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Efi Arazi School of Computer Science

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Cultural Evolutionary Dynamics with Success and Influence Bias

by

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Saar Egozi

Supervised by Dr. Yoav Ram

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School of Zoology, Faculty of Life Sciences, Tel Aviv University, Tel Aviv 6997801, Israel

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1 Abstract

18 Copying role-models can be an efficient method for acquiring knowledge. A common bias when
choosing a role-model to copy is success bias: copying whoever appears more successful. This bias
20 depends on the performance of the role-model alone, with no other factors. We propose an additional
bias that may be prevalent in cultural transmission: influence bias, in which role-model choice is
22 affected by the number of individuals that have already copied each potential role-model. We combine
success and influence bias together to a “prestige bias” and analyze its effects on cultural-evolutionary
24 dynamics using mathematical analysis and stochastic simulations. We find analytic approximations
to our stochastic model, facilitating further mathematical analysis and reducing the computational
26 complexity of simulations. We validate these approximations using simulations, and demonstrate
their robustness to model assumptions. We also find approximations to the fixation probability and the
28 fixation time of an invading favored (by bias) cultural trait, in both constant and changing environments,
which resemble Kimura’s approximations for population-genetic models. These approximations show
30 that success bias effectively plays the part of natural selection, whereas influence bias effectively
reduces the population size. Influence bias also accelerates the evolutionary dynamics, as can be
32 expected in a *rich-getting-richer* process. Our model may provide a good description of cultural
transmission, especially in human societies where social media is popular. Further work is needed
34 to test if this model could predict various phenomena in cultural evolution when extended with the
effects of selection and innovation.

This work is in preparation for submission to a high-impact journal.

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54 2 Introduction

Cultural transmission. In cultural transmission, individuals transmit cultural traits (i.e., behavior, beliefs, norms) to one another, typically via learning and demonstrating (Cavalli-Sforza and Feldman, 1981). Examples for cultural traits in humans are behavioral patterns, such as personalities and habits, transmitted via both verbally and by observations (O'Brien et al., 2010). Although cultural transmission is most common in humans, it is also observed in other animals such as chimpanzees (Horner et al., 2010; Kendal et al., 2015), dolphins and whales (Whitehead, 2017). In elephants, McComb et al. (2001) showed that once a matriarch is removed from the group, the group's survival instincts are inferior and that "the possession of enhanced discriminatory abilities by the oldest individual [matriarch] in a group can influence the social knowledge of the group as a whole." By playing audio recordings of African elephants, they showed that groups with a matriarch recognize and react better to hostile or friendly calls than groups without a matriarch. Battesti et al. (2012) showed that choice of oviposition site in fruit flies is culturally transmitted: inexperienced flies that spent some time with experienced flies chose the same type of oviposition site even without directly observing this behavior. How the information is transmitted is still an open question, but it has been suggested that flies may use olfactory cues like other animals, such as rodents and bees.

Direction of transmission. Similar to genetic transmission, culturally transmitted traits can be transmitted from parents to offspring, and their effects of can be physiological rather than behavioral. For example, parents can "teach" their children to be strong or tall, within some biological limits, by instructing them to maintain a specific diet and engage in physical activity. Contrary to genetic transmission, cultural transmission can be non-vertical, that is, traits may be transmitted via social learning from non-parental individuals, and even unrelated individuals such as teachers, leaders, media, or any stranger that interacts with the learning individual. Thus, cultural transmission may combine vertical transmission, where parents transmit to their offspring; oblique transmission, where adults transmit traits to unrelated offspring; and horizontal transmission, where peers from the same age cohort transmit to one another. Vertical transmission is also possible in the opposite direction: parents may copy traits from their offspring (Cavalli-Sforza and Feldman, 1981; Creanza et al., 2017).

Transmission biases. In social learning, transmission biases cause a trait to have a disproportionate probability to be transmitted compared to its frequency in the population. Although more common in cultural transmission, transmission biases do occur in genetic transmission. For example, *wtf* genes in yeast bias their transmission to the gamete by secreting a long life-expectancy poison together with a short life-expectancy antidote, so that a gamete without the gene will perish because the poison will outlive the antidote (Eickbush et al., 2019). Importantly, even when a trait is disfavored by natural selection, it may still spread in a population due to transmission biases that are strong enough to overcome selection (Boyd and Richerson, 1988, Ch. 8 pg. 279). Cohen et al. (2021) show that cooperative behavior can evolve in an individual due to horizontal transmission bias even when there is no benefit to it, or when it benefits its competitors.

Success bias. Rendell et al. (2010) have conducted a tournament between learning strategies. Each strategy defines when individuals observe and copy from others, and when they engage in individual learning, in which an individual learns a cultural trait on his own. The best strategies had a high frequency of social learning relative to individual learning, even when the transmission error was almost 50%. From these results we understand that all the winning strategies were mostly based on success biased social learning, meaning it contributed more to the general success of the population than individual learning. However, all winning strategies included individual learning to some degree, implying that success-biased learning alone isn't the best way to advance, even when success is measured accurately.

Evaluating success. Boyd and Richerson (1988, Ch. 5) suggest that the evaluation of success can be divided into three groups: *direct bias*, *indirect bias* and *frequency-dependent bias*. A direct bias occurs when a variation of a trait is more attractive than others, and is evaluated by *directly* testing the variation of the trait. For example, an individual observing a Ping-Pong match can attempt both of the observed paddle grips to determine which grip is better. An indirect bias occurs when an individual uses the value of one trait to determine the attractiveness of another, so it *indirectly* evaluates the attractiveness of the role-model. For example, an observer may copy the paddle grip of the Ping-Pong player who scored more points in the match, thus indirectly evaluating the grip by the points scored. A frequency-dependent bias occurs when an individual has a probability to copy a variant of the trait that higher or lower than trait's frequency among demonstrators. For example, when an individual is 80% likely to copy the common paddle grip even when only 60% of the population is using it, it is said to be frequency-biased, or in this case, conformist. Frequency bias could be negative, i.e., non-conformist bias. Conformity and non-conformity are well-known biases in cultural transmission (Molleman et al., 2013), and its effect on cultural evolution have been studied with both models (Denton et al., 2020a,b) and experiments (Aljadeff et al., 2020).

Prestige. Prestige means having a good reputation or high esteem, therefore does not directly signify success (although it may imply it), making it an indirect bias. Both Boyd and Richerson (1988, Ch. 8) and Fogarty et al. (2017) suggest that prestige biases are probably more common in humans than success biases. Boyd and Richerson (1988, Ch. 8) add that maladaptive traits may spread widely in a population if indirect biases are strong enough. They suggest that such biases could lead to a runaway process caused by a cultural equivalent of sexual selection (Andersson, 1994). On the other hand, Henrich and Broesch (2011) suggest that prestige biases, over generations, can lead to cultural adaptations, and that although prestige can lead to maladaptive traits spreading in the population, it can also accelerate the spread of adaptive traits. Prestige is often mentioned in the cultural-evolution literature, but seldom modeled.

Influence bias. Today, social media provides an easy way to estimate the social and cultural influence individuals have over others, and therefore may have an effect on decision making. Online social networks such as *Facebook* or *Instagram* are known to affect the influence of individuals (Anagnostopoulos et al., 2008; Peng et al., 2018; Diga and Kelleher, 2009), and specific marketing practices were invented to capitalize on this effect (Lee et al., 2012). Here, we model such influence as an

130 indirect bias in cultural transmission, in which the choice of a role-model depends on the choices
 made by other individuals that have already chosen a role-model. In addition to using influence bias as
 132 an easy way to approximate role-models worth, it can also be a used to approximate it better than the
 copier’s own estimation. This bias can save the copier costs: time, effort etc, and it can also improve
 134 its choice of role-model.

This bias depends on the state of a role-model rather than on its trait, in contrast to frequency biases
 136 such as conformity (Denton et al., 2020a), which depend on the frequency of a trait in the population
 or in a sample of role-models. We define a model of cultural transmission with prestige bias that
 138 combines both success and influence biases, provide analytic approximations for this model, and
 analyze its dynamics.

140 3 Models and methods

We begin with a continuous trait model with indirect bias suggested by Boyd and Richerson (1988),
 142 develop an extension with influence bias, and then develop a model with a dichotomous trait. We
 implemented our stochastic models and approximations, performed statistical analyses, and produced
 144 figures using Python (Van Rossum et al., 2007) with NumPy (Van Der Walt et al., 2011) and Matplotlib
 (Hunter, 2007). Source code is available at <https://github.com/yoavram-lab/PrestigeBias>.

