1 - \beta), \quad V(x' - x) \approx x(1 - x) \left(\frac{1}{\alpha N + (1 - \alpha)} \right). \quad (17)$$

286 This analysis gives a surprising result relating the parameters α and β to parameters of the classical
 Wright-Fisher model from population genetics: the selection coefficient s , a measure of the effect of
 288 natural selection on the change in frequency of genotypes, and the effective population size, N_e , a
 measure of the effect of random genetic drift on the change in frequency of genotypes. In a diffusion-
 290 equation approximation of the classical Wright-Fisher model, the expectation and variance of the
 change in frequency are $E[x' - x] = x + x(1 - x)s + o(s)$ and $V[x' - x] = x(1 - x)/N_e$ [19, eq. 7],
 292 respectively. Therefore, we have the following result.

294 **Result 4** (Effective selection coefficient and population size). *The effective selection coefficient s and*
effective population size N_e can be written in terms of the success coefficient β (eq. (5)), the bias
 296 *weight α (eq. (10)), and the population size N as*

$$s = 1 - \beta(A), \quad N_e = \alpha N + (1 - \alpha). \quad (18)$$

298 Note that when $N \gg 1$, $N_e \approx \alpha N$, resulting in a very convenient expression.

300 Using our effective selection coefficient, $1 - \beta$, and effective population size, N_e , with the population-
 genetics fixation probability approximation given by [19, eq. 8], we obtain:

302 **Result 5** (Fixation probability). *The fixation probability is approximately*

$$\pi(x) = \frac{1 - e^{-2(1-\beta)N_e x}}{1 - e^{-2(1-\beta)N_e}}, \quad (19)$$

304 *where x is the initial frequency of the favored phenotype \hat{A} .*

Similarly, we can use $1 - \beta$ and N_e in the population-genetics fixation time approximation given by
 306 [45, eq. 17].

308 **Result 6** (Fixation time). *The expected fixation time (conditioned on fixation) from an initial frequency*
 x is approximately

$$T(x) = J_1(x) + \frac{1 - \pi(x)}{\pi(x)} \cdot J_2(x), \quad (20)$$

where $N_e = \alpha N + (1 - \alpha)$, $S = N_e(1 - \beta)$, and

$$\begin{aligned} J_1(x) &= \frac{2}{(1 - \beta)(1 - e^{-2S})} \int_x^1 \frac{(e^{2S\xi} - 1)(e^{-2S\xi} - e^{-2S})}{\xi(1 - \xi)} d\xi, \\ J_2(x) &= \frac{2}{(1 - \beta)(1 - e^{-2S})} \int_0^x \frac{(e^{2S\xi} - 1)(1 - e^{-2S\xi})}{\xi(1 - \xi)} d\xi. \end{aligned} \quad (21)$$

Note that these integrals cannot be solved in closed form, and are estimated numerically.

Numerical validation. We compare our approximations (eqs. (19) and (20)) with results of simulations of our dichotomous model using various α and β values, as well as simulations of the Wright-Fisher model, using the effective selection coefficient, $1 - \beta$, and effective population size, $N_e = \alpha N + (1 - \alpha)$. We find see that the two models have similar dynamics, and both are well approximated by our approximations (Figure 1).

Changing environment . After finding a good approximation in a constant environment, where the favorable trait is always \hat{A} , we proceeded to find an approximation for when the environment changes. Following [21], we denote k as the number of generations in which the invading phenotype is favored by success bias, and l as the number of generations in which the resident phenotype is favored by success bias. We then proceed to find expressions for the expectation and variance of the change in frequency between $n = k + l$ generations. The proof is in Appendix C.

Result 7 (Drift and diffusion terms in a changing environment). *Let x be the initial frequency of the invading phenotype and X_t the number of individuals with that phenotype after n generation. Then,*

$$E[X_n/N - x] \simeq x(1 - x)S_n/N_e, \quad \text{and} \quad V(X_n/N - x) \simeq nx(1 - x)/N_e, \quad (22)$$

where $S_n = \sum_{t=1}^n N(1 - \beta_t)$.

Note that here, we have the average selection coefficient during a cycle of n generations as the selection coefficient in eq. (19). Using the drift and diffusion terms and following [21], we can approximate the fixation probability in a changing environment using

$$\tilde{\pi}(x) = \frac{1 - e^{-2\frac{S_n}{n}N_ex}}{1 - e^{-2\frac{S_n}{n}N_e}}. \quad (23)$$

Numerical validation. Comparing our approximation (eq. (23)) to simulations, we find that the approximation fits simulation results well for variable bias weights, α , which corresponds to the effective population size (Figure 2A).

However, the approximation is more sensitive to the value of the success bias coefficient β (Figure 2B). We suspect that when β is too small, there will not be many cycles in the simulations, because either the population reaches a high frequency of the fitter phenotype after just a few cycles, or the fitter

