On the interpretation of the operation of natural selection in class-structured populations

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Abstract

Biological adaptation is the outcome of allele-frequency change by natural selection. At the same time, populations are usually class structured as individuals occupy different states such as age, sex, stage or habitat. This is known to result in the differential transmission of alleles called class transmission, and thus also affects allele-frequency change even in the absence of selection. How does one then isolate the allele-frequency change due to selection from that owing to class transmission? We show how reproductive values can be used to decompose arithmetic allele-frequency change between any two distant generations of the evolutionary process in terms of effects of selection and class transmission. This provides a missing relationship between multigenerational allele-frequency change and the operation of selection. It also allows to define an appropriate measure of fitness summarizing the effect of selection in a multigenerational evolutionary process, which connects asymptotically to invasion fitness.

Keywords: natural selection, class structure, reproductive values, allele-frequency change.

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Introduction

Consider the following situation you may encounter as an evolutionary biologist. Suppose you observe a population between two distant points in time, and empirically measure at each census point the total number of individuals in the population and the alleles they carry at some locus of interest. Suppose further you can also measure the survival and number of descendants of these individuals, and that these measurements can be subdivided into different reproductive classes the individuals carrying the alleles can be in, such as the sex, age, stage or habitat. The overall time of observation is moreover assumed short enough to neglect the appearance of new mutations and the population is closed and large enough to neglect the effect of migration and genetic drift. Then, any change in allele frequency must have occurred due to natural selection and/or the non-selective process of class transmission, where the latter is the differential reproductive success of an individual owing to differential classes in which individuals reproduce and survive, also known to alter allele frequencies in class-structured populations even in the absence of selection [e.g., Grafen, 2006, Leturque and Rousset, 2002, Stubblefield and Seger, 1990, Taylor, 1990]. However, it is only natural selection that can cause allelic fixations and hence is the only evolutionary force that shapes biological adaptations [Barton et al., 2007, Fisher, 1930, Futuyama, 2017, Lynch and Walsh, 2018]. It is therefore natural to ask how much of the measured change in allele frequency is caused by natural selection and how much by class transmission, and how much of the overall change can be attributed to each demographic time step of the evolutionary process? To answer this question requires a careful account of the operation of selection and class transmission in class-structured populations.

Most previous theoretical work on evolution in class-structured populations, however, has focused on biological scenarios where class transmission has a negligible effect on the evolutionary dynamics [e.g., Barfield et al., 2011, Caswell, 2000, Engen et al., 2014, Gardner, 2015, Grafen, 2006, 2015, Leturque and Rousset, 2002, Lion, 2018, Lion and Gandon, 2022, Priklopil and Lehmann, 2020, Rousset, 2004, Taylor, 1990]. This is the case, for instance, in a large-time limit when either survival and reproduction is frequency- and density-independent [Engen et al., 2014, Grafen, 2006, 2015] or when selection is assumed weak [Barfield et al., 2011, Leturque and Rousset, 2002, Lion, 2018, Lion and Gandon, 2022, Priklopil and Lehmann, 2020, Rousset, 2004, Rousset and Ronce, 2004, Taylor and Frank, 1996]. In this work, the asymptotic evolutionary success of an allele is characterised in terms of a weighted allele frequency (or weighted trait average) with weights as reproductive values, which can loosely be interpreted as genetic contributions of individuals to the future of the population [e.g., Barton and Etheridge, 2011]. The main justification that has been given for using reproductive values as weights is that the dynamics of weighted averages behave 'nicely' in that they cancel any allele-frequency change caused by non-heritable fitness differences [Grafen, 2006]. The resulting dynamics governed purely by reproductive-value weighted fitness differentials is then taken as a measure of selection [Engen et al., 2014, Grafen, 2006, 2015, Leturque and Rous-

set, 2002, Lion, 2018, Lion and Gandon, 2022, Rousset, 2004, Rousset and Ronce, 2004, Taylor and Frank, 1996]. However, in this previous work it is not clear how the reproductive-value weighted frequency connects to the standard arithmetic average allele frequency describing the unfolding of the evolutionary process. As a consequence, no explicit formal nor verbal biological reason has been given in why reproductive-value weighted allele-frequency is an appropriate measure of selection, and how to interpret it in terms of the arithmetic allele frequency. Further, for non-asymptotic finite-time evolutionary processes, class transmission will contribute to allele-frequency change and hence cannot be ironed away by using reproductive values as weights.

The aim of this paper is to give an answer to these questions by providing an operational decomposition of the contribution of natural selection and that of class transmission to the arithmetic average allele-frequency change in a class-structured population, where individuals may experience frequency- and density dependent interactions as well as environmental fluctuations. In this decomposition, we consider a change over an arbitrary number of demographic time steps and allocate fractions of the average allele-frequency change to each step of this evolutionary process. Our analysis shows, in particular, that the previously used reproductive-value weighted allele-frequency change is exactly the arithmetic allele-frequency change caused by selection when 'assessed' at the end of the observed process. We also provide the expression for the previously unaccounted allele-frequency change due to class transmission, such that the sum of these two contributions gives the total arithmetic allele-frequency change attributed to any given generation but assessed at the end of the observed process. These calculations imply, perhaps counter-intuitively, that the allele-frequency change caused by selection and class transmission during any demographic time step is tied to the entire evolutionary process of interest and hence cannot be studied in isolation. Finally, we provide a detailed and biologically explicit definition of reproductive value, and provide a representation of fitness summarizing the effect of selection and class transmission in the multiple time-step evolutionary process.

Our analysis proceed in two main steps. In order to motivate the formalization of allele-frequency change over an evolutionary process spanning multiple demographic time steps, we first consider the more traditional approach in calculating the allele-frequency change over a single time-step that is still widely used in evolutionary analysis. Second, we turn to the multiple time-step evolutionary process, which forces us to reconsider some of the intuition gained from the singe time-step change. Here, we derive our main results, discuss the connected literature, and then connect our results to earlier work on asymptotic evolutionary dynamics.

Single Generational Process in Class-Structured Populations

The Model

For simplicity but without loss of generality, we consider a population of haploid individuals that reproduce asexually, each of which is characterized by one of a finite number of alleles that segregate in the population. The population is assumed class-structured so that each individual belongs to one of a finite number of classes (age, stage etc.) and can possibly transition between the classes, e.g., via survival, maturation or physiological development. We furthermore assume that reproduction and class transition occurs at discrete demographic time steps, that there are no mutations, and that the population is closed and large enough to ignore the effect of migration and genetic drift. Then, the state of the population can be fully characterized by the vector $\mathbf{n}_t$ collecting elements of the form $n_t(a,i)$, which stands for the number of individuals in class a with allele i at time t. This number satisfies the recursion

$$n_{t+1}(a,i) = \sum_b w_t(a \mid b,i) n_t(b,i), \tag{1}$$

where we use the shorthand notation $w_t(a \mid b,i) = w_t(a \mid b,i,\mathbf{n}_t)$ to represent the class-specific individual fitness of a carrier of allele i. The class-specific individual fitness $w_t(a \mid b,i)$ is defined as the expected number of settled 'offspring' in class a with allele i at $t+1$ produced by a single 'parent' with allele i in class b at t including the surviving self (hence quotation marks), and thus gives the number of gene copies a at time $t+1$ descending from a parent b carrying allele i and alive at t. Because the class-specific individual fitness may depend in an arbitrary way on the population state $\mathbf{n}_t$, the model allows for arbitrarily complicated frequency- and density-dependent interactions between individuals and because it is indexed by t it allows for arbitrary extrinsic environmental fluctuations affecting reproduction and class transition. We sum over all classes in eq. (1) because parents in any class may possibly produce offspring of any other class, and we note that all equations throughout hold for all segregating alleles.

Allele-Frequency Change

To analyze allele-frequency change in the model, we need to introduce the following notations (see Table 1 for a summary of all notations). First, we denote by $n_t(i) = \sum_a n_t(a,i)$ the total number of individuals carrying allele i, by $n_t(a) = \sum_i n_t(a,i)$ the total number of individuals in class a and by $n_t = \sum_{a,i} n_t(a,i)$ the total number of individuals in the population. From these quantities, $p_t(i) = n_t(i)/n_t$ is the frequency of allele i, $p_t(a) = n_t(a)/n_t$ is the frequency of class a individuals, $p_t(a \mid i) = n_t(a,i)/n_t(i)$ is the frequency of class a individuals amongst those with allele i and $p_t(i \mid a) = n_t(a,i)/n_t(a)$ is the frequency of allele i within class a. From this, and summing eq. (1) over all classes and alleles, we have that $n_{t+1} = \bar{w}_t n_t$, where $\bar{w}_t = \sum_{a,b} \bar{w}_t(a \mid b) p_t(b)$ is the average fitness in the population, which is here expressed in

terms of the class-specific average fitness $\bar{w}_t(a \mid b) = \sum_i w_t(a \mid b, i) p_t(i \mid b)$ over alleles, while the average fitness of allele i itself is $\bar{w}_t(i) = \sum_{a,b} w_t(a \mid b, i) p_t(b \mid i)$.

The change in frequency $\Delta p_t(i) = p_{t+1}(i) - p_t(i)$ of allele i over a single time step $[t, t+1]$, which we refer to as 'generation' t, is then

$$\Delta p_t(i) = \frac{1}{n_{t+1}} \left(\bar{w}_t(i) - \bar{w}_t\right) n_t(i) = \left(\frac{\bar{w}_t(i) - \bar{w}_t}{\bar{w}_t}\right) p_t(i) \tag{2}$$

(Appendix A1.1). The first equality makes the cause of allele-frequency change in generation t explicit: $\bar{w}_t(i) - \bar{w}_t$ gives the additional number of offspring produced by a single allele i carrier compared to an average individual from the total population. Multiplying this with the total number of parents i at t and dividing by the total number of offspring at $t+1$ we obtain the change in allele-frequency i in generation t. The second equality in eq. (2) is the standard representation of allele-frequency change in the absence of mutation and genetic-drift (e.g., Gillespie, 1991, eq. 4.1, Nagylaki, 1992, eq. 2.8 for models without class structure). Indeed, an allele can only increase in frequency if it propagates through the population faster than alleles do on average: allele i increases in frequency in generation t whenever $\bar{w}_t(i)/\bar{w}_t > 1$.

While it would be tempting to conclude that natural selection is responsible for all the allele-frequency change in eq. (2), as is the case in populations without class structure (Figure 1; Gillespie, 1991), this is not true in class-structured populations. Indeed, one can see this by considering a situation where every allele in each class has the same class-specific fitness $w_t(a \mid b, i) = w_t(a \mid b)$ for all i segregating in the population at all times. This thus defines a neutral process whereby eq. (2) reduces to

$$\Delta p_t^{\mathrm{ct}}(i) = \frac{1}{n_{t+1}} \sum_a \sum_b w_t(a \mid b) \Big[p_t(b \mid i) - p_t(b)\Big] n_t(i), \tag{3}$$

where we used the superscript 'ct' to indicate that all change in allele frequency $\Delta p_t(i) = \Delta p_t^{\mathrm{ct}}(i)$ is caused by class transmission only (Appendix A1.1). Equation (3) shows that non-selective allele-frequency change is due to a non-uniform distribution of alleles across classes and occurs until all alleles are fully transmitted through all the classes resulting in $p_t(b \mid i) = p_t(b)$, a point at which there is zero allele-frequency change.

Disentangling Selection from Class Transmission

How then should one disentangle the effect of natural selection from the effect of class transmission when there are heritable differences in survival and reproduction in class structured populations, i.e. when $w_t(a \mid b, i) \neq w_t(a \mid b, j)$ for different alleles i and j? Because alleles can be found in different classes and selection on allele i should reflects its reproductive success as compared to all segregating alleles in the population, we are led to the following

partitioning of allele-frequency change

$$\Delta p_t(i) = \Delta p_t^{\text{sel}}(i) + \Delta p_t^{\text{ct}}(i), \tag{4a}$$

where the effect of selection on allele-frequency change is

$$\Delta p_t^{\text{sel}}(i) = \frac{1}{n_{t+1}} \sum_a \sum_b \Big[w_t(a \mid b, i) - \bar{w}_t(a \mid b) \Big] p_t(b \mid i) n_t(i) = \left(\frac{\bar{w}_t(i) - \bar{\bar{w}}_t(i)}{\bar{w}_t} \right) p_t(i), \tag{4b}$$

while the effect of class transmission on allele-frequency change is

$$\Delta p_t^{\text{ct}}(i) = \frac{1}{n_{t+1}} \sum_a \sum_b \Big[\bar{w}_t(a \mid b) - \frac{1}{n_{\mathcal{C}}} \bar{w}_t \Big] p_t(b \mid i) n_t(i) = \left(\frac{\bar{\bar{w}}_t(i) - \bar{w}_t}{\bar{w}_t} \right) p_t(i), \tag{4c}$$

where $\bar{\bar{w}}_t(i) = \sum_{a,b} \bar{w}_t(a \mid b) p_t(b \mid i)$ is the fitness of an allele i carrier if it were to reproduce as an average (reference) individual in each class, and $n_{\mathcal{C}}$ is the number of classes in the population. This partitioning follows because by definition different evolutionary forces have distinct effects on allele frequency, and, each force must conserve allele frequencies so that a change in frequency of any one allele must be balanced by the change in other alleles (Appendix A1.1, Figure 1B).

The first equality in eq. (4b) says that the effect of selection in each class is proportional to the difference between the class-specific fitness $w_t(a \mid b, i)$ of an individual carrying i as compared to the class specific average fitness $\bar{w}_t(a \mid b)$ in that class, which is thus the reference fitness below and above which selection occurs. Summing over all classes then produces the second equality in eq. (4b), which says that allele i is favoured by selection whenever it has a greater fitness than if it were to reproduce as an average individual within a class, i.e. $\bar{w}_t(i)/\bar{\bar{w}}_t(i) > 1$. By contrast, the first equality in eq. (4c) says that the effect of class transmission in each class is proportional to the difference between the class-specific average fitness $\bar{w}_t(a \mid b)$ and the class-specific fitness in the absence of class-specific differences in reproduction $\bar{w}_t/n_{\mathcal{C}}$ (where reproduction within and between classes is identical). Summing over all classes, allele i is thus favoured by class transmission whenever its fitness is greater if it were to reproduce as an average individual within a class as compared to an average individual in the total population, i.e. $\bar{\bar{w}}_t(i)/\bar{w}_t > 1$, and this occurs whenever alleles are non-uniformly distributed across classes (see eq. A7 in Appendix A1.1). We also note that this force of class transmission is not the outcome of a neutral process only, since the fitness of allele i under class transmission $\bar{\bar{w}}_t(i)$ depends on $p_t(b \mid i)$ and is thus calculated from the full evolutionary process where $w_t(a \mid b, i) \neq w_t(a \mid b, j)$. Whenever the process is neutral, i.e. $w_t(a \mid b, i) = w_t(a \mid b)$ for all i, then $\Delta p_t^{\text{sel}}(i) = 0$ and $\Delta p_t^{\text{ct}}(i)$ reduces to eq. (3). A partitioning equivalent to eq. (4) but expressed in terms of phenotypic change was derived by Lion [2018, eq. 2] from the Price equation.

