

Prestige as a Driving Force in Cultural Transmission

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Abstract

Copying our role-models have always been an efficient method of acquiring knowledge. Copying successful role-model is one of the methods of cultural transmission of traits. In this paper, we study the various biases and their effects of the population and it's evolution. The most common bias when choosing a role-model to copy is *success bias*, i.e copying whoever appears successful to us. This estimation is based on the performance of the role-model alone, without any other factors. Here, we study another factor we believe aids to better model the cultural inheritance of traits in a large population. *Influence bias* is a bias evaluated by the number of copiers a role-model already has. In our model we combine these components to what we call the **Prestige bias** and analyze its relationship to the dynamics of the population. We successfully found mathematical approximations to our model, easing the mathematical analysis and the computation power required for simulations. We show the value of these approximations using simulations, and their robustness to variations such as mutation and other relaxations required for the mathematical proofs. In the binary form of our model, we found alternatives to *Kimura's* equations for approximating fixation probability and time to fixation of an invading advantageous trait, in both a constant and changing environment. We show that *Influence* solely affects the effective population size. We found that influence acts as an accelerator for a state of the population, matching the *rich getting richer* it was based on. We believe such model better describes how humans acquire knowledge from one another, mainly in the last years where social networks are very popular. Social networks allow easy access to estimate number of copiers a role-model has, with little to no effort.

Introduction

Traits transmission is when an individual passes on a trait, genetic or behavioral, to another individual. Transmission in nature manifests in two main ways: genetic and cultural. Genetic transmission is when an individual, or several, transmit their genes to their offspring by duplication of their own cells. Cultural transmission is the way individuals transmit cultural traits (i.e behavior) from one another, typically via teaching and demonstrating. Cultural transmission is most common in humans (Cavalli-Sforza and Feldman, 1981, pg. 3) and in primates like chimpanzees (Horner et al., 2010; Kendal et al., 2015). The common cultural traits in humans are behavioral patterns, like personalities and habits, transmitted via observations and verbal discussions. Henrich and McElreath (2007) suggest that cultural learning may be particular to humans, but McComb et al. (2001) suggest that it appears in other mammals as well, elephants for example:

... 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.

They showed that once a matriarch is removed from the group, the group's survival instincts are inferior. They support their hypothesis by exacting an experiment: playing audio recordings of African elephants, showing that groups with a matriarch recognize and react better to hostile or

friendly calls than the groups without one. Moreover, cultural transmission appears in other species,
even simpler than mammals, such as *Drosophila*. Battesti et al. (2012) show that oviposition site
choice in fruit flies is culturally transmitted. They showed that flies without experience in choosing
sites, after spending some time with "experienced" flies, chose the same type of site without directly
observing this behavior. Battesti et al. (2012) mention that how the information is transferred is
still an open question, but suggest that the flies may use olfactory cues, like other animals such as
rodents and bees.

Cultural transmission is similar to genetic transmission in many ways, while different in others.
Similar to genetic transmission, the effects of culturally transmitted traits can be physiological
rather than behavioral, and transmitted from parents to offspring. For example, parents can teach
their children to be strong or tall, within some biological limits, by instructing them to maintain a
healthy diet and engage in physical activity. Contrary to genetic transmission, the sources of the
traits can be many, and not only parents. They can even be unrelated, like teachers, celebrities,
coaches, the media, or any stranger that comes in contact with them. Cultural transmission can
be vertical, where parents transmit to their children, but also oblique, where other adults transmit
traits to children (not their own). Horizontal transmission is also possible, where peers transmit
traits to one another. Lastly, vertical transmission in the opposite direction is possible too, where
parents copy traits from their children (e.g. playing video games) as Cavalli-Sforza and Feldman
(1981) and Creanza et al. (2017) suggest. In addition, even when a cultural trait is disfavored by
natural selection, it still may spread across a population given transmission biases strong enough
to negate the selection bias (Boyd and Richerson, 1988, Ch. 8 pg. 279).

Transmission bias occurs when a trait has a disproportionate probability from its frequency in
the population to be transmitted. For example, Eickbush et al. (2019) show that there are genes
of yeast called *wtf genes*, that bias their transmission to the gametes. They secrete a long life ex-
pectancy poison, together with a short life expectancy antidote, so a gamete without the gene will
perish (the poison will outlive the antidote). Transmission biases, though exist in genetic transmis-
sion, are probably more common in cultural transmission. Much like mutation in genetic evolution,
one could learn behavioral patterns or traits on his own, usually referred to as *innovation*, also called
individual learning, and just like mutation, without it humans might have been remained at the
stone age, or even go extinct. Rendell et al. (2010) suggest that success biased social transmission
contribute more to the general success of the population than individual learning. They conducted
a tournament for developing learning strategies of a population, where each participant need to
devise a strategy. Each strategy must define when individuals should observe and copy from others,
and when to engage in individual learning. The best strategies contained a high percentage of social
learning relative to individual learning, even when the error when copying was as high as almost
0.5. It is important to add that all of the strategies include some percentage of individual learning,
and without it the results would be a lot worse. In addition to Rendell et al. (2010), Fogarty et al.

(2017) define different types of transmission biases based on success. They define several types of role-model choosing methods, all assuming that the copier correctly identifies the successful ones. Both studies assume that individuals can successfully evaluate successful individuals. 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 is 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 between two others can try both of the paddle grips it observed, and decide what grip is better for it. An indirect bias is 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. Continuing with the example, a bystander could copy the paddle grip of the Ping-Pong player who scored more points in the match. A frequency-dependent bias is when an individual has a probability to copy a variant of the trait that is nonlinear to the trait's frequency in the parent's generation. Continuing with the 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.

Frequency bias could be negative too. Aljadeff et al. (2020) show that societies under competitive conditions are likely to develop diversity in foraging specialization rather than uniformity.

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) claim 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 the indirect bias is strong enough. They claim the bias could lead to a *runaway process*, caused by a cultural equivalent of *sexual selection* (Andersson, 1994). On the other hand, Henrich and Broesch (2011) claim that prestige biases, over generations, can lead to cultural adaptations. According to them, prestige can make a maladaptive trait spread in the population, but can also accelerate the spread of adaptive traits as well. *Prestige bias* is often mentioned in the literature, but seldom modeled. Boyd and Richerson (1988) have modeled the prestige bias, but didn't include the effects the copiers of a role-model has on the probability of other individuals to choose the same role model.

This effect is similar to *conformity* (Denton et al., 2020), which is usually modeled as a different bias. *Conformist learning* (imitating locally common behaviors) is a known bias in cultural transmission (Molleman et al., 2013), and we suggest that prestige bias is made up by both indirect bias and a new type of conformity. Our new component, *influence*, is assigned to a role-model, contrary to conformity, which refers to the frequency of a trait in the population, regardless which individuals posses it. **The goal of this study is to define a more realistic model for prestige bias and analyze the dynamics of the population it causes.**

Today, due to social media, it is easier than ever to estimate the influence individuals have over others, therefore it is probably a major part of humans decision-making process. For example, the number of *followers* a person has in the mobile application *Instagram* may significantly affect

how his beliefs are perceived by the population. We want to create a model that better fits reality and simulate scenarios that better mimic cultural transmission dynamics. With a more accurate model of prestige bias, we may understand better how cultural traits are transmitted, and why. Moreover, we could better explain the cause for the spread of maladaptive traits, or the acceleration of adaptive traits often seen in humans.

Models and Methods

Reminder: A *Wright–Fisher model* is a mathematical model meant to describe a genetic drift process. This model assumes that generations do not overlap and that each copy of the gene found in the new generation is drawn independently at random from all copies of the gene in the old generation.