146 3.1 Continuous trait

We follow the model of Boyd and Richerson (1988), assuming only oblique transmission of the trait
 148 and omitting the indirect trait in order to reduce model complexity. We consider a population of N
 individuals, described by a single trait with a continuous value. Each generation, N naive individuals,
 150 or copiers, choose an individual from the previous generation, or role-models, from which they will
 copy their trait. Similar to a Wright-Fisher model, we assume non-overlapping generations such that
 152 the entire population is replaced in each generation. The population at time t can be described by
 $\mathbf{A}(t) = (A_1(t), \dots, A_N(t))$ where $A_i(t)$ is trait value of individual i at time t . We assume the initial
 154 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

$$156 \quad A_i(t + 1) = F_i(\mathbf{A}(t)) . \quad (1)$$

Success bias. Boyd and Richerson (1988, Ch. 8, p. 247-249) describe a blended transmission algo-
 158 rithm by defining F as a weighted average of the traits of all role-models,

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

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

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

162 $A_{i,j}$ is the absolute trait value copier i estimates for role-model j with some error $e_i \sim N(0, \eta^2)$,

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

164 and $\beta(\cdot)$ is the bias function that quantifies the success bias of a role-model,

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

166 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 , equivalent to relative
168 fitness in evolutionary-genetic transmission models.

Boyd and Richerson (1988) note that the deterministic blended transmission algorithm they use has
170 alternatives. We thus develop a similar stochastic model with transmission from a single random role-model. Instead of eq. (2), we define the transmission function F as a random variable with its
172 distribution given by

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

174 such that $G_{i,j}$ gives the probability of copier i to choose to copy the trait of role-model j .

Influence bias. Here we introduce a new element to the model. We assume that in each generation,
176 copiers choose their role-models one by one. We denote $K_{i,j}$ as the number of copiers that chose role-model j after copier i chose a role-model. Thus, i out of N copiers already chose a role-model,
178 $\sum_{j=1}^N K_{i,j} = i$, and there are $N - i$ copiers that have yet to choose a role-model. The stochastic process of role-model choice,

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

is described by the recurrence equation

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

where $S_{i,j} = 1$ if the i -th copier chose role-model j and 0 otherwise, and the initial state is $K_{0,j} =$
184 0.

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

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

188 The prestige $G_{i,j}$ of role-model j in the eyes of copier i is determined by the estimated biased trait value $\beta(A_{i,j})$ and the number of copiers that chose role-model j before copier i , $K_{i-1,j}$, replacing
190 eq. (3) of Boyd and Richerson (1988) with

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

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

We assume every individual evaluates the importance of success and influence differently. Addition-
 196 ally, we assume every role-model displays his influence and success individually, for example - a
 person with more followers but lack of actual skill may emphasize the number of his followers rather
 198 than his actual skill. We therefore modeled α_{ij} to be the relation between every copiers intrinsic
 significance of estimation, and every role-models personal emphasis.

200 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 $\sum_{j=1}^N G_{i,j} = 1$.

202 3.2 Dichotomous trait

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

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

210 where C is the number of role-models with trait \hat{A} and $K_{i,A}$ is the number of copiers that already chose
 A when copier i chooses a role-model and α' is the odd ratio of the bias weight $\alpha' = \frac{\alpha}{1-\alpha}$.

212 We prove this equation later, based on the proof of the Dirichlet-Multinomial approximation.

Initially, we assume the population has a single individual with phenotype \hat{A} and $N - 1$ individuals
 214 with phenotype A . The rest of the details follow the continuous trait model.

4 Results

216 4.1 Approximations

Our model is defined by two nested stochastic processes. Change over multiple generations is described
 218 by the phenotype distribution at each generation, $\{\mathbf{A}(t)\}_t$. 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-
 220 model, $\{\mathbf{K}_i\}_{i=1}^N$. We emphasize that the models are nested: $\mathbf{A}(t + 1)$ can be computed from $\mathbf{A}(t)$
 by evaluating \mathbf{K}_N . However, the former requires iterating over eqs. (8) and (9). Thus, we sought to
 222 find an equivalent stochastic process that has the same joint distribution as \mathbf{K}_N . We found two such
 approximations, summarized here and explained in detail below. In both we assume either α_j is a

224 trait of role-model j only (contrary to α_{ij} that included the relation with copier i), or a completely homogeneous α .

226 1. The number of copiers of a specific role-model at each step, $K_{i,j}$, follows the *generalized binomial distribution* (Drezner and Farnum, 1993) and therefore,

228 (a) 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 $i = 1, \dots, N$). This means that there's no actual estimation error in the population, just a fixed bias in every copiers estimation.

232 (b) 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.

236 2. 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 there's no meaning for the order of copiers. Therefore, the number of copiers of all role-models, $\mathbf{K}_i = (K_{i,1}, \dots, K_{i,N})$, follows a Dirichlet-Multinomial distribution, $\mathbf{K}_i \sim DM(N, \mathbf{G}_1)$, where $\mathbf{G}_1 = (G_{1,1}, \dots, G_{1,N})$ is the prestige vector of all role-models in the "eyes" of the first copier. Note that here $G_{i,j}$ is only a function of the trait values A_j and the bias weights α_j , as the estimation error is uniform, meaning all copiers are identical.

4.2 Generalized binomial distribution

244 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 parameterized by
246 $GBD(n, p, \theta)$ 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).

248

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

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

$$254 \quad Q_j(k, i) = P_j(S_{i,j} = 1 \mid k-1, i-1) \cdot Q_j(k-1, i-1) + P_j(S_{i,j} = 0 \mid k, i-1) \cdot Q_j(k, i-1), \quad (12)$$

where $S_{i,j} = 1$ when the i -th copier chooses role-model j . Equation (12) is equivalent to eq. (2.1) by
256 Drezner and Farnum (1993), which completes the proof.

Corollary 1. $E[K_{N,j}] = N \cdot G_{1,j}$.

258 *Proof.* Drezner and Farnum (1993, eq. (2.3)) show that $E[k] = N \cdot Q_j(1, 1)$ (modified from their
notation). $Q_j(1, 1)$ is the initial probability to choose role-model j , before any role-model choices are
260 made. $Q_j(1, 1) = G_{1,j}$ by definition, which completes the proof.

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

Proof. appendix A

264 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

$$266 \quad E[K_{Nj}] = N \cdot \frac{\alpha \cdot \beta(A_j + e)}{\sum_{m=1}^N \alpha \cdot \beta(A_m + e)} = \beta(A_j + e) \left/ \overline{\beta(A + e)} \right., \quad (13)$$

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

$$270 \quad E[K_{Nj}] = L \cdot \beta(A_j + e). \quad (14)$$

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

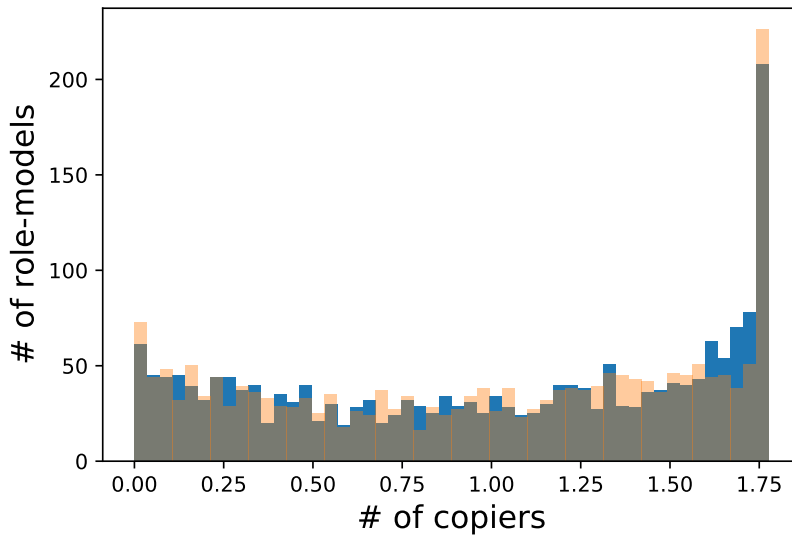


Figure 1: Numerical validation of the GBD approximation. The approximation (orange) fits simulation results (blue) well when using 1,000 simulations for both models. Here, population size, $N = 2,000$; bias weight, $\alpha = 0.1$; idea phenotype value, $\hat{A} = 1$; role-model traits $\mathbf{A} \sim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

Although basic, fig. 1 shows good fit of the GBD approximation. This validation is initial, and the
 276 more extensive validations we do on the Dirichlet-Multinomial approximation, because it is what we
 will use in our analysts.

278 4.3 Dirichlet-Multinomial distribution

Pólya urn model. This stochastic process consists of N draws from an urn with an initial amount of
 280 colored balls of M colors. When a ball is drawn, it is then placed back in the urn together with an
 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
 282 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 0 otherwise. The probability that $S_{i,j} = 1$ given \mathbf{U}_{i-1} is

$$284 \quad P(S_{i,j} = 1 \mid \mathbf{U}_{i-1}) = \frac{u_{i-1,j}}{\sum_{m=1}^M u_{i-1,m}} = \frac{o_j + w_{i-1,j}}{\sum_{m=1}^M o_m + w_{i-1,m}} = \frac{o_j + w_{i-1,j}}{i-1 + \sum_{m=1}^M o_m}, \quad (15)$$

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

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

Proof. Denote $\alpha' = \frac{\alpha}{1-\alpha}$ as the bias weight ratio, and $A'_j = A_j + e$. From eq. (10) and because
 292 $\sum_{j=1}^N K_{i,j} = i$, we have

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

294 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
 proof.