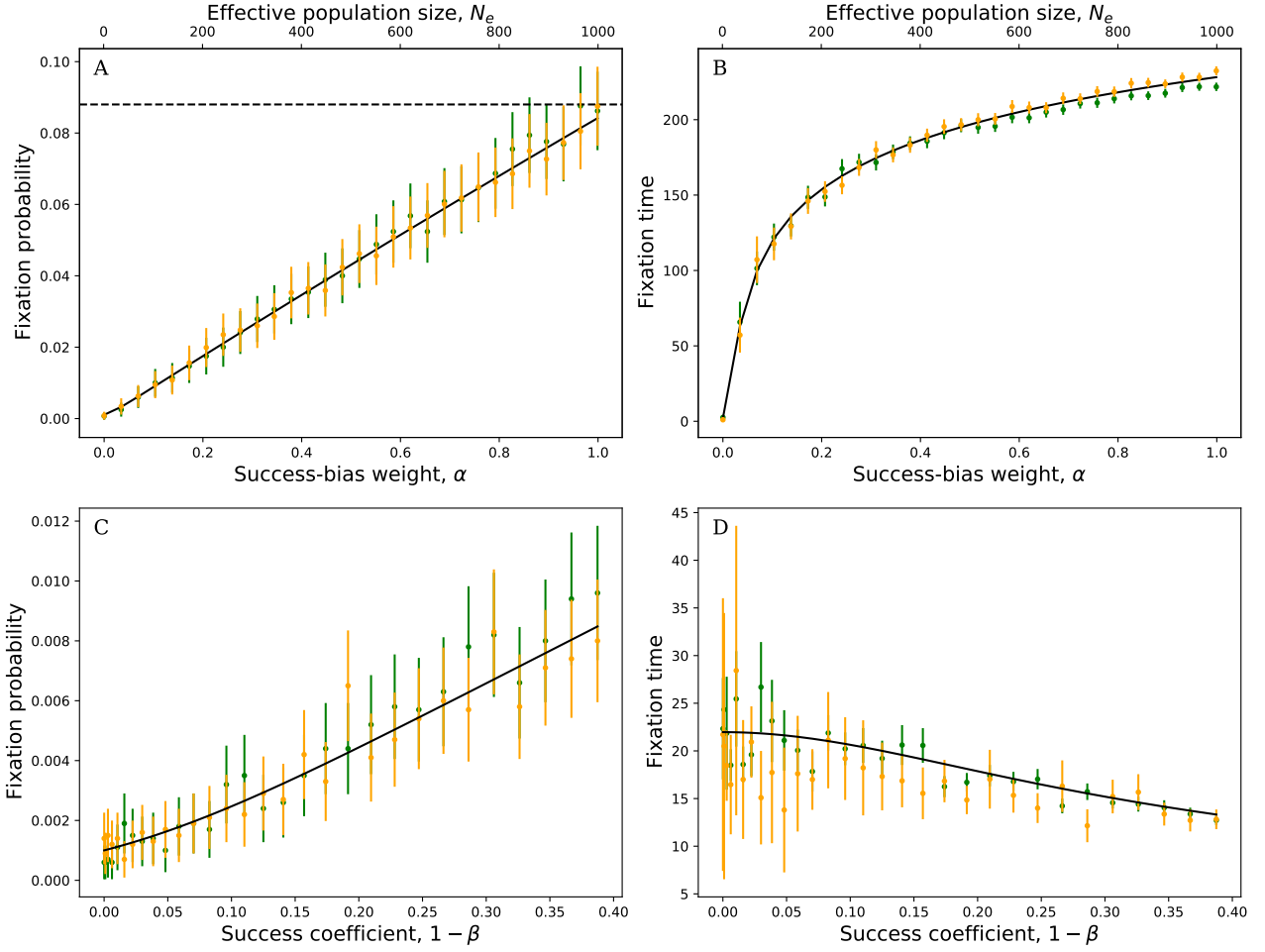


Figure 1: Fixation probability and time in a constant environment. Fixation probability and time (in generations) as a function of the success-bias weight α (bottom x-axis), or effective population size N_e (top x-axis) in the top row, and as a function of the success coefficient, $1 - \beta$, on the bottom row. The approximation (black; eq. (19)) agrees with both DM simulations (green) and Wright-Fisher simulation (orange). Fixation probability (A) is bounded by $2(1 - \beta)$ (blue). Markers are averages of 10,000 simulations, error bars show 95% confidence intervals for panels A and B and 75% for panels C and D. Here, Population size, $N = 1,000$; phenotype values, $\hat{A} = 1$, $A = 0.7$ (panels A and B), $A = a \cdot \hat{A}$ with $0.01 \leq a \leq 0.99$ (panels C and D); success coefficient, $1 - \beta = s = 0.044$ (panels A and B); success-bias weight, $\alpha = 0.01$ (panels C and D).

phenotype goes extinct very quickly. For such β values (below 0.65), the fixation probability exceeds even the constant environment approximation (which is the upper limit). We note that the diffusion-equation approximation assumes weak selection, or in our case, weak success bias.

We found that for a large k/l ratio (with a constant cycle length, $n = k + l = 100$), the changing environment approximation (eq. (23)) converges to the constant environment approximation (eq. (19)), see Figure 2C and Figure 2D.

The approximation follows the trend of the simulation results for all α values. On increasing the success coefficient α to more than 0.15, the simulation results were located above the changing environment approximation, and below the constant environment approximation. We believe the reason is the structure of the cycle. Our proof and approximation in the changing environment are for a large number of cycles, and when the success coefficient α is too high, there might be very few cycles.

Either the ideal trait is copied by enough copiers so that the influence is sufficient to negate the success
 bias when the cycle changes (and the trait favored by the bias becomes the disfavored), or the opposite
 happens, and the ideal trait goes extinct before there are enough copiers that copied it. We then tried to
 change the ratio between the number of cycles where \hat{A} is favored and disfavored. We showed that the
 approximation fits well regardless of the ratio, but when the ratio of favored generations to disfavored
 ones is very high, it is very similar to a constant environment model.