A *Moran model* assumes overlapping generations. At each time step, one individual is chosen to reproduce and one individual is chosen to die. In our models we harness these two models and modify them to describe new mathematical models that we use to expand the basic indirect bias model Boyd and Richerson (1988) suggest.

Continuous Model

Consider a population of N individuals, each individual has one trait on a continuous scale. Every generation, N naive individuals (*copiers*) must choose a trait to copy from one of the individuals of the previous generation (*role-models*). Similar to a Wright–Fisher model, we assume the generations don’t overlap. We base our model on the model of Boyd and Richerson (1988), by assuming only oblique transmission of the traits (*Indicator trait* - A). Unlike their model, we omit a second trait called **Indirectly biased trait** to lower complexity. The model’s state at time t can be described by:

$$\vec{A}_t = (A_{t,1}, \dots, A_{t,N}) \quad (1)$$

where \vec{A}_t is a vector describing the indicator traits at time t , and \vec{A}_0 is drawn from a standard normal distribution. Each individual from generation $t + 1$, a *copier*, inherits traits like so:

$$A'_i = F_i(\vec{A}_t) \quad (2)$$

where A'_i is the indicator and indirect trait values correspondingly, that copier i acquires. We use A'_i as an alias for $A_{i,(t+1)}$ for simplicity for the transition between generations $t \rightarrow t + 1$. F is a function over the t generation traits vector, and is defined differently for every implementation of the **Generic model**.

Success bias. Boyd and Richerson (1988, Ch.8, p.247-249) describe a method of inheritance using a *blend*, i.e weighted average of the trait of the entire generation. They define F as a weighted

average of the role-models' traits in a single generation:

$$F_i(\vec{X}) = \sum_{j=1}^N (G_{ij} \cdot X_{ij}) \quad (3)$$

where $G_{i,j}$ is:

$$G_{ij} = \frac{\beta(A_{ij})}{\sum_{l=1}^N \beta(A_{il})} \quad (4)$$

We define G_{ij} to be the *Success bias* of role-model j in the eyes of copier i . $A_{i,j}$ is the absolute indicator trait value copier i estimates role-model j has:

$$A_{i,j} = A_j + e_i, \quad (5)$$

where e_i is the copier's error of estimation, $e \sim N(0, \frac{1}{\eta^2})$. $\beta(X)$ is the bias function, meant to quantify the success bias of a role-model:

$$\beta(A_{i,j}) = b \cdot \exp\left(-\frac{(A_{i,j} - \hat{A})^2}{2J}\right), \quad (6)$$

where \hat{A} is the optimal indicator value and J, b are model parameters to control the "strength" of the bias. $G_{i,j}$ is therefore the relative success score copier i assigns to role-model j , resembling *relative fitness* in genetic transmission models.

Random choice transmission. Boyd and Richerson (1988) note that the method of transmission they use in their model has alternatives. We follow their suggestion and create a model similar to theirs, with random choice as a transmission method: The probability of copier i to choose role-model j as his role-model to copy its traits from is $G_{i,j}$. Once a copier chose its role-model, it will copy both its traits only from his role-model, instead of a weighted average of the entire role-model generation:

$$A'_i = A_{i,j} \quad (7)$$

Influence bias. Copiers choose their role-models one by one. After copier i chose a role-model, we denote K_{ij} as the number of copiers that chose role-model j until that point, such that $\sum_{j=1}^N K_{i,j} = i$. The stochastic process of role-model choice,

$$\{\vec{K}_i\}_{i=1}^N, \quad \vec{K}_i = (K_{i1}, \dots, K_{iN}), \quad (8)$$

is described by the recurrence equation

$$K_{i,j} = K_{i-1,j} + S_{i,j}, \quad i, j = 1, 2, \dots, N \quad (9)$$

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

190 The probability that the i -th copier chose role-model j

$$G_{i,j} = P(S_{i,j} = 1 | S_{1,j}, S_{2,j}, \dots, S_{i-1,j}) \quad (10)$$

192 is the prestige of role-model j in the eyes of copier i . This prestige $G_{i,j}$ is determined as follows.
 First, role-model j is characterized by its indicator value A_j as before, and the estimated indicator
 194 value by copier i , $A_{i,j}$ remains as eq. (5). Finally, the prestige $G_{i,j}$ of role-model j in the eyes of
 copier i is determined by the estimated biased indicator value $\beta(A_{i,j})$ and the number of copiers
 196 that chose role-model j before copier i , $K_{i-1,j}$,

$$G_{i,j} = \frac{\alpha_j \cdot \beta(A_{i,j}) + (1 - \alpha_j) \cdot K_{i-1,j}}{W_i}, \quad (11)$$

198 where the weight α_j is a characteristic of role-model j that determines the relative significance of the
 indicator and the influence in the prestige, and W_i is a normalizing factor to ensure $\sum_{j=1}^N G_{i,j} = 1$,

$$200 \quad W_i = \sum_{j=1}^N \left(\alpha_j \cdot \beta(A_{i,j}) + (1 - \alpha_j) \cdot K_{i-1,j} \right). \quad (12)$$

Binary model

202 The indicator trait can now manifest in only two phenotypes, and for simplicity we define they
 can be either \hat{A} or A . In the binary model, the influence is determined by the number of copiers
 204 already chosen **any** role-model with either A or \hat{A} , as all role-models with A will contribute to the
 probability of the trait to be inherited just the same (can be proved with simple induction). Simply
 206 put, assuming there are two role-models with the A trait, the probability a copier will copy from
 either role-model will be the same, and the probability the A trait will be inherited is the sum of
 208 both role-models. In the general case, the probability of the i -th individual to inherit trait A , based
 on eq. (22) is:

$$210 \quad P_{i,A} = \frac{(N - X)\alpha'\beta(A) + K_A}{i - 1 + (N - X)\alpha'\beta(A) + X\alpha'\beta(\hat{A})} = \frac{(N - X)\alpha'\beta(A) + K_A}{i - 1 + (N - X)\alpha'\beta(A) + \alpha'X} \quad (13)$$

where X is the number of role-models with trait \hat{A} and K_A is the number of copiers that already
 212 chose A .

The model begins with the first generation having a single individual with \hat{A} , and the rest have A .
 214 The process itself is the same stochastic process as the continuous model.

Methods

216 The main methods we used to experiment and compare our models is using computer generated
 simulations. In order to establish our claims and base our mathematical approximations of our

models, we used the χ^2 test for the full continuous model, and the Kimura's equations of fixation probability and time to fixation for the binary model.

Results

Approximations

Currently $\{\vec{K}_i\}_{i=1}^N$ is a stochastic process where each state depends on the previous state, i.e a Markov chain. We wanted to find an equivalent stochastic process that has the same joint distribution on $\{\vec{K}_i\}_{i=1}^N$, but it is possible to evaluate the joint distribution directly without evaluating all the marginal conditional distributions: eq. (9), eq. (10).

We found two approximations to our process, which are summarized here and explained in detail later on:

1. $K_{i,j}$ follows the general binomial distribution defined by Drezner and Farnum (1993). Moreover, $\mathbb{E}[K_{N,j}] = N \cdot G_{1,j}$ if $e = e_l = e_m$ for all l, m . That is, 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. In addition, we find that when α is homogeneous, $\alpha_l = \alpha_m$ for all l, m , then $\mathbb{E}[K_{N,j}] = \beta(A'_j) / \overline{\beta(A')}$, where A'_j is the estimated indicator value $A'_j = A_j + e$, and $\overline{\beta(A')}$ is the population mean estimated indicator value. That is, the expected number of copiers of a role-model equals its relative biased indicator value, similar to the role of relative fitness in population-genetic models.
2. The role-model choice process eq. (8) is equivalent to a Pólya urn model if $e_l = e_m$ for all l, m . Therefore, $\vec{K}_i = (K_{i,1}, \dots, K_{i,N})$ follows a Dirichlet-Multinomial distribution,

$$\vec{K}_i \sim DM(N, \vec{G}_1), \quad (14)$$

where $\vec{G}_1 = (G_{1,1}, \dots, G_{1,N})$. Note that here $G_{i,j}$ is only a function of the indicator values A_j and the weights α_j .

