Quantifying Random Drift in a Multi-level Selection Model

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Abstract

Random drift – stochastic effects leading to evolutionary change – is one of the major forces within evolution. Its effects are more significant for smaller populations. Since it has been shown that group-structured populations undergoing multi-level selection have a significantly lower *effective* population size (N_e), one would expect to see a more significant impact of random drift in these type of systems. Although there are some quantities available that are greatly influenced by drift, *e.g.* fixation probability or the fluctuations around a mutation-selection equilibrium, random drift has not often been quantified directly.

The aim of this study is to quantify random drift in a group-structured population undergoing multi-level selection. First, we will present a new framework based on Price's equation that is able to do quantify both random drift and natural selection on multiple levels. Secondly, we will apply this framework on a model based on Traulsen and Nowak (2006). Then we will study how the fixation probability of a mutant and the fluctuations around a mutation-selection equilibrium change for varying number of groups in the group-structured population of our model. Finally, we will try to explain these effects using the terms from our newly presented framework.

We have found that our framework is able to properly describe the evolutionary change due to drift in our model. Furthermore, we can identify some trends in the patterns of within-group and among-group drift corresponding to the behaviour of the system and are able to explain these. However, it has still proven difficult to explain directly how changes in fixation probability are affected directly by the drift terms. Future research could study the implications of the different terms from our framework more extensively, considering more quantities of random drift or perhaps studying the terms in more models.

Summary

In the theory of evolution, two major forces can be distinguished: natural selection and random drift. Natural selection is a deterministic force which considers individuals having higher reproductive success or having higher survival chances due to how well they are adapted. Random drift is a stochastic force which considers random processes. It describes individuals having higher reproductive success or survival chances due to random chance. One of the most important aspects of random drift is that its impact is greater in smaller populations.

Evolution is often considered to take place on a single level, for example selection on organisms in a population. However there is a theory which proposes that evolution can act on multiple levels, called multi-level selection theory. Within multi-level selection theory, evolution is considered on multiple levels, for example selection acting on organisms in a population, but also selection acting between different populations at the same time.

In previous research, it has been found that in a population that is divided into groups undergoing multi-level selection, the *effective* population size is greatly decreased. The effective population size is a quantity describing how a complex population, for example when it is divided into groups, behaves when it would have been a simple population. Considering the effective size of populations can make it easier to compare a complex system to a simple system and predict what kind of behaviour we could expect in this complex system. Since the effective population size of a group-structured population undergoing multi-level selection has been found to be lower, we could expect random drift to have a greater impact in such a system, considering its impact is greater in smaller populations.

Considering random drift might have a more significant impact in a system undergoing multi-level selection, we are interested in quantifying random drift in such a system. Therefore, in this study, we formulate a framework that is able to quantify random drift in a multi-level selection model. This framework is based on Price's equation, which is an important equation within evolutionary theory and it describes evolutionary change over time. We applied our newly presented framework on a model considering a group-structured population which is undergoing multi-level selection. In this model, we consider two levels of selection since we consider individuals (within-group level) that are divided into groups (among-group level). We found that the framework was able to properly describe evolutionary change in this model.

Furthermore, we studied how the behaviour of the model changes when we vary the number of groups in the group-structured population. We are able to see a changing pattern of random drift on both levels for a varying number of groups. Additionally, we are able to explain these patterns in the random drift resulting from our framework. However, it still proved to be difficult to directly explain the behaviour of the system based on these patterns in random drift. Further research

could explore more models or systems on which our framework could be applied to increase our understanding of the role of random drift in multi-level selection theory.

1 Introduction

In the theory of evolution, random drift – stochastic effects leading to evolutionary change – is one of the most important concepts, besides natural selection. Random drift can have significant effects on evolutionary change by decreasing genetic variation or by affecting the success of new mutations. These effects are known to be more significant in smaller populations and thus decrease with population size. In populations that are spatially structured and undergoing group-events, however, the 'effective population size' may be much smaller than the true population size. Moreover, if a population is subdivided into groups and these groups act as units of selection themselves (multi-level selection), the effective population size might be strongly affected. Therefore, it might be useful to study the effects of random drift in multi-level selection models where the population is subdivided into groups and groups are undergoing group-events, like extinction-events. Are we then able to determine the evolutionary forces on these multiple levels, and specifically, can we define and quantify random drift in such a group-structured population undergoing multi-level selection?