Multigenerational Process in Class-Structured Populations

Framing Allele-Frequency Change Decomposition

Suppose now the process (eq. 1) runs over multiple generations between some initial time t_0 and final time t_f where $\mathcal{T} = [t_0, t_\mathrm{f}]$ will denote this interval and contain the generation t discussed in eqs. (2-4). Our next aim is to ascertain how much of the total allele-frequency change $\Delta p_\mathcal{T}(i) = p_{t_\mathrm{f}}(i) - p_{t_0}(i)$ that has occurred during $\mathcal{T}$ is due to natural selection and class transmission, and what fractions of this should be attributed to each generation of the multigenerational process. That is, we seek to find a decomposition

$$\Delta p_\mathcal{T}(i) = \Delta p^{\mathrm{sel}}_\mathcal{T}(i) + \Delta p^{\mathrm{ct}}_\mathcal{T}(i), \tag{5a}$$

where

$$\Delta p^{\mathrm{sel}}_\mathcal{T}(i) = \sum_{t=t_0}^{t_\mathrm{f}-1} \Delta p^{\mathrm{sel}}_{t|\mathcal{T}}(i) \qquad \Delta p^{\mathrm{ct}}_\mathcal{T}(i) = \sum_{t=t_0}^{t_\mathrm{f}-1} \Delta p^{\mathrm{ct}}_{t|\mathcal{T}}(i) \tag{5b}$$

are, respectively, the cumulative fractions of allele-frequency change over $\mathcal{T}$ that are attributed to selection and class transmission, and where $\Delta p^{\mathrm{sel}}_{t|\mathcal{T}}(i)$ and $\Delta p^{\mathrm{ct}}_{t|\mathcal{T}}(i)$ represent, respectively, the fractions of these changes that can be attributed to selection and class transmission occurring in generation t. The fraction of the total cumulative change attributed to generation t is thus $\Delta p^{\mathrm{sel}}_{t|\mathcal{T}}(i) + \Delta p^{\mathrm{ct}}_{t|\mathcal{T}}(i)$.

Because $\Delta p^{\mathrm{sel}}_{t|\mathcal{T}}(i)$ and $\Delta p^{\mathrm{ct}}_{t|\mathcal{T}}(i)$ are assessed at the final time t_f and conditioned on the process starting at the initial time t_0, they can not match the partitioning in eq. (4) of the single-generational process. Indeed, $\Delta p^{\mathrm{ct}}_t(i)$ is not in general equal to $\Delta p^{\mathrm{ct}}_{t|\mathcal{T}}(i)$ because $\Delta p^{\mathrm{ct}}_t(i)$ is conditioned on the state of the population at t and hence counts also offspring that are produced by parents who themselves were produced by selection in the previous generation(s) $[t_0, t]$. Likewise, $\Delta p^{\mathrm{sel}}_t(i)$ is not in general equal to $\Delta p^{\mathrm{sel}}_{t|\mathcal{T}}(i)$ because $\Delta p^{\mathrm{sel}}_t(i)$ does not take into account that the descendants of the selected offspring undergo the process of class transmission during $[t+1, t_\mathrm{f}]$ thus altering the magnitude of the frequency assessed at t_f. As a consequence, the fraction $\Delta p^{\mathrm{sel}}_{t|\mathcal{T}}(i) + \Delta p^{\mathrm{ct}}_{t|\mathcal{T}}(i)$ of the cumulative change attributed to generation t is also not in general equal to $\Delta p^{\mathrm{sel}}_t(i) + \Delta p^{\mathrm{ct}}_t(i)$. The question then is, how does one calculate the contributions in eq. (5)? To that end, we must first introduce the concept of an individual reproductive value.

Individual Reproductive Value

We now define $n^\circ_t(a, i)$ as the number of a, i individuals at time t that satisfy the recursion

$$n^\circ_{t+1}(a, i) = \sum_b \bar{w}_t(a \mid b) n^\circ_t(b, i) \tag{6}$$

from t_0 onward, with initial condition $n^{\circ}_{t_0}(a,i) = n_{t_0}(a,i)$ for all a and i. The process induced by eq. (6) is said to be non-selective because every allele within a class reproduces equally according to the class-specific fitness $\bar{w}_t(a \mid b)$ of a randomly sampled allele ('average allele') in each class, and hence no allele is being selected for. We emphasise that the choice of this non-selective process is not arbitrary, and is defined precisely to give the dynamics of an allele as if it were to reproduce as an average allele, so that $\bar{w}_t(a \mid b)$ is used as a reference fitness to disentangle selection from class transmission (see eq. 4). The class-specific fitness $\bar{w}_t(a \mid b)$ is thus calculated under the full observed evolutionary process with selection (i.e. the process defined by eq. 1), whereby the population is not monomorphic, and for this reason we refrained from calling the non-selective process the 'neutral process'. All variables with a superscript $\circ$ will then stand for variables that are determined by this non-selective process from time t_0 onwards (Appendix A1.2). Formally, eq. (6) is the adjoint equation to the backward in time process

$$v_t(a) = \sum_b v_{t+1}(b)\bar{w}_t(b \mid a), \tag{7}$$

and we set the final condition to $v_{t_f}(a) = 1$ for all a (Box A). We can then interpret $v_t(a)$ as the *number of individuals alive at the final time t_f that under the non-selective process where individuals survive and reproduce as average individuals within each class between $[t, t_f]$ descend from a single individual of class a alive at time t*. We call $v_t(a)$ the reproductive value of an (average) individual of class a (i.e. of a randomly sampled allele in class a). This is a representation of the classic notion of individual reproductive value [Fisher, 1930, Grafen, 2006, Leslie, 1948, Taylor, 1990, Tuljapurkar, 1989b, such non-asymptotic reproductive values have also been previously called 'genetic contributions', Barton and Etheridge, 2011], which in a multi-type process has indeed been evaluated from the average fitness within a class [Lessard and Soares, 2016, Lion, 2018]. We denote by $\bar{v}_t(i) = \sum_a v_t(a)p_t(a \mid i)$ the average reproductive value of a carrier of allele i. We also define a population-wide average reproductive value $\bar{v}_t$ from $\bar{v}_t = \bar{v}_{t+1}\bar{w}_t$ which is an adjoint equation to the process of population growth $n_{t+1} = \bar{w}_t n_t$, thus underpinning the non-selective process of populations without class structure. The interpretation of $\bar{v}_t$ is the number of individuals at t_f that descend under the process of population growth from an average individual in the population at time t (i.e. $\bar{v}_t = \prod_{t=t_0}^{t_f-1} \bar{w}_t$).

Disentangling Selection from Class Transmission

We can now represent the contribution of selection attributed to generation t as

$$\Delta p^{\text{sel}}_{t|\mathcal{T}}(i) = \frac{1}{n_{t_f}} \sum_a \sum_b v_{t+1}(a)\Big[w_t(a \mid b,i) - \bar{w}_t(a \mid b)\Big]p_t(b \mid i)n_t(i) = \left(\frac{\bar{w}^{\text{v}}_t(i) - \bar{v}_t(i)}{\bar{v}_t}\right) p_t(i), \tag{8}$$

where $\bar{w}^{\text{v}}_t(i) = \sum_a \sum_b v_{t+1}(a)w_t(a \mid b,i)p_t(b \mid i)$ is the reproductive-value weighted average individual fitness giving the number of individuals at t_f that descend under the non-selective

processes (eqs. 6-7) from all the offspring produced by a single individual i at t (Appendix A1.2). Because $w_t(a \mid b, i) - \bar{w}_t(a \mid b)$ gives the additional number of offspring produced by i as compared to the average individual in the class during $[t, t+1]$, each of which leave $v_{t+1}(a)$ descendants under the non-selective process (eqs. 6-7), the summation over classes in eq. (8) isolates the generational effect of selection in an otherwise non-selective process (Figure 1B).

Eq. (8) is equal to the frequency of individuals measured at t_f that descend under the non-selective process from all offspring at $t+1$ that were produced due to selection during $[t, t+1]$ by all parents i at t (Figure 2B). This is the interpretation of the effect of selection attributed to generation t in a multigenerational evolutionary process. Because $\bar{v}_t(i)$ is always positive, selection favours allele i in a multigenerational process at t whenever $\bar{w}_t^\mathrm{v}(i)/\bar{v}_t(i) > 1$, where $\bar{w}_t^\mathrm{v}(i)/\bar{v}_t(i)$ is interpreted as the relative number of individuals at t_f that descend under the non-selective process from all offspring produced by a single individual i at t, relative to the number of individuals at time t_f that would descend from this individual under the non-selective process only (from a single individual i at t). The fraction $\bar{w}_t^\mathrm{v}(i)/\bar{v}_t(i)$ is thus the relative fitness attributed to selection at t in a multigenerational context.

Next, the contribution of class transmission that is attributed to the generation t is

$$\Delta p_{t|\mathcal{T}}^{\mathrm{ct}}(i) = \frac{1}{n_{t+1}} \sum_a \sum_b \left[\bar{w}_t(a \mid b) - \frac{1}{n_\mathcal{C}} \bar{w}_t \right] p_t^\circ(b \mid i) n_t^\circ(i) = \left(\frac{\bar{w}_t^\circ(i) - \bar{w}_t}{\bar{w}_t} \right) r_t^\circ(i) p_t(i), \quad (9)$$

where $\bar{w}_t^\circ(i) = \sum_{a,b} \bar{w}_t(a \mid b) p_t^\circ(b \mid i)$ is the average fitness of an individual i if it were to reproduce as an average individual of the class in which it resides at time t. In eq. (9), such an individual itself comes from a lineage of non-selected individuals during $[t_0, t]$ since $r_t^\circ(i) = n_t^\circ(i)/n_t(i)$ is the fraction of individuals i at t among those carrying i that descend from a lineage of individuals that have undergone only the non-selective process between $[t_0, t]$ (Appendix A1.2). Indeed, $\bar{w}_t^\circ(i) - \bar{w}_t$ gives the average number of offspring at $t+1$ produced by an individual i at t if it were to reproduce as an average individual in its class as compared to a population-wide average individual (compare with eq. 4c), which, when multiplied with the number of non-selected parents $n_t^\circ(b, i) = p_t^\circ(b \mid i) n_t^\circ(i)$ and divided by the total population size produces $\Delta p_{t|\mathcal{T}}^{\mathrm{ct}}(i)$, as required by the partitioning of total allele-frequency change (eq. 5). Note that we do not weight the offspring at $t+1$ with reproductive values because we would then also count events of class transmission at later generations and not only at the generation t of interest.

Eq. (9) is equal to the frequency of individuals measured at t_f that descend under the non-selective process from all offspring measured at $t+1$ that were produced due to class transmission during $[t, t+1]$ by all non-selected parents i at t (Figure 2C). This is the interpretation of the effect of class transmission attributed to generation t in a multigenerational evolutionary process. Because $\bar{w}_t$ is always positive, class transmission favours allele i in a multigenerational process in generation t whenever $\bar{w}_t^\circ(i)/\bar{w}_t > 1$. Here, $\bar{w}_t^\circ(i)/\bar{w}_t$ gives the number of offspring at $t+1$ produced due to the non-selective processes $\bar{w}_t^\circ(i)$ (see eq. 6)

relative to the number of offspring produced due to the non-selective process of population growth only $\bar{w}_t$ by a single non-selected parent i at t. The fraction $\bar{w}_t^{\circ}(i)/\bar{w}_t$ is thus the relative fitness attributed to class transmission at t in a multigenerational context.

Connection to Previous Work

We have produced a decomposition for allele-frequency change in a multigenerational process (eq. 5), where such change can be partitioned into generation-specific contributions caused by natural selection $\Delta p^{\text{sel}}_{t|\mathcal{T}}(i)$ (eq. 8) and class transmission $\Delta p^{\text{ct}}_{t|\mathcal{T}}(i)$ (eq. 9). These calculations are consistent with the partitioning of the single-generation effects of selection and class transmission, since eq. (4) is recovered by setting $t = t_0$ and $t + 1 = t_{\text{f}}$ in eq. (5) and eqs. (8)-(9), and they connect to a number of previous studies. To discuss these, let us denote by $p^{\alpha}_t(i) = \sum_a \alpha_t(a) p_t(i \mid a)$ the class reproductive-value weighted allele i frequency at t where $\sum_a \alpha_t(a) = 1$ (see eq. A16 for the representation of $\alpha_t(a)$). Then,

$$\Delta p^{\text{sel}}_{t|\mathcal{T}}(i) = \Delta p^{\alpha}_t(i) \tag{10}$$

(eq. A16). The right-hand side of eq. (8) is therefore conceptually equivalent to eq. (10) of Grafen [2015] for allele-frequency change in a panmictic population, to eq. (7) of Lion [2018] for the phenotypic change in a panmictic population, to eq. (5) of Lion and Gandon [2022] for the allele-frequency change in periodically fluctuating environments, and to eq. (69) of Priklopil and Lehmann [2021] for allele-frequency change in a spatially structured population. This previous work, however, did not provide the biological interpretation of the change $\Delta p^{\alpha}_t(i)$ in terms of contributions to final frequencies in a (finite or infinite-time) multigenerational process, i.e. it did not discuss the left-hand side of eq. (10), which is interpreted as the change in the arithmetic average allele frequency due to selection in generation t but assessed at the end of the observed evolutionary process. Also, it did not provide the corresponding expression for the allele-frequency change $\Delta p^{\text{ct}}_{t|\mathcal{T}}(i)$ caused by class transmission. The cumulative contribution of selection for phenotypic change (here corresponding to $\Delta p^{\text{sel}}_{\mathcal{T}}(i)$) was in turn discussed in Gardner [2015]. However, this previous work focused on the large-time behavior of populations ($t_{\text{f}} \to \infty$), and moreover, it did not define operationally the reproductive-value weights and instead appealed to Taylor [1990] who considers a reference fitness that is subject to a neutral process only (i.e. it is the fitness in a monomorphic population for the wild-type or resident allele). However, the recursion for reproductive value eq. (7) should be expressed in terms of the average class-specific fitness (the fitness of a randomly sampled allele in each class) in the observed focal population subject to selection (as explicitly emphasized in Lessard and Soares [2016], Lion [2018]), and so it is not clear to what type of evolutionary process the formalization of Gardner [2015] really applies to. Likewise, the cumulative change $\Delta p^{\text{sel}}_{\mathcal{T}}(i)$ was considered in Lehmann and Rousset [2014, footnote 3], but here too, the reproductive-value weights were not operationalised. We here ascertained that

the non-selective process must be evaluated under the average population process (eq. 6) for $\Delta p^{\text{sel}}_{\mathcal{T}}(i)$ to represent the cumulative contribution of selection in the observed population.