General Binomial Distribution Approximation

The general binomial distribution (GBD) is achieved by a series of Bernoulli experiments, with possible dependency between experiments.

Proposition: The number of copiers $K_{i,j}$ follows the GBD, $K_{i,j} \sim GBD(i, \alpha_i \cdot \beta(A'_j))$, when $e_l = e_m$ for all $l, m \in N$ and $A'_j = A_j + e$

Proof: We'll denote $Q_j(k, i) = P(K_{i,j} = k | K_{i-1,j})$ as the probability that exactly k out of i copiers choose role-model j , using conditional probability and eq. (9):

$$Q_j(k, i) = P_j(S_{i,j} = 1 | k-1, i-1) \cdot Q_j(k-1, i-1) + P_j(S_{i,j} = 0 | k, i-1) \cdot Q_j(k, i-1) \quad (15)$$

where $S_{i,j} = 1$ when the i -th copier chooses role-model j .

250 We see that eq. (15) is equivalent to eq. (2.1) that Drezner and Farnum (1993) define. $Q_j(k, N)$
is the probability that k out of N copiers choose role-model j at the end of the process, which by
252 our previous notation is $k = K_{N,j}$. By describing the process of eq. (8) as (Drezner and Farnum,
1993) did, we've completed the proof.

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

In (Drezner and Farnum, 1993, equation 2.3), they show that the expected value of k is:

256 $\mathbb{E}[k] = N \cdot Q_j(1, 1)$ (using different notations). $Q_j(1, 1)$ is the initial probability to choose role-
model j , before any choices are made. $Q_j(1, 1) = G_{1,j}$ by definition, therefore we can say that
258 $\mathbb{E}[K_{N,j}] = N \cdot G_{1,j}$.

260 **Corollary 2:** $\mathbb{E}[K_{N,j}] = \alpha_j \cdot \beta(A'_j) / \overline{\alpha \cdot \beta(A')}$.

Proof: The initial prestige of role-model j based on eq. (11) is:

$$262 \quad G_{1,j} = \frac{\alpha_j \cdot \beta(A'_j)}{\sum_{m=1}^N \alpha_m \cdot \beta(A'_m)} \quad (16)$$

The denominator of eq. (16) can also be formulated as:

$$264 \quad \sum_{m=1}^N \alpha_m \beta(A'_m) = N \cdot \overline{\alpha \cdot \beta(A')} \quad (17)$$

where $\overline{\alpha \beta(A')}$ is the mean value of $\alpha_m \cdot \beta(A'_m)$ for all m . Using eq. (17) we get:

$$266 \quad \mathbb{E}[K_{N,j}] = \alpha_j \cdot \beta(A'_j) / \overline{\alpha \cdot \beta(A')} \quad (18)$$

, completing our proof.

268 The special case where $\alpha = \alpha_l = \alpha_m$ for all $l, m \in N$ is interesting, because we can evaluate the
expected number of copiers using a linear equation:

$$270 \quad \mathbb{E}[K_{N,j}] = N \cdot \frac{\alpha \cdot \beta(A'_j)}{\sum_{m=1}^N \alpha \cdot \beta(A'_m)} = \beta(A'_j) / \overline{\beta(A')} \quad (19)$$

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

$$\mathbb{E}[K_{Nj}] = L \cdot \beta(A'_j) \quad (20)$$

Dirichlet-Multinomial Distribution Approximation

Reminder: *Pólya urn model* is a stochastic process that is defined as such: The process consists of N draws from an urn with an initial amount of 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 colour. Let $\vec{U}_i = \{u_{i,1}, u_{i,2}, \dots, u_{i,M}\}$ 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 0 otherwise. The probability that $S_{i,j} = 1$ given U_{i-1} is:

$$\begin{aligned} P(S_{i,j} = 1 | U_{i-1}) &= \frac{u_{i-1,j}}{\sum_{m=1}^M u_{i-1,m}} = \frac{o_j + w_{i-1,j}}{\sum_{m=1}^M o_m + w_{i-1,m}} \\ &= \frac{o_j + w_{i-1,j}}{i - 1 + \sum_{m=1}^M o_m} \end{aligned} \quad (21)$$

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

Proposition: process $\{\vec{K}_i\}_{i=1}^N$ is equivalent to a *Pólya urn model* when $e = e_i = e_j$ and $\alpha = \alpha_j = \alpha_i$ for all $i, j \in N$.

Proof: We denote α' as the odds ratio between the weights of the indicator and the influence ($\alpha' = \frac{\alpha}{1-\alpha}$). Using eq. (11) we get:

$$\begin{aligned} G_{i,j} &= \frac{\alpha \cdot \beta(A'_j) + (1 - \alpha) \cdot K_{i-1,j}}{W_i} \cdot \frac{1 - \alpha}{1 - \alpha} \\ &= \frac{\alpha' \beta(A'_j) + K_{i-1,j}}{\sum_{m=1}^N \alpha' \beta(A'_m) + K_{i-1,m}} \\ &= \frac{\alpha' \beta(A'_j) + K_{i-1,j}}{i - 1 + \sum_{m=1}^N \alpha' \beta(A'_m)} \end{aligned} \quad (22)$$

We see that eq. (21) and eq. (22) are equivalent when setting $M = N$, $o_j = \alpha' \beta(A'_j)$, $w_{i,j} = K_{i,j}$, completing the proof.

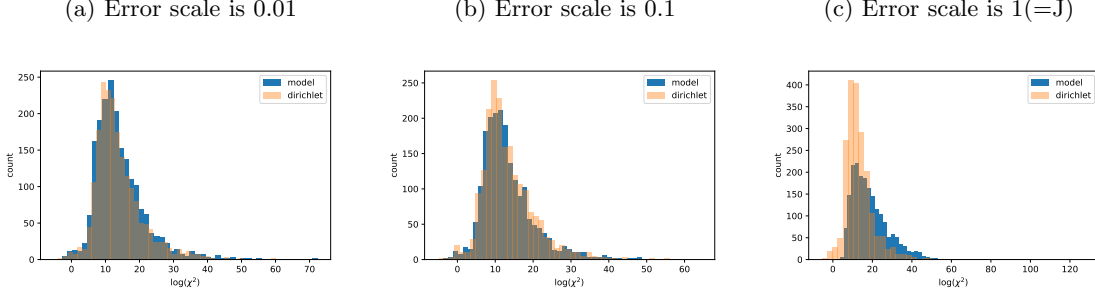


Figure 1: Demonstrates the similarities between the χ^2 metric of the DM approximation and the full model, showing the approximation is good until a very high error rate. Population size $N = 2000$. 400 simulations per figure

Corollary 1: In their paper, Frigyük et al. (2010, section 2) prove that the proportion of different colored balls in a *Pólya urn model* will converge to the Dirichlet distribution as the number of draws approaches infinity, based on *Martingale Convergence Theorem* (Durrett, 1999). We therefore have an approximation for the relative "weight" or the proportion each role-model has when evaluated as a role-model. Drawing from a Multinomial distribution where the parameters are the modified weights gained from the Dirichlet distribution is viable for selecting the role-model for the next generation. We can therefore sample from a Dirichlet-Multinomial distribution to approximate how many copiers each of the role-models will have: $\vec{K}_i \sim DM(N, \vec{G}_1)$.