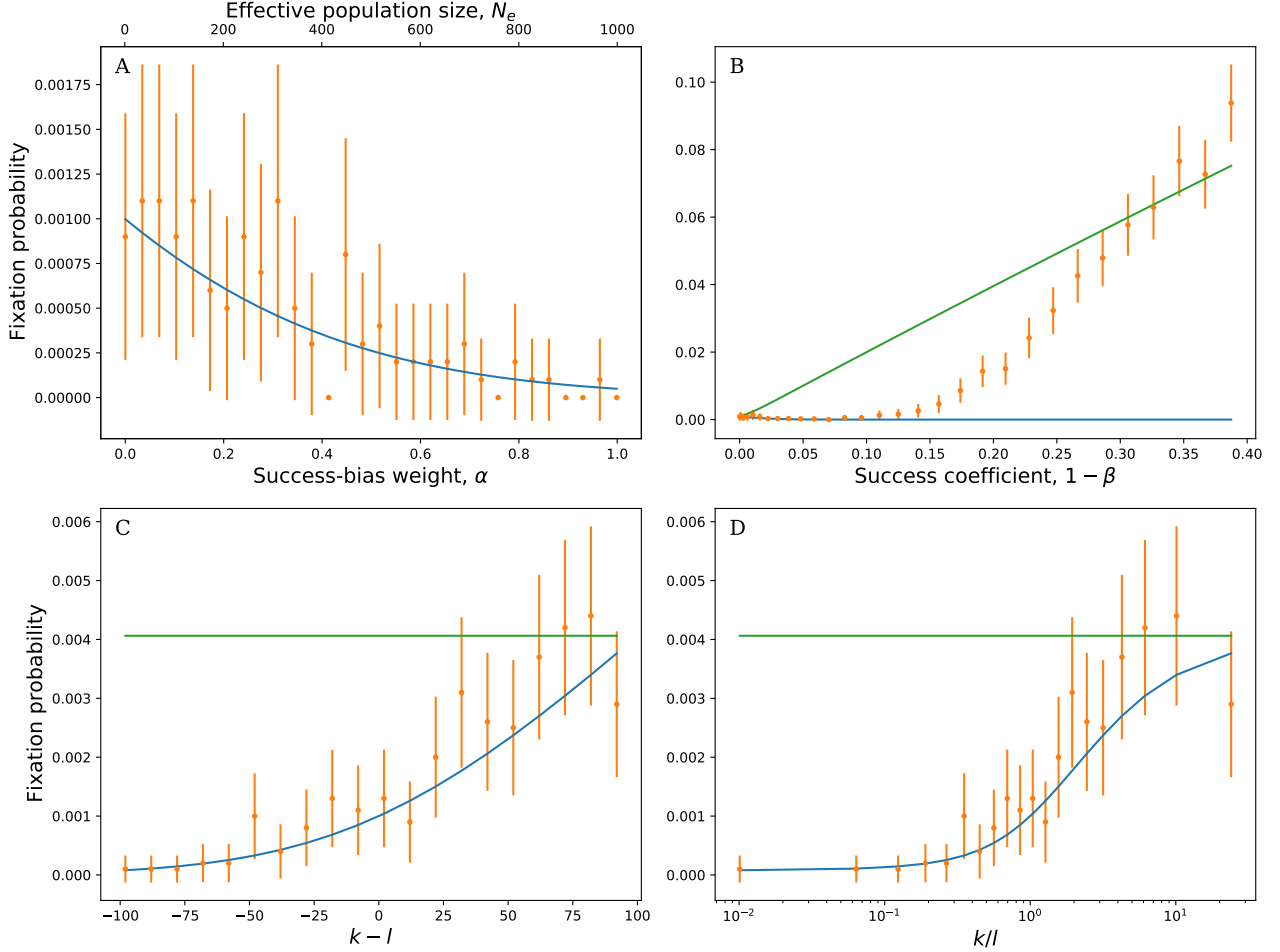


Figure 2: Fixation probability in a changing environment. (A) Fixation probability decreases with the success-bias weight (bottom x-axis) and effective population size (top x-axis). The approximation (blue; eq. (23)) agrees with simulation results (orange). (B) Fixation probability increases with the 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". (C,D) The approximation (blue) is robust to changes in environmental cycle length, as it agrees with simulations (orange) for different sizes of the changing environment cycle, where k and l are the number of generations each trait value is under success bias. When $k > l$, the approximation and the simulations are both very close to the constant environment approximation (green), because the more generations the rare phenotype is favored, the more similar it is to the constant environment model, where it is always favored by the success bias. Markers show average of 10,000 simulations, error bars show 75% (panels A, C, and D) and 95% (panel B) confidence intervals. Here, population size, $N = 1,000$; phenotype values, $\hat{A} = 1$ with $A = 0.9$ (panels A and B) and $A = 0.8$ (panels C and D); In panel A, the success coefficient is $1 - \beta = s = 0.005$; In panels B, C, and D, the success-bias weight is $\alpha = 0.1$.

Adaptive success-bias weight

358 We ran simulations of the role-model choice process during a single generation in which every
copier evaluates its own optimal success-bias weight, α^* , which minimizes the expected squared error
360 between the estimated and the ideal trait values,

$$\alpha^* = \operatorname{argmin} \sum_{j=1}^N \frac{\alpha A_j + (1 - \alpha) K_j}{\sum_{l=1}^N \alpha A_l + (1 - \alpha) K_l} (\hat{A} - A_j)^2, \quad (24)$$

362 where A_j is the trait of role-model j and K_j the number of copiers that already chose role-model
 j .

364 We find that when copiers choose their success-bias weight, it decreases with the number of copiers
that have already chosen a role-model (Figure 3). Moreover, their estimation error is much lower
366 compared to a constant success-bias weight, which gives roughly the same high estimation error to all
copiers (compare Figure 3B and C): in this example, the adaptive weight estimation error converges
368 to 0.046, whereas a constant weight gives values > 0.74 .

Discussion

370 Some cultural traits or cultural role-models may be copied more often than others due to transmission
biases. One such bias is success bias, in which copiers are more likely to copy a successful role-model.
372 Although many models assume that success can be accurately estimated, it has been suggested that
because it is hard to estimate success, a more common bias is *prestige bias*—a bias towards role-models
374 perceived to be successful. This perceived success can be determined by performance with respect to
another trait (indirect) [5, 24], or by the influence an individual has on others [26, 31].

376 We developed a cultural-evolution model with prestige bias that includes both indirect success and
influence biases, where the latter is a bias towards role-models with many copiers and hence is the
378 same as conformity bias. We model these biases using a stochastic role-model choice process:
each copier, in turn, randomly chooses a role-model, and this choice is affected both by the estimated
380 success of each potential role-model and the number of copiers that already chose each role-model
(eq. 10).

382 Hence, our model has two “nested” stochastic processes: the role-model choice process within each
generation, and the cultural-evolutionary process between generations. To simplify the mathematical
384 and computational analysis, we developed analytic approximations for the role-model choice process
using the *generalized binomial distribution* (GBD, Result 1) and the *Dirichlet-Multinomial dis-*
386 *tribution* (DM, Corollary 3). The latter is especially useful, as it approximates the entire role-model
choice process and only requires us to assume that the relative effect of success and influence is a
388 characteristic of the role-model and not the copier.

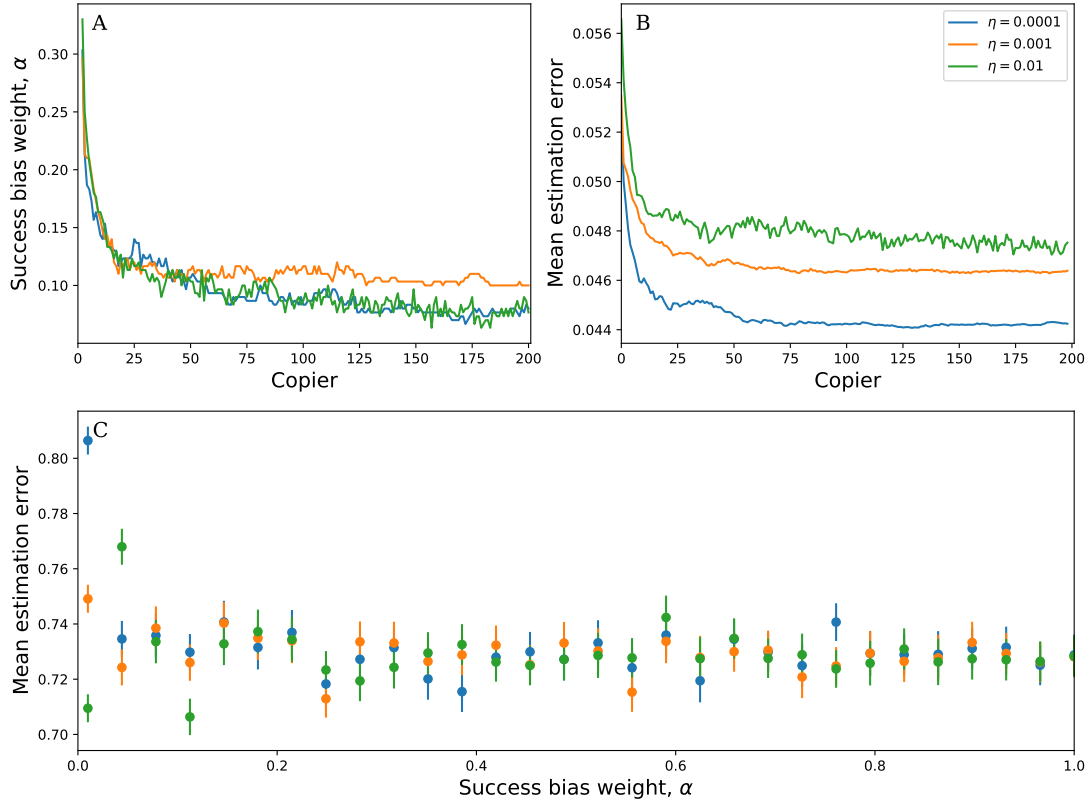


Figure 3: Advantage of an adaptive success-bias weight. Both success-bias weight α (A) and estimation error (B) decrease during the role-model choosing process, demonstrating that influence becomes more favored as more copiers have made their choice. However, when α is homogeneous (C), the mean estimation error doesn't decrease, regardless of α or η . The mean estimation error in the homogeneous α model is larger by a factor of 10 than the adaptive α model. Here, population size $N = 200$; estimation error is normally distributed $e \sim N(0, \eta^2)$ with standard deviation $\eta = 0.0001$ (blue), 0.001 (orange), 0.01 (green), plots are average of 300 simulations.