In a series of two-allele models under weak selection induced by weak phenotypic deviations, the cumulative contribution of selection was considered in populations of small (finite) size under the form of the probability of fixation [Leturque and Rousset, 2002, Rousset and Ronce, 2004]. Under weak selection, it is sufficient to evaluate reproductive values under the neutral process determined by the wild-type or resident population only (see Rousset, 2004 for applications to general demographic situations). Furthermore, and finally, in large populations and under weak phenotypic deviation, the effect of class transmission vanishes asymptotically (as $t_{\text{f}} \to \infty$). In this case for sufficiently large t the reproductive-value weighted allele-frequency change is approximately equal to the change in the arithmetic allele frequency [Priklopil and Lehmann, 2021], namely

$$\Delta p_t(i) \approx \Delta p^{\text{sel}}_{t|\mathcal{T}}(i) = \Delta p^{\alpha}_t(i), \tag{11}$$

which thus fully characterizes allele-frequency change in a class-structured population. Here too, it is sufficient to evaluate the reproductive values under the neutral process determined by the resident population only (e.g., Priklopil and Lehmann, 2020; Appendix A3.2). The term $\Delta p^{\alpha}_t(i)$ has long been in use in phenotypic models to describe reproductive-value weighted allele-frequency change under weak selection [e.g., Lion, 2018, Priklopil and Lehmann, 2020, Rousset, 2004, Roze and Rousset, 2004, Stubblefield and Seger, 1990, Taylor, 1990, 1996]. Eq. (11) thus connects this allele-frequency change under weak selection back to the final frequencies and the full frequency change at generation t of a multigenerational process. The correspondence $\Delta p_t(i) \approx \Delta p^{\alpha}_t(i)$ in eq. (11) was implicitly reached before in class-structured models for phenotypic change in panmictic populations [Barfield et al., 2011, Lion, 2018] and was explicitly discussed for allele-frequency change in spatially subdivided populations [Priklopil and Lehmann, 2021].

Geometric Mean Fitness

Having identified the contributions of selection and class transmission in a multigenerational process, it seems natural to ask whether one can summarize the evolutionary process by a single number – a representation of mean fitness – that would predict whether the allele frequency increases or decreases as a result of selection and/or class transmission? To that end, let us introduce the geometric mean fitness

$$\overline{W}_{\mathcal{T}}(i) = \overline{W}^{\text{sel}}_{\mathcal{T}}(i)\overline{W}^{\text{ct}}_{\mathcal{T}}(i), \tag{12}$$

where

$$\overline{W}^{\text{sel}}_{\mathcal{T}}(i) = \left(\prod_{t=t_0}^{t_{\text{f}}-1} W^{\text{sel}}_{t|\mathcal{T}}(i)\right)^{1/(t_{\text{f}}-t_0)} \quad \text{with} \quad W^{\text{sel}}_{t|\mathcal{T}}(i) = \frac{\bar{w}^{\text{v}}_t(i)}{\bar{v}_t(i)} \tag{13}$$

and

$$\overline{W}^{\mathrm{ct}}_{\mathcal{T}}(i) = \left(\prod_{t=t_0}^{t_f-1} W^{\mathrm{ct}}_{t|\mathcal{T}}(i)\right)^{1/(t_f-t_0)} \quad \text{with} \quad W^{\mathrm{ct}}_{t|\mathcal{T}}(i) = \frac{\bar{w}^{\circ}_t(i)}{\bar{w}_t}. \tag{14}$$

Here, $W^{\mathrm{sel}}_{t|\mathcal{T}}(i)$ is the relative fitness of a randomly sampled allele i carrier at t, which is attributed to selection at t, and $W^{\mathrm{ct}}_{t|\mathcal{T}}(i)$ is the relative fitness of a randomly sampled non-selected individual i at t, which is attributed to class transmission at t. Whenever $W^{\mathrm{sel}}_{t|\mathcal{T}}(i) > 1$, selection thus favours allele i in generation t and whenever $W^{\mathrm{ct}}_{t|\mathcal{T}}(i) > 1$ class transmission favours allele i in generation t (see Appendix A2).

Over the entire time-interval $\mathcal{T}$, selection thus favours allele i whenever $\overline{W}^{\mathrm{sel}}_{\mathcal{T}}(i) > 1$, while class transmission favours allele i whenever $\overline{W}^{\mathrm{ct}}_{\mathcal{T}}(i) > 1$. We have thus obtained a partitioning of the total geometric mean fitness into the means $\overline{W}^{\mathrm{sel}}_{\mathcal{T}}(i)$ and $\overline{W}^{\mathrm{ct}}_{\mathcal{T}}(i)$ summarizing the multi-generational contribution of selection and class transmission for allele-frequency change, respectively. Importantly, it is not a conclusion that if allele i is favored by evolution, $\overline{W}_{\mathcal{T}}(i) > 1$, it is also favored by selection, $\overline{W}^{\mathrm{sel}}_{\mathcal{T}}(i) > 1$, nor vice versa. This suggests that one should worry about the effect of class transmission on the evolutionary process if one is interested in understanding the exact effect of selection in class-structured populations. Yet the theoretical literature routinely uses representations of mean geometric fitness to characterize evolutionary stable population states thus attributing such effects entirely to selection (e.g., Caswell, 2000, Ferrière and Gatto, 1995, Svardal et al., 2015). These representations are justified because they consider the spread of a rare allele in the population (Box B; Appendix A3.1). In this case, selection is the determining evolutionary force because class transmission converges in a large time limit to its steady state and will no longer contribute to allele-frequency change. The same is true for the characterization of the dynamics of alleles that express closely similar phenotypes leading to weak selection (recall eq. 11, see also Appendix A3.2). Finally we note that one can also express $W^{\mathrm{sel}}_{\mathcal{T}}(i)$ in terms of the $\bar{w}_t(i)$'s, but then the generation-specific partitioning is incorrect and one must nevertheless define it relative to the same reference allele as in eqs. (12)-(14) to account for the effect of class transmission (Appendix A2.2).

Discussion

We analyzed allele-frequency change in a class-structured population with the aim to decompose the changes caused by natural selection and the non-selective process of class transmission allowing for frequency-dependence, density-dependence, and time-dependent environmental changes. Three main messages arise from our analysis.

First, we presented the standard representation for the single-generation change in allele frequency and then calculated the contributions of selection and class transmission to this change (eqs. 4b–4c). We showed that selection acting on an allele must be defined relative to the average fitness in each class. This reference fitness, which can be thought as the fitness of a randomly sampled allele in a given class, also defines the effect of class transmission

affecting allele frequencies whenever the distribution of alleles across classes is not uniform. These single-generation contributions, as our paper reveals, should not be however used as contributions in a multigenerational context where the measurements are taken over multiple time steps. This is so because, on one hand, the contribution of class transmission contains the contributions of selection in the past, and hence in a multigenerational context it conflates the effect of class transmission with past effects of selection. On the other hand, the contribution of selection fails to take into account that the descendants of the selected offspring undergo class transmission in the future thus altering the magnitude of this allele-frequency change, and hence does not take into account that non-heritable survival and reproduction differences affect the evolutionary process in class-structured populations. Hence, the single-generational allele-frequency change that is still widely used to describe the essence of natural selection (e.g., the review of Queller, 2017 p. 347) does not generally capture the essence of selection in a multigenerational context in class structured populations. Yet all allele frequency change leading to adaptation is certainly multigenerational and populations are generally class structured.

Second, we provided the expressions for the contribution of selection and class transmission attributed to generation t in a multigenerational process spanning between some initial time t_0 and final time t_f (eqs. 8–9). We showed that these contributions must be defined in the context of the entire span of the evolutionary process under focus and requires a careful account of the notion of reproductive value for which we provided a biological definition in the context of a finite-time process (see eq. 7). Based on our analysis we suggest the following definition for the effect of selection acting on allele i and attributed to a specific demographic time step $[t, t+1]$ of interest: it is the difference between two frequencies measured at the end of the observed evolutionary process at time t_f, (i) a frequency of allele i if it were to descend from a lineage that first underwent selection and class transmission during $[t, t+1]$ but thereafter selection was 'turned off' and all descendants underwent only the process of class transmission, and (ii) a frequency of allele i if it were to descend from a lineage that underwent only class transmission from t onward. This definition thus isolates the one generational effect of selection at t from an otherwise non-selective evolutionary process governed by class transmission. Because these effects attributed to generation t are assessed at t_f they are in general different to evolutionary changes in the single-generation context assessed at $t+1$ (eq. 4b). It may therefore be the case that while the single-generation effect of selection contributes negatively to allele-frequency change, the multigenerational effect may be positive and vice versa. For weak selection resulting from individuals expressing closely similar phenotypes, a simpler picture emerges as class-transmission becomes negligible in distant future. Then, all allele frequency change in the present is captured by the reproductive-value weighted allele-frequency change, and this also gives the present effect of selection in terms of a frequency assessed in the distant future. In this case the reproductive-value weighted allele-frequency can be interpreted as a measure that aligns the current effect of selection

with both current and future allele-frequency change thereby bridging single-generational and multigenerational perspectives of selection (eq. 11).

Third, we summarized the contributions of selection and class transmission over the entire evolutionary process in terms of geometric mean fitness's (eqs. 13-14). The representation of fitness that summarizes the multigenerational effect of selection is the relative reproductive-value weighted average individual fitness (eq. 13), which gives the mean number of offspring measured at the end of the multigenerational process that descend under the non-selective process from all offspring produced by all parents throughout the entire evolutionary process. While this fitness is generally not sufficient to predict the direction of evolution, it should do so over long time scales ($t_{\mathrm{f}} \to \infty$) where the class-transmission often vanishes. In particular, this is the case and underlies the widespread use of invasion fitness as a representation of fitness summarizing the effect of selection (Box B). This is also the case in populations where class-transmission is a much faster process than selection, as for instance under weak selection. In both cases the class-specific genetic structure converges fast under class transmission to its steady state and the long-term dynamics is governed purely by selection (see Appendix A3.1 for details). In biological scenarios where these two assumptions are not met exactly, we also expect that the geometric mean for selection calculated over sufficiently many generations gives a good approximation for the effect of selection and can be used to predict the evolutionary trajectory of an allele beyond the time-frame of observation.

We formulated all these results for haploid asexual populations, but our analysis can in a straightforward manner be generalized to more complex life-cycles and sexually reproducing populations. Likewise, we considered only panmictic populations, but the main results are bound to carry over to spatially structured populations. Our interpretations of allele frequency changes due to natural selection in class-structured populations should thus apply regardless of the details of the underlying population processes. Overall, we hope to have given a satisfactory answer to the question posed in the introduction and clarified the operation of natural selection in class-structured populations.

A1 Allele-Frequency Change in Class-Structured Populations

A1.1 Single Generational Process

We here derive eqs. (2)–(4). First, note that

$$\begin{aligned}\Delta p_t(i) = p_{t+1}(i) - p_t(i) &= \frac{n_{t+1}(i)}{n_{t+1}} - \frac{n_t(i)}{n_t} = \frac{n_{t+1}(i)}{n_{t+1}} - \frac{\bar{w}_t n_t(i)}{\bar{w}_t n_t} = \frac{n_{t+1}(i)}{n_{t+1}} - \frac{\bar{w}_t n_t(i)}{n_{t+1}} \\ &= \frac{1}{n_{t+1}} \left(n_{t+1}(i) - \bar{w}_t n_t(i) \right),\end{aligned} \tag{A1}$$

and substituting $n_{t+1}(i) = \bar{w}_t(i) n_t(i)$ (obtained by summing eq. 1 over all classes) into the last term yields the first equality in eq. (2). The second equality in eq. (2) is obtained by substituting $n_{t+1} = \bar{w}_t n_t$ (obtained by summing eq. 1 over all classes and alleles).

Let us now write the change in allele frequency (eq. A1 or eq. 2) as

$$\begin{aligned}\Delta p_t(i) &= \frac{1}{n_{t+1}} \left(\bar{w}_t(i) - \bar{w}_t \right) n_t(i) \\ &= \frac{1}{n_{t+1}} \sum_{a,b} \Big(w_t(a \mid b, i) p_t(b \mid i) - \sum_j w_t(a \mid b, j) p_t(b, j) \Big) n_t(i).\end{aligned} \tag{A2}$$

Supposing that all alleles have exactly the same fitness, i.e. $w_t(a \mid b, i) = w_t(a \mid b)$ for all i, this allele-frequency change reduces to

$$\Delta p_t(i) = \frac{1}{n_{t+1}} \sum_{a,b} w_t(a \mid b) \Big(p_t(b \mid i) - p_t(b) \Big) n_t(i), \tag{A3}$$

where we used $p_t(b) = \sum_j p_t(b, j)$ and which proves eq. (3).

Next, we consider the case where $w_t(a \mid b, i) \neq w_t(a \mid b, j)$ and prove that selection acting on an individual carrying allele i in a given class must be defined relative to the average individual fitness within that class. To show this, we first note that different evolutionary forces have distinct effects on allele frequency, and adopt the following two definitions. (1) Natural selection is defined as the only evolutionary force changing allele frequencies as a result of differential reproductive success caused by genetic differences, and so we will assume that the average excess of i individuals in class a produced by b individuals due to selection is proportional to $w_t(a \mid b, i) - f_t(a \mid b)$, where $f_t(a \mid b)$ is a reference measure of reproductive success to be derived from the analysis. (2) Class transmission is defined as the only evolutionary force changing allele frequencies where differential reproductive success is caused by differences in classes in which individuals reproduce and/or survive. Since this is independent of inherited fitness differences, it is purely a consequence on how alleles are distributed across classes. Now inserting $f_t(a \mid b) p_t(b \mid i) n_t(i) - f_t(a \mid b) p_t(b \mid i) n_t(i) = 0$ into

the parenthesis of the second equality in eq. (A2), we directly get

$$\Delta p_t(i) = \Delta p_t^{\text{sel}}(i) + \Delta p_t^{\text{ct}}(i), \tag{A4}$$

with

$$\begin{aligned} \Delta p_t^{\text{sel}}(i) &= \frac{1}{n_{t+1}} \sum_a \sum_b \Big[w_t(a \mid b, i) - f_t(a \mid b) \Big] p_t(b \mid i) n_t(i) \\ \Delta p_t^{\text{ct}}(i) &= \frac{1}{n_{t+1}} \sum_a \sum_b \Big[f_t(a \mid b) - \frac{1}{n_{\mathcal{C}}} \bar{w}_t \Big] p_t(b \mid i) n_t(i) \end{aligned} \tag{A5}$$

which give the changes in frequency of i caused by selection ('sel'), with yet to be established $f_t(a \mid b)$, and class transmission ('ct'). Next, summing over i in the first line of eq. (A5) produces

$$\sum_i \Delta p_t^{\text{sel}}(i) = \frac{1}{n_{t+1}} \sum_{a,b} [\bar{w}_t(a \mid b) - f_t(a \mid b)] n_t(b). \tag{A6}$$

Consistency requires that $\sum_i \Delta p_t^{\text{sel}}(i) = 0$ since total allele frequency must be conserved under the action of an evolutionary force. Thus, we must have $f_t(a \mid b) = \bar{w}_t(a \mid b)$ for all a, b, which is a choice that also satisfies the consistency relation $\sum_i \Delta p_t^{\text{ct}}(i) = 0$ and therefore proves eq. (4). We finally note that by substituting $f_t(a \mid b) = \bar{w}_t(a \mid b)$ into the second equation in eq. (A5) and re-arranging we get

$$\Delta p_t^{\text{ct}}(i) = \frac{1}{n_{t+1}} \sum_{a,b} \bar{w}_t(a \mid b) \Big(p_t(b \mid i) - p_t(b) \Big) n_t(i), \tag{A7}$$

thus confirming the above eq. (A3) saying that class transmission is induced by the non-uniform distribution of alleles across classes.