296 Frigýik et al. (2010, section 2) prove that the proportion of different colored balls in a Pólya urn
 model converges to the Dirichlet distribution as the number of draws approaches infinity, based on
 298 the *Martingale Convergence Theorem* (Durrett, 1999). We therefore have an approximation for the
 relative prestige each role-model has when evaluated by copiers. Thus, choosing the role-models for
 300 all copiers is equivalent to drawing from a Multinomial distribution where the parameters are the
 modified weights from a Dirichlet distribution and we have the following corollary.

302

Corollary 3. *The number of copiers of each role-model follows a Dirichlet-Multinomial distribution,
 304 $\mathbf{K}_i \sim DM(N, \mathbf{G}_1)$, under the conditions of Result 2.*

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 the full model. First, we computed an observed distribution of the number of copiers from the average empirical distribution of multiple simulations. We then compared this observed distribution with the expected theoretical DM distribution as can be seen in fig. 2 (a). The difference in distributions was not perceived when plotting both distributions on the same figure, so we used the difference instead. The maximum difference is 0.5 role-models, which indicate 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 of the DM distribution itself, as seen in fig. 2 (b). We see that the negative log likelihood of the observed data is much higher than any other shuffled version of the parameters vector, supporting our approximation more.

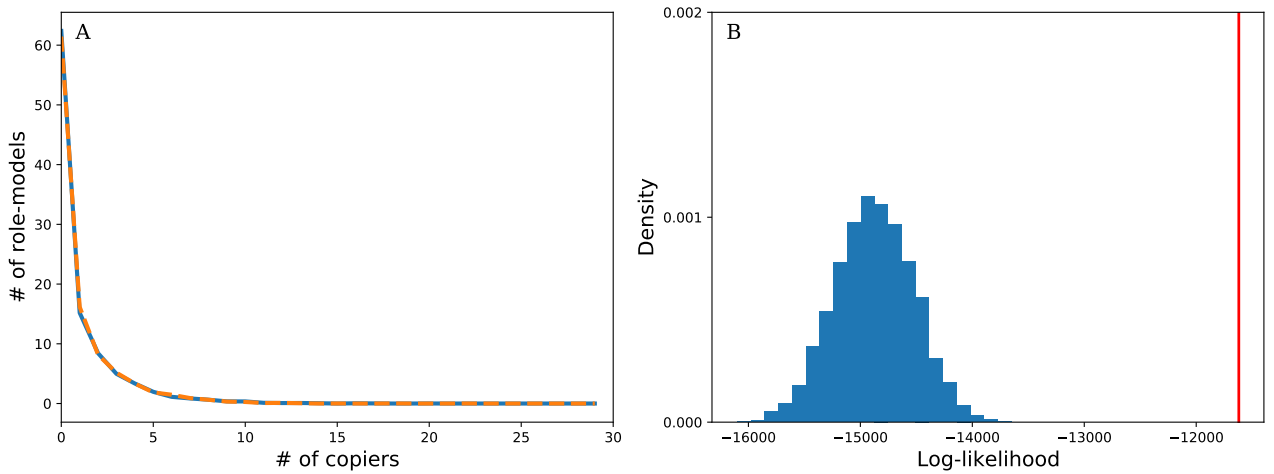


Figure 2: Numerical validation of the DM approximation. We performed computational "experiments" of the role-model choice process and compared them to the DM distribution. **(A)** The difference between the DM distribution (orange) and the empirical distribution of the experiments (blue) is very small. **(B)** The log-likelihood of the DM distribution for results of the experiments (red vertical line) is much higher compared to the log-likelihood of permutations of experiments (blue histogram). Here, population size, $N = 100$; number of experiments, $m = 100$; 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.

Next, we examined the fixation probability and fixation time of a favored phenotype \hat{A} when invading a population of phenotype A and compared results from the full model and the DM approximation. We find that the number of simulations needed to sufficiently approximate our model with the DM approximation is roughly 1,000 (Figure 3). Next, we examined the robustness of the DM 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 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 standard deviation is 0.1, the fixation probability and time is similar (fig. 4). 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 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 of the full
 328 model (fig. 5).

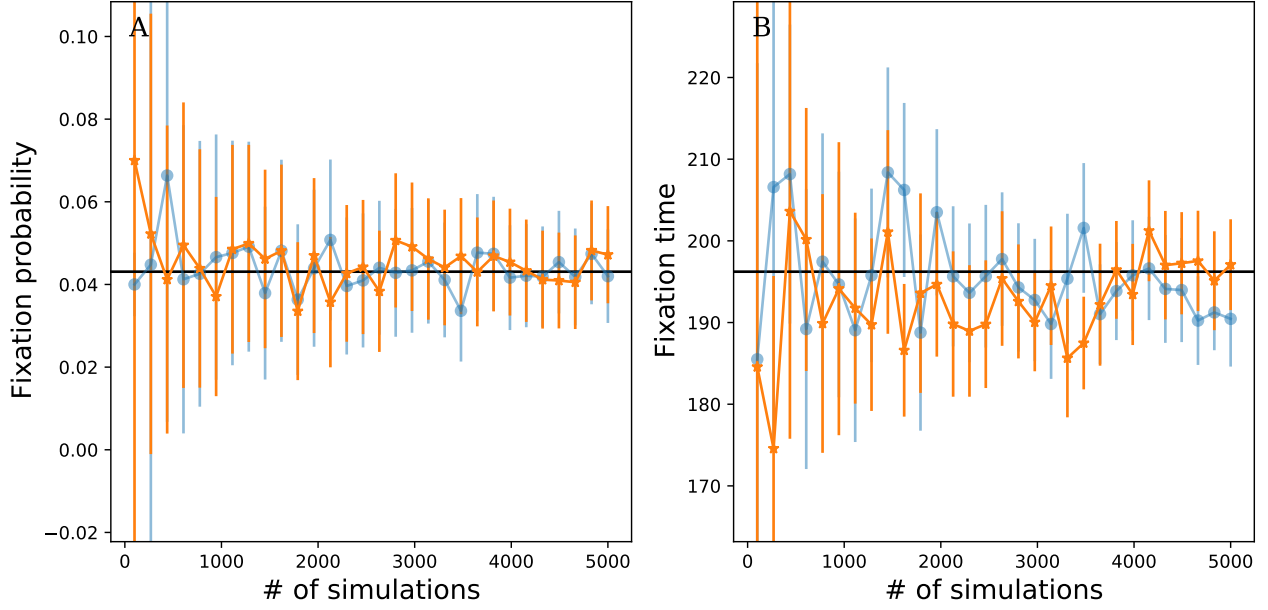


Figure 3: DM Approximation precision as function of number of simulations. Our DM approximation (orange) agrees with stochastic simulation results (blue) when using 1,000 or more simulations. Both fluctuate around the analytic fixation probability approximation (black; eq. (19)). Markers are averages 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, $\beta(A) = 0.956$.

4.4 Fixation probability and time

330 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
 332 on the conditional fixation probability and conditioned fixation time (conditioned on the population
 reaching fixation) of a favored phenotype, using a diffusion-equation approximation approach, similar
 334 to analyses of population-genetic models (Kimura, 1962; Kimura and Ohta, 1969; Otto and Whitlock,
 2006). We are mainly interested in the effect of the bias weight, α , which determines the relative
 336 effect of success and influence on prestige bias, given by eq. (10). For 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
 338 in our model is approximately DM distributed (corollary 3 and eq. (16)).

We start by finding the expectation and variance of the change in frequency from one generation to
 340 the next, which are the drift and diffusion terms of the diffusion equation.