Numeric validation: We showed our process is DM (Dirichlet-Multinomial) distributed when there are no errors when copying or evaluating the traits, and when α is homogeneous in the population. To test if our process is still DM distributed when there are copying errors in the population, we ran 400 simulations for three different error scales (η). To check the resemblance of the DM approximation to the original iterative process, we measure the χ^2 statistic of both processes and the results can be seen in fig. 1. Even with a relatively high error scales (1% and 10% of J) we can see the distributions of the χ^2 metrics are very similar. With a higher η (e.g. $\eta = J$), which is approximately 100% error when evaluating a trait, the distributions are noticeably different.

In addition to the chi-squared test, we want to observe how well does the Dirichlet-Multinomial distribution approximates our entire model, and not just one generation in it. To do that we simplify our model to a binary model, so the simulations of the model to run in a feasible amount of time.

Numeric comparisons

We're interesting in studying the difference between the real binary model as we defined in eq. (13), and the Dirichlet-Multinomial approximation. Specifically, we're interesting in the fixation probability of the favored trait (\hat{A}) and its time to fixation.

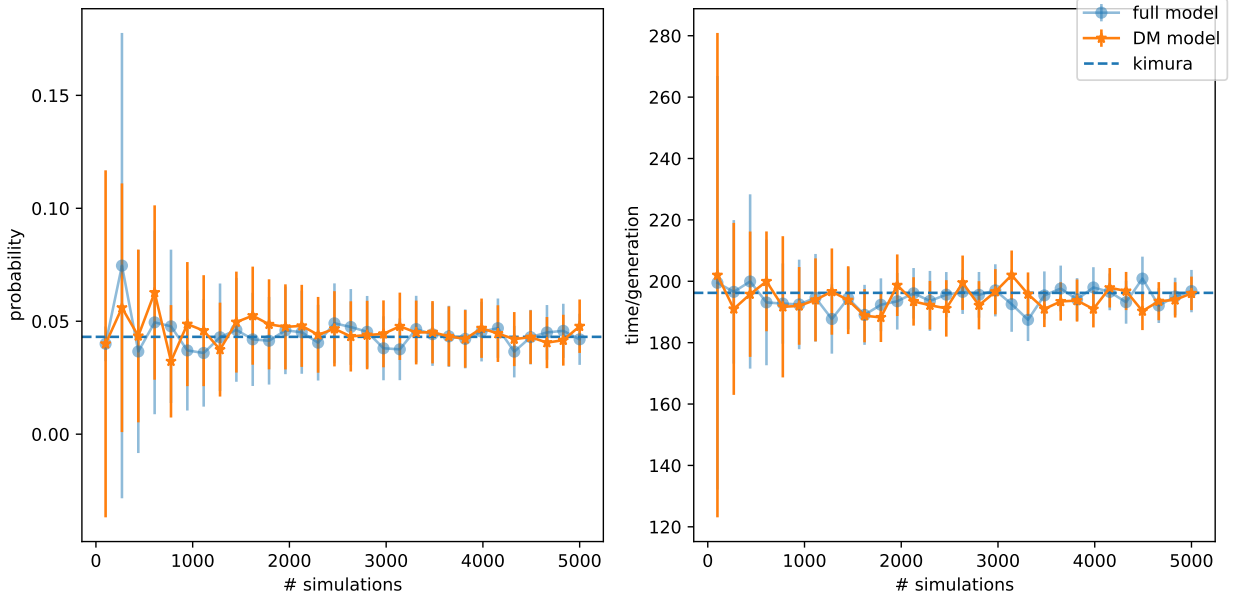


Figure 2: The number of simulations needed to get a good approximation. At 1,000 the approximation is good enough. Error bars represent 95% confidence interval. Population size $N = 1000$, $\alpha = 0.5$, $J = 1$, $\hat{A} = 1$, $A = 0.7$, $\beta(A) = 0.956$.

The first step was to find the number of simulations needed to sufficiently approximate the real
 318 model with the DM approximation. From fig. 2 we see that 1000 simulations or higher is enough.

The next step was to see how the observed metrics (fixation probability and time) varies when
 320 relaxing our assumptions we used to prove the DM approximation. First we relaxed our assumption
 of no mutation. To include mutation in the binary model, it needs to be redefined, since in the
 322 original model it was based on the fact the traits are drawn from a continuous scale. In the binary
 model mutation will be manifested as an error when evaluating the bias itself. This is easily done
 324 by using a heterogeneous J parameter, which controls the strength of the success bias in eq. (6).

In fig. 3 we see the comparison when heterogeneous mutation is applied to both models. When
 326 mutation is applied, we sample J_i for each copier i from a normal distribution with varying scale
 (variance). We can see that even when the standard deviation is 0.1, the metrics of both models
 328 are both similar, and close to the Kimura approximation (more details in the next section).

In fig. 4 we relaxed our assumption of a homogeneous α , and used a heterogeneous α instead.
 330 Similar to the mutation comparison, we drew α_j for each role-model j from a normal distribution
 with varying scale. We again see that the metrics of both models are similar in the entire spectrum
 332 of our x-axis, and the Kimura approximation is within both confidence intervals.

Fixation probability and time - binary model

334 **Kimura's approximation:** After establishing a case in the favor of our DM approximation, we
 wanted to use it to examine the behavior of the population. Specifically, we wanted to analyze the
 336 influence of the indicator weight (α) on the fixation probability and time to fixation of the favored

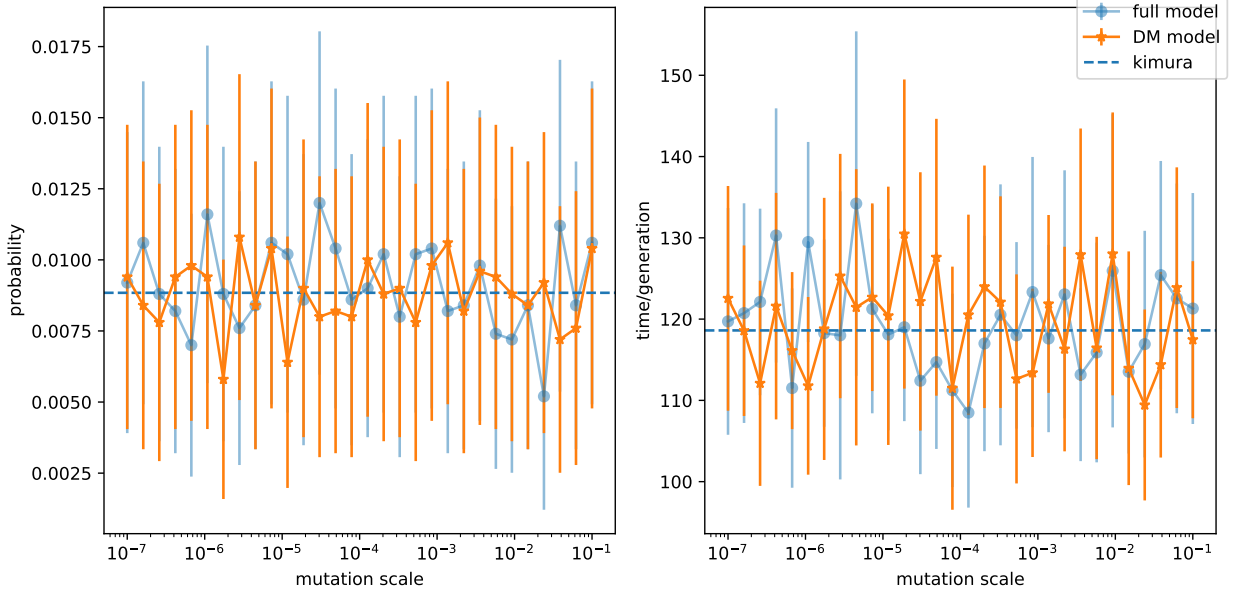


Figure 3: Comparison of the DM approximation and the full model when mutation is included. Even high mutation rate doesn't worsen the approximation, and the data points are close to the mathematical estimation (Kimura's). Error bars are 95% confidence intervals, and are condensed (± 0.01 probability and ± 40 generations) 5000 simulations per data point, $N = 1000$, $\alpha = 0.1$, $\hat{A} = 1$, $A = 0.7$, $J \sim N(1, x^2)$ where x is the mutation scale in the x-axis.