Analyzing the model with the DM distribution, we found approximations for the fixation probability and fixation time of a cultural trait under biased transmission in a constant environment. Our approximations are similar to Kimura's evolutionary-genetic approximations, in that (i) the difference between the resident and invading cultural trait values, $1 - \beta(A)$, is equivalent to the selection coefficient in favor of a beneficial allele, s , and (ii) increasing the relative weight of influence versus success bias, α , decreases the effective population size, N_e (Figure 1).

We also analyzed a cyclic changing environment in which the identity of the success-biased trait switches after a fixed amount of generations (Figure 2). We find that, similarly to the constant environment approximation, a change in the success-bias weight α has no negative effects on the goodness-of-fit of the approximation to simulation results. We also showed that this approximation is more sensitive to changes in the success coefficient β than the constant environment approximation, and a lower value is required to have a good fit. The ratio between the number of generations in which

the rare phenotype is under positive transmission bias and the number of generations in which it is
402 under negative bias does not affect the goodness-of-fit of the approximation.

We also examined a scenario in which copiers can adapt their success-weight bias, α , to minimize their
404 copying error, i.e., copy trait values closer to the optimal value. We found that as the role-model choice
process proceeds (that is, more copiers make their choices), both the success-bias weight (chosen by
406 copiers) and the estimation error decrease. The latter is significantly lower than in a population using
a constant, fixed success-bias weight, regardless of the value of the constant weight (Figure 3). This
408 suggests that the later a copier makes its choice, the more it should rely on choices of previous copiers,
and the less it should rely on its own estimation. The rationale, then, is that the more information a
410 copier has, e.g., by using others as information sources, the more informative and effective his choice
can be.

412 Chudek et al. [31] report the first direct tests in children that suggest the existence of prestige bias,
defined as the tendency to learn from individuals to whom others have preferentially attended, learned,
414 or deferred. Their definition of prestige is similar to our influence bias. They showed that the odds
of 3-4 years-old children learning from an adult role-model to whom bystanders had previously
416 preferentially attended for 10 seconds were more than twice those of learning from a role model
whom bystanders ignored. They also note that prestige effects are domain sensitive: they found that
418 prestigious role-models were attended more when demonstrating artifact use, whereas role-models
presenting food preferences had less attendants, suggesting that the domain itself (artifact use vs.
420 food preference) can affect the attendance, and hence the prestige of the role-model. This led to the
suggestion that when the trait is costly to learn individually, prestige will have a stronger bias [31]. It
422 would be interesting to include costs in our model to try and observe these effects and dynamics in a
large population.

424 According to [24], natural selection has favored the emergence of psychological biases for learning
from those individuals most likely to possess adaptive information. They studied Fijian villages to
426 examine if and how such biases emerge in a small-scale society. They found that Fijian villagers are
more likely to learn from role-models perceived as more successful/knowledgeable, both within and
428 across domains. Their research thus suggests that copying from those perceived as successful, rather
than who are actually successful, is a common phenomenon. They show that the social networks
430 representing copier–role-model relationships are centralized, suggesting that it is consistent with
the prediction that people substantially share notions about who is a good cultural model, but that
432 individuals’ role-model selections are influenced by multiple factors.

Prestige bias also occurs in more modern domains such as western medicine. Norredam and Album
434 [28] examined literature from 1950 to 2005 on the effects of prestige on medicinal practices. They
found that active, specialized, biomedical, and high-technological types of medicine on organs in
436 the upper part of the bodies of young and middle-aged people were accorded high levels of prestige,
whereas medicine and practices with opposite characteristics had low levels of prestige. For example,
438 they found that surgery counts as the most prestigious specialty, while psychiatry is the least prestigious.
In addition, doctors tend to rank practices that require more time to master as more prestigious, while

other procedures that are considered easier to master are less prestigious. This means that there may be very important practices that are neglected due to prestige bias. They concluded that such differences in prestige may affect for actual priority setting in healthcare systems.

Prestige bias can help to cheaply estimate and acquire knowledge, which may facilitate survival and reproduction. However, it is not always the case, and there could be negative repercussions to this bias, such as invasion of maladaptive traits. Takahashi and Ihara [27] mention that social learning not only takes the form of random copying of other individuals, but also involves learners' choice of what to learn and from whom to learn. They suggest a best-of- k model where an individual samples k role-models and chooses the one he deems most "successful". They mention that a previous mathematical analysis has shown that it may sometimes result in maladaptive cultural evolution when the payoffs associated with cultural variants vary stochastically. In such a case, learners may be selectively disfavored and in the long run replaced by unbiased learners, who simply copy someone chosen at random. They developed new mathematical models that are simpler and mathematically tractable. They found that best-of- k learning, unlike unbiased learning, can facilitate the invasion of an on average inferior variant that sometimes gives a very high payoff (see Fogarty et al. [56] and references there). Our model, which includes influence bias, is consistent with this claim. When a maladaptive trait is "piggybacking" on a role-model with high influence, the former could spread in the population. In addition, best-of- k learning can be stable against invasion by unbiased learning if social learning is sometimes combined with individual learning [27]. Our model includes only social learning, and not individual learning, but it could be interesting to combine it with individual learning and see how it affects the dynamics.

Prestige bias can also accelerate reversal of harmful traditions such as child marriage and domestic violence. Efferson et al. [25] suggest a *spillover* mechanism, in which an intervention affects a large enough group in a target population, so that others not included in the intervention also change their behavior. They find that there are individuals who act as *agents*, who are often observed, and therefore they are ideal targets for interventions. This is similar to influential role-models in our model, where a prestigious individual will be copied more often, and will therefore spread their trait faster and wider in the population. They also suggest a way to use this phenomenon to change existing traditions in a population. It is very clear however, that just as it can be used to end harmful traditions, the same agents could start harmful traditions.

Dunbar [30] hypothesized that larger, more complex brains can store and manage more information and in turn, this information can support the costs of a larger brain. Following this, Muthukrishnan and Henrich [29] suggested that prestige can directly affect human physical evolution. They present a concept called *cultural brains*—brains that evolved primarily for the acquisition of adaptive knowledge. They then develop a model that predicts a strong relationship between brain size and group size, because group size also provides access to more adaptive knowledge. They also presented the *cumulative cultural brain* hypothesis, which proposes that human brains have evolved with an ability and tendency for selective, high-fidelity social learning. As part of this process, there are a variety of strategies and biases that have evolved to hone in on the most adaptive knowledge. These strategies

and biases include direct and indirect cues of the popularity of cultural traits (e.g. success and prestige
480 biases). They suggest that one of the reasons for the extreme increase in brain size in humans is the
ability to "cheaply" acquire adaptive knowledge via transmission biases such as prestige.