342 **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 is the success coefficient
 344 of phenotype A , $\beta = \beta(A) < \beta(\hat{A}) = 1$. Then,*

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

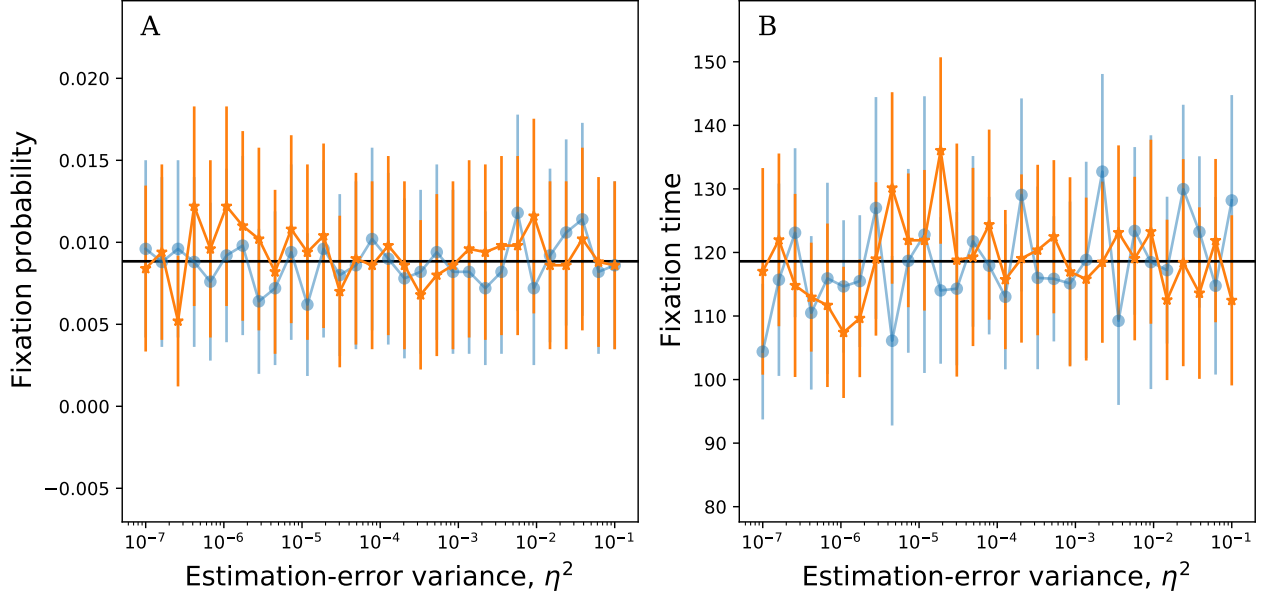


Figure 4: Robustness of DM approximations to success estimation error. Both the DM approximation (orange) and our approximation (black) agree with the stochastic simulations (blue), even with a high estimation error. Markers are averages across simulations, error bars are 95% confidence intervals. 5,000 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 $\eta \in [10^{-7}, 10^{-1}]$.

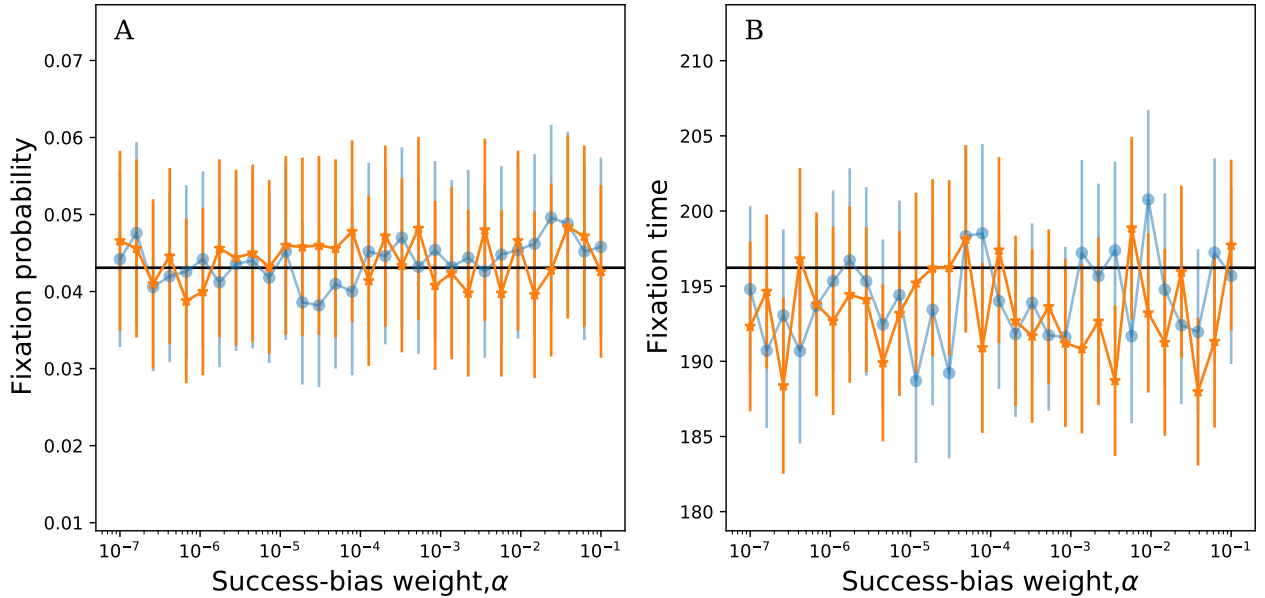


Figure 5: Robustness of DM approximations to variation in the bias weight α . Both the DM approximation (orange) and Kimura's equation (black line) fit the stochastic simulations (blue) well even with a high variation in success bias weight. Markers for average across 5,000 simulations, error bars are 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, $\beta(A) = 0.956$.

This analysis gives a surprising result relating the parameters α and β to parameters of the classical
 348 Wright-Fisher model from population genetics: the selection coefficient s , a measure of the effect of
 natural selection on the change in frequency of genotypes, and the effective population size, N_e , a
 350 measure of the effect of random genetic drift on the change in frequency of genotypes. In a diffusion-
 equation approximation of the classical Wright-Fisher model, the expectation and variance of the
 352 change in frequency are $E[x' - x] = x + x(1 - x)s + o(s)$ and $V[x' - x] = x(1 - x)/N_e$ (Kimura, 1962,
 eq. 7). Therefore, we have the following result.

354

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

$$358 \quad s = 1 - \beta(A), \quad N_e = \alpha N + (1 - \alpha) . \quad (18)$$

Using our effective selection coefficient, $1 - \beta$, and effective population size, N_e , with the population-
 360 genetics fixation probability approximation given by Kimura (1962, eq. 8), we get the following result.
 It's interesting to notice that when $N \gg 1$, $N_e \approx \alpha N$, resulting in a very convenient expression.

362

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

$$364 \quad \pi = \frac{1 - e^{-2(1-\beta)N_e x}}{1 - e^{-2(1-\beta)N_e}} \quad (19)$$

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

366 Similarly, we can use $1 - \beta$ and N_e in the population-genetics fixation time approximation given by
 Kimura and Ohta (1969, eq. 17).

368

Result 6 (Fixation time).

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

370 where, given $S = N_e(1 - \beta)$ and $x = \frac{1}{N_e}$,

$$u(x) = \frac{1 - e^{-2Sx}}{1 - e^{-2S}} \quad (21)$$

372 and,

$$J_1 = \frac{2}{(1 - \beta)(1 - e^{-2S})} \int_x^1 \frac{(e^{2S\xi} - 1)(e^{-2S\xi} - e^{-2S})}{\xi(1 - \xi)} d\xi, \quad (22)$$

374

$$J_2 = \frac{2}{(1-\beta)(1-e^{-2S})} \int_0^P \frac{(e^{2S\xi} - 1)(1 - e^{-2S\xi})}{\xi(1-\xi)} d\xi \quad (23)$$

376

$$T = \frac{1-\pi}{1-\beta} \int_0^x \frac{e^{2(1-\beta)\xi} - 1}{\xi(1-\xi)} d\xi + \frac{\pi}{1-\beta} \int_x^1 \frac{1 - e^{-2(1-\beta)(1-\xi)}}{\xi(1-\xi)} d\xi \quad (24)$$

Note that these integrals cannot be solved in closed form, so we can only estimate them numerically.

Numerical validation. We compare our approximations (eqs. (19) and (24)) 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, $s_e = 1 - \beta$, 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 our approximations (Figure 6).

Changing environment . After finding a good approximation in constant environment, where the favorable trait is always \hat{A} , we proceeded to find an approximation for a changing environment. Following Ram et al. (2018), we find the following expressions for the expectation and variance of the change in frequency between t generations.

388

Result 7 (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,*

$$E[X_t/N - x] \simeq x(1-x)S_t/N_e, \quad \text{and} \quad V(X_t/N - x) \simeq tx(1-x)/N_e, \quad (25)$$

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

Proof. appendix C

Using the drift and diffusion terms and following Ram et al. (2018), we can approximate the fixation probability in a changing environment using

$$\tilde{\pi} = \frac{1 - e^{-2\frac{S_n}{n}N_ex}}{1 - e^{-2\frac{S_n}{n}N_e}} \quad (26)$$

where $\frac{S_n}{n} = \frac{k-l}{k+l}(1 - \beta)$ and $n = k + l$. That is, we use the average selection coefficient during a cycle of $k + l$ generations as the selection coefficient eq. (19).

Numerical validation. Comparing our approximation, eq. (26) to numerical simulations, we find that the approximation fits simulations results well for variable bias weights, α , which corresponds to the effective population size (Figure 7A).