When there is no class structure, i.e. $w_t(a \mid b, i) = w_t(i)$ for all a and b, we have $\bar{w}_t(a \mid b) = \bar{w}_t = \sum_j w_t(j) p_t(j)$. Then, $\Delta p_t^{\text{ct}}(i) = 0$ and eq. (A4) reduces to

$$\Delta p_t(i) = \left(\frac{w_t(i) - \bar{w}_t}{\bar{w}_t} \right) p_t(i) \tag{A8}$$

which is the standard representation of allele-frequency change in populations without class structure (Gillespie, 1991, eq. 4.1, Nagylaki, 1992, eq. 2.8).

A1.2 Multigenerational Process

We here derive eq. (8) and eq. (9). To that end, we define $n_{t|h}(\cdot)$ and $p_{t|h}(\cdot)$ as the state variables at t that underwent the full evolutionary process between $[t_0, h]$ and that from time h onward have undergone the non-selective process where individuals reproduce as average individuals from the population. In the main text, we use the short-hand notation $n_t^\circ(\cdot) = n_{t|t_0}(\cdot)$ and $p_t^\circ(\cdot) = p_{t|t_0}(\cdot)$ for variables that have undergone the non-selective process right from the onset (i.e. the initial time t_0), but we must define the more general state variables in this appendix to derive the results. In particular, $n_{t|h}(a, i)$ gives the number of individuals

a, i at time t that descend from a lineage of individuals that underwent the full evolutionary process between $[t_0, h]$ and the non-selective process between $[h, t]$. For $h \leq t < t_{\mathrm{f}}$, this state variable thus satisfies the recursion

$$n_{t+1|h}(a, i) = \sum_b \bar{w}_t(a \mid b) n_{t|h}(b, i) \tag{A9}$$

(compare with eq. 6 in the main text) with initial condition $n_{h|h}(a, i) = n_h(a, i)$, which is the final state of the state variable $n_t(a, i)$ that has undergone the full evolutionary process (eq. 1) between $[t_0, h]$. Next, we introduce the state variable

$$p_{t|h}(a, i) = \frac{n_{t|h}(a, i)}{n_t}, \tag{A10}$$

which gives the proportion of individuals in the population at time t that descend from a lineage of a, i individuals that underwent the full evolutionary process between $[t_0, h]$ and that from time h onward have undergone a non-selective process (and recall that $n_t = n_{t|t}$ and hence this proportion is relative to the total number of individuals under the full evolutionary process). We can equivalently interpret $p_{t|h}(a, i)$ as the frequency of individuals of type a, i at the final time t_{f} that descend from a lineage of individuals that underwent selection and class transmission between $[t_0, h]$ and then only class transmission between $[h, t]$ (relative to the number of individuals that underwent the full evolutionary process from t_0 onward).

A1.2.1 Disentangling Selection from the Evolutionary Process

We are now ready to derive eq. (8). First, by using eq. (A10) we observe that in a multigenerational process over $\mathcal{T}$, the effect of selection in generation t on allele frequency can be defined for all t as

$$\Delta p^{\mathrm{sel}}_{t|\mathcal{T}}(i) = p_{t_{\mathrm{f}}|t+1}(i) - p_{t_{\mathrm{f}}|t}(i). \tag{A11}$$

Indeed, the variable $p_{t_{\mathrm{f}}|t+1}(i)$ gives the frequency of individuals i at t_{f} that descend from individuals that underwent selection and class transmission until $t+1$ and then class transmission until t_{f}. Hence, subtracting from $p_{t_{\mathrm{f}}|t+1}(i)$, the allele frequency $p_{t_{\mathrm{f}}|t}(i)$ where selection acts only until time t, we isolate in eq. (A11) one iteration of selection $[t, t+1]$ from an otherwise class-transmission process during $[t, t_{\mathrm{f}}]$. Applying eq. (A11) recursively, we get

$$p_{t_{\mathrm{f}}|t_{\mathrm{f}}}(i) = \sum_{t=t_0}^{t_{\mathrm{f}}-1} \Delta p^{\mathrm{sel}}_{t|\mathcal{T}}(i) + p_{t_{\mathrm{f}}|t_0}(i). \tag{A12}$$

Then, by using the consistency relation $p_{t_{\mathrm{f}}|t_{\mathrm{f}}}(i) = p_{t_{\mathrm{f}}}(i)$ and by reorganizing the terms gives

$$p_{t_{\mathrm{f}}}(i) - p_{t_{\mathrm{f}}|t_0}(i) = \sum_{t=t_0}^{t_{\mathrm{f}}-1} \Delta p^{\mathrm{sel}}_{t|\mathcal{T}}(i). \tag{A13}$$

Because $p_{t_f|t_0}(i)$ is the frequency of i at time t_f if only class transmission was in play over the entire $\mathcal{T}$ (and $p_{t_f}(i) = p_{t_f|t_f}(i)$ if both selection and class transmission was in play), we have obtained that $\Delta p^{\text{sel}}_{\mathcal{T}}(i) = p_{t_f}(i) - p_{t_f|t_0}(i)$ gives the fraction of the total allele-frequency change that is due to selection with $\Delta p^{\text{sel}}_{t|\mathcal{T}}(i)$ as the contribution of selection in generation t.

Next, we evaluate $\Delta p^{\text{sel}}_{t|\mathcal{T}}(i)$ as defined by eq. (A11). For this, we note the identity

$$p_{t_f|t}(i) = \frac{1}{n_{t_f}} \bar{v}_t(i) n_t(i), \tag{A14}$$

where we used the definition for reproductive values (eq. 7) and

$$\bar{v}_t(i) = \sum_a v_t(a) p_t(a \mid i) \tag{A15}$$

is the average reproductive value of i at time t as defined in the main text. Notice that eq. (A14) can also be written as

$$\begin{aligned} p_{t_f|t}(i) &= \frac{1}{n_{t_f}} \sum_a v_t(a) p_t(a \mid i) p_t(i) n_t \\ &= \frac{1}{n_{t_f}} \sum_a v_t(a) p_t(a) p_t(i \mid a) n_t \\ &= \sum_a \alpha_t(a) p_t(i \mid a), \end{aligned} \tag{A16}$$

where $\alpha_t(a) = (n_t / n_{t_f}) v_t(a) p_t(a)$ is the class reproductive value satisfying $\sum_a \alpha_t(a) = 1$ since $n_{t_f} = \bar{v}_t n_t$. Hence, $p_{t_f|t}(i)$ is the (class) reproductive-value weighted allele frequency used in the evolutionary analysis of class-structured populations (e.g., Lion, 2018, Priklopil and Lehmann, 2021, Rousset, 2004, Rousset and Ronce, 2004, Taylor, 1990, 1996).

Now, the weighted allele frequency (eq. A14) satisfies

$$\begin{aligned} p_{t_f|t+1}(i) &= \frac{1}{n_{t_f}} v_{t+1}(i) n_{t+1}(i) = \frac{1}{n_{t_f}} \sum_a v_{t+1}(a) n_{t+1}(a, i) \\ &= \frac{1}{n_{t_f}} \sum_a \sum_b v_{t+1}(a) \Big[w_t(a \mid b, i) - \bar{w}_t(a \mid b) \Big] p_t(b \mid i) n_t(i) + \\ &+ \frac{1}{n_{t_f}} \sum_a \sum_b v_{t+1}(a) \bar{w}_t(a \mid b) p_t(b \mid i) n_t(i) \\ &= p_{t_f|t}(i) + \frac{1}{n_{t_f}} \sum_a \sum_b v_{t+1}(a) \Big[w_t(a \mid b, i) - \bar{w}_t(a \mid b) \Big] p_t(b \mid i) n_t(i), \end{aligned} \tag{A17}$$

where we applied eq. (A15) in the second equality, eq. (1) in the third equality, and eq. (7) and eq. (A14) in the fourth equality. From the definition in eq. (A11) this thus proves the first equality in eq. (8).

The second equality in eq. (8) can be obtained by noting that $n_{t_f} = \bar{v}_t n_t$ where $\bar{v}_t =$

$\prod_{h=t}^{t_f-1} \bar{w}_h$, in which case we can write eq. (A14) equivalently as

$$p_{t_f|t}(i) = \frac{\bar{v}_t(i)}{\bar{v}_t} p_t(i), \tag{A18}$$

and hence

$$\begin{aligned}
\Delta p^{\text{sel}}_{t|\mathcal{T}}(i) &= \frac{1}{\bar{v}_t} \sum_a \sum_b v_{t+1}(a) \Big[w_t(a \mid b, i) - \bar{w}_t(a \mid b) \Big] p_t(b \mid i) p_t(i) \\
&= \frac{1}{\bar{v}_t} \Big[\sum_a \sum_b v_{t+1}(a) w_t(a \mid b, i) p_t(b \mid i) - \sum_a \sum_b v_{t+1}(a) \bar{w}_t(a \mid b) p_t(b \mid i) \Big] p_t(i) \\
&= \frac{1}{\bar{v}_t} \Big[\sum_a \sum_b v_{t+1}(a) w_t(a \mid b, i) p_t(b \mid i) - \sum_b v_t(b) p_t(b \mid i) \Big] p_t(i) \\
&= \left(\frac{\bar{w}^{\text{v}}_t(i) - \bar{v}_t(i)}{\bar{v}_t} \right) p_t(i),
\end{aligned} \tag{A19}$$

where in the third equality we applied eq. (7) and in the fourth equality the definition of $\bar{v}_t(i)$ and

$$\bar{w}^{\text{v}}_t(i) = \sum_a \sum_b v_{t+1}(a) w_t(a \mid b, i) p_t(b \mid i). \tag{A20}$$

A1.2.2 Disentangling Class Transmission from the Evolutionary Process

We here derive eq. (9). We observe that in a multigenerational process over $\mathcal{T}$ the effect of class transmission in generation t on allele frequency can be defined for all t as

$$\Delta p^{\text{ct}}_{t|\mathcal{T}}(i) = p_{t+1|t_0}(i) - p_{t|t_0}(i). \tag{A21}$$

Indeed, $p_{t+1|t_0}(i)$ gives the frequency of i individuals that underwent class transmission until $t+1$, and hence by subtracting from this the frequency $p_{t|t_0}(i)$ of i individuals that underwent class transmission until t, we isolate one iteration of class transmission during $[t, t+1]$. Moreover, because the non-selective process of population growth does not alter allele frequencies, $\Delta p^{\text{ct}}_{t|\mathcal{T}}(i)$ is also the frequency of individuals at t_f that descend under the process of population growth from offspring produced due to class transmission during $[t, t+1]$, thus in a multigenerational context giving the effect of class transmission in generation t. Now, by setting $t = t_f - 1$ into eq. (A21), we have

$$p_{t_f|t_0}(i) = \Delta p^{\text{ct}}_{t_f-1|\mathcal{T}}(i) + p_{t_f-1|t_0}(i) \tag{A22}$$

and a recursive substitution produces

$$p_{t_f|t_f}(i) = \sum_{t=t_0}^{t_f-1} \Delta p^{\text{ct}}_{t|\mathcal{T}}(i) + p_{t_0|t_0}(i). \tag{A23}$$

Then, by noting that $p_{t_0|t_0}(i) = p_{t_0}(i)$ and by reorganizing the terms gives

$$p_{t_f|t_0}(i) - p_{t_0}(i) = \sum_{t=t_0}^{t_f-1} \Delta p^{\text{ct}}_{t|\mathcal{T}}(i). \tag{A24}$$

Because $p_{t_f|t_0}(i)$ is the frequency of i at time t_f if only class transmission was in play over the entire time-interval $\mathcal{T}$, we have obtained that the total change in allele frequency due to class transmission is $\Delta p^{\text{ct}}_{\mathcal{T}}(i) = p_{t_f|t_0}(i) - p_{t_0}(i)$ and $\Delta p^{\text{ct}}_{t|\mathcal{T}}(i)$ is the contribution of class transmission in generation t.

Next, we evaluate $\Delta p^{\text{ct}}_{\mathcal{T}}(i)$ as defined by eq. (A21). Using eq. (A10), we can write the recursion

$$\begin{aligned} p_{t+1|t_0}(i) &= \frac{n_{t+1|t_0}(i)}{n_{t+1}} = \frac{1}{n_{t+1}} \sum_a n_{t+1|t_0}(a,i) \\ &= \frac{1}{n_{t+1}} \sum_a \sum_b \left[\bar{w}_t(a \mid b) - \frac{1}{n_{\mathcal{C}}} \bar{w}_t \right] n_{t|t_0}(b,i) + \frac{1}{n_{t+1}} \bar{w}_t n_{t|t_0}(i) \\ &= \frac{1}{n_{t+1}} \sum_a \sum_b \left[\bar{w}_t(a \mid b) - \frac{1}{n_{\mathcal{C}}} \bar{w}_t \right] n_{t|t_0}(b,i) + p_{t|t_0}(i), \end{aligned} \tag{A25}$$

where in the third equality we used eq. (A9) (eq. 6 in the main text) and in the fourth equality $n_{t+1} = \bar{w}_t n_t$ and eq. (A10). Reorganization and using $r^{\circ}_t(i)$ as defined in the main text as well as recalling the shortcut notation $n_{t|t_0}(\cdot) = n^{\circ}_t(\cdot)$ and $p_{t|t_0}(\cdot) = p^{\circ}_t(\cdot)$ yields eq. (9).

A1.2.3 Reduction to Population Models Without Class Structure

We now show that our derivation is consistent with the standard population genetic model without class structure where $w_t(i) = w_t(a \mid b, i)$ for all a, b. Substituting this into eq. (9) gives $\Delta p^{\text{ct}}_{t|\mathcal{T}}(i) = 0$ and when substituting it into eq. (8) yields

$$\begin{aligned} \Delta p^{\text{sel}}_{t|\mathcal{T}}(i) &= \frac{1}{n_{t_f}} \sum_a \sum_b v_{t+1}(a) \Big[w_t(a \mid b, i) - \bar{w}_t(a \mid b) \Big] p_t(b \mid i) n_t(i) \\ &= \frac{1}{n_{t_f}} \sum_a \sum_b v_{t+1}(a) \Big[w_t(i) - \bar{w}_t \Big] p_t(b \mid i) n_t(i) \\ &= \frac{1}{n_{t_f}} \bar{v}_{t+1} \Big[w_t(i) - \bar{w}_t \Big] n_t(i), \end{aligned} \tag{A26}$$

where we used $\bar{v}_t = \sum_a v_t(a)$ and $1 = \sum_b p_t(b \mid i)$. Using $\bar{v}_t = \prod_{h=t}^{t_f-1} \bar{w}_h$ we can write $n_{t_f} = \bar{v}_t n_t = \bar{v}_{t+1} \bar{w}_t n_t$, and substituting into eq. (A26) shows that the fraction of allele-frequency change attributed to selection in generation t is equal to the right-hand side of eq. (A8) and thus we have in force of eq. (A4) (but where class transmission has no effect) that for populations without class structure

$$\Delta p_t(i) = \Delta p^{\text{sel}}_t(i) = \Delta p^{\text{sel}}_{t|\mathcal{T}}(i). \tag{A27}$$

However, in a multigenerational context, we can interpret $\Delta p^{\text{sel}}_{t|\mathcal{T}}(i)$ as the fraction of individuals as measured at t_{f} that descend form all the offspring produced in generation t under the non-selective process of population growth. This is a novel interpretation of allele frequency change in the standard model and justifies the use of reproductive values in Figure 1A.