482 One path forward is an analysis of the dynamics of the adaptive success-bias weight model, in which
every copier chooses its α . It would be interesting to see the if the mean estimation error and the
484 adaptive weight, α^* , converge to specific values, and how they are affected by the model parameters. It
may also be possible to relax the assumptions required for our approximations, such as homogeneous
486 estimation error and success-bias weight. Lastly, it would be interesting to analyze the continuous
model and determine how much it differs from the dichotomous model.

488 Another way to expand our model is to account for the two types of prestige or leadership suggested
by Van Vugt and Smith [23] that are attributed to Confucius and Machiavelli. Confucius viewed
490 leaders as role-models who exercise influence through possessing superior knowledge, skills, and
(outstanding) personal qualities. This fits the success bias in our model. In contrast, Machiavelli
492 viewed leaders as rulers who exercise influence by imposing costs through (the threat of) punishment
and violence. Van Vugt and Smith suggest that these opposing views are both partially supported by
494 the available evidence but each one on its own offers an incomplete view of the complex and dynamic
concept of leadership. Several adjustments could be made so that our model reflects these leadership
496 styles, such as assuming there is a correlation between phenotype and leadership style. The resulting
cultural-evolutionary dynamics and their dependence on the costs and benefits are intriguing.

498 **Conclusions.** We studied a model of cultural evolution under two transmission biases: the commonly
studied success bias, together with influence bias, which has so far received less attention. We found
500 approximations for this complex dynamics. We then showed that success bias affects the evolutionary
dynamics much like natural selection does, whereas influence bias has a similar effect to random
502 genetic drift. We also find a clear advantage to individuals that can choose the relative weight of the
two biases.

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Appendices

Appendix A General binomial distribution approximation

Proving $E[K_{Nj}] = \alpha_j \cdot \beta(A_j + e) / \overline{\alpha \cdot \beta(A + e)}$, where the average in the denominator is over the role-models index, j .

Proof. The initial prestige of role-model j based on eq. (10) is

$$G_{1,j} = \frac{\alpha_j \cdot \beta(A_j + e)}{\sum_{m=1}^N \alpha_m \cdot \beta(A_m + e)}. \quad (\text{A1})$$

The denominator of eq. (A1) can also be formulated as:

$$\sum_{m=1}^N \alpha_m \beta(A_m + e) = N \cdot \overline{\alpha \cdot \beta(A + e)}, \quad (\text{A2})$$

where $\overline{\alpha \beta(A + e)}$ is the mean value of $\alpha_m \cdot \beta(A_m + e)$. Using eq. (A2) and **Corollary 1** we get,

$$E[K_{Nj}] = \alpha_j \cdot \beta(A_j + e) \left/ \overline{\alpha \cdot \beta(A + e)} \right., \quad (\text{A3})$$

Appendix B Drift and diffusion in a constant environment

Proving drift and diffusion terms in a constant environment. Let x and x' be the frequency of type \hat{A} in a population with N individuals in the current and next generation, and β be the success coefficient of phenotype A , $\beta = \beta(A) < \beta(\hat{A}) = 1$. Then,

$$E[x' - x] \approx x(1 - x)(1 - \beta), \quad V(x' - x) \approx x(1 - x) \left(\frac{1}{\alpha N + (1 - \alpha)} \right).$$

Proof. Let X be the number of individuals of type \hat{A} such that $x = X/N$. X' is the number of individuals with \hat{A} in the next generation. The expected number of individuals is (due to the DM approximation),

$$E[X'] = N \frac{\alpha_1}{\alpha_1 + \alpha_2}, \quad (\text{B1})$$

where $\alpha_1 = \alpha'X$ and $\alpha_2 = \alpha'(N - X)\beta$, from eq. (11). To use frequencies instead of counts, $E[x'] = E[X'/N] = \frac{1}{N}E[X']$. Putting it together,

$$\begin{aligned} E[x'] &= \frac{1}{N}N \frac{\alpha'xN}{\alpha'xN + \alpha'N(1-x)\beta} = \frac{x}{x + (1-x)\beta} \\ &= \frac{x}{x + (1-x) - (1-x) + (1-x)\beta} = x \frac{1}{1 - (1-x)(1-\beta)} \\ &= x(1 + (1-x)(1-\beta) + o(1-\beta)) = x + x(1-x)(1-\beta) + o(1-\beta), \end{aligned} \quad (\text{B2})$$

following Durrett [20, p. 253, ch 7.2] and because $1/(1-y) = 1 + y + y^2 + \dots$

We therefore have

$$E[x' - x] = E[x'] - E[x] = x(1-x)(1-\beta) + o(1-\beta), \quad (\text{B3})$$

which gives us the drift term of the diffusion equation.

Using the variance of the DM distribution,

$$V(X') = N \frac{\alpha_1}{\alpha_1 + \alpha_2} \left(1 - \frac{\alpha_1}{\alpha_1 + \alpha_2}\right) \left(\frac{N + \alpha_1 + \alpha_2}{1 + \alpha_1 + \alpha_2}\right). \quad (\text{B4})$$

Again, we want to use frequencies so we have $V(X'/N) = \frac{1}{N^2}V(X')$. Putting it together with our model notations,

$$V(x') = \frac{1}{N^2}N \frac{x}{x + (1-x)\beta} \left(1 - \frac{x}{x + (1-x)\beta}\right) \left(\frac{N + \alpha'xN + \alpha'N(1-x)\beta}{1 + \alpha'xN + \alpha'N(1-x)\beta}\right). \quad (\text{B5})$$

Following Durrett [20, ch 7.2], we assume $\beta \approx 1$, such that

$$\frac{x}{x + (1-x)\beta} \approx x \quad (\text{B6})$$

and for the entire variance expression we get

$$V(x') \approx \frac{1}{N}x(1-x) \left(\frac{N + \alpha'xN + \alpha'N - \alpha'xN}{1 + \alpha'xN + \alpha'N - \alpha'xN}\right) = x(1-x) \left(\frac{1 + \alpha'}{1 + \alpha'N}\right). \quad (\text{B7})$$

Now because x is a constant, $V(x) = 0$, and therefore

$$V(x' - x) = V(x') - V(x) \approx x(1-x) \left(\frac{1 + \alpha'}{1 + \alpha'N}\right). \quad (\text{B8})$$

α' is the odds ratio of the bias weight,

$$\alpha' = \frac{\alpha}{1 - \alpha}. \quad (\text{B9})$$

Combining eq. (B8) and eq. (B9) we get:

$$V(x' - x) \approx x(1 - x) \left(\frac{1 + \frac{\alpha}{1-\alpha}}{1 + \frac{\alpha}{1-\alpha}N} \right) = x(1 - x) \left(\frac{1}{\alpha N + (1 - \alpha)} \right). \quad (\text{B10})$$

This gives the diffusion term of the diffusion equation.