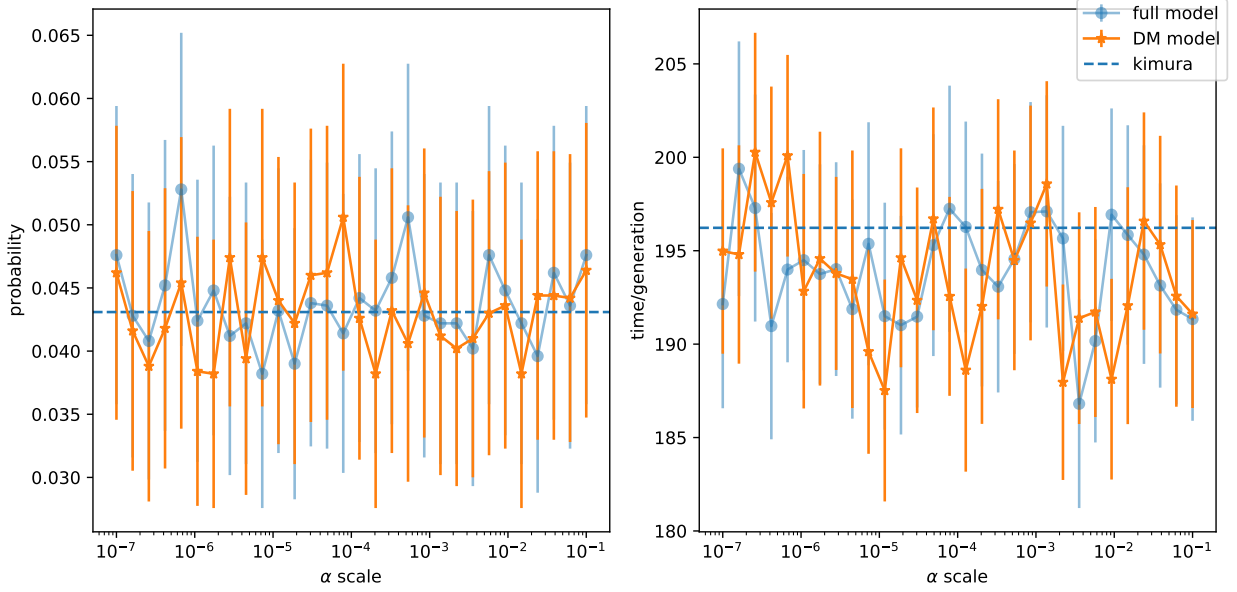


Figure 4: Comparison of the DM approximation and the full model when success weight is heterogeneous. High success weight variance distances the approximation and the full model of generations to fixation from the Kimura's approximation, but not by much (confidence intervals still cover it). Error bars are 95% confidence intervals, and are less condensed (± 0.03 probability and ± 40 generations) 5000 simulations per data point, $N = 1000$, $\alpha \sim N(0.5, x^2)$, $\hat{A} = 1$, $A = 0.7$, $J = 1$, $\beta(A) = 0.956$.

phenotype in a binary model. For simplicity, we don't include mutation rate in the binary model
 338 approximations. Following Durrett (2008), we used our DM approximation of the model to find
 the effective population size. From eq. (13) we can derive that the process of inheritance in our
 340 binary model is DM distributed with a parameters vector of size two: $\vec{V} = (\alpha'X, (N - X)\alpha'\beta(A))$.

Proposition: $1 - \beta(A)$ is equivalent to the selection coefficient s in a classic Wright-Fisher model
 342 in the diffusion equations meant to approximate the fixation probability and time of the advanta-
 geous trait.

Proof: Let x be the frequency of type \hat{A} in the population with N individuals. Let X be the
 number of individuals of type \hat{A} so $x = X/N$. X' is the number of individuals with \hat{A} in the next
 346 generation and x' their frequency. By definition $\beta(\hat{A}) = 1$, and for simplicity we'll denote $\beta(A) = \beta$
 ($\beta < 1$).

348 The expected number of individuals of a DM distribution is:

$$E[X'] = N \frac{\alpha_1}{\alpha_1 + \alpha_2}, \quad (23)$$

350 where $\alpha_1 = \alpha'X$ and $\alpha_2 = \alpha'(N - X)\beta$, from eq. (13). We want to use frequencies instead of
 quantities to follow Durrett's process so:

$$352 \quad E[x'] = E\left[\frac{X'}{N}\right] = \frac{1}{N}E[X'] \quad (24)$$

Putting it together we get:

$$\begin{aligned} E[x'] &= \frac{1}{N}N \frac{\alpha'xN}{\alpha'xN + \alpha'N(1-x)\beta} \\ 354 \quad &= \frac{x}{x + (1-x)\beta} \end{aligned} \quad (25)$$

which is identical to the equation in the top of page 253, chap 7.2 in Durrett (2008). We
 356 therefore use the same approximation and say that:

$$\begin{aligned} E[x'] &= \frac{x}{x + (1-x)\beta} = \frac{x}{x + (1-x)(1-s)} = \\ &= x + x(1-x)s + o(s) \\ &= x + x(1-x)(1-\beta) + o(1-\beta) \end{aligned} \quad (26)$$

358 By definition, x is constant, so $E[x] = x$. We continue to calculate $E[x' - x]$:

$$E[x' - x] = E[x'] - E[x] = x(1-x)(1-\beta) + o(1-\beta) \quad (27)$$

360 where when substituting $1 - \beta$ with s , we get the same result as Durrett (2008) which is the desired result.

362 **Proposition:** $Ne = \alpha N + (1 - \alpha)$, where Ne is the effective population size of our binary model.

Proof: The variance of a DM distribution is:

$$364 \quad V(X') = N \frac{\alpha_1}{\alpha_1 + \alpha_2} \left(1 - \frac{\alpha_1}{\alpha_1 + \alpha_2}\right) \left(\frac{N + \alpha_1 + \alpha_2}{1 + \alpha_1 + \alpha_2}\right) \quad (28)$$

And again, we want to use frequencies so:

$$366 \quad V\left(\frac{X'}{N}\right) = \frac{1}{N^2} V(x') \quad (29)$$

Putting it together with our model's notations:

$$368 \quad V(x') = \frac{1}{N^2} N \frac{x}{x + (1 - x)\beta} \left(1 - \frac{x}{x + (1 - x)\beta}\right) \left(\frac{N + \alpha' x N + \alpha' N(1 - x)\beta}{1 + \alpha' x N + \alpha' N(1 - x)\beta}\right) \quad (30)$$

Like Durrett, we'll use the zero order of the approximation when $\beta \approx 1$, so:

$$370 \quad \frac{x}{x + (1 - x)\beta} \approx x \quad (31)$$

and we also use $\beta \approx 1$ for the entire variance expression and get:

$$372 \quad \begin{aligned} V(x') &\approx \frac{1}{N} x(1 - x) \left(\frac{N + \alpha' x N + \alpha' N - \alpha' x N}{1 + \alpha' x N + \alpha' N - \alpha' x N}\right) \\ &= x(1 - x) \left(\frac{1 + \alpha'}{1 + \alpha' N}\right) \end{aligned} \quad (32)$$