Random drift

In evolutionary theory, random drift (or just 'drift' or 'genetic drift') is often considered to cover all evolutionary change due to stochastic factors (Okasha, 2006). Random drift opposes natural selection, which is deterministic, although it can be difficult to distinguish the effects of the two in an evolutionary scenario (Beatty, 1984). Specifically, two major effects of random drift on evolution have been studied extensively (Gillespie, 1998). Firstly, random drift can decrease the amount of genetic variation in a population, acting as a dispersive force (Wright, 1931). However, in most natural populations, the effects of this dispersive force are very weak. Secondly, random drift affects the probability that a new mutation in a population is able to survive and perhaps even fix in the population (Fisher, 1922).

Multi-level selection

To understand the effects of random drift in multi-level selection models, it is important to cover what multi-level selection theory entails. According to multi-level selection theory, the Darwinian principles that are necessary for evolution – character variation, associated fitness differences and heritability – can be applied on multiple levels (Okasha, 2006). Therefore, multi-level selection makes the notion that selection itself does not occur only at a single level, but at multiple levels. Consider a two-level example, where individuals, the lower-level units, are divided over groups, the higher-level units (Fig. 1). In this example, multi-level selection theory would apply (1) when the individuals vary in a certain heritable character, which leads to differences in fitness and (2) when the groups have a heritable character of their own which leads to differences in fitness of these groups. Note that the terms 'individual' and 'group' are, in biology, easily interpreted as organisms in a population. However multi-level selection theory describes any hierarchical setting considering lower- and higher-level units. Okasha (2006) emphasises this notion by using the abstract terms 'particles' and 'collectives', which are adopted from Hamilton (1975) and Kerr and Godfrey-Smith (2002).
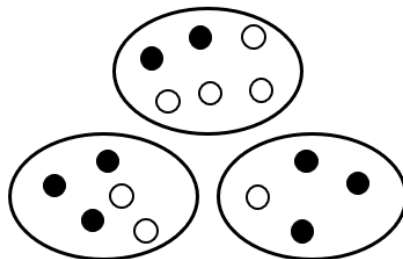

Figure 1: Schematic representation of two types of individuals, divided over groups

A very important distinction to make, is the nature of this heritable character of the groups. This heritable group character can either originate from the heritable character of the individuals, or the group character can be completely independent from the individual's character (Okasha, 2006). For this first case, we can distinguish between a group character that is simply the average of the individual's character in the corresponding group and a group character that is dependent

on the individual's character indirectly (Grantham, 1995; Lloyd, 1988; Okasha, 2006). These type of group characters are called 'aggregate' characters and 'emergent' characters, respectively.

Additionally, when considering the group's fitness, there are two ways to define this fitness (Damuth & Heisler, 1988). Firstly, the group's fitness can be defined as the average fitness of all the individuals within this group. Secondly, the group's fitness can be defined as the number of offspring groups it produces, similarly to how a individual's fitness is often defined as the number of offspring individuals it produces. To distinguish between these two definitions, they are referred to as 'group fitness$_1$' and 'group fitness$_2$', respectively (following Okasha (2006)).

The distinction into 'group fitness$_1$' and 'group fitness$_2$' is important for the understanding of multi-level selection, since the two definitions lead to two distinct concepts of multi-level selection. The distinction rests on the question whether the individual or the group level are the 'focal' level of selection (Damuth & Heisler, 1988; Okasha, 2006). Firstly, when the interest lies on the frequencies of different individual character types and these individuals happen to be subdivided into groups, the individual level is the 'focal' level of selection. Secondly, when the interest lies on groups as well, considering them as Darwinian entities on their own, the group level (or both levels) might be the 'focal' level of selection. These two different ideas are referred to as multi-level selection 1 (MLS1) and multi-level selection 2 (MLS2), respectively, following Damuth and Heisler (1988). In MLS1, 'group fitness$_1$' is considered as the fitness of groups, while in MLS2, 'group fitness$_2$' is considered as the fitness of groups. For this paper, MLS1 is considered and this is referred to when multi-level selection is mentioned

Effective population size

To understand why studying subdivided populations could produce interesting results, we need to consider the concept of 'effective population size'.