Appendix C Drift and diffusion in a changing environment

Proving drift and diffusion terms in a changing environment. Let x be the initial frequency of the invading phenotype and X_t is the number of individuals with the phenotype at time t . Then,

$$E[X_t/N - x] \simeq x(1 - x)S_t/N_e, \quad \text{and} \quad V(X_t/N - x) \simeq tx(1 - x)/N_e,$$

where $S_t = \sum_{i=1}^t N(1 - \beta_i)$.

Proof. Let $s_t = N(1 - \beta_t)$, and $S_n = \sum_{i=1}^n s_i$, where β_t is $\beta(A)$ at generation t . We prove by induction both terms in eq. (22). From eq. (B3) we know that

$$E \left[\frac{X_{t+1}}{N} - \frac{X_t}{N} \middle| X_t \right] = \frac{X_t}{N} \left(1 - \frac{X_t}{N} \right) (1 - \beta_{t+1}) = \frac{1}{N} \frac{X_t}{N} \left(1 - \frac{X_t}{N} \right) s_{t+1}. \quad (\text{C1})$$

Also note that using the definition of $V(y) = E[y^2] - (E[y])^2$

$$\begin{aligned} E \left[\frac{X_t}{N} \left(1 - \frac{X_t}{N} \right) \right] &= E \left[\frac{X_t}{N} - \left(\frac{X_t}{N} \right)^2 \right] = E \left[\frac{X_t}{N} \right] - E \left[\left(\frac{X_t}{N} \right)^2 \right] \\ &= E \left[\frac{X_t}{N} \right] - V \left(\frac{X_t}{N} \right) - \left(E \left[\frac{X_t}{N} \right] \right)^2. \end{aligned} \quad (\text{C2})$$

We can now use the induction assumption of $V(\frac{X_t}{N})$ to get

$$E \left[\frac{X_t}{N} \left(1 - \frac{X_t}{N} \right) \right] \simeq E \left[\frac{X_t}{N} \right] \left(1 - E \left[\frac{X_t}{N} \right] \right) - \frac{1}{N_e} tx(1 - x). \quad (\text{C3})$$

From eq. (C1) we know that

$$\begin{aligned} E \left[\frac{X_{t+1}}{N} - \frac{X_t}{N} \right] &= \frac{1}{N} s_{t+1} E \left[\frac{X_t}{N} \left(1 - \frac{X_t}{N} \right) \right] \simeq \frac{1}{N} s_{t+1} \left(E \left[\frac{X_t}{N} \right] \left(1 - E \left[\frac{X_t}{N} \right] \right) - \frac{1}{N_e} tx(1 - x) \right) \\ &\simeq \frac{1}{N} s_{t+1} \cdot E \left[\frac{X_t}{N} \right] \left(1 - E \left[\frac{X_t}{N} \right] \right) - \frac{1}{N_e N} s_{t+1} tx(1 - x). \end{aligned} \quad (\text{C4})$$

Now we omit $O(\frac{1}{Ne \cdot N})$ and get

$$E \left[\frac{X_{t+1}}{N} - \frac{X_t}{N} \right] \simeq \frac{1}{N} s_{t+1} \cdot E \left[\frac{X_t}{N} \right] \left(1 - E \left[\frac{X_t}{N} \right] \right) . \quad (C5)$$

We now look at the induction assumption to see that

$$E \left[\frac{X_t}{N} - x \right] = E \left[\frac{X_t}{N} \right] - E[x] = E \left[\frac{X_t}{N} \right] - x , \quad (C6)$$

so using the assumption we get

$$\begin{aligned} E \left[\frac{X_t}{N} \right] &\simeq \frac{1}{N} S_t x (1 - x) + x , \\ 1 - E \left[\frac{X_t}{N} \right] &\simeq 1 - \frac{1}{N} S_t x (1 - x) + x . \end{aligned} \quad (C7)$$

We use both expressions in eq. (C5) and get

$$\begin{aligned} E \left[\frac{X_{t+1}}{N} - \frac{X_t}{N} \right] &\simeq \frac{1}{N} s_{t+1} \left(\frac{1}{N} S_t x (1 - x) + x \right) \left(1 - \frac{1}{N} S_t x (1 - x) + x \right) \\ &\simeq \frac{1}{N} s_{t+1} \cdot x (1 - x) , \end{aligned} \quad (C8)$$

after again omitting $O(\frac{1}{N^2})$ terms. To conclude the proof, we note that

$$E \left[\frac{X_{t+1}}{N} - x \right] = E \left[\frac{X_{t+1}}{N} - \frac{X_t}{N} \right] + E \left[\frac{X_t}{N} - x \right] , \quad (C9)$$

so again using the induction assumption, together with eq. (C8) we get

$$\begin{aligned} E \left[\frac{X_{t+1}}{N} - x \right] &\simeq \frac{1}{N} s_{t+1} \cdot x (1 - x) + \frac{1}{N} S_t \cdot x (1 - x) \\ &\simeq \frac{1}{N} x (1 - x) (S_t + s_{t+1}) \simeq \frac{1}{N} S_{t+1} x (1 - x) , \end{aligned} \quad (C10)$$

which proves the drift term.

For the diffusion term, we use a property of variance,

$$V \left(\frac{X_{t+1}}{N} \right) = E \left[V \left(\frac{X_{t+1}}{N} \middle| X_t \right) \right] + V \left(E \left[\frac{X_{t+1}}{N} \middle| X_t \right] \right) . \quad (C11)$$

Using eq. (C1) we see that

$$\begin{aligned} E \left[\frac{X_{t+1}}{N} \middle| X_t \right] - E \left[\frac{X_t}{N} \middle| X_t \right] &= \frac{1}{N} s_{t+1} \frac{X_t}{N} \left(1 - \frac{X_t}{N} \right) \\ E \left[\frac{X_{t+1}}{N} \middle| X_t \right] &= \frac{X_t}{N} + \frac{1}{N} s_{t+1} \frac{X_t}{N} \left(1 - \frac{X_t}{N} \right) . \end{aligned} \quad (C12)$$

Using eq. (B10) we get

$$V\left(\frac{X_{t+1}}{N}\middle|X_t\right) = \frac{1}{N_e} \frac{X_t}{N} \left(1 - \frac{X_t}{N}\right), \quad (\text{C13})$$

and using the equation $y'(1 - y') \simeq y(1 - y)$ on the first part of eq. (C11) we get

$$E\left[V\left(\frac{X_{t+1}}{N}\middle|X_t\right)\right] = \frac{1}{N_e} E\left[\frac{X_t}{N} \left(1 - \frac{X_t}{N}\right)\right] \simeq \frac{1}{N_e} x(1 - x). \quad (\text{C14})$$

Moving on to simplify the second part of eq. (C11) using eq. (C12),

$$V\left(E\left[\frac{X_{t+1}}{N}\middle|X_t\right]\right) = V\left(\frac{X_t}{N} + \frac{1}{N} s_{t+1} \frac{X_t}{N} \left(1 - \frac{X_t}{N}\right)\right) \quad (\text{C15})$$