Again following Durrett we want to calculate:

$$374 \quad V(x' - x) = V(x') - V(x) \approx x(1 - x) \left(\frac{1 + \alpha'}{1 + \alpha' N}\right) \quad (33)$$

because x is a constant so $V(x) = 0$

376 In our model, α' is the odds ratio of a parameter we called "indicator weight", denoted in our model as α , so:

$$378 \quad \alpha' = \frac{\alpha}{1 - \alpha} \quad (34)$$

And combining with the previous equations we get:

$$\begin{aligned}
V(x' - x) &\approx x(1 - x) \left(\frac{1 + \frac{\alpha}{1-\alpha}}{1 + \frac{\alpha}{1-\alpha}N} \right) \\
&= x(1 - x) \left(\frac{\frac{1-\alpha+\alpha}{1-\alpha}}{\frac{1-\alpha+\alpha N}{1-\alpha}} \right) \\
&= x(1 - x) \left(\frac{1}{1 - \alpha(1 - N)} \right) \\
&= x(1 - x) \left(\frac{1}{\alpha N + (1 - \alpha)} \right) \\
&= x(1 - x) \frac{1}{N_e}
\end{aligned} \tag{35}$$

Using our substitute for a selection coefficient, $1 - \beta$, and the effective population size N_e , we can estimate the fixation probability and time of our binary model.

The fixation probability derived from Kimura is therefore:

$$P_{fix} = \frac{1 - e^{-2(1-\beta)N_e x}}{1 - e^{-2(1-\beta)N_e}} \tag{36}$$

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

The time to fixation can be estimated by:

$$T_{fix} = \frac{1 - P_{fix}}{1 - \beta} \int_0^x \frac{e^{2(1-\beta)\xi} - 1}{\xi(1 - \xi)} d\xi + \frac{P_{fix}}{1 - \beta} \int_x^1 \frac{1 - e^{-2(1-\beta)(1-\xi)}}{\xi(1 - \xi)} d\xi \tag{37}$$

where the integrals cannot be solved in closed form, so we can only estimate them numerically.

To validate our math we ran multiple simulations comparing our binary model with the classic Wright-Fisher model, using different α and β each time, and using the corresponding values of s and N_e for the WF simulations. In fig. 5 we changed α (and N_e accordingly) and used a constant β . In fig. 6 we changed β and used a constant α . In both cases we can see that the two models behave similarly, and both are approximated well by the Kimura's equations: eq. (36) and eq. (37).

Changing environment

After finding good estimations for our model in a constant environment, when the favorable trait is always \hat{A} , we want to find an estimation for our model in a changing environment.

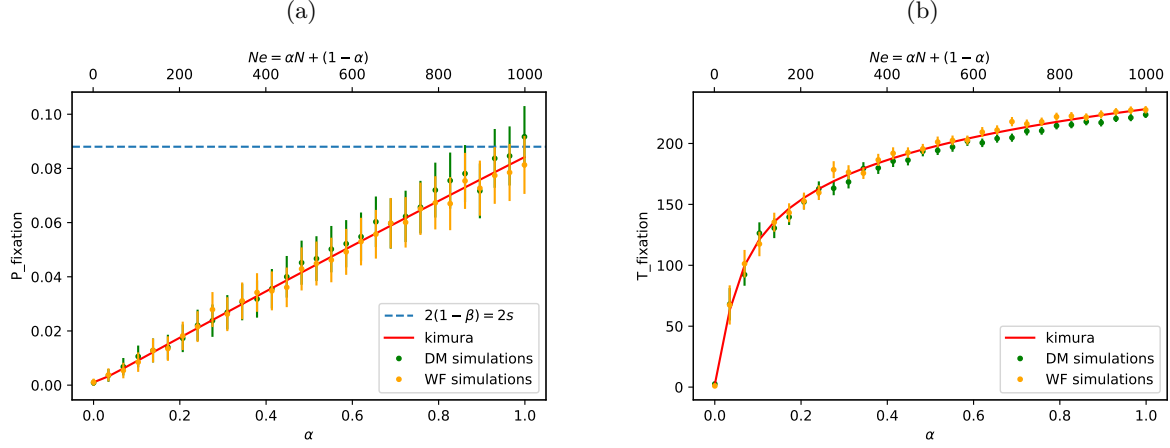


Figure 5: Comparison of the DM approximation and the WF model for different values of the effective population size. The approximation seems very good, and is also condensed around the mathematical equation expectancy. Error bars are 95% confidence intervals. Effective population calculated by $N_e = \alpha N + (1 - \alpha)$. 5,000 simulations per data point, $N = 1,000$, $\hat{A} = 1$, $A = 0.7$, $J = 1$, $1 - \beta = s = 0.044$.

For that we will find an expression for the expected and variance of the change in frequency
 398 between t generations. Let $s_t = N(1 - \beta_t)$, and $S_n = \sum_{i=1}^n s_i$, where β_t is $\beta(A)$ at time/generation t .

Proposition: $E[\frac{X_t}{N} - x] \simeq \frac{1}{N} S_t x(1 - x)$, $V(\frac{X_t}{N}) \simeq \frac{1}{N_e} t x(1 - x)$, where x is the initial frequency
 400 of the favorable/invasive trait and X_t is the number of individuals with the trait at time t .

The proof is based on the proof of Ram et al. (2018), proving a similar scenario.

402 **Proof by induction:** From eq. (27) we know that

$$\begin{aligned}
 E \left[\frac{X_{t+1}}{N} - \frac{X_t}{N} \middle| X_t \right] &= \frac{X_t}{N} \left(1 - \frac{X_t}{N} \right) (1 - \beta_{t+1}) \\
 &= \frac{1}{N} \frac{X_t}{N} \left(1 - \frac{X_t}{N} \right) s_{t+1}
 \end{aligned} \tag{38}$$

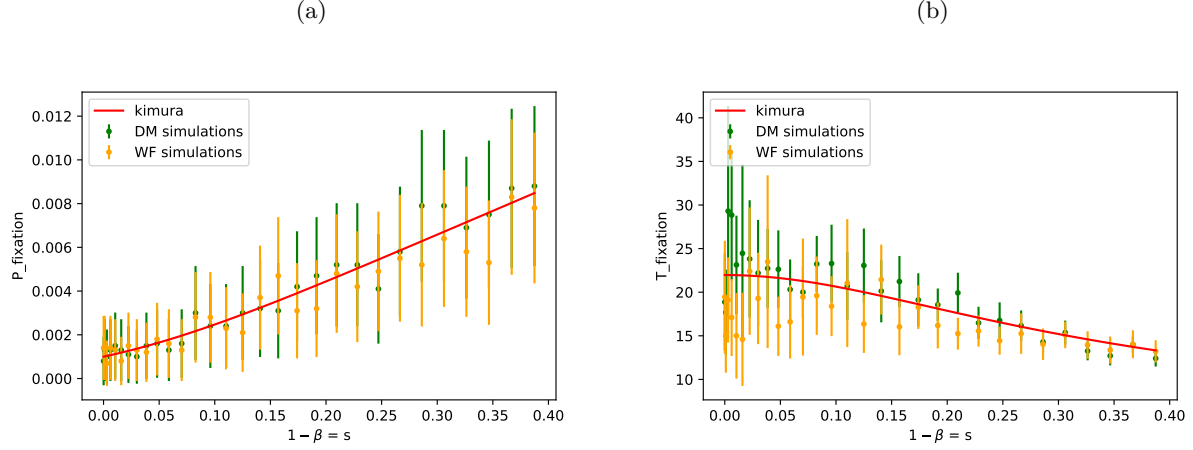


Figure 6: Comparison of the DM approximation and the WF model for different values of the selection coefficient, manifested as success bias in our model. The approximation seems good, and is also condensed around the mathematical equation expectancy. Error bars are 95% confidence intervals. Effective population calculated by $N_e = \alpha N + (1 - \alpha)$. 5,000 simulations per data point, $N = 1,000$, $\hat{A} = 1$, $A = 0.7, J = 1, \alpha = 0.01$.