In the field of population dynamics, often idealised populations are considered, making certain assumptions to simplify calculations, *e.g.* random mating and constant population sizes (S. Rice, 2004). However, in reality, systems are more complex and the assumptions of an idealised population are often not met. In order to still be able to use calculations and equations derived for simple systems in more complicated situations, the size of an idealised population that would behave similar to the complex system is calculated. This calculated population size is called the effective population size (N_e), originally devised by Wright (1931), and can be used to substitute the actual population size in equations for a simple system.

A subdivided population is an example of such a complex system and therefore the effective population size can be used to more accurately describe the dynamics of such a population. When considering N_e for a simple subdivided population, like the finite island model, it is found that subdividing a population increases the effective size (S. Rice, 2004). However, a study by Whitlock and Barton (1997), found that subdividing a population usually decreases the effective population size, due to differing sizes and contributions of subdivisions.

Additionally, effective population size can be further affected by group-level events in subdivided populations. The effect of group-events, like extinction and recolonisation, on the effective population size has been studied in so-called meta-populations. A meta-population is defined as a population of multiple subpopulations, called demes, and evolution in these type of populations has been studied extensively (Pannell & Charlesworth, 2000). Such a meta-population model can be extended to consider extinction and recolonisation (whenever a deme goes extinct, it is recolonised by individuals from other demes) which was originally proposed by Slatkin (1977), resembling a simple 'island-model'. Whitlock and Barton (1997) found that the effective population size of such a model is greatly reduced as a result of extinction-events. Most importantly, this is due to colonists occupying the empty space, which arises following an extinction event, having much higher reproductive success as opposed to individuals in full demes (Wang & Caballero, 1999; Whitlock & Barton, 1997).

Considering both subdividing a population as well as group-events affect effective population size, we may expect evolutionary forces to be affected as well. Since the impact of random drift decreases with increasing population size and we expect a smaller effective population size from extinction-events and possibly from subdividing a population as well, it is especially interesting to see how evolution is affected.

Quantifying evolution

In order to understand an evolutionary process it can be very useful to quantify the effect of selection in this process. This can be done using Price's equation (Price, 1972).

Price's equation describes the change in the mean of any phenotypic character in a very general way, without considering any biological assumptions (Frank, 1995, 1998). The basic Price equation does this by describing the change in the population average of this phenotypic character, which from now on we will call ϕ. The population average then is notated as $\overline{\phi}$. The change in $\overline{\phi}$ is determined by two terms, according to Price's equation. Firstly, it considers change in $\overline{\phi}$ due to selection. This term is based on individuals with a certain value for ϕ, generally having a higher or lower fitness w, the number of offspring an individual gets. Secondly, Price's equation considers change in $\overline{\phi}$ due to parents getting offspring which has a different value for ϕ then their parent. This is called transmission bias. Considering these two forces, the basic Price equation looks as follows:

$$\overline{w}\Delta\overline{\phi} = \underbrace{\text{Cov}\left(w_i, \phi_i\right)}_{\text{Selection}} + \underbrace{\overline{w_i\Delta\phi_i}}_{\text{Transmission Bias}} . \tag{1}$$

In this equation, $\Delta\overline{\phi}$ is the change in the population average of ϕ, which is weighted by the population average fitness $\overline{w}$. Moreover, the first term on the right-hand side shows the covariance between the fitness w_i and phenotype value ϕ_i for every individual i and represents natural selection. The second term on the right-hand side shows the average, or expected value, of the fitness w_i times the difference in ϕ between a parent and their offspring, $\Delta\phi_i$, for every individual i. This represents the change due to the transmission bias.

Price's equation has also been used to describe multi-level evolutionary systems (Hamilton, 1975; Price, 1972), which will be described later in this article. Additionally, an extension on Price's equation has also been proposed to quantify drift within a single-level system (Grafen, 2000), and will be covered later as well.

Quantifying drift

Although it is possible to quantify random drift using Price's equation, there are also other ways to quantify (the effects of) random drift within an evolutionary system.