A2 Geometric Mean Fitness

A2.1 Geometric Mean in terms of multigenerational relative fitness

We here derive eqs. (12)-(14). First, we calculate eq. (13). Using eq. (A10) we obtain the recursion

$$\begin{aligned} p_{t_{\text{f}}|t+1}(i) = \frac{1}{n_{t_{\text{f}}}} v_{t+1}(i) n_{t+1}(i) &= \frac{1}{n_{t_{\text{f}}}} \sum_a v_{t+1}(a) n_{t+1}(a,i) \\ &= \frac{1}{n_{t_{\text{f}}}} \sum_a \sum_b v_{t+1}(a) w_t(a \mid b,i) p_t(b \mid i) n_t(i) \\ &= \frac{1}{\bar{v}_t(i)} \sum_a \sum_b v_{t+1}(a) w_t(a \mid b,i) p_t(b \mid i) p_{t_{\text{f}}|t}(i), \end{aligned} \tag{A28}$$

where in the third equality we used eq. (1) and in the final equality we used the relation $n_t(i) = p_{t_{\text{f}}|t}(i) n_{t_{\text{f}}} / \bar{v}_t(i)$, which was obtained from $p_{t_{\text{f}}|t}(i) = n_{t_{\text{f}}|t}(i)/n_{t_{\text{f}}}$ (using eq. A10) and the identity $n_{t_{\text{f}}|t}(i) = \bar{v}_t(i) n_t(i)$. Then, using the definition of $\bar{w}^{\text{v}}_t(i)$ produces

$$p_{t_{\text{f}}|t+1}(i) = \frac{\bar{w}^{\text{v}}_t(i)}{\bar{v}_t(i)} p_{t_{\text{f}}|t}(i). \tag{A29}$$

Because $p_{t_{\text{f}}|t+1}(i)$ is the frequency of i at t_{f} that descend from a lineage of i that underwent selection and class transmission until $t+1$ and thereafter only class transmission, and $p_{t_{\text{f}}|t}(i)$ is the frequency of i at t_{f} if selection acted only until t, then $W^{\text{sel}}_{t|\mathcal{T}}(i) = \bar{w}^{\text{v}}_t(i)/\bar{v}_t(i)$ is the relative fitness attributed to only selection in generation t. Setting $t+1 = t_{\text{f}}$ on the left hand side in eq. (A29) and iterating backward in time yields

$$p_{t_{\text{f}}|t_{\text{f}}}(i) = \prod_{t=t_0}^{t_{\text{f}}-1} W^{\text{sel}}_{t|\mathcal{T}}(i) p_{t_{\text{f}}|t_0}(i). \tag{A30}$$

Because $p_{t_{\text{f}}|t_0}(i)$ is the allele frequency at time t_{f} in a process without selection and $p_{t_{\text{f}}|t_{\text{f}}}(i) = p_{t_{\text{f}}}(i)$ is the frequency at t_{f} with selection, the product in eq. (A30) summarizes the fitness excess over $\mathcal{T}$ caused by selection only. Taking the geometric mean of the product in eq. (A30) then together with eq. (A29) proves eq. (13).

Second, we calculate eq. (14). Consider the recursion

$$\begin{aligned} p_{t+1|t_0}(i) = \frac{n_{t+1|t_0}(i)}{n_{t+1}} &= \frac{1}{n_{t+1}} \sum_a n_{t+1|t_0}(a,i) \\ &= \frac{1}{n_{t+1}} \sum_a \sum_b \bar{w}_t(a \mid b) n_{t|t_0}(b,i) \\ &= \sum_a \sum_b \frac{\bar{w}_t(a \mid b) p_{t|t_0}(b \mid i)}{\bar{w}_t} p_{t|t_0}(i) \\ &= \frac{\bar{w}_{t|t_0}(i)}{\bar{w}_t} p_{t|t_0}(i), \end{aligned} \tag{A31}$$

where we used eq. (A9) (eq. 6 in the main text) and

$$\bar{w}_{t|t_0}(i) = \sum_{a,b} \bar{w}_t(a \mid b) p_{t|t_0}(b \mid i). \tag{A32}$$

This is the fitness of a single i at t coming from a lineage of non-selected individuals and will be different for different alleles if alleles are initially distributed differently between classes: $p_{t_0}(b \mid i) \neq p_{t_0}(b)$. Note that in the main text we used the shorthand notation $\bar{w}_t^{\circ}(i) = \bar{w}_{t|t_0}(i)$. Because $p_{t+1|t_0}(i)$ is the frequency of i at $t+1$ that descend from a lineage of i that underwent class transmission between $[t_0, t+1]$ and $p_{t|t_0}(i)$ is the frequency of i at t whose lineage underwent class transmission between $[t_0, t]$, then $W^{\mathrm{ct}}_{t|\mathcal{T}}(i) = \bar{w}_{t|t_0}(i)/\bar{w}_t$ is the relative fitness attributed to only class transmission in generation t. Setting $t+1 = t_{\mathrm{f}}$ on the left hand side in eq. (A31) and iterating backwards in time yields

$$p_{t_{\mathrm{f}}|t_0}(i) = \prod_{t=t_0}^{t_{\mathrm{f}}-1} W^{\mathrm{ct}}_{t|\mathcal{T}}(i) p_{t_0|t_0}(i). \tag{A33}$$

Because $p_{t_0|t_0}(i) = p_{t_0}(i)$ is the initial allele frequency at t_0 and $p_{t_{\mathrm{f}}|t_0}(i)$ is the final frequency under class transmission only, the product in eq. (A33) summarizes the fitness excess over $\mathcal{T}$ caused by class transmission (see below further discussion on the relative fitness attributed to class transmission in generation t). Taking the geometric mean of the product in eq. (A33) then together with eq. (A31) proves eq. (14).

Finally, we calculate eq. (12). Substituting eq. (A33) into eq. (A30), and by using $p_{t_{\mathrm{f}}|t_{\mathrm{f}}}(i) = p_{t_{\mathrm{f}}}(i)$ and $p_{t_0|t_0}(i) = p_{t_0}(i)$ we get

$$p_{t_{\mathrm{f}}}(i) = \left(\prod_{t=t_0}^{t_{\mathrm{f}}-1} W^{\mathrm{sel}}_{t|\mathcal{T}}(i) \right) \left(\prod_{t=t_0}^{t_{\mathrm{f}}-1} W^{\mathrm{ct}}_{t|\mathcal{T}}(i) \right) p_{t_0}(i), \tag{A34}$$

where $W^{\mathrm{sel}}_{t|\mathcal{T}}(i) = \bar{w}_t^{\mathrm{v}}(i)/\bar{v}_t(i)$ and $W^{\mathrm{ct}}_{t|\mathcal{T}}(i) = \bar{w}_{t|t_0}(i)/\bar{w}_t$. Taking the geometric means shows eq. (12).

As noted above, $W^{\mathrm{ct}}_{t|\mathcal{T}}(i) = \bar{w}_{t|t_0}(i)/\bar{w}_t$ in eq. (A34) is the relative fitness for class transmission of a single i individual at t in a multigenerational process over $\mathcal{T}$, given we have sampled

an individual at t who is itself a product of class transmission. If we want to condition on the realized population state at some later generation h, we can use the fact that

$$p_{h|t_0}(i) = \prod_{t=t_0}^{h-1} W^{\mathrm{ct}}_{t|\mathcal{T}}(i) p_{t_0}(i) \tag{A35}$$

and substituting this into (A34) we have

$$\begin{aligned} p_{t_\mathrm{f}}(i) &= \left(\prod_{t=t_0}^{t_\mathrm{f}-1} W^{\mathrm{sel}}_{t|\mathcal{T}}(i)\right)\left(\prod_{t=h}^{t_\mathrm{f}-1} W^{\mathrm{ct}}_{t|\mathcal{T}}(i)\right)\prod_{t=t_0}^{h-1} W^{\mathrm{ct}}_{t|\mathcal{T}}(i) p_{t_0}(i) \\ &= \left(\prod_{t=t_0}^{t_\mathrm{f}-1} W^{\mathrm{sel}}_{t|\mathcal{T}}(i)\right)\left(\prod_{t=h}^{t_\mathrm{f}-1} W^{\mathrm{ct}}_{t|\mathcal{T}}(i)\right) p_{h|t_0}(i) \end{aligned} \tag{A36}$$

and using the identity $p_{h|t_0}(i) = r^\circ_h(i) p_h(i)$ we get

$$\begin{aligned} p_{t_\mathrm{f}}(i) &= \left(\prod_{t=t_0}^{t_\mathrm{f}-1} W^{\mathrm{sel}}_{t|\mathcal{T}}(i)\right)\left(\prod_{t=h}^{t_\mathrm{f}-1} W^{\mathrm{ct}}_{t|\mathcal{T}}(i)\right) r^\circ_h(i) p_h(i) \\ &= \left(\prod_{t=t_0}^{t_\mathrm{f}-1} W^{\mathrm{sel}}_{t|\mathcal{T}}(i)\right)\left(\prod_{t=h+1}^{t_\mathrm{f}-1} W^{\mathrm{ct}}_{t|\mathcal{T}}(i)\right) W^{\mathrm{ct}}_{h|\mathcal{T}}(i) r^\circ_h(i) p_h(i). \end{aligned} \tag{A37}$$

This shows that $W^{\mathrm{ct}}_{h|\mathcal{T}}(i) r^\circ_h(i)$ is the relative fitness for class transmission of a single randomly sampled i individual in generation h.

A2.2 Alternative Representation of Geometric Mean for Selection

Here we show that one can write the geometric mean for selection (eq. 13) also in terms of individual fitness functions as

$$\overline{W}^{\mathrm{sel}}_{\mathcal{T}}(i) = \left(\prod_{t=t_0}^{t_\mathrm{f}-1} \frac{\bar{w}_t(i)}{\bar{w}_{t|t_0}(i)}\right)^{1/(t_\mathrm{f}-t_0)}, \tag{A38}$$

and recall that in the main text we use the shorthand notation $\bar{w}^\circ_t(i) = \bar{w}_{t|t_0}(i)$. To show this, we first observe that the cumulative fitness of i over $\mathcal{T}$ caused by selection only is $p_{t_\mathrm{f}}(i)/p_{t_\mathrm{f}|t_0}(i)$ (compare with eq. A13). To obtain $p_{t_\mathrm{f}}(i)$, we can use the recursion $p_{t+1}(i) = p_t(i)\bar{w}_t(i)/\bar{w}_t$ recursively over $\mathcal{T}$ and we get

$$p_{t_\mathrm{f}}(i) = \prod_{t=t_0}^{t_\mathrm{f}-1} \frac{\bar{w}_t(i)}{\bar{w}_t} p_{t_0}(i). \tag{A39}$$

Now, substituting this and the frequency $p_{t_\mathrm{f}|t_0}(i)$ from eq. (A33) into $p_{t_\mathrm{f}}(i)/p_{t_\mathrm{f}|t_0}(i)$, and taking the geometric mean, gets us eq. (A38).

Next, we show that eq. (A38) and eq. (13) are indeed equivalent. To do this, we first derive

a recursion for $p_{h|t}(a \mid i)$ over $[t, t_{\mathrm{f}}]$ as

$$p_{h+1|t}(a \mid i) = \frac{n_{h+1|t}(a,i)}{n_{h+1|t}(i)} = \frac{1}{\bar{w}_{h|t}(i)} \sum_b \bar{w}_t(a \mid b) p_{h|t}(b \mid i), \tag{A40}$$

where we applied eq. (A9) (eq. 6 in the main text) and $n_{h+1|t}(i) = \bar{w}_{h|t}(i) n_{h|t}(i)$ with $\bar{w}_{h|t}(i) = \sum_{a,b} \bar{w}_t(a \mid b) p_{h|t}(b \mid i)$, and where the initial condition satisfies $p_{t|t}(a \mid i) = p_t(a \mid i)$. Then, we produce

$$\begin{aligned} \bar{v}_t(i) &= \sum_a v_t(a) p_{t|t}(a \mid i) \\ &= \sum_a \sum_b v_{t+1}(b) \bar{w}_t(b \mid a) p_{t|t}(a \mid i) \\ &= \sum_b v_{t+1}(b) p_{t+1|t}(a \mid i) \bar{w}_{t|t}(i), \end{aligned} \tag{A41}$$

where the first equality follows from the definition of $\bar{v}_t(i)$, and in the second equality we used eq. (7) and in the third equality we used the relation $p_{h+1|t}(a \mid i) \bar{w}_{h|t}(i) = \sum_b \bar{w}_t(a \mid b) p_{h|t}(b \mid i)$ obtained from eq. (A40). Applying the logic in eq. (A41) recursively we get

$$\bar{v}_t(i) = \prod_{h=t}^{t_{\mathrm{f}}-1} \bar{w}_{h|t}(i) \sum_a v_{t_{\mathrm{f}}}(a) p_{t_{\mathrm{f}}|t}(a \mid i), \tag{A42}$$

and by noting that $v_{t_{\mathrm{f}}}(a) = 1$ for all a and $1 = \sum_a p_{t_{\mathrm{f}}|t}(a \mid i)$ produces

$$\bar{v}_t(i) = \prod_{h=t}^{t_{\mathrm{f}}-1} \bar{w}_{h|t}(i). \tag{A43}$$

We can then write

$$\begin{aligned} \bar{w}_t^{\mathrm{v}}(i) n_t(i) &= \sum_a \sum_b v_{t+1}(a) w_t(a \mid b, i) n_t(b, i) \\ &= \sum_a v_{t+1}(a) n_{t+1}(a, i) \\ &= \sum_a v_{t+1}(a) p_{t+1}(a \mid i) n_{t+1}(i) \\ &= \bar{v}_{t+1}(i) \bar{w}_t(i) n_t(i), \end{aligned} \tag{A44}$$

where the first equality follows from the definition of $\bar{w}_t^{\mathrm{v}}(i)$, and in the second equality we used eq. (1) and in the final equality we applied the definition of $\bar{v}_t(i)$ and $n_{t+1}(i) = \bar{w}_t(i) n_t(i)$. We have thus produced the identity

$$\bar{w}_t^{\mathrm{v}}(i) = \bar{v}_{t+1}(i) \bar{w}_t(i). \tag{A45}$$

We can substitute this into

$$\begin{aligned}\prod_{t=t_0}^{t_f-1}\frac{\bar{w}_t^{\mathrm{v}}(i)}{\bar{v}_t(i)} &= \prod_{t=t_0}^{t_f-1}\frac{\bar{v}_{t+1}(i)\bar{w}_t(i)}{\bar{v}_t(i)} \\ &= \prod_{t=t_0}^{t_f-1}\frac{\bar{w}_t(i)}{\bar{v}_{t_0}(i)} = \prod_{t=t_0}^{t=t_f-1}\frac{\bar{w}_t(i)}{\bar{w}_{t|t_0}(i)},\end{aligned} \tag{A46}$$

where in the second equality we used $\bar{v}_{t_f}(i) = 1$ $(= \sum_a v_{t_f}(a)p_{t_f}(a \mid i) = \sum_a p_{t_f}(a \mid i)$ by assumption), and in the final equality we applied eq. (A43). This shows that the eqs. (13) and (A38) are indeed equivalent.