Now, because $\frac{X_t}{N}$ is a frequency, i.e $0 \leq X_t/N \leq 1$, we know that $V\left(\frac{X_t}{N} \left(1 - \frac{X_t}{N}\right)\right) \leq \frac{1}{4}$. We therefore find that

$$V\left(\frac{1}{N} s_{t+1} \frac{X_t}{N} \left(1 - \frac{X_t}{N}\right)\right) \leq \frac{1}{4N^2} s_{t+1}^2, \quad (\text{C16})$$

and so it can be ignored. Combining our equations we get

$$V\left(E\left[\frac{X_{t+1}}{N}\middle|X_t\right]\right) = V\left(\frac{X_t}{N}\right) + O\left(\frac{1}{N^2}\right) \simeq V\left(\frac{X_t}{N}\right). \quad (\text{C17})$$

Using the induction assumption and eq. (C14),

$$V\left(\frac{X_{t+1}}{N}\right) \simeq \frac{1}{N_e} x(1 - x) + \frac{1}{N_e} t x(1 - x) \simeq \frac{1}{N_e} x(1 - x)(t + 1) \quad (\text{C18})$$

which proves the diffusion term.

Supplementary Figures

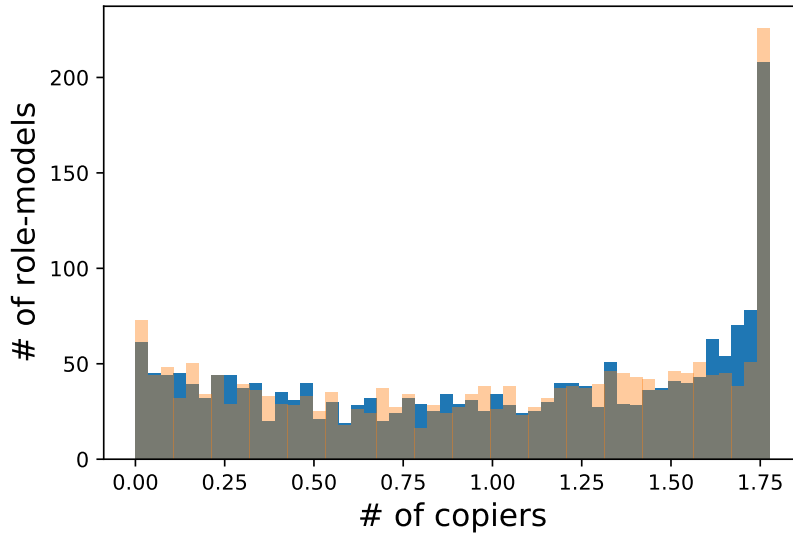


Figure S1: Numerical validation of the GB approximation. The approximation (orange) fits simulation results (blue) well when using 1,000 simulations for both models. Here, population size, $N = 2,000$; bias weight, $\alpha = 0.1$; ideal phenotype value, $\hat{A} = 1$; role-model traits $\mathbf{A} \sim N(0, 1)$; success bias value, $\beta(A) = 0.956$.

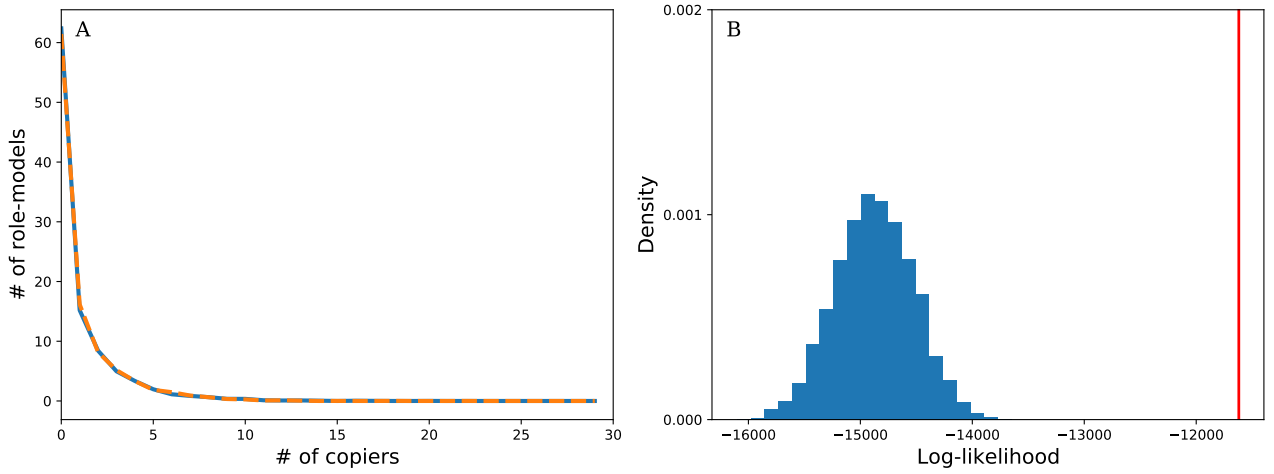


Figure S2: Numerical validation of the DM approximation. We performed computational simulations of the role-model choice process and compared them to the DM distribution. **(A)** The difference between the DM distribution (orange) and the empirical distribution of the simulations (blue) is very small. **(B)** The log-likelihood of the DM distribution 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.