As mentioned earlier, one way random drift affects evolution is via its effects on survival of new mutations. Therefore, the fixation probability of a new mutant within a population is a quantitative measure indicating the effects of random drift to some extent. In earlier models of evolution, like the Wright-Fisher model, fixation probability is the probability of a certain allele taking over the entire population (Gillespie, 1998). The Wright-Fisher model considers a population of N diploid individuals, thus considering $2N$ alleles. Alleles have no fitness effects on individuals. A new generation is created by randomly selecting an allele from the $2N$ alleles and putting an exact copy of this allele in the new generation. This is repeated $2N$ times, leading again to a population of $2N$ alleles. The probability of fixation of a single allele, i.e. the probability that a certain allele will be the only type of allele in the population, is simply $1/(2N)$. More generally, the fixation probability of an allele in a neutral setting is the number of copies of this allele in the population i, divided by the total number of alleles, $i/(2N)$. If a certain allele in a population has a fitness advantage, it is obvious that its fixation probability is higher than in a neutral situation. Similarly, an allele with a fitness disadvantage has a lower fixation probability than in a neutral situation, but has a non-zero fixation probability nonetheless. Finally, the fixation probability of an allele with a fitness disadvantage, relative to the fixation probability of the other alleles, increases with a smaller population size N.

When considering a population that is in equilibrium, we can study the fluctuations around this equilibrium since these indicate the effects of drift to some extent. When mutations are present, a (multi-level) system can move towards an equilibrium where natural selection and mutation balance each other out, called the mutation-selection equilibrium (S. Rice, 2004). However, when in equilibrium, there is often still quite some variation found where the system fluctuates around this equilibrium. Considering that mutation and selection keep the system in equilibrium, it is due to the effects of random drift, that the system is still fluctuating. These fluctuations around an equilibrium have been found in group-structured populations, even when the total population size was quite large and one might not expect these large effects of drift (Hermsen, 2022).

Knowing that it is possible to quantify drift itself within a single-level system using Price's equation and that there are some quantities available that are greatly influenced by the effects of drift, it might be possible to gain more knowledge of drift within a multi-level system. This leads to the following questions which will be covered in this report. How can we quantify random drift in group-structured multi-level selection models? And how can we use these quantities to understand the behaviour of these type of models?

Firstly, we will take Price's equation and expand on it by incorporating both multi-level selection as well as random drift. Secondly, we consider a simple multi-level selection model, which was adapted from Traulsen and Nowak (2006). We will study its behaviour in terms of both fixation probability as well as fluctuations around a mutation-selection equilibrium. Finally, we will examine how changing the number of groups affects the behaviour of the system in terms of these aspects. We will then try to explain this using the newly presented framework for quantifying drift in a multi-level system.

2 Results

2.1 Extending Price's equation

As mentioned in the introduction, Price's equation is able to quantify the contribution of selection as well as transmission bias on the change in a certain phenotypic character. Since at first we will consider a version of the model in which mutation is excluded, we can ignore the transmission bias for now. This version of Price's equation, ignoring transmission bias, takes the following form:

$$\overline{w}\Delta\overline{\phi} = \text{Cov}\left(w_i, \phi_i\right). \tag{2}$$

In this current form, Price's equation does not consider separate terms for within- and among-group selection or random drift. Therefore, we will extend on the original Price equation to measure these separate terms.

Adding random drift to Price's equation

The first step for expanding on Price's equation we will take, is by adding random drift, based on work by Grafen (2000).

In order to add random drift, we must acknowledge that realised fitness of individual i, w_i, might differ from the expected fitness of individual i, w_i^*. The expected fitness of an individual is the number of offspring we would expect this individual to produce based on the probabilities of getting a certain number of offspring. (See the Appendix for the calculation of these probabilities and the expected fitness for our specific model). The expected fitness more accurately represents 'fitness' – an individual is more fit than another individual if we *expect* the former one to get more offspring. Deviations from this expected number of offspring are the source of random drift. Within a simulation, we indeed expect some deviation within a time step from this expected fitness. For example, for every time step, all individuals have some value for expected fitness, however, if only one individual is allowed to reproduce per time step, there will be some deviation from this expected fitness for almost all individuals within a single time step.

By recognising both an expected and a realised fitness, we can define a deviation δ_i for individual i from its expected fitness:

$$w_i = w_i^* + \delta_i \tag{3}$$

This δ_i now describes the randomness in a single time step for every individual, and thus tells us something about the drift in a time step.

By substituting eq. 3 into eq. 2, we get

$$\overline{w}\Delta\overline{\phi} = \underbrace{\text{Cov}\left(w_i^*, \phi_i\right)}_{\text{Selection}} + \underbrace{\text{Cov}\left(\delta_i, \phi_i\right)}_{\text{Random Drift}}. \tag{4}$$

In this equation, the first term on the right-hand side now describes the change in mean phenotype due to selection, while the second term on the right-hand side now describes the change in mean phenotype due to random drift. The drift term describes the covariance of the deviation of expected and realised fitness for individual i and the phenotype value of individual i.