If one is only interested in the net geometric mean, then one can use eq. (A38) instead of eq. (13). In fact, eq. (A38) may in some situations be easier to apply because each factor $\bar{w}_t(i)/\bar{w}_{t|t_0}(i)$ only depends on the past events whereas in eq. (13) each factor $\bar{w}_t^{\mathrm{v}}(i)/\bar{v}_t(i)$ requires calculating also the future states of the population via reproductive values. However, the per generation contributions $\bar{w}_t(i)/\bar{w}_{t|t_0}(i)$ in eq. (A38) and $\bar{w}_t^{\mathrm{v}}(i)/\bar{v}_t(i)$ in eq. (13) are not equal, and only the latter is the correct fitness describing the effect of selection in generation t in a multigenerational context. Nevertheless, both approaches give the same geometric means and in both approaches one must use the same non-selective process (eq. 6) to tease out the effect of selection from class transmission (i.e. both use the same average reference allele). Finally, and similarly to the above calculations of geometric means for selection, we can write

$$\begin{aligned}p_{t_f}(i) &= \prod_{t=t_0}^{t_f-1} W_{t|\mathcal{T}}^{\mathrm{sel}}(i)W_{t|\mathcal{T}}^{\mathrm{ct}}(i)p_{t_0}(i) = \prod_{t=t_0}^{t_f-1}\frac{\bar{w}_t^{\mathrm{v}}(i)}{\bar{v}_t(i)}\frac{\bar{w}_{t|t_0}(i)}{\bar{w}_t}p_{t_0}(i) \\ &= \prod_{t=t_0}^{t_f-1}\frac{\bar{w}_t(i)}{\bar{v}_{t_0}(i)}\frac{\bar{w}_{t|t_0}(i)}{\bar{w}_t}p_{t_0}(i) = \prod_{t=t_0}^{t_f-1}\frac{\bar{w}_t(i)}{\bar{w}_t}p_{t_0}(i),\end{aligned} \tag{A47}$$

where in the third equality we used eq. (A46) and in the fourth equality eq. (A43). This calculation shows, in particular, that the contribution $\bar{w}_t(i)/\bar{w}_t$ is not equal to $(\bar{w}_t^{\mathrm{v}}(i)/\bar{v}_t(i))(\bar{w}_{t|t_0}(i)/\bar{w}_t) = W_{t|\mathcal{T}}^{\mathrm{sel}}(i)W_{t|\mathcal{T}}^{\mathrm{ct}}(i)$ and only the latter gives the fitness describing the effect of selection and class transmission in generation t on the final frequency in a multigenerational context.

A3 Asymptotic Evolutionary Process

A3.1 Invasion Fitness

Here we derive the equations for Box B. Recall the definition of the invasion exponent of allele i when the initial number of such alleles is $n_{t_0}(i)$:

$$\rho = \lim_{t_f\to\infty}\frac{1}{t_f - t_0}\ln\frac{n_{t_f}(i)}{n_{t_0}(i)} \tag{A48}$$

(e.g., Ferrière and Gatto, 1995, Metz et al., 1992, Tuljapurkar, 1989b). Since we are interested in the growth of i when rare, we suppose that the model contains a steady state where i is

absent (and while one can calculate invasion fitness for very general population attractors, we will focus on equilibria). We thus suppose an equilibrium $\hat{\mathbf{n}} = (\hat{n}(a,j))_{a,j}$ characterizing the population when i is absent (i.e. the 'resident' population) where $\hat{n}(a,i) = 0$ for all a and $\hat{n}(a,j) > 0$ for all $j \neq i$ and all a, and that $\hat{\mathbf{n}}$ is asymptotically stable along the invariant (multidimensional) axis where allele i is absent (i.e. where $\hat{n}(a,i) = 0$ for all a). More specifically, we have $0 = \hat{n}(a,i) = \hat{p}(a \mid i)\hat{n}(i)$ for all a implying that $\hat{n}(i) = 0$. In this section and henceforth, the hat notation indicates that the quantity (state variable or a function) is evaluated at the equilibrium $\hat{\mathbf{n}}$.

We now calculate eq. (A48). First, from eq. (A34) we get

$$p_{t_\mathrm{f}}(i) = \left(\prod_{t=t_0}^{t_\mathrm{f}-1} \frac{\bar{w}_t^{\mathrm{v}}(i)}{\bar{v}_t(i)} \frac{\bar{w}_{t|t_0}(i)}{\bar{w}_t} \right) p_{t_0}(i). \tag{A49}$$

By multiplying both sides by $n_{t_\mathrm{f}} = \prod_{t=t_0}^{t_\mathrm{f}-1} \bar{w}_t n_{t_0}$ we obtain

$$n_{t_\mathrm{f}}(i) = \left(\prod_{t=t_0}^{t_\mathrm{f}-1} \frac{\bar{w}_t^{\mathrm{v}}(i)}{\bar{v}_t(i)} \frac{\bar{w}_{t|t_0}(i)}{\bar{w}_t} \frac{\bar{w}_t}{1} \right) n_{t_0}(i). \tag{A50}$$

We then divide both sides by $n_{t_0}(i)$ and Taylor expand the function $n_{t_\mathrm{f}}(i)/n_{t_0}(i)$ about the steady state $\hat{\mathbf{n}}$ (we need to expand the whole trajectory of vectors $\mathbf{n}_{t_0}, \ldots, \mathbf{n}_{t_\mathrm{f}-1}$), which results in the linearized equation

$$\frac{n_{t_\mathrm{f}}(i)}{n_{t_0}(i)} = \prod_{t=t_0}^{t_\mathrm{f}-1} \frac{\hat{\bar{w}}^{\mathrm{v}}(i)}{\hat{\bar{v}}(i)} + \text{h.o.t.} = \left(\frac{\hat{\bar{w}}^{\mathrm{v}}(i)}{\hat{\bar{v}}(i)} \right)^{t_\mathrm{f}-t_0} + \text{h.o.t.} \tag{A51}$$

where the h.o.t. refers to terms of order $|\mathbf{n}_t - \hat{\mathbf{n}}|$ for all $t \in \mathcal{T}$. The first equality in eq. (A51) follows from evaluating $\bar{w}_t$ and $\bar{w}_{t|t_0}(i) = \bar{w}_t^{\circ}(i)$ in eq. (A50) at $\hat{\mathbf{n}}$: $\hat{\bar{w}} = 1$ follows from the definition of an equilibrium (i.e. $\hat{n} = \hat{\bar{w}}\hat{n}$ implies $\hat{\bar{w}} = 1$), and $\hat{\bar{w}}^{\circ}(i) = 1$ follows from the equality $1 = \hat{\bar{w}} = \sum_{a,b} \hat{\bar{w}}(a \mid b)\hat{p}(b) = \sum_{a,b} \hat{\bar{w}}(a \mid b)\hat{p}^{\circ}(b \mid i) = \hat{\bar{w}}^{\circ}(i)$, where we used the fact that at the equilibrium $\hat{\mathbf{n}}$ the identity $\hat{p}^{\circ}(a \mid i) = \hat{p}(a)$ holds for all a. One can see this by comparing the recursion in eq. (A40) and $p_{t+1}(a) = \sum_b \bar{w}_t(a \mid b)p_t(b)/\bar{w}_t$, but we ought to emphasise that the identity $\hat{p}^{\circ}(a \mid i) = \hat{p}(a)$ holds only for allele i and only at the equilibrium $\hat{\mathbf{n}}$ where allele i is absent. Furthermore, in the expressions $\hat{\bar{w}}^{\mathrm{v}}(i) = \sum_{a,b} \hat{v}(a)\hat{\bar{w}}(a \mid b,i)\hat{p}(b \mid i)$ and $\hat{\bar{v}}(i) = \sum_a \hat{v}(a)\hat{p}(a \mid i)$ the vector $\hat{\mathbf{v}}$ is calculated from eq. (7) and evaluated at $\hat{\mathbf{n}}$ and the vector $\hat{\mathbf{p}}(i)$ with elements $\hat{p}(a \mid i)$ is calculated from the recursion

$$p_{t+1}(a \mid i) = \frac{n_{t+1}(a,i)}{n_{t+1}(i)} = \frac{1}{\bar{w}_t(i)} \sum_b w_t(a \mid b,i)p_t(b \mid i), \tag{A52}$$

evaluated at $\hat{\mathbf{n}}$ (obtained by using the definition of $p_t(a \mid i)$, eq. (1) and the recursion $n_{t+1}(i) = \bar{w}_t(i)n_t(i)$). Notice that whereas $\hat{\mathbf{p}}^{\circ}(i)$ with elements $\hat{p}^{\circ}(a \mid i)$ is calculated under a non-selective process from eq. (A40), the vector $\hat{\mathbf{p}}(i)$ is calculated under the full evolutionary process with selection (eq. A52), and hence in general $\hat{\mathbf{p}}^{\circ}(i) \neq \hat{\mathbf{p}}(i)$.

Now, we can substitute eq. (A51) into eq. (A48) which leads to

$$\rho = \ln \frac{\hat{\bar{w}}^{\mathrm{v}}(i)}{\hat{\bar{v}}(i)}. \tag{A53}$$

In this final step we used the fact that as $t_{\mathrm{f}} \to \infty$ the h.o.t. present in eq. (A51) converge to 0. Moreover, $\exp \rho$ can be shown to be the leading eigenvalue of the fitness matrix with elements $\hat{w}(a \mid b, i)$ and that its corresponding eigenvector is $\hat{\mathbf{p}}(i)$. These are standard results about ρ and have been proved elsewhere (e.g., Caswell, 2000, Tuljapurkar, 1989b) with the representation of ρ given in eq. (A53) appearing previously too [Lehmann and Rousset, 2020, Lehmann et al., 2016].

Finally, we show that any arbitrarily weighted fitness function could be used in eq. (A53). To this end, define an arbitrarily weighted fitness function

$$\bar{w}_t^q(i) = \sum_a \sum_a q_{t+1}(a) w_t(a \mid b, i) p_t(b \mid i) \tag{A54}$$

with arbitrary weights $q_t(a)$ that follow some arbitrary system of recursions. Then, we produce an analogues identity to eq. (A45), which reads as

$$\bar{w}_t^q(i) = \bar{q}_{t+1}(i) \bar{w}_t(i), \tag{A55}$$

where $q_{t+1}(i) = \sum_a q_{t+1}(a) p_{t+1}(a \mid i)$. At the resident equilibrium we hence necessarily have that

$$\frac{\hat{\bar{w}}^q(i)}{\hat{\bar{q}}(i)} = \frac{\hat{\bar{q}}(i)\hat{\bar{w}}(i)}{\hat{\bar{q}}(i)} = \hat{\bar{w}}(i), \tag{A56}$$

thus proving eq. (B.1) of Box B.

A3.2 Evolutionary Dynamics under Weak Selection

Here we derive eq. (11) and show that over sufficiently large $\mathcal{T}$ only the multigenerational partitioning (eqs. 8-9) is consistent with weak-selection approximations, namely, that reproductive-value weighted selection-term governs the slow phase of allele-frequency change after the initial allele-frequency change caused by class transmission has become negligible. For this, we consider models where alleles encode for closely similar phenotypes and our derivation is an adaptation from Priklopil and Lehmann [2020, 2021] who analysed continuous-time population models.

For simplicity but without a loss of generality, let us further suppose that only two alleles segregate in the population, and that one of the two alleles, say allele i, is derived by mutation from the other allele, say j. We further suppose that the effect of the mutation on the phenotypic expression of some trait is class-specific so that the phenotypic profile of i can be written as $\mathbf{z}(i) = \mathbf{z}(j) + \delta\boldsymbol{\eta}$, where $\mathbf{z}(k)$, with elements $z(a, k)$, is the phenotypic profile

of allele $k = i, j$ such that when the allele is in class a it expresses phenotype $z(a, k)$ and where $\boldsymbol{\eta}$ gives the direction of the effect of the mutation, with the effect in class a being $\eta(a)$. Assuming the fitness functions to be continuous, a small parameter δ implies i and j having closely similar phenotypes, and hence having closely similar fitness functions. In particular, for $\delta = 0$, the mutant i and the resident (wild-type) j fitness's are equal, i.e. we have the consistency relation

$$w_t(a \mid b, i) = w_t(a \mid b, j) = w_t(a \mid b), \tag{A57}$$

where $w_t(a \mid b)$ is a function that is independent of allele frequency (see also eqs. A3 for the notation).