However, the approximation is more sensitive to the value of the success bias coefficient β (Figure 7B). We suspect that when β is too small, there will not be many cycles in the simulations, because either

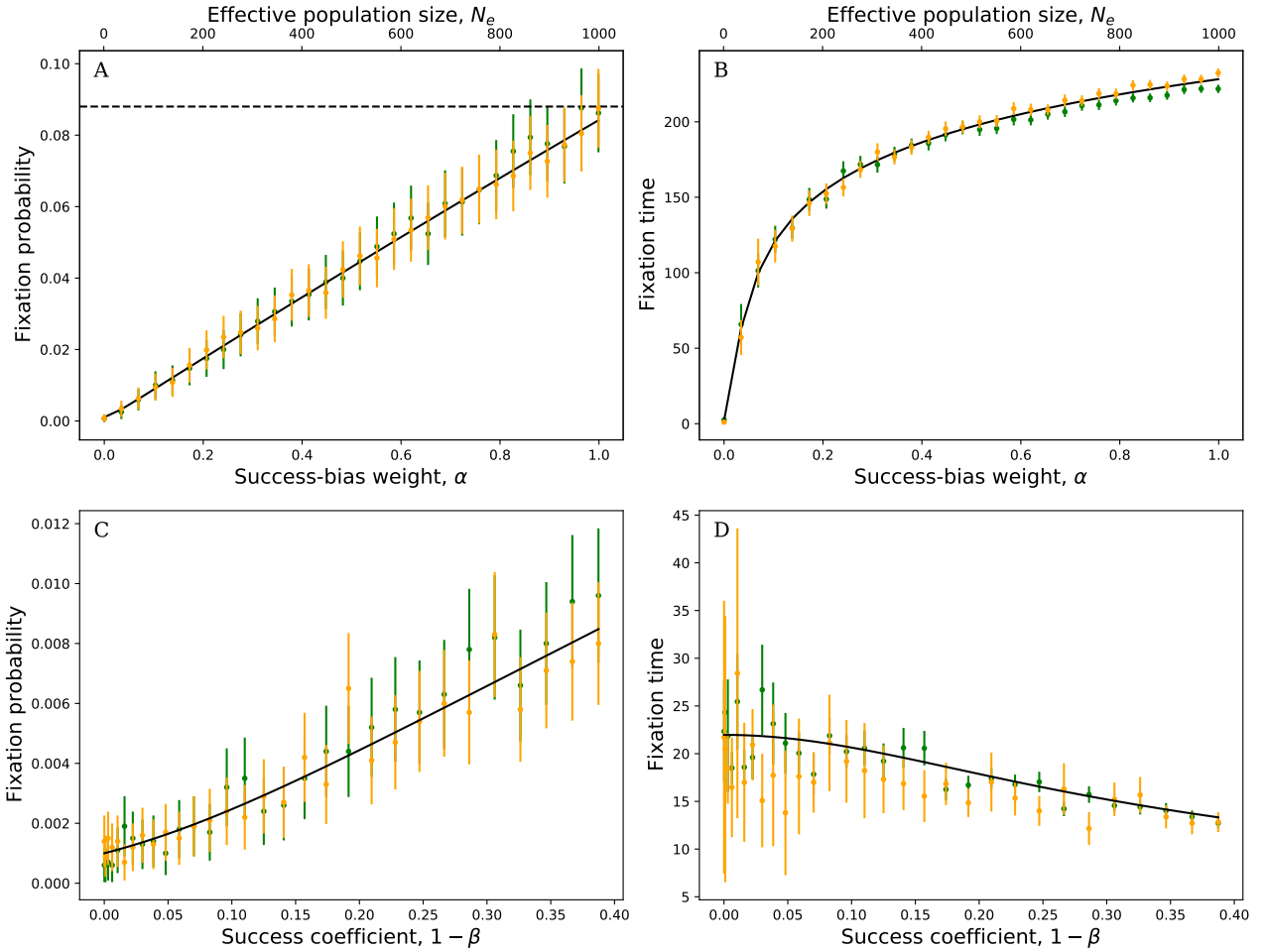


Figure 6: Fixation probability and time in a constant environment. Fixation probability and time (in generations) as a function of the success-bias weight α (bottom x-axis), or effective population size N_e (top x-axis) in the top row, and as a function of the success coefficient, $1 - \beta$, on the bottom row. The approximation (black; eq. (19)) agrees with both DM simulations (green) and Wright-Fisher simulation (orange). Fixation probability (A) is bounded by $2s_e = 2(1 - \beta)$ (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, $\hat{A} = 1$, $A = 0.7$ (A and B), $A = a \cdot \hat{A}$ with $0.01 \leq a \leq 0.99$ (panels C and D); success coefficient, $1 - \beta = s = 0.044$ (A and B); success-bias weight, $\alpha = 0.01$ (panels C and D).

the population reaches a high frequency of the fitter phenotype after just a few cycles, or the fitter phenotype becomes extinct very quickly. For the β values (0.65 and below), the fixation probability exceeds even the constant environment approximation (which is the upper limit). However, this is to be expected, because the diffusion-equation approximations assume weak selection (i.e., low selection coefficient s).

When k is the number of generations where the invading phenotype is favored, and l when the original trait is, we found that for large k -to- l ratio (while keeping constant total cycle length, $n = k + l = 100$), the changing environment approximation, eq. (26) converges to the constant environment approximation, eq. (19), see Figure 7C and Figure 7D.

Result 8. *The effective population size doesn't affect the goodness of fit of the approximation. The success coefficient however, must be even lower than before for the approximation to fit.*

The proof is seen in Figure 7A,B. The approximation follows the trend of the simulation results
416 for all α values. When increasing the success coefficient to more than 0.15, the simulation results
were located above the changing environment approximation, and below the constant environment
418 approximation. We believe the reason is the structure of the cycle. Our proof and approximation in
the changing environment are for a large amount of cycles, and when the success coefficient is too
420 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
422 bias becomes the disfavored), or the opposite happens, and the ideal trait gets extinct before there were
enough copiers that copied it. We then tried to change the ratio between the number of cycles where
424 \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
426 environment model.

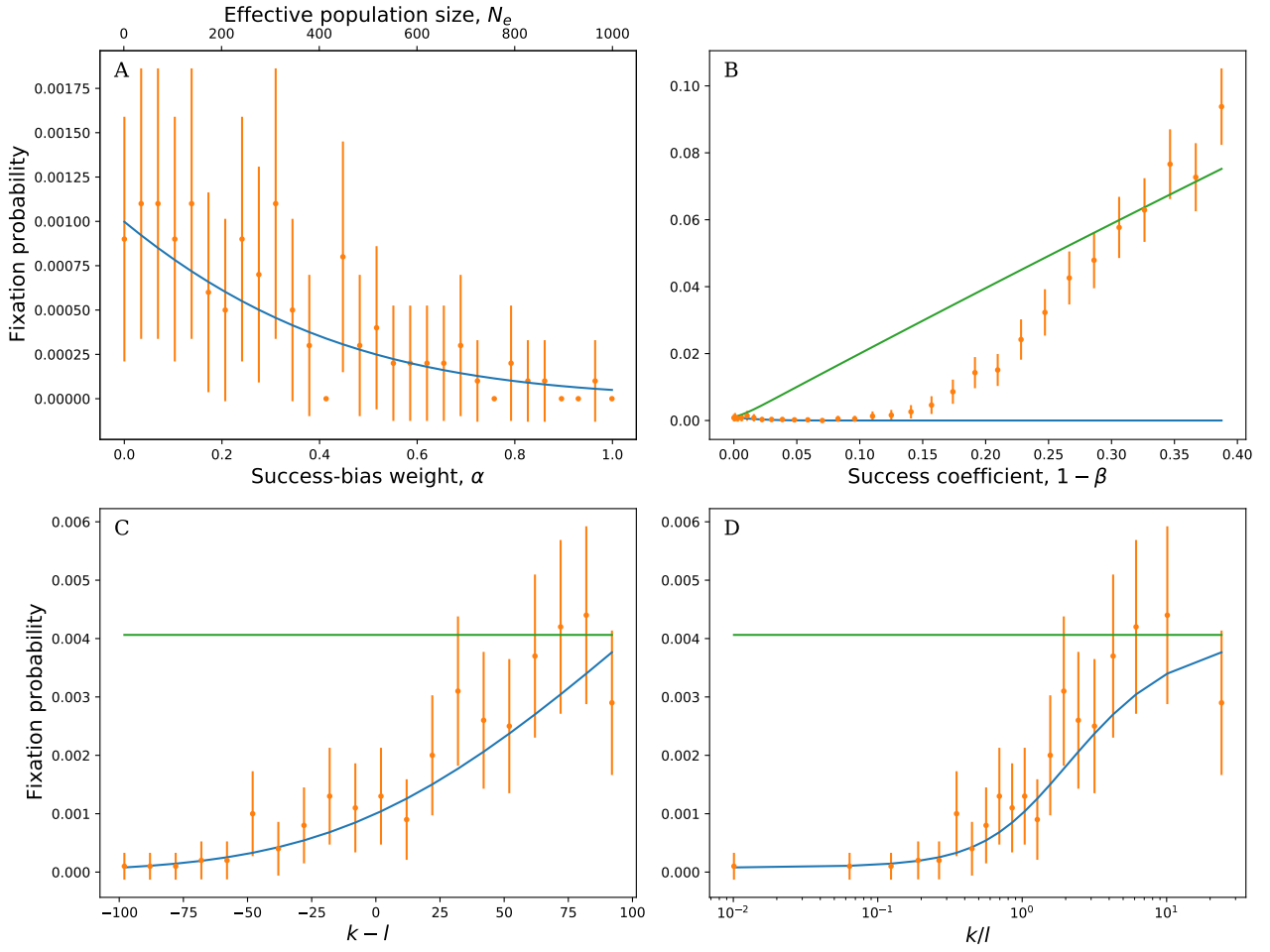


Figure 7: Fixation probability in a changing environment. (A) Fixation probability decreases with the the success-bias weight (bottom x-axis) and effective population size (top x-axis). The approximation (blue; eq. (26)) agrees with simulation results (orange). (B) Fixation probability increases with 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. (26)). 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% (A, C, and D) and 95% (B) confidence intervals. Here, population size, $N = 1,000$; phenotype values, $\hat{A} = 1$, $A = 0.9$ (A and B), $A = 0.8$ (C and D); In (A), the success coefficient is: $1 - \beta = s = 0.005$; In (B, C, and D) the success-bias weight is $\alpha = 0.1$.