It is important to realise that not all deviation of realised fitness from the expected fitness leads to a change in the population average of ϕ. This is only the case when individuals with a certain phenotype value tend to have more/less deviation from expected fitness than other individuals. In that case, $\text{Cov}\left(\delta_i, \phi_i\right)$ is non-zero. This accurately represents that random drift itself is neutral, but it can have an effect, when due to chance it affects certain individuals/genes/part of the population.

Adding within- and among-group selection to Price's equation

As mentioned before, in multi-level selection theory, we can identify two levels of selection (the among-group and the within-group level). Price's equation can be used to describe such a multi-level scenario, as shown by Hamilton (1975) and Price (1972). Recall the covariance between the realised fitness and phenotype of an individual as shown in eq. 2. Using the Law of Total Covariance, we are able to decompose this covariance into a within-selection term and a among-selection term, as we will show now.

In order to introduce this decomposition, it is useful to use a certain notation concerning averaging over individuals or over groups, as used by Hermsen (2022). Consider ϕ_{ij}, which is the value of a certain character ϕ of individual i in group j. The mean of ϕ within group j, $\{\phi; j\}_\mathrm{w}$, can be calculated as follows:

$$\{\phi; j\}_\mathrm{w} \equiv \frac{\sum_{i=1}^{n_j} \phi_{ij}}{n_j}, \tag{5}$$

where n_j is the number of individuals in group j. In $\{\phi; j\}_\mathrm{w}$, the 'w' stands for 'within', indicating we are averaging over a certain value within a single group. Note that the j in this notation, sometimes will be dropped if it is not essential for the understanding of an equation.

Additionally, let Φ be a character of groups. We can define $\langle\Phi\rangle_\mathrm{a}$ as the mean of Φ among the groups where the value of each group gets weighted by its size n_j. $\langle\Phi\rangle_\mathrm{a}$ is calculated as follows:

$$\langle\Phi\rangle_\mathrm{a} \equiv \frac{\sum_{j=1}^{m} n_j \Phi_j}{N}, \tag{6}$$

where m is the number of groups and N is the total number of individuals. Now, the 'a' in $\langle\Phi\rangle_\mathrm{a}$ stands for 'among', indicating that we are averaging over a character of groups.

Finally, we are able to conclude that

$$\langle\{\phi\}_\mathrm{w}\rangle_\mathrm{a} = \overline{\phi}. \tag{7}$$

In other words, we can conclude that when we take the within-group mean of ϕ for every group and we weigh these within-means for the size of its group, this results in the population average of ϕ (Hermsen, 2022).

In previous work by Hamilton (1975) and Price (1972) the selection-term in Price's equation, as seen in eq. 2, has been decomposed into a within- and an among-group term using the Law of Total Covariance. We can perform this decomposition on the selection term from eq. 4, which considers expected offspring. Considering the notations described above, this decomposition looks as follows:

$$\mathrm{Cov}\left(w_i^*, \phi_i\right) = \underbrace{\mathrm{Cov}_\mathrm{a}\left(\{w_i^*\}_\mathrm{w}, \{\phi_i\}_\mathrm{w}\right)}_{\text{Among-group Selection}} + \underbrace{\langle\mathrm{Cov}_\mathrm{w}\left(w_i^*, \phi_i; j\right)\rangle_\mathrm{a}}_{\text{Within-group Selection}}. \tag{8}$$

In this equation, the first term on the right-hand side shows the among-group selection term. Considering MLS1, we define the group fitness as the mean of the fitness of the individuals that group encompasses. Additionally, we define the phenotypic trait of groups as the mean of the phenotypic trait of the individuals in that group. Therefore, the among-group selection is the covariance of the within mean of fitness and the within-group mean of the phenotypic character of all groups. The second term on the right-hand side shows the within-group selection term. This term takes the covariance of individual phenotype and individual fitness for every group, and takes the among-group mean of these values (thus the covariances of every group are weighted by its size).