Now, consider the multigenerational partitioning (eqs. 8-9) as prescribed in the main text $\Delta p_{t|\mathcal{T}}(i) = \Delta p^{\text{sel}}_{t|\mathcal{T}}(i) + \Delta p^{\text{ct}}_{t|\mathcal{T}}(i)$ with

$$\begin{aligned} \Delta p^{\text{sel}}_{t|\mathcal{T}}(i) &= \frac{1}{n_{t_{\text{f}}}} \sum_a \sum_b v_{t+1}(a) \Big[w_t(a \mid b, i) - \bar{w}_t(a \mid b) \Big] n_t(b, i) \\ \Delta p^{\text{ct}}_{t|\mathcal{T}}(i) &= \frac{1}{n_{t+1}} \sum_a \sum_b \bar{w}_t(a \mid b) \left[p_{t|t_0}(b \mid i) - p_t(b) \right] n_{t|t_0}(i), \end{aligned} \tag{A58}$$

where these expressions follows from rearrangement using the definition of individual fitness functions. As we are interested in the dynamics for small values of δ, we Taylor expand eq. (A58) about $\delta = 0$ to get

$$\Delta p_{t|\mathcal{T}}(i) = \Delta p^{\text{ct}}_{t|\mathcal{T}}(i) \Big|_{\delta=0} + \delta \frac{\text{d}}{\text{d}\delta} \Delta p^{\text{sel}}_{t|\mathcal{T}}(i) \Big|_{\text{s.s.}} + \text{h.o.t.}, \tag{A59}$$

where h.o.t. refers to 'higher order terms' (in the above equation these terms are of order δ^2) and where the first-order term is evaluated at the steady state ('s.s.') of the resident or wild-type population where $\delta = 0$ (see below for explanation). First, we note that in eq. (A59) the zero-order term is governed purely by class transmission because the selection-term $\Delta p^{\text{sel}}_{t|\mathcal{T}}(i)|_{\delta=0}$ is 0 due to the fact that for $\delta = 0$ we have $w_t(a \mid b, i) = \bar{w}_t(a \mid b)$ (eq. A57). The zero-order term in eq. (A59) reads

$$\Delta p^{\text{ct}}_{t|\mathcal{T}}(i) \Big|_{\delta=0} = \frac{1}{n_{t+1}} \sum_a \sum_b w_t(a \mid b) \left[p_{t|t_0}(b \mid i) - p_t(b) \right] n_{t|t_0}(i) \Big|_{\delta=0}, \tag{A60}$$

where we again used eq. (A57) and where all terms on the right-hand-side are calculated for $\delta = 0$. In contrast, and second, we note that the first-order term in eq. (A59) is governed purely by selection. This is because both variables $p_{t|t_0}(b \mid i)$ and $p_t(b)$ in eq. (A58) follow the exact same recursion $y_{t+1}(b) = (\sum_b \bar{w}_t(a \mid b) y_t(b)) / (\sum_{a,b} \bar{w}_t(a \mid b) y_t(b))$, where $y_t(b) = p_{t|t_0}(b \mid i)$ or $y_t(b) = p_t(b)$, implying that (i) their derivatives are equal, and that (ii) their steady states are also equal and hence these variables will be δ-distance away from each other after some initial phase of evolutionary dynamics, i.e. after some finite time t^*. Because timescale-separation methods [Priklopil and Lehmann, 2020] allow us to substitute this steady state into first-order terms, we obtain that the entire derivative of class transmission

$\frac{\mathrm{d}}{\mathrm{d}\delta}\Delta p^{\mathrm{ct}}_{t|\mathcal{T}}(i)|_{\mathrm{s.s.}}$ is 0. This is the reason why the first-order term in eq. (A59) is given only by the term $\frac{\mathrm{d}}{\mathrm{d}\delta}\Delta p^{\mathrm{sel}}_{t|\mathcal{T}}(i)\Big|_{\mathrm{s.s.}}$ and this can further be expressed as

$$\frac{\mathrm{d}}{\mathrm{d}\delta}\Delta p^{\mathrm{sel}}_{t|\mathcal{T}}(i)\Big|_{\mathrm{s.s.}} = (1-p_t(i))p_t(i)\delta\sum_a\sum_b \hat{v}(a)\partial_{z(b,i)}\hat{w}(a\mid b)\eta(b)\hat{p}(b). \tag{A61}$$

The hat notation here indicates these terms have been evaluated at the resident or wild-type steady state and $\partial_{z(b,i)}$ refers to a partial derivative with respect to the phenotypic expression of the focal individual whose fitness function it is (calculations not shown here, see Priklopil and Lehmann 2020 for details).

Equations (A58)-(A61) thus show that the initial change in allele frequency is dominated purely by class transmission, that is, $\Delta p_{t|\mathcal{T}}(i) = \Delta p^{\mathrm{ct}}_{t|\mathcal{T}}(i)|_{\delta=0} + \text{h.o.t.}$. If the time of observation $\mathcal{T}$ is sufficiently large so that it contains the time point t^* after which class transmission becomes negligible, however, then the first-order term takes over the dynamics and at later times the allele-frequency is dominated purely by selection. That is, after t^* the change in allele frequency follows $\Delta p_{t|\mathcal{T}}(i) = \Delta p^{\mathrm{sel}}_{t|\mathcal{T}}(i) + \text{h.o.t.} = \delta\Delta\frac{\mathrm{d}}{\mathrm{d}\delta}\Delta p^{\mathrm{sel}}_{t|\mathcal{T}}(i)|_{\mathrm{s.s.}} + \text{h.o.t.}$. Furthermore, because any allele frequency with arbitrary weights is approximately equal to the reproductive-value weighted allele frequency and hence also $p^{\mathrm{sel}}_{t|\mathcal{T}}(i)$ [Priklopil and Lehmann, 2021], we also have the approximation $\Delta p_{t|\mathcal{T}}(i) = \Delta p_t(i) + \text{h.o.t.}$, which justifies eq. (11). Note also that the sum in eq. (A61) is a constant and defines the selection gradient for this model, and because the term in-front of the sum is sign-equivalent, the sign of the selection gradient determines whether the allele frequency increases or decreases monotonically until the allele either goes to fixation or goes extinct (Priklopil and Lehmann, 2021 for details).

Finally, we contrast the above calculation obtained from the multigenerational partitioning to that obtained from the single-generation partitioning by Taylor expanding eq. (4) about $\delta = 0$ to get

$$\Delta p_t(i) = \Delta p^{\mathrm{ct}}_t(i)\Big|_{\delta=0} + \delta\frac{\mathrm{d}}{\mathrm{d}\delta}\left(\Delta p^{\mathrm{ct}}_t(i) + \Delta p^{\mathrm{sel}}_t(i)\right)_{\mathrm{s.s.}} + \text{h.o.t.} \tag{A62}$$

where

$$\Delta p^{\mathrm{ct}}_t(i)\Big|_{\delta=0} = \frac{1}{n_{t+1}}\sum_a\sum_b w_t(a\mid b)\left[p_t(b\mid i) - p_t(b)\right]n_t(i) \tag{A63}$$

and

$$\begin{aligned}\left(\Delta p^{\mathrm{ct}}_t(i) + \Delta p^{\mathrm{sel}}_t(i)\right)_{\mathrm{s.s.}} = &\sum_a\sum_b \hat{w}(a\mid b)\frac{\mathrm{d}}{\mathrm{d}\delta}\left[p_t(b\mid i) - p_t(b)\right]_{\mathrm{s.s.}} p_t(i) + \\ &+ (1-p_t(i))p_t(i)\sum_a\sum_b \partial_{z(b,i)}\hat{\bar{w}}(a\mid b,i)\eta(b)\hat{p}(b).\end{aligned} \tag{A64}$$

In eq. (A63) all terms on the right-hand-side are calculated for $\delta = 0$. In eq. (A64), the first term on the right-hand-side does not vanish because $p_t(b\mid i)$ and $p_t(b)$ do not follow the same dynamical equation for non-zero δ and hence the derivative inside the brackets is non-zero, which is in contrast to $p_{t|t_0}(b\mid i)$ and $p_t(b)$ in eq. A60 (and note that all other derivatives are zero because they are multiplied by the term inside the brackets evaluated at $\delta = 0$ which

does vanish). This shows that the slow dynamics depends on the perturbation of the genetic structure (first term in eq. A64) and confirms that $\Delta p_t^{\mathrm{ct}}(i)$ is not governed by class transmission only in the context of a multigenerational process over $\mathcal{T}$: in the single-generation partitioning one conditions on the state at time t and hence counts also the ancestors of individuals at t that underwent selection in the past $[t_0, t]$. Moreover, using eqs. (A58)-(A61), we have that $\frac{\mathrm{d}}{\mathrm{d}\delta}\Delta p_{t|\mathcal{T}}^{\mathrm{sel}}(i)\Big|_{\mathrm{s.s.}} = \left(\Delta p_t^{\mathrm{ct}}(i) + \Delta p_t^{\mathrm{sel}}(i)\right)_{\mathrm{s.s.}} + \text{h.o.t.}$ which implies that the reproductive values in the multigenerational partitioning contain the deviation term caused by genetic structure in the single-generation partitioning. While one can in principle use both eqs. (A64) and (A61) to approximate allele-frequency change under small phenotypic deviations, eq. (A61) is considerably easier to calculate. To conclude, we have confirmed that the expressions $\Delta p_t^{\mathrm{ct}}(i)$ and $\Delta p_t^{\mathrm{sel}}(i)$ in eq. (4) do not give the correct contributions of class transmission and selection in a multigenerational evolutionary process.

Symbol	Definition
$n_t(a,i)$	Number of individuals in class a carrying allele i at time t
$n_t(i) = \sum_a n_t(a,i)$	Total number of individuals carrying allele i at time t
$n_t(a) = \sum_i n_t(a,i)$	Total number of individuals in class a at time t
$p_t(i) = n_t(i)/n_t$	Frequency of individuals in the population carrying allele i at time t
$p_t(a \mid i) = n_t(a,i)/n_t(i)$	Frequency of individuals in class a amongst all the individuals that carry allele i in the population at time t
$p_t(i \mid a) = n_t(a,i)/n_t(i)$	Frequency of individuals carrying allele i amongst all the individuals in class a at time t
$w_t(a \mid b,i)$	Expected number of offspring of class a produced over the time step $[t,t+1]$ by a single parent in class b carrying allele i
$\bar{w}_t(a \mid b) = \sum_i w_t(a \mid b,i)p_t(i \mid b)$	Expected number of offspring of class a produced over the time step $[t,t+1]$ by a single average parent in class b
$\bar{w}_t(i) = \sum_{a,b} w_t(a \mid b,i)p_t(b \mid i)$	Expected number of offspring produced over the time step $[t,t+1]$ by a single average parent i in the population
$\bar{w}_t = \sum_{a,b} \bar{w}_t(a \mid b)p_t(b)$	Expected number of offspring produced over the time step $[t,t+1]$ by a single average parent in the population
$v_t(a)$	Reproductive value of an individual a at time t in a multigenerational process over $\mathcal{T}$, defined as the expected number of individuals at time t_f that descend under the non-selective process from that individual
$\bar{v}_t(i) = \sum_a v_t(a)p_t(a \mid i)$	Reproductive value of an average i at time t in a multigenerational process over $\mathcal{T}$
$\bar{v}_t = \sum_i \bar{v}_t(i)p_t(i)$	Reproductive value of an average individual in the population at time t in a multigenerational process over $\mathcal{T}$
$\bar{\bar{w}}(i) = \sum_{a,b} \bar{w}_t(a \mid b)p_t(b \mid i)$	Expected number of offspring produced over the time step $[t,t+1]$ by a single i at time t if it were to survive and reproduce as an average individual in the class
$n_t^\circ(a,i)$	Total number of individuals i in class a at time t in a non-selective process where all individuals between $[t_0,t]$ survive and reproduce as average individuals of their class
$n_t^\circ(i)$	Total number of individuals i at time t in a non-selective process where all individuals between $[t_0,t]$ survive and reproduce as average individuals in the class
$p_t^\circ(a \mid i)$	Frequency of a at t amongst all the individuals that carry allele i in a non-selective process that started at time t_0
$\bar{w}_t^\circ(i) = \sum_{a,b} \bar{w}_t(a \mid b)p_t^\circ(b \mid i)$	Expected number of offspring produced over the time step $[t,t+1]$ by a single i if it were to reproduce as an average individual in the class and that comes from a lineage of non-selected individuals between $[t_0,t]$
$\bar{w}_t^\mathrm{v}(i) = \sum_{a,b} v_t(a)w_t(a \mid b,i)p_{t+1}(b \mid i)$	Expected number of individuals at time t_f that descend under a non-selective process from all offspring produced during $[t,t+1]$ by a single i carrier

Symbol	Definition
$r^{\circ}(i) = n_t^{\circ}(i)/n_t(i)$	Fraction of i at t that come from a lineage of non-selected individuals during $[t_0, t]$
$n_{\mathcal{C}}$	Total number of classes in the class-structured population
$q_t(a)$	Arbitrary weight of individuals in class a at time t
$q_t(i) = \sum_a q_t(a) p_t(a \mid i)$	Arbitrary weight of an average individual i in the population at time t
$\bar{w}^q(i) = \sum_{a,b} q_{t+1}(a) w_t(a \mid b, i) p_{t+1}(b \mid i)$	Expected number of offspring produced during $[t, t+1]$ by a single i when each offspring in each class is weighted by an arbitrary weight $q_{t+1}(a)$

Table 1: Definitions of the variables and main quantities. See main text for further explanations.