4.5 Adaptive success-bias weight

428 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

430 between the estimated and the ideal trait values,

$$\alpha^* = \underset{\alpha}{\operatorname{argmin}} \sum_{j=1}^N \frac{\alpha A_j + (1 - \alpha) K_j}{\sum_{l=1}^N \alpha A_l + (1 - \alpha) K_l} \cdot (\hat{A} - A_j)^2, \quad (27)$$

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

434 We find that when copiers adapt their success-bias weight, it decreases with the number of copiers
 436 that have already chosen a role-model (Figure 8). Moreover, their estimation error is much lower
 438 compared to a constant success-bias weight, which gives roughly the same high estimation error to all
 copiers (compare Figure 8B and C): in this example, the adaptive weight estimation error converges
 to 0.046, whereas a constant weight gives values > 0.74 .

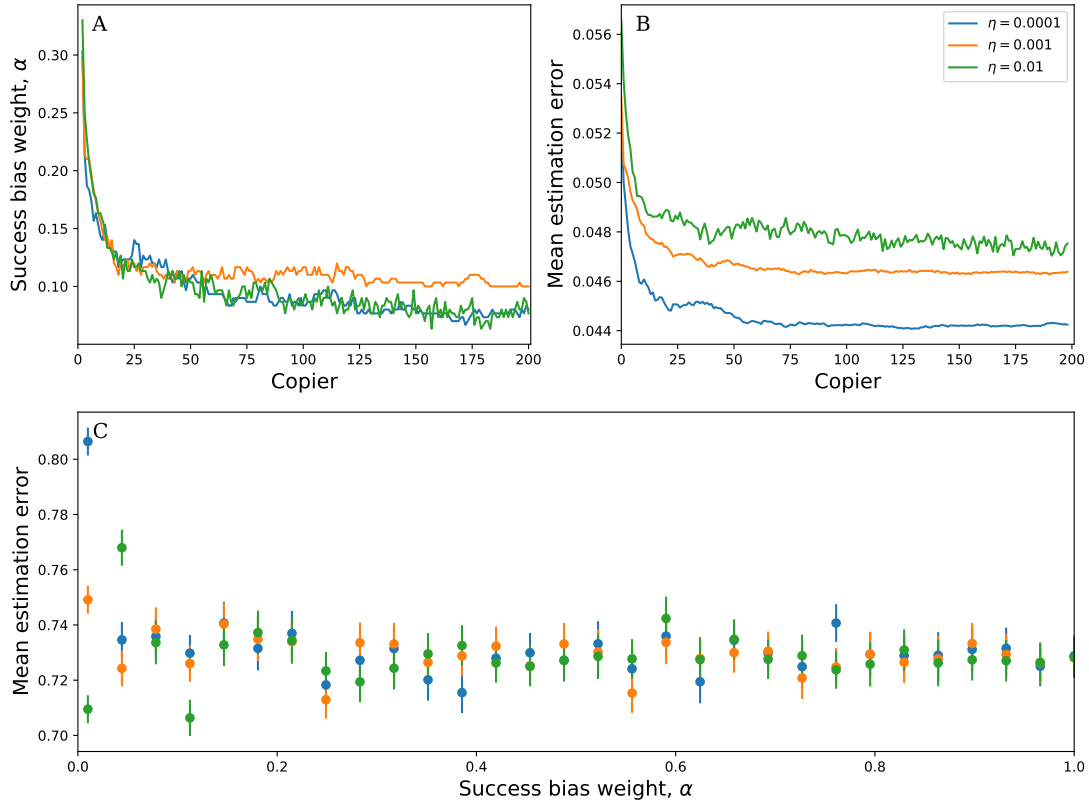


Figure 8: Advantage of an adaptive success-bias weight. Both success-bias weight α (A) and estimation error (B) decrease during the role-model choosing process, demonstrating that influence becomes more favored as more copiers have made their choice. However, when α is homogeneous (C), the mean estimation 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.

5 Discussion

During cultural transmission, cultural traits such as attitudes, values, beliefs, and behavioral patterns are transmitted between individuals, for example via copying and social learning. Some cultural traits or cultural role-models may be copied more often due to transmission biases. A common bias is success bias, in which copiers are more likely to copy a successful role-model. Many models assume that success can be accurately estimated. However, it has been suggested that because it is hard to estimate success, a more common bias is *prestige bias*—a bias towards role-models perceived to be successful in other traits (Henrich and Broesch, 2011).

Inspired by a model by Boyd and Richerson (1988), we developed a cultural-evolution model with prestige bias that includes both success and influence biases, where the latter is a bias towards role-models with many copiers. This is accomplished by a role-model choice process: each copier, in its turn, chooses a role-model, and that choice is affected both by the estimated success of each potential role-model and the number of copiers that already chose each role-mode (eq. 10).

This resulted in a model with two "nested" stochastic processes: the role-model choice process within each generation, and the cultural-evolutionary process between generations. To simplify the mathematical 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 distribution* (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 characteristic of the role-model, rather than the copier.

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, such 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 6).

We also analyzed a cyclic changing environment in which the identity of the success-biased trait switches after a fixed amount of generations (Figure 7). 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 generation in which the rare phenotype is under positive transmission bias and the number of generations in which it is 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 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

476 (adapted by copiers) and the estimation error decrease. The latter is significantly lower compared to a
population using a constant, fixed success-bias weight, regardless of the value of the constant weight
478 (Figure 8). This 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
480 more information a copier has, e.g. by using others as information sources, the more informative and
effective his choice can be.

482 **Prestige in the literature.** According to King and Cowlishaw (2009), there are two main approaches
to group decision making in nature: leadership and consensus. Leaders would usually be high-ranking
484 members of the group: elders, individuals with many kin relations, or individuals possessing other
dominant traits. King and Cowlishaw (2009) describe benefits for the closest associates of a dominant
486 baboon, such as protection from predators. In some species, like the females of *Eulemur fulvus rufus*
(Red lemur), leaders may arise due to nutritional needs, and not due to possessing superior traits
488 (Erhart and Overdorff, 1999). In humans, leadership also has its costs and benefits. Leaders can
make decisions that would most benefit them and their closest followers, while still maintaining group
490 cohesion. However, wrong decision making that harms the group could result in negative effects
for the leader. In modern society, many humans strive for prestigious positions, as they may reap
492 rewards greater than the risk and costs to achieve them, or due to individual personality and pressure
or education from the family.

494 Henrich and Gil-White (2001) suggested that there are two types of leadership: prestige-based and
dominance-based leadership. In the latter, social status is acquired through aggression, intimidation
496 and violence. It is also more common than prestige in non-human animals. Their definition of prestige
seems to overlap with ours. They suggest prestige is composed of estimation in the eyes of other people
498 (similar to our success bias) and commanding position in people's minds, i.e, the number of followers
other people think one has, which they define as *influence*, similar to our influence bias. Henrich and
500 Gil-White (2001) show that prestige can evolve via natural selection as an efficient process to extract
reproductive benefit from the flow of socially transmitted information. They back up their claims by
502 creating testable predictions and using evidence from the literature and experiments of social sciences.
Simply put, prestige can naturally evolve when social learning already exists to save costs of individual
504 learning.

Furthermore, according to Boyd and Henrich (2002), the process of cultural evolution doesn't require
506 accurate replication of cultural traits, addressed as "representation" in their paper. They base their
assumption on three claims: mental representations are non-discrete, cultural transmission is highly
508 inaccurate, and mental representations are not replicated, but rather are 'reconstructed' through an
inferential process that is strongly affected by cognitive 'attractors.' They describe three different
510 models to support their points. We see a high similarity between their model and ours. Like them, we
treat the cultural trait as non-discrete (in the main model, before simplifying it to facilitate analysis).
512 We also assume error in estimation, such that copiers do not precisely replicate their role-models, but
rather reconstruct them to create a potentially different trait, which is their representation of the role-

514 model's trait. In addition, the inferential process that they describe as strongly affected by cognitive
 attractors may include our definition of influence bias.