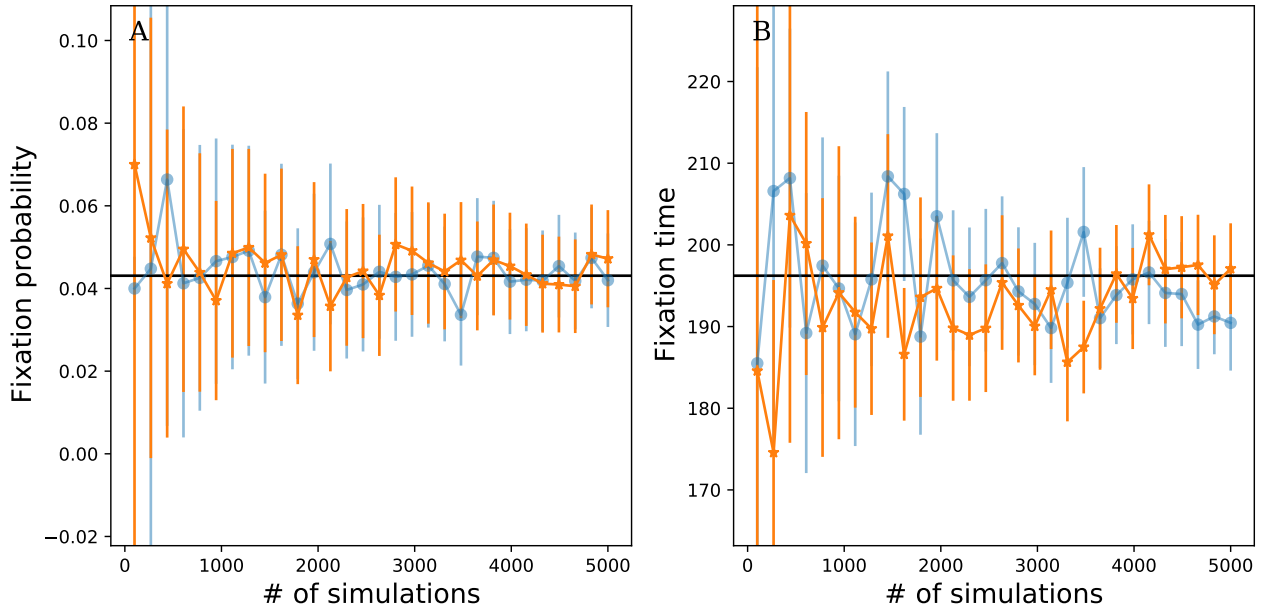


Figure S3: DM Approximation precision as function of number of simulations. Our DM approximation (orange) agrees with stochastic simulation results (blue) when using 1,000 or more simulations. Both fluctuate around the analytic fixation probability approximation (black; eq. (19)). Markers are averages 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, $\beta(A) = 0.956$.

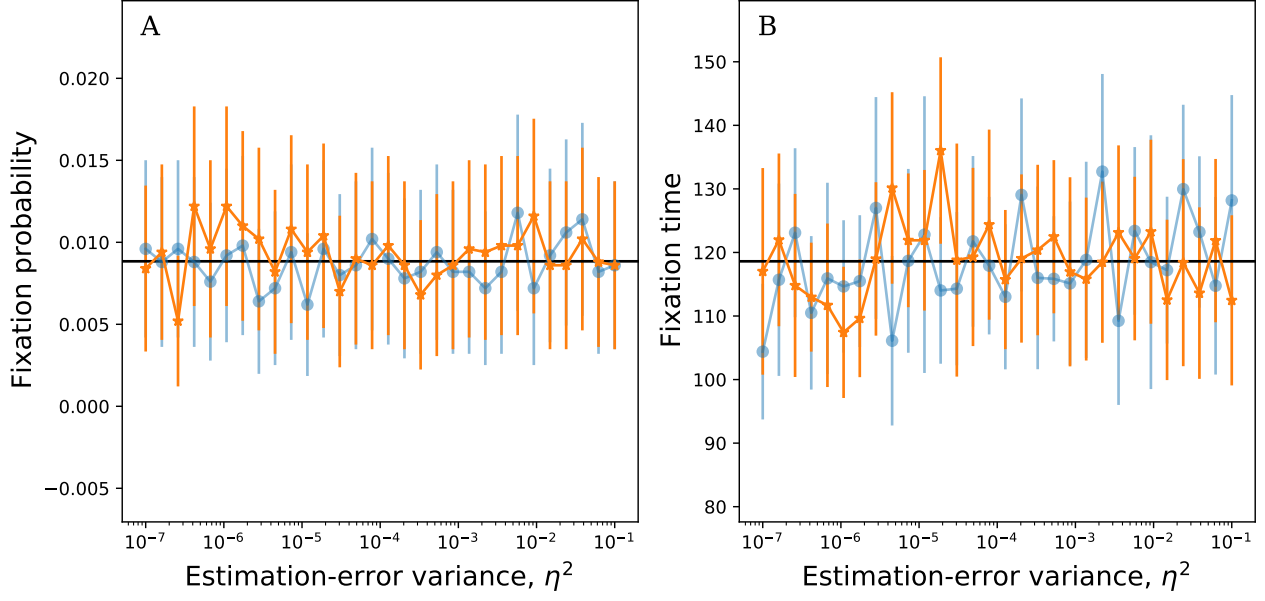


Figure S4: Robustness of DM approximations to success estimation error. Both the DM approximation (orange) and our approximation (black) agree with the stochastic simulations (blue), even with a high estimation error. Markers are averages across simulations, error bars are 95% confidence intervals. 5,000 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 in on the x-axis.

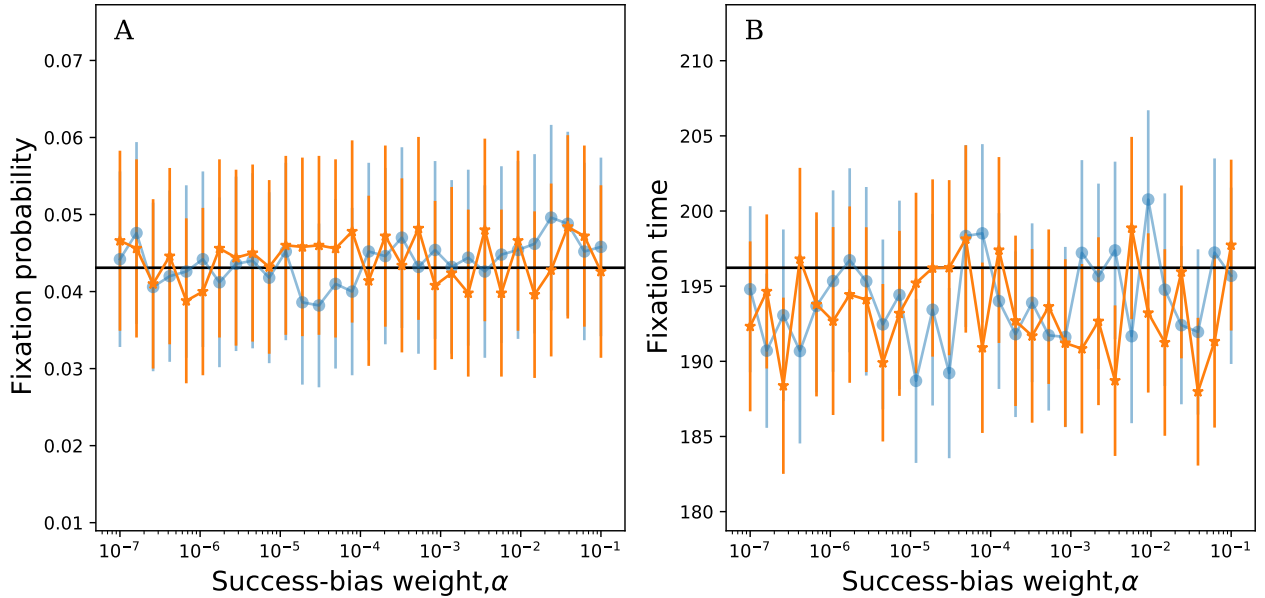


Figure S5: Robustness of DM approximations to variation in the bias weight α . Both the DM approximation (orange) and Kimura's equation (black line) fit the stochastic simulations (blue) well even with a high variation in success bias weight. Markers for average across 5,000 simulations, error bars are 95% confidence intervals. Here, population size, $N = 1000$; success bias weight normally distributed, $\alpha \sim N(0.5, x^2)$; phenotype values $\hat{A} = 1, A = 0.7$; success bias value, $\beta(A) = 0.956$.