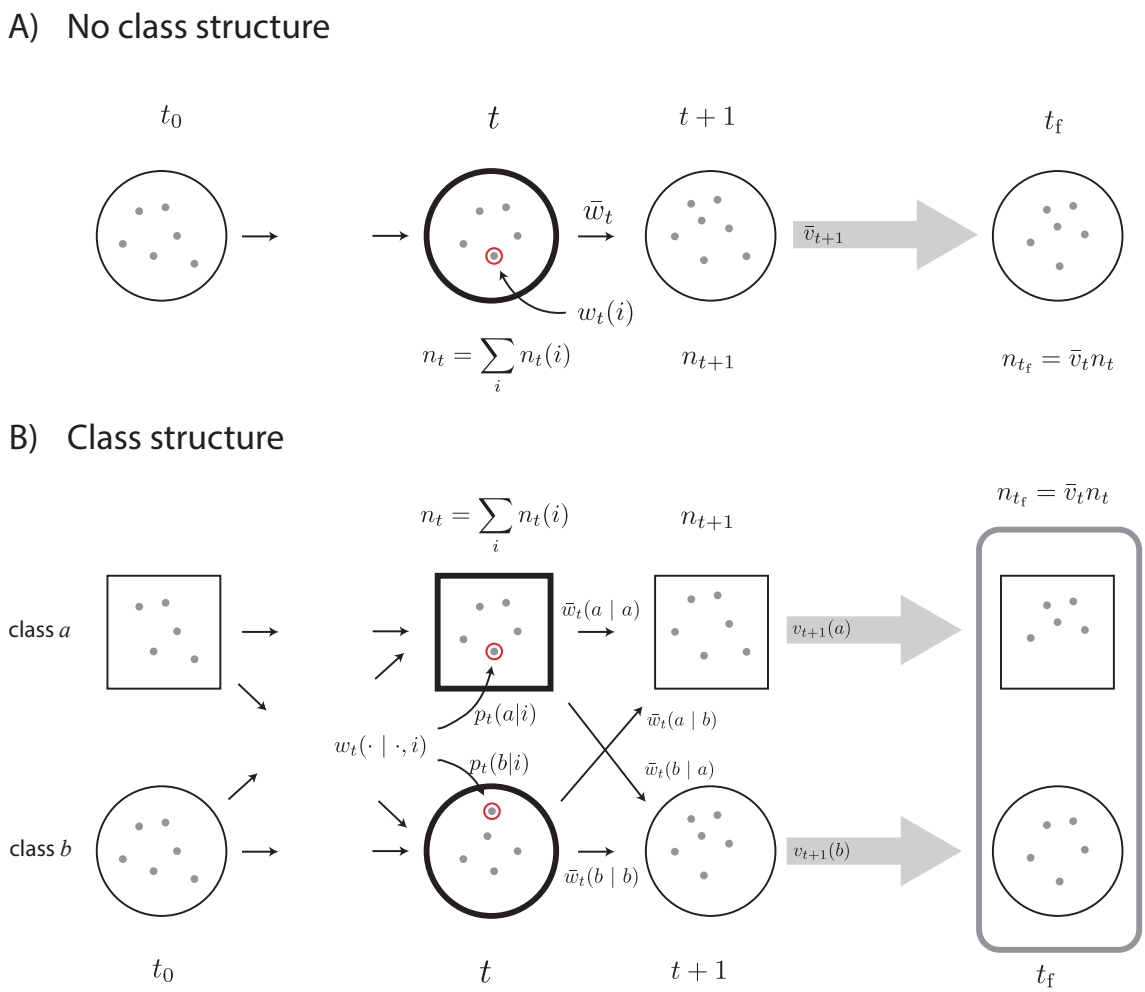

Figure 1: **Panel A)** Evolutionary dynamics in a population without class structure where $w_t(a \mid b, i) = w_t(i)$ for all a, b (Appendix A1.2.3). The big circles represent a population at different time points t, and the grey dots represent individuals. Allele i (red circle) is favoured by selection during $[t, t+1]$ if its fitness exceeds that of the average individual. The change in frequency during this demographic time period is $\Delta p_t(i) = \Delta p_t^{\text{sel}}(i) = \Delta p_{t|\mathcal{T}}^{\text{sel}}(i) = n_t(i)(w_t(i) - \bar{w}_t)/n_{t+1}$, which can be interpreted as the fraction of the total frequency of i measured at the final time t_f that is attributed to generation t (see eq. A27 of the Appendix). This is so because in the absence of selection during $[t+1, t_f]$ (grey thick arrow) the descendants of the selected and average individuals propagate equally fast and hence do not alter allele frequencies. **Panel B)** Evolutionary dynamics in a class-structured population where at each point in time t the population is now separated into two classes a (squares) and b (circles) between which the alleles can transition. Because alleles can reside in either of the two classes, allele i is now favoured by selection during $[t, t+1]$ if its class-specific fitness exceeds that of an average individual within its class. The change in frequency during this demographic time period due to selection is thus $\Delta p_t^{\text{sel}}(i) = (1/n_{t+1}) \sum_{x,y \in \{a,b\}} (w_t(x \mid y, i) - \bar{w}_t(x \mid y)) p_t(y \mid i) n_t(i)$ as given in eq. (4b). To obtain the frequency $\Delta p_{t|\mathcal{T}}^{\text{sel}}(i)$ we must weight each offspring i produced due to selection during $[t, t+1]$ by their class-specific reproductive values giving the number of their descendants at t_f under class transmission only during $[t+1, t_f]$, and then compare this to the total number of individuals at t_f. This yields $\Delta p_{t|\mathcal{T}}^{\text{sel}}(i) = (1/n_{t_f}) \sum_{x,y \in \{a,b\}} v_{t+1}(x)(w_t(x \mid y, i) - \bar{w}_t(x \mid y)) p_t(y \mid i) n_t(i)$ as given in eq. (8).

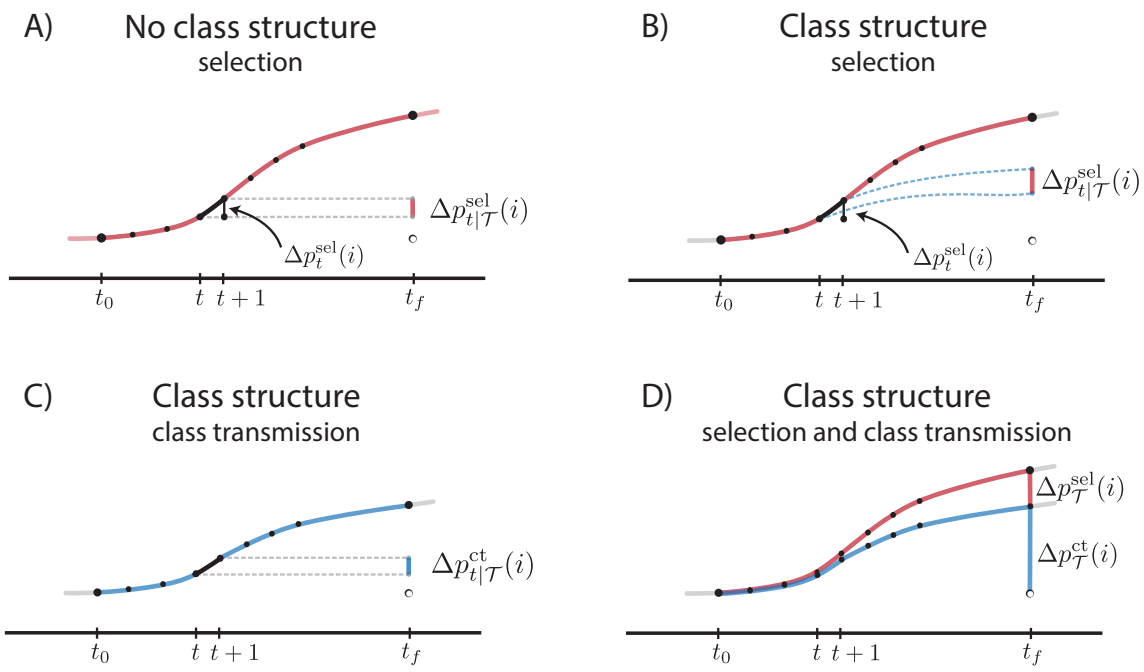

Figure 2: Partitioning of the allele-frequency change $\Delta p_{\mathcal{T}}(i) = p_{t_{\mathrm{f}}}(i) - p_{t_0}(i)$ into fractions caused by selection $\Delta p^{\mathrm{sel}}_{\mathcal{T}}(i) = \sum_{t=t_0}^{t_{\mathrm{f}}-1} \Delta p^{\mathrm{sel}}_{t|\mathcal{T}}(i)$ and class transmission $\Delta p^{\mathrm{ct}}_{\mathcal{T}}(i) = \sum_{t=t_0}^{t_{\mathrm{f}}-1} \Delta p^{\mathrm{ct}}_{t|\mathcal{T}}(i)$. **Panel A)** Allele-frequency change in a population without class structure where $w_t(a \mid b, i) = w_t(i)$ for all a, b (Appendix A1.2.3). The black dots along the red curve indicate the observed allele frequencies in different generations. The fraction $\Delta p^{\mathrm{sel}}_{t|\mathcal{T}}(i)$ of individuals observed at time t_{f} gives the difference between two frequencies (indicated by the short vertical red line): the frequency of all i that underwent the full evolutionary process with selection until $t+1$ and thereafter reproduced and survived under a non-selective process (top grey dashed line), and the frequency of all i that underwent the full evolutionary process only until time t and thereafter reproduced and survived under a non-selective process (bottom grey dashed line). These gray lines are horizontal because in populations without class structure $\Delta p_t(i) = \Delta p^{\mathrm{sel}}_t(i) = \Delta p^{\mathrm{sel}}_{t|\mathcal{T}}(i)$ (eq. A27). **Panel B)** Allele-frequency change due to selection in a class-structured population. The explanation is identical to panel A, except that in a class-structured population class transmission can also alter allele frequencies (blue dashed curve). Because of this, we have in general $\Delta p^{\mathrm{sel}}_t(i) \neq \Delta p^{\mathrm{sel}}_{t|\mathcal{T}}(i)$ (compare eqs. 4b and 8). **Panel C)** Allele-frequency change over $\mathcal{T}$ due to class transmission in a class-structured population. The fraction $\Delta p^{\mathrm{ct}}_{t|\mathcal{T}}(i)$ of individuals gives the difference between two frequencies (indicated by the short vertical blue line): the frequency of all i that underwent class transmission until $t+1$ and thereafter reproduced and survived under the non-selective process of population growth (top grey dashed line), and the frequency of all i that underwent class transmission only until t and thereafter reproduced and survived under the non-selective process of population growth (bottom grey dashed line). Because we are conditioning on a (hypothetical) lineage of alleles that have underwent class transmission only (blue curve), the dots along the blue curve are not the observed frequencies and must be calculated. This also implies that in general $\Delta p^{\mathrm{ct}}_t(i) \neq \Delta p^{\mathrm{ct}}_{t|\mathcal{T}}(i)$ (compare eqs. 4c and 9), and explains why $\Delta p^{\mathrm{ct}}_t(i)$ is not depicted. **Panel D)** The total multigenerational change in allele frequency over $\mathcal{T}$ caused by selection $\Delta p^{\mathrm{sel}}_{\mathcal{T}}(i)$ and class transmission $\Delta p^{\mathrm{ct}}_{\mathcal{T}}(i)$ in a class-structured population. The sums $\Delta p^{\mathrm{sel}}_{\mathcal{T}}(i) = \sum_t \Delta p^{\mathrm{sel}}_{t|\mathcal{T}}(i)$ and $\Delta p^{\mathrm{ct}}_{\mathcal{T}}(i) = \sum_t \Delta p^{\mathrm{ct}}_{t|\mathcal{T}}(i)$ are obtained from panels B and C.

BOX A. Adjoint system and the dynamics of reproductive value

Consider an arbitrary population process during $\mathcal{T}$,

$$x_{t+1}(a) = \sum_b f_t(a \mid b) x_t(b), \tag{A.1}$$

where $f_t(a \mid b)$ gives the number of type a individuals produced by a single type b individual at time t and $x_t(b)$ specifies the number of individuals of type b at time t under this process. In particular, this process may or may not include selection. The so-called adjoint system (e.g., Athans and Falb, 2007, p. 147) of eq. (A.1) can then be expressed as

$$y_t(a) = \sum_b y_{t+1}(b) f_t(b \mid a), \tag{A.2}$$

where $\mathbf{y}_t = (y_t(a))$ is called an adjoint variable (associated to the vector $\mathbf{x}_t = (x_t(a))$). A useful property of adjoint systems is that $\sum_a x_t(a) y_t(a)$ is constant and equal for all t, and the exact value depends on the initial and final conditions $\mathbf{x}_{t_0}$ and $\mathbf{y}_{t_\mathrm{f}}$. In fact, the specification of the final condition also suggests a biological interpretation for the adjoint variable $\mathbf{y}_t$. For instance, suppose that the final condition satisfies $y_{t_\mathrm{f}}(a) = 1$ for all a. Then, we have $\sum_a x_t(a) y_t(a) = x_{t_\mathrm{f}}$ for all t where $x_{t_\mathrm{f}} = \sum_a x_{t_\mathrm{f}}(a)$ is the total population size at the final time t_f under this arbitrary population process. The adjoint variable $y_t(a)$ can be interpreted, under this arbitrary process, as the *number of individuals alive at time t_f that are the descendants of a single type a individual alive at time t*. Indeed, this definition follows from the recursion: the number of individuals at t_f that descend from a single individual a at t – the left hand-side of eq. (A.2) – is equal to the number $f_t(b \mid a)$ of offspring-individuals b that this parent individual a produces and where each offspring-individual at $t+1$ is multiplied by the number $x_{t+1}(b)$ of its descendants alive at t_f, and then we sum over all classes of offspring. Note that the final condition $y_{t_\mathrm{f}}(a) = 1$ is consistent with this interpretation because the 'descendant' alive at t_f and its 'ancestor' alive at t_f must be one and the same individual, and hence the number of individuals at t_f that 'descend' from an individual alive at t_f must be 1. In the main text $f_t(a \mid b)$ is defined as the class-specific fitness $\bar{w}_t(a \mid b)$, in which case eq. A.2 defines the dynamics of reproductive values under the non-selective process. Representing reproductive value dynamics as an adjoint system is also discussed e.g. in Lion [2018, eq. 14].

BOX B. Invasion fitness

Here we connect the partitioning of the recursion for a multigenerational process (eq. 5) as well as the partitioning of the geometric mean (eqs. 13-14) to the asymptotic evolutionary trajectory of a rare allele. Recall that the invasion exponent of allele i is defined (under some technical conditions) as $\rho = \lim_{t_f \to \infty} 1/(t_f - t_0) \ln(n_{t_f}(i)/n_{t_0}(i))$ giving the asymptotic exponential rate of growth of allele i, which has been widely used as a summary measure of selection since at least Fisher [1930] and is often called the Malthusian growth rate. Suppose that all alleles but i coexist at some asymptotically stable equilibrium, which we call the resident equilibrium (the assumption of an equilibrium is not necessary as the calculations carry over to more complex attractors of the resident population e.g. Ferrière and Gatto, 1995, Metz et al., 1992, Tuljapurkar, 1989a). Then, the invasion fitness for allele i, defined as $\hat{\bar{W}}(i) = e^{\rho}$, and giving the expected number of offspring produced asymptotically per generation per parent i, can be expressed as

$$\hat{\bar{W}}(i) = \frac{\sum_{a,b} \hat{q}(a)\hat{w}(a \mid b, i)\hat{p}(b \mid i)}{\sum_a \hat{q}(a)\hat{p}(a \mid i)} = \frac{\hat{\bar{w}}^q(i)}{\hat{\bar{q}}(i)} \tag{B.1}$$

(Appendix A3.1). Here, $\hat{q}(a)$ is an arbitrary weight of an individual in class a evaluated at the resident equilibrium (all hats hereafter indicate evaluation at an equilibrium), $\hat{\bar{w}}^q(i) = \sum_{a,b} \hat{q}(a)\hat{\bar{w}}(a \mid b)\hat{p}(b \mid i)$ is an arbitrarily weighted fitness of i and $\hat{\bar{q}}(i) = \sum_a \hat{q}(a)\hat{p}(a \mid i)$. The fact that eq. (B.1) is equal for arbitrary weights implies that only selection is in play in calculations of invasion fitness. Indeed, on one hand, by setting $\hat{q}(a) = \hat{v}(a)$ for all a, the invasion fitness can be represented as the asymptotic geometric mean for selection $\hat{\bar{W}}(i) = \lim_{t_f \to \infty} \overline{W}^{\text{sel}}_{\mathcal{T}}(i) = \hat{\bar{w}}^{\text{v}}(i)/\hat{\bar{v}}(i)$ (Appendix A3.1). On the other hand, by setting $\hat{q}(a) = 1$ for all a, the invasion fitness can be represented as the asymptotic geometric mean fitness $\hat{\bar{W}}(i) = \lim_{t_f \to \infty} \overline{W}_{\mathcal{T}}(i) = \hat{\bar{w}}(i)$ (Appendix A3.1). This confirms that the asymptotic evolutionary trajectory of a rare allele i is fully determined by a measure of fitness where only selection is in play. Or even more precisely, upon the introduction of the allele i the evolutionary trajectory is subject to both class transmission and selection but then converges to the leading eigenvector with elements $\hat{p}(a \mid i)$, along which class transmission vanishes and the rate of growth is given by the invasion fitness determined by selection only (Appendix A3.1). We note that the two representations of invasion fitness, $\hat{\bar{w}}(i)$ and $\hat{\bar{w}}^{\text{v}}(i)/\hat{\bar{v}}(i)$, extend to spatially structured populations and $\hat{\bar{w}}^{\text{v}}(i)/\hat{\bar{v}}(i)$ forms the basis of the inclusive fitness representation of invasion fitness [Lehmann and Rousset, 2020, Lehmann et al., 2016].

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