While the decomposition of the selection term has been performed before (Hamilton, 1975; Price, 1972), we will now also make a similar decomposition for the drift term from eq. 4. This results in the following equation:

$$\mathrm{Cov}\left(\delta_i, \phi_i\right) = \underbrace{\mathrm{Cov}_\mathrm{a}\left(\{\delta_i\}_\mathrm{w}, \{\phi_i\}_\mathrm{w}\right)}_{\text{Among-group Drift}} + \underbrace{\langle\mathrm{Cov}_\mathrm{w}\left(\delta_i, \phi_i; j\right)\rangle_\mathrm{a}}_{\text{Within-group Drift}}. \tag{9}$$

Here, similar to the selection terms, the first term on the right-hand side represents the among-group drift and the second term on the right-hand side represents the within-group drift.

Now, we can finally complete our full extension of Price's equation by substituting eq. 8 and eq. 9 into eq. 4 and making the decomposition of :

$$\overline{w}\Delta\overline{\phi} = \underbrace{\text{Cov}_{\text{a}}\left(\{w_i^*\}_{\text{w}}, \{\phi_i\}_{\text{w}}\right)}_{\text{Among-group Selection}} + \underbrace{\langle\text{Cov}_{\text{w}}\left(w_i^*, \phi_i; j\right)\rangle_a}_{\text{Within-group Selection}}$$
$$+ \underbrace{\text{Cov}_{\text{a}}\left(\{\delta_i\}_{\text{w}}, \{\phi_i\}_{\text{w}}\right)}_{\text{Among-group Drift}} + \underbrace{\langle\text{Cov}_{\text{w}}\left(\delta_i, \phi_i; j\right)\rangle_{\text{a}}}_{\text{Within-group Drift}}. \quad (10)$$

In this new extension of Price's equation, the among-group selection term is the among-group covariance (for calculating the covariance, groups are weighted by their size) of the group's fitness and the group's phenotypic character. As mentioned, for our model we consider the group's fitness to be the within-group mean fitness of all its individuals and the group's phenotypic character to be the within-group mean phenotypic character of all its individuals. Therefore, these within-group means are used in the among-group selection term. To illustrate: if groups with a high average phenotype value tend to have a *high* average expected fitness compared to other groups, the among-group selection becomes positive. However, if groups with a high average phenotype value tend to have a *low* average expected fitness compared to other groups, the among-group selection becomes negative

The within-group selection term is the among-group mean of the within-group covariances of the individuals' expected fitness and the individuals' phenotype value for all groups. Again to illustrate: if individuals with a high phenotype value from a certain group tend to have a *high* expected number of offspring compared to other individuals in that group, the within-group selection becomes positive. However, if individuals with a high phenotype value from a certain group tend to have a *low* expected number of offspring compared to other individuals in that group, the within-group selection becomes negative.

The most important difference between the among- and the within-group selection terms is that for the among-group term we are comparing average offspring of groups to the average offspring of other groups, while for the within-group term we are comparing offspring of individuals from a certain group to offspring of other individuals *within that same group.*

The among-group drift term describes the among-group covariance of the within-group mean deviation (of the realised fitness from the expected fitness) and the within-group mean phenotypic character. To illustrate: if groups with a high average phenotype value tend to have a *positive* average deviation (*i.e.* on average, these individuals have produced a greater number of offspring than expected), while other groups have zero average deviation (*i.e.* on average, these individuals have produced the exact number of offspring as expected), the among-group drift becomes positive. However, if groups with a high average phenotype value and tend to have a *negative* average deviation (*i.e.* on average, these individuals have produced a lesser number of offspring than expected) while other groups have zero average deviation (*i.e.* on average, these individuals have produced the exact number of offspring as expected), the among-group drift becomes negative.

Regarding this among-group drift term, it is important to note that group-events can have a significant impact. If group-reproduction and -extinction would be absent, we expect the within-group means of δ to be small. Specifically, if groups are full and an individual is able to reproduce, this reproduction goes at the expense of another individual in that group, so that the within-group mean of δ is zero. Therefore, we expect the among-group drift term, which is the covariance of the within-group mean of δ and the within-group mean of ϕ, to be small. However, when we do consider a group-extinction event, the deviations of all individuals within this group become negative, which results in a large negative within-group mean of δ. This can then lead to a significant value of the among-group drift term, especially when all individuals within that group have a similar phenotype value.