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

$$\begin{aligned}
 E \left[\frac{X_t}{N} \left(1 - \frac{X_t}{N} \right) \right] &= E \left[\frac{X_t}{N} - \left(\frac{X_t}{N} \right)^2 \right] \\
 &= E \left[\frac{X_t}{N} \right] - E \left[\left(\frac{X_t}{N} \right)^2 \right] \\
 &= E \left[\frac{X_t}{N} \right] - V \left(\frac{X_t}{N} \right) - \left(E \left[\frac{X_t}{N} \right] \right)^2
 \end{aligned} \tag{39}$$

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

$$E \left[\frac{X_t}{N} \left(1 - \frac{X_t}{N} \right) \right] \simeq E \left[\frac{X_t}{N} \right] \left(1 - E \left[\frac{X_t}{N} \right] \right) - \frac{1}{N_e} t x (1 - x) \tag{40}$$

408 From eq. (38) we know that

$$\begin{aligned}
E \left[\frac{X_{t+1}}{N} - \frac{X_t}{N} \right] &= \frac{1}{N} s_{t+1} E \left[\frac{X_t}{N} \left(1 - \frac{X_t}{N} \right) \right] \\
&\simeq \frac{1}{N} s_{t+1} \left(E \left[\frac{X_t}{N} \right] \left(1 - E \left[\frac{X_t}{N} \right] \right) - \frac{1}{N_e} t x (1 - x) \right) \\
&\simeq \frac{1}{N} s_{t+1} \cdot E \left[\frac{X_t}{N} \right] \left(1 - E \left[\frac{X_t}{N} \right] \right) - \frac{1}{N_e N} s_{t+1} t x (1 - x)
\end{aligned} \tag{41}$$

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

$$E \left[\frac{X_{t+1}}{N} - \frac{X_t}{N} \right] \simeq \frac{1}{N} s_{t+1} \cdot E \left[\frac{X_t}{N} \right] \left(1 - E \left[\frac{X_t}{N} \right] \right) \tag{42}$$

412 We'll now look at the induction assumption to see that

$$E \left[\frac{X_t}{N} - x \right] = E \left[\frac{X_t}{N} \right] - E[x] = E \left[\frac{X_t}{N} \right] - x, \tag{43}$$

414 so using the assumption we get

$$\begin{aligned}
E \left[\frac{X_t}{N} \right] &\simeq \frac{1}{N} S_t x (1 - x) + x \\
1 - E \left[\frac{X_t}{N} \right] &\simeq 1 - \frac{1}{N} S_t x (1 - x) + x
\end{aligned} \tag{44}$$

416 we'll use both expressions in eq. (42) and get

$$\begin{aligned}
E \left[\frac{X_{t+1}}{N} - \frac{X_t}{N} \right] &\simeq \frac{1}{N} s_{t+1} \left(\frac{1}{N} S_t x (1 - x) + x \right) \left(1 - \frac{1}{N} S_t x (1 - x) + x \right) \\
&\simeq \frac{1}{N} s_{t+1} \cdot x (1 - x)
\end{aligned} \tag{45}$$

418 after again omitting $O(\frac{1}{N^2})$ parts of the equation. To conclude our proof, we see that

$$E \left[\frac{X_{t+1}}{N} - x \right] = E \left[\frac{X_{t+1}}{N} - \frac{X_t}{N} \right] + E \left[\frac{X_t}{N} - x \right] \tag{46}$$

420 so again using the induction assumption, together with eq. (45) we get

$$\begin{aligned}
E \left[\frac{X_{t+1}}{N} - x \right] &\simeq \frac{1}{N} s_{t+1} \cdot x(1-x) + \frac{1}{N} S_t \cdot x(1-x) \\
&\simeq \frac{1}{N} x(1-x)(S_t + s_{t+1}) \\
&\simeq \frac{1}{N} S_{t+1} x(1-x)
\end{aligned} \tag{47}$$

422 which proves the first part of our preposition.

For the second part, we'll use a property of variance:

$$424 \quad V \left(\frac{X_{t+1}}{N} \right) = E \left[V \left(\frac{X_{t+1}}{N} \middle| X_t \right) \right] + V \left(E \left[\frac{X_{t+1}}{N} \middle| X_t \right] \right) \tag{48}$$

using eq. (38) we see that:

$$\begin{aligned}
E \left[\frac{X_{t+1}}{N} \middle| X_t \right] - E \left[\frac{X_t}{N} \middle| X_t \right] &= \frac{1}{N} s_{t+1} \frac{X_t}{N} \left(1 - \frac{X_t}{N} \right) \\
426 \quad E \left[\frac{X_{t+1}}{N} \middle| X_t \right] &= \frac{X_t}{N} + \frac{1}{N} s_{t+1} \frac{X_t}{N} \left(1 - \frac{X_t}{N} \right)
\end{aligned} \tag{49}$$

Using eq. (35) we get:

$$428 \quad V \left(\frac{X_{t+1}}{N} \middle| X_t \right) = \frac{1}{N_e} \frac{X_t}{N} \left(1 - \frac{X_t}{N} \right) \tag{50}$$

and using the equation $y'(1-y') \simeq y(1-y)$ on the first part of eq. (48) we get:

$$430 \quad E \left[V \left(\frac{X_{t+1}}{N} \middle| X_t \right) \right] = \frac{1}{N_e} E \left[\frac{X_t}{N} \left(1 - \frac{X_t}{N} \right) \right] \simeq \frac{1}{N_e} x(1-x) \tag{51}$$

and moving on to simplify the second part of eq. (48) using eq. (49):

$$432 \quad V \left(E \left[\frac{X_{t+1}}{N} \middle| X_t \right] \right) = V \left(\frac{X_t}{N} + \frac{1}{N} s_{t+1} \frac{X_t}{N} \left(1 - \frac{X_t}{N} \right) \right) \tag{52}$$

434 and now, because $\frac{X_t}{N}$ is a frequency, i.e $0 \leq \frac{X_t}{N} \leq 1$, we know that $V \left(\frac{X_t}{N} \left(1 - \frac{X_t}{N} \right) \right) \leq \frac{1}{4}$. We therefore see that:

$$V \left(\frac{1}{N} s_{t+1} \frac{X_t}{N} \left(1 - \frac{X_t}{N} \right) \right) \leq \frac{1}{4N^2} s_{t+1}^2 \tag{53}$$

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

$$V \left(E \left[\frac{X_{t+1}}{N} \middle| X_t \right] \right) = V \left(\frac{X_t}{N} \right) + O \left(\frac{1}{N^2} \right) \simeq V \left(\frac{X_t}{N} \right) \tag{54}$$