516 **Empirical evidence of prestige bias** Chudek et al. (2012) report the first direct tests in children that
 suggest the existence of prestige bias, defined as the tendency to learn from individuals to whom
 518 others have preferentially attended, learned, 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
 520 to whom bystanders had previously preferentially attended for 10 seconds were more than twice those
 of their learning from a role-models whom bystanders ignored. They also note that prestige effects are
 522 domain sensitive: they found that prestigious role-models were attended more when demonstrating
 artifact use, whereas role-models presenting food preferences had less attendants, suggesting that the
 524 domain itself (artifact use vs. food preference) can affect the attendance, and hence the prestige of the
 role-model. This lead Chudek et al. (2012) to suggest that when the trait is costly to learn individually,
 526 prestige will have a stronger bias. It would be interesting to include costs in our model to try and
 observe these effects and dynamics in a large population.

528 According to Henrich and Broesch (2011), evolutionary theorists propose that natural selection has
 favored the emergence of psychological biases for learning from those individuals most likely to
 530 possess adaptive information. Thus, they studied Fijian villages to examine if and how such biases
 emerge in a small-scale society. They found that Fijian villagers are more likely to learn from role-
 532 models perceived as more successful/knowledgeable, both within and across domains. Their research
 thus suggests that copying from those perceived as successful, rather than actually are successful, is a
 534 common phenomena. They show that the social networks representing copier–role-model relationships
 are centralized, suggesting that it is consistent with the prediction that people substantially share
 536 notions about who is a good cultural model, but that individuals' role-model selections are influenced
 by multiple factors.

538 We can also find prestige bias in more modern domains such as western medicine. Norredam and
 Album (2007) examined literature from 1950 to 2005 on the effects of prestige on medicinal practices.
 540 They found that active, specialized, biomedical, and high-technological types of medicine on organs
 in the upper part of the bodies of young and middle-aged people were accorded high levels of prestige,
 542 whereas medicine and practices with opposite characteristics had low levels of prestige. For example,
 they found that surgery counts as the most prestigious specialty, while psychiatry is the less prestigious.
 544 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
 546 very important practices that are neglected due to prestige bias. They concluded that such differences
 in prestige may bear consequences for actual priority setting in healthcare systems.

548 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
 550 bias, such as invasion of maladaptive traits. Takahashi and Ihara (2019) mention that social learning
 not only takes the form of random copying of other individuals, but also involves learners' choice of
 552 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 mentioned that a previous
554 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
556 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
558 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. Our model, which includes
560 influence bias, is consistent with this claim. When a maladaptive trait is "piggybacking" a role-model
with high influence, this trait could spread in the population. In addition, they show that best-of- k
562 learning can be stable against invasion by unbiased learning if social learning is sometimes combined
with individual learning. Our model only includes social learning, and not individual learning, but it
564 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
566 violence. Efferson et al. (2020) 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
568 their behavior. They found that there are individuals who act as *agents*, who are often looked upon,
and therefore they are ideal targets for interventions. This is similar to influential role-models in our
570 model, where a prestigious individual will be copied more often, and will therefore spread his trait
faster and wider in the population. They also suggest a way to use this phenomena to change existing
572 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 (2009) hypothesized that larger, more complex brains can store and manage more information
574 and in turn, this information can support the costs of a larger brain. Following up on this, Muthukrishna
and Henrich (2016) offered that prestige can directly affect human physical evolution. They present a
576 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,
578 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
580 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
582 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.

586 **Further work.** 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
588 error and the adaptive weight, α^* , are converging 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,
590 such as homogeneous 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.

592 Another way to expand our model is to account for the two types of prestige or leadership suggested
by Van Vugt and Smith (2019) that are attributed to Confucius and Machiavelli. Confucius viewed
594 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
596 viewed leaders as rulers who exercise influence by imposing costs through (the threat of) punishment
and violence. Van Vugt and Smith (2019) suggest that these two opposing views are both partially
598 supported by 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
600 these leadership styles, such as assuming there is a correlation between phenotype to leadership style.
The emerging cultural-evolutionary dynamics and their dependence on the costs and benefits are
602 intriguing.

Conclusions. Here, we presented support for the existence of prestige biases in cultural transmission,
604 including the commonly studied success bias. We introduced an influence bias, which has so far
received less attention. We believe the combination of these biases may be a strong driving force in
606 cultural evolution. We show that the relative effect of the two biases changes the effective population
size such that the increasing the weight individuals give to influence bias, decreases the effective
608 population size. We also find a clear advantage to individuals that can choose the relative weight of
the two biases.

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A General Binomial Distribution approximation proof

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

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

$$G_{1,j} = \frac{\alpha_j \cdot \beta(A_j + e)}{\sum_{m=1}^N \alpha_m \cdot \beta(A_m + e)} . \quad (28)$$

The denominator of eq. (28) can also be formulated as:

$$\sum_{m=1}^N \alpha_m \beta(A_m + e) = N \cdot \overline{\alpha \cdot \beta(A + e)} , \quad (29)$$

where $\overline{\alpha \beta(A + e)}$ is the mean value of $\alpha_m \cdot \beta(A_m + e)$ for all m . Using eq. (29) and **Corollary 1** we get,

$$E[K_{Nj}] = \alpha_j \cdot \beta(A_j + e) / \overline{\alpha \cdot \beta(A + e)} , \quad (30)$$

B Drift and diffusion in a constant environment proof

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 is 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),

$$E[X'] = N \frac{\alpha_1}{\alpha_1 + \alpha_2} , \quad (31)$$

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,

$$\begin{aligned} E[x'] &= \frac{1}{N} N \frac{\alpha'xN}{\alpha'xN + \alpha'N(1-x)\beta} = \frac{x}{x + (1-x)\beta} \\ &= \frac{x}{x + (1-x) - (1-x) + (1-x)\beta} = x \frac{1}{1 - (1-x)(1-\beta)} \\ &= x(1 + (1-x)(1-\beta) + o(\beta)) = x + x(1-x)(1-\beta) + o(\beta) , \end{aligned} \quad (32)$$

following Durrett (2008, p. 253, ch 7.2) and because $1/(1 - y) = 1 + y + y^2 + \dots$

By definition, x is constant, so $E[x] = x$. We therefore have

$$E[x' - x] = E[x'] - E[x] = x(1 - x)(1 - \beta) + o(1 - \beta), \quad (33)$$

which gives us the drift term of the diffusion equation.

Using the variance of the DM distribution,

$$V(X') = N \frac{\alpha_1}{\alpha_1 + \alpha_2} \left(1 - \frac{\alpha_1}{\alpha_1 + \alpha_2}\right) \left(\frac{N + \alpha_1 + \alpha_2}{1 + \alpha_1 + \alpha_2}\right). \quad (34)$$

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,

$$V(x') = \frac{1}{N^2} N \frac{x}{x + (1 - x)\beta} \left(1 - \frac{x}{x + (1 - x)\beta}\right) \left(\frac{N + \alpha'xN + \alpha'N(1 - x)\beta}{1 + \alpha'xN + \alpha'N(1 - x)\beta}\right). \quad (35)$$

Following Durrett (2008, ch 7.2), we assume $\beta \approx 1$, such that

$$\frac{x}{x + (1 - x)\beta} \approx x \quad (36)$$

and for the entire variance expression we get

$$V(x') \approx \frac{1}{N} x(1 - x) \left(\frac{N + \alpha'xN + \alpha'N - \alpha'xN}{1 + \alpha'xN + \alpha'N - \alpha'xN}\right) = x(1 - x) \left(\frac{1 + \alpha'}{1 + \alpha'N}\right). \quad (37)$$

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

$$V(x' - x) = V(x') - V(x) \approx x(1 - x) \left(\frac{1 + \alpha'}{1 + \alpha'N}\right). \quad (38)$$

α' is the odds ratio of the bias weight,

$$\alpha' = \frac{\alpha}{1 - \alpha}. \quad (39)$$

Combining eq. (38) and eq. (39) we get:

$$V(x' - x) \approx x(1 - x) \left(\frac{1 + \frac{\alpha}{1 - \alpha}}{1 + \frac{\alpha}{1 - \alpha}N}\right) = x(1 - x) \left(\frac{1}{\alpha N + (1 - \alpha)}\right). \quad (40)$$

This gives the diffusion term of the diffusion equation.