(a) success bias/selection coefficient is: $1 - \beta = s = 0.005$

(b) success weight is: $\alpha = 0.1$

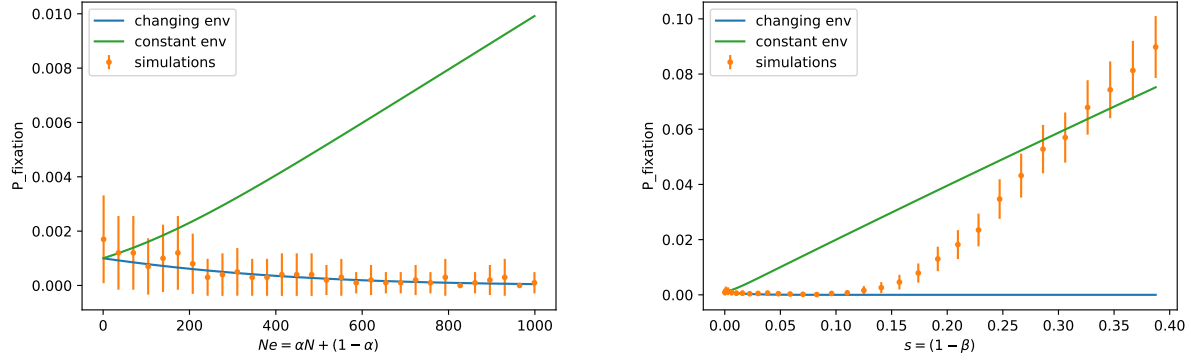


Figure 7: Model simulations compared with both the constant environment and the changing environment equations with different effective populations sizes and selection coefficients. Changing the effective population size doesn't affect the approximation, and it is condensed the mathematical expected values across all values. High values of success bias ($s > 0.1$) will distance the simulations from the changing environment expected values. Very high values ($s > 0.35$) will even deviate from the constant environment expected values. This is expected because Kimura's approximation are only viable for low selection coefficient values. 10,000 simulations per data point, $N = 1,000$, $\hat{A} = 1$, $A = 0.9$, $J = 1$.

438 Using the induction assumption and eq. (51):

$$V\left(\frac{X_{t+1}}{N}\right) \simeq \frac{1}{N_e}x(1-x) + \frac{1}{N_e}tx(1-x) \simeq \frac{1}{N_e}x(1-x)(t+1) \quad (55)$$

440 proving the second part of our preposition.

Following our proof, we can say that after many cycles, we can use a modified version of our
442 fixation probability:

$$P_{fix} = \frac{1 - e^{-2\frac{S_n}{n}N_ex}}{1 - e^{-2\frac{S_n}{n}N_e}} \quad (56)$$

444 where $\frac{S_n}{n} = \frac{k-l}{k+l}(1 - \beta)$, $n = k + l$. Put into words, we use the average selection coefficient of a
cycle ($k + l$) as the selection coefficient in our original equation. In our proof we showed that the
446 expected change in frequency and variance is only manifested in the selection coefficient S_n , and
that we can use those modified equation as a base for Kimura's equation.

448 We wanted again to validate our results, using simulations. This time, the number of parameters
increased: in addition to α, β , there are also k, l as model parameters.

450 We again tried different variations of the parameters, changing only one of them at a time. In
fig. 7 we can see that α on it's own doesn't cause any deviation for the the estimation. β however
452 affects the results greatly.

We plotted along the modified estimation the original Kimura's estimation, as a limiter. We
454 suspect that when β is too large, there won't be many cycles in the simulations. This might
happen if either the population reaches a high frequency of the ideal trait after only a few cycles,

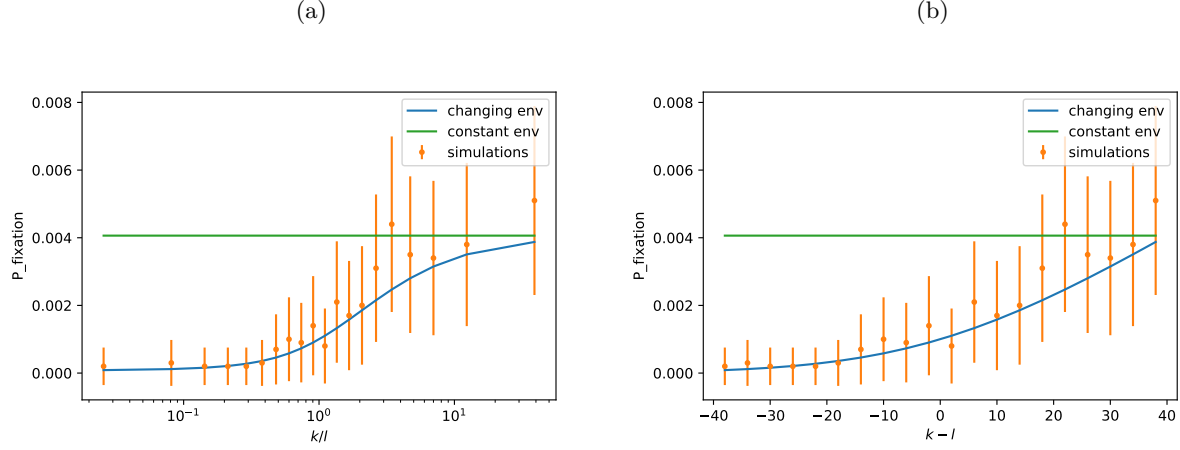


Figure 8: Model simulations compared with both the constant environment and the changing environment equations for different compositions of the environment cycle. When $k < l$ the approximation is good. When $k > l$, the approximation and the simulations are both very close to the constant environment approximation. 10,000 simulations per data point, $N = 1,000$, $\hat{A} = 1$, $A = 0.8$, $J = 1$, $1 - \beta = s = 0.02$, $\alpha = 0.1$.

or it get extinct very quickly, because the advantage it had in the k generations wasn't sufficient, and the same s becomes a greater disadvantage when the environment changes, resulting in a fast extinction.

In the larger values of β we even see a deviation from the original estimation environment, but it's to be expected, because Kimura's equations are only viable for small s values.

We then also tried changing the composition of the cycle, by keeping a constant $n = 40$, but changing k, l accordingly.

In fig. 8 we see that the larger k relative to l , the closer the modified equation is to the original estimation of the constant environment. When using higher values of n , the simulation results doesn't fit the equation result as with lower values. This is due to the fact that our proof, and therefore our equation is more accurate when more cycles occur. When n is high, there will be less cycles, and the simulations will get closer to the constant environment equation.

Discussion

Cultural transmission is the phenomenon of which cultural elements, in the form of attitudes, values, beliefs, and behavioral patterns, are transmitted between individuals, typically via copying. Some cultural traits can be more likely to be copied by others, regardless of their frequency in the population. Such transmission biases are common in cultural transmission processes. Many models are based on the assumption that success can be correctly identified, and easily copied. Here we assume that success isn't correctly identified, therefore individuals may use other indicators to try and estimate the success of potential role-models. We believe, as Fogarty et al. (2017) suggest, that *prestige biases* are more common in nature than success biases, since estimating success is harder. We believe prestige is composed of two main components: a trait that indicates success

478 (but doesn't guarantee it), and the influence the individual already has on others, i.e number of
individuals already chose him as a role-model. We suggest a model for *prestige bias*, inspired by
480 the model Boyd and Richerson (1988) have suggested, and added the *influence bias* to it. We
approximated our models using various distributions, and compared them to the original model
482 using simulations. We showed that a *Rich getting richer* type of model can be approximated well
by the general binomial distribution and the dirichlet multinomial distribution. We experimented
484 with constant and changing environment in our model, and created a variation of a binary model
for easier mathematical and computational analysis. We believe that in this era of social media it
486 is easy to estimate one's influence over others. It is therefore crucial to model the cultural biases
more realistically than success bias based model, and we believe including influence is crucial for
488 that purpose.

With a more realistic model of a common cultural transmission bias, we may be able to better
490 understand decision-making processes in humans, including life-changing choices such as occupation
or a life partner. Our model can be expanded in multiple ways: observing the effects of different
492 bias functions, including errors in estimating the influence, combining factors of cost when copying
from an influential role model (not all could afford to copy from the most popular role-model),
494 and analyzing the differences when including several optimal values for the indicator trait (multiple
preference traits in the population).

496 **Appendix A - Time table**

Today - Oct 2021: Find approximation replacing Durrett's equations for the time to fixation.

498 **Nov - Mar 2021:** Combining the findings to a paper and a thesis.

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