C Drift and diffusion in a changing environment proof

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. (25). From eq. (33) we know that

$$E \left[\frac{X_{t+1}}{N} - \frac{X_t}{N} \middle| X_t \right] = \frac{X_t}{N} \left(1 - \frac{X_t}{N} \right) (1 - \beta_{t+1}) = \frac{1}{N} \frac{X_t}{N} \left(1 - \frac{X_t}{N} \right) s_{t+1}. \quad (41)$$

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

$$\begin{aligned} E \left[\frac{X_t}{N} \left(1 - \frac{X_t}{N} \right) \right] &= E \left[\frac{X_t}{N} - \left(\frac{X_t}{N} \right)^2 \right] = E \left[\frac{X_t}{N} \right] - E \left[\left(\frac{X_t}{N} \right)^2 \right] \\ &= E \left[\frac{X_t}{N} \right] - V \left(\frac{X_t}{N} \right) - \left(E \left[\frac{X_t}{N} \right] \right)^2. \end{aligned} \quad (42)$$

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

$$E \left[\frac{X_t}{N} \left(1 - \frac{X_t}{N} \right) \right] \simeq E \left[\frac{X_t}{N} \right] \left(1 - E \left[\frac{X_t}{N} \right] \right) - \frac{1}{N_e} tx(1-x). \quad (43)$$

From eq. (41) we know that

$$\begin{aligned} E \left[\frac{X_{t+1}}{N} - \frac{X_t}{N} \right] &= \frac{1}{N} s_{t+1} E \left[\frac{X_t}{N} \left(1 - \frac{X_t}{N} \right) \right] \simeq \frac{1}{N} s_{t+1} \left(E \left[\frac{X_t}{N} \right] \left(1 - E \left[\frac{X_t}{N} \right] \right) - \frac{1}{N_e} tx(1-x) \right) \\ &\simeq \frac{1}{N} s_{t+1} \cdot E \left[\frac{X_t}{N} \right] \left(1 - E \left[\frac{X_t}{N} \right] \right) - \frac{1}{N_e N} s_{t+1} tx(1-x). \end{aligned} \quad (44)$$

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

$$E \left[\frac{X_{t+1}}{N} - \frac{X_t}{N} \right] \simeq \frac{1}{N} s_{t+1} \cdot E \left[\frac{X_t}{N} \right] \left(1 - E \left[\frac{X_t}{N} \right] \right). \quad (45)$$

We now look at the induction assumption to see that

$$E \left[\frac{X_t}{N} - x \right] = E \left[\frac{X_t}{N} \right] - E[x] = E \left[\frac{X_t}{N} \right] - x, \quad (46)$$

so using the assumption we get

$$\begin{aligned} E \left[\frac{X_t}{N} \right] &\simeq \frac{1}{N} S_t x (1-x) + x, \\ 1 - E \left[\frac{X_t}{N} \right] &\simeq 1 - \frac{1}{N} S_t x (1-x) + x. \end{aligned} \quad (47)$$

We use both expressions in eq. (45) and get

$$\begin{aligned} E \left[\frac{X_{t+1}}{N} - \frac{X_t}{N} \right] &\simeq \frac{1}{N} s_{t+1} \left(\frac{1}{N} S_t x (1-x) + x \right) \left(1 - \frac{1}{N} S_t x (1-x) + x \right) \\ &\simeq \frac{1}{N} s_{t+1} \cdot x (1-x), \end{aligned} \quad (48)$$

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

$$E \left[\frac{X_{t+1}}{N} - x \right] = E \left[\frac{X_{t+1}}{N} - \frac{X_t}{N} \right] + E \left[\frac{X_t}{N} - x \right], \quad (49)$$

so again using the induction assumption, together with eq. (48) we get

$$\begin{aligned} E \left[\frac{X_{t+1}}{N} - x \right] &\simeq \frac{1}{N} s_{t+1} \cdot x (1-x) + \frac{1}{N} S_t \cdot x (1-x) \\ &\simeq \frac{1}{N} x (1-x) (S_t + s_{t+1}) \simeq \frac{1}{N} S_{t+1} x (1-x), \end{aligned} \quad (50)$$

which proves the drift term.

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

$$V \left(\frac{X_{t+1}}{N} \right) = E \left[V \left(\frac{X_{t+1}}{N} \middle| X_t \right) \right] + V \left(E \left[\frac{X_{t+1}}{N} \middle| X_t \right] \right). \quad (51)$$

Using eq. (41) we see that

$$\begin{aligned} E \left[\frac{X_{t+1}}{N} \middle| X_t \right] - E \left[\frac{X_t}{N} \middle| X_t \right] &= \frac{1}{N} s_{t+1} \frac{X_t}{N} \left(1 - \frac{X_t}{N} \right) \\ E \left[\frac{X_{t+1}}{N} \middle| X_t \right] &= \frac{X_t}{N} + \frac{1}{N} s_{t+1} \frac{X_t}{N} \left(1 - \frac{X_t}{N} \right). \end{aligned} \quad (52)$$

Using eq. (40) we get

$$V \left(\frac{X_{t+1}}{N} \middle| X_t \right) = \frac{1}{N_e} \frac{X_t}{N} \left(1 - \frac{X_t}{N} \right), \quad (53)$$

and using the equation $y'(1-y') \simeq y(1-y)$ on the first part of eq. (51) we get

$$E \left[V \left(\frac{X_{t+1}}{N} \middle| X_t \right) \right] = \frac{1}{N_e} E \left[\frac{X_t}{N} \left(1 - \frac{X_t}{N} \right) \right] \simeq \frac{1}{N_e} x (1-x). \quad (54)$$

Moving on to simplify the second part of eq. (51) using eq. (52),

$$V\left(E\left[\frac{X_{t+1}}{N}\middle|X_t\right]\right) = V\left(\frac{X_t}{N} + \frac{1}{N}s_{t+1}\frac{X_t}{N}\left(1 - \frac{X_t}{N}\right)\right) \quad (55)$$

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

$$V\left(\frac{1}{N}s_{t+1}\frac{X_t}{N}\left(1 - \frac{X_t}{N}\right)\right) \leq \frac{1}{4N^2}s_{t+1}^2, \quad (56)$$

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

$$V\left(E\left[\frac{X_{t+1}}{N}\middle|X_t\right]\right) = V\left(\frac{X_t}{N}\right) + O\left(\frac{1}{N^2}\right) \simeq V\left(\frac{X_t}{N}\right). \quad (57)$$

Using the induction assumption and eq. (54),

$$V\left(\frac{X_{t+1}}{N}\right) \simeq \frac{1}{N_e}x(1-x) + \frac{1}{N_e}tx(1-x) \simeq \frac{1}{N_e}x(1-x)(t+1) \quad (58)$$

which proves the diffusion term.

תקציר

העתקה של מודל לחיקוי יכולה להיות שיטה יעילה לרכישת ידע. כאשר נדרשים לבחור מודל לחיקוי, ישנה הטייה ידועה הנקראת הטייה מבוססת הצלחה: כלומר, להעתיק מהמודל לחיקוי שנראה המצליח ביותר. הטייה זאת מבוססת על ביצועיו ויכולותיו של המודל לחיקוי בלבד, ללא גורמים נוספים. אנחנו מציעים הטייה נוספת שייתכן שהינה נפוצה בתהליכי תורשה תרבותית: הטייה מבוססת השפעה, כלומר, הבחירה במודל לחיקוי מושפעת מכמות המעתיקים שכבר בחרו מודל לחיקוי. במודל שלנו אנחנו משלבים את ההטיות לכדי הטייה אחת שאנו קוראים לה "הטיית יוקרה" ואנו מנתחים את ההשפעות של הטייה זו על הדינמיקות של אבולוציה תרבותית, באמצעות שימוש באנליזה מתמטית וסימולציות סטוכסטיות.

במחקר זה מצאנו שיערוכים מתמטיים לתהליך הסטוכסטי שלנו, אשר סייעו לנו בפיתוח מתמטיים מורכבים יותר של המודל, וביעול החישוביות של הסימולציות בסדר גודל. אנו מאששים שיערוכים אלה באמצעות סימולציות, ובודקים את חוסנם כנגד הנחות מקלות שבאמצעותן מצאנו שיערוכים אלו. בנוסף, מצאנו שיערוכים ל"הסתברות קיבעון" (ההסתברות שאלמנט תרבותי יתפשט באוכלוסיה כולה) ו"זמן לקיבעון", בסביבות קבועות ומשתנות, אשר דומים לשיערוכי קימורה למודלים של אבולוציה גנטית. שיערוכים אלו מראים שהטייה מבוססת הצלחה דומה לבחירה הטבעית, והטייה מבוססת השפעה מקטינה את גודל האוכלוסייה האפקטיבי. הטייה מבוססת השפעה גם מאיצה את הדינמיקות של האבולוציה, כמו שניתן לצפות ממודל "עשירים מתעשרים". המודל שלנו יכול לתאר בצורה טובה תהליכי תורשה תרבותית, במיוחד בתרבויות של בני האדם, בהן רשתות המדיה החברתית פופולריות. עובדה נוספת נדרשת בכדי לבחון אם מודל זה יכול לחזות תופעות כלשהן באבולוציה תרבותית, כאשר מעשירים אותו בהשפעות של בחירה טבעית, ויוזמה אישית.

עבודה זו בוצעה בהדרכתו של דר' יואב רם מבי"ס לזואולוגיה, הפקולטה למדעי החיים, אוניברסיטת תל אביב.