The within-group drift term describes the among-group mean of the within-group covariances of the individuals' deviation (of the realised fitness from the expected fitness) and the individual's phenotype value for all groups. Again to illustrate: if individuals with a high phenotype value from a certain group tend to have a *positive* deviation, while other individuals from that group have zero deviation, the within-group drift becomes positive. However, if individuals with a high phenotype value from a certain group tend to have a *negative* deviation, while other individuals from that group have zero deviation, the within-group drift becomes negative.

Again, the most important difference between the among- and the within-group drift terms, is that for the among-group term we are comparing average deviation of collectives to the average deviation of other groups, while for the within-group term we are comparing deviation of individuals from a certain group to the deviation of other individuals *within that same group.*

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This new extension of Price's equation can now be used to describe both selection and drift on both among-group and within-group level in a single time step in any evolutionary model

2.2 A simple multi-level model

In order to use this newly presented framework for quantifying drift and selection on two levels, we adopt a simple multi-level selection model from Traulsen and Nowak (2006). By choosing a simple model, it is easier to perform the new calculations and use those to analyse the behaviour of multi-level selection model.

The model considers a population of individuals that is divided into groups. Every timestep, a single individual is allowed to reproduce. The probability of a certain individual being chosen to reproduce, is calculated using a pay-off matrix from an evolutionary game. The intensity of selection in this evolutionary game is given by a selection parameter w. Offspring of a reproducing individual remains within the same group as its parent. Groups are considered to have limited space and only have place for n individuals. Whenever a group exceeds this number of individuals, this group will either divide into two groups with a probability q, or a random individual from this group will be eliminated with probability $1 - q$. Whenever a group divides, the individuals are distributed randomly over the two new groups and another group, chosen at random, is eliminated in order to keep the number of groups constant. This constant number of groups is given by m. From these rules, it follows that the total population size (total number of individuals) varies between m and mn. A schematic representation of the model can be seen in figure 2.

Interestingly, although the model only describes the reproduction of individuals, the model also contains group-level selection since groups that contain individuals that have a higher chance to reproduce reach size n quicker, allowing them to divide more frequently. Therefore, group-level selection originates from only individual-level dynamics. Since the model considers group-level selection it is suitable for our research and the extended Price equation.

Additionally, Traulsen and Nowak (2006) consider two type of individuals within their model: cooperators and defectors. Cooperators pay a cost c, but give all other individuals in their group a benefit b. On the other hand, defectors pay no cost but still benefit from cooperators in their group. Traulsen and Nowak (2006) used this set-up for understanding under what conditions cooperation can evolve. For our study, however, we modified this set-up slightly. Specifically, we do not consider cooperators and defectors, but a wildtype and a mutant type. The wildtypes pay a cost c, without giving any benefits to others, while the mutants do not pay this cost. This way, mutants have a fitness advantage over the wildtypes.
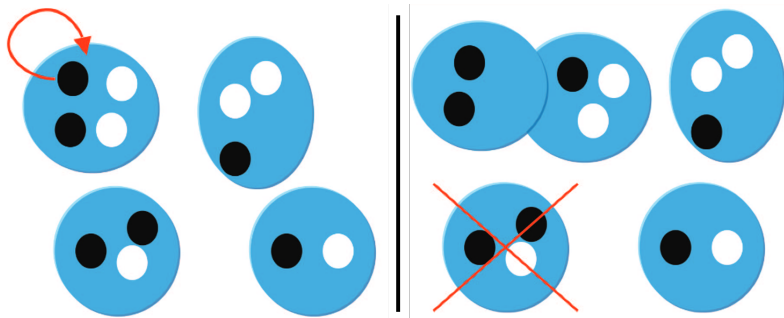

Figure 2: Schematic representation of the model from Traulsen and Nowak (2006). individuals are divided into groups. The number of groups, m is constant. Every time step a single individual is allowed to reproduce. All groups can contain n individuals maximum. When a group is full, it can divide into two groups with probability q or a single individual is chosen to be eliminated with probability $1 - q$. Figure is adopted from Traulsen and Nowak (2006).

2.3 Fixation probability in a multi-level model

We are now able to take our extension of Price's equation and apply this on the simple multi-level selection model. We can try to understand its behaviour, in terms of drift on the within- and the among-group level.

In a multi-level selection model, we can consider two population sizes, the number of individuals in a group and the number of groups. Intuitively, we would expect that having large groups decreases the effects of within-group drift. Inversely, we would expect that having a large number

of groups would decrease the effects of among-group drift. Both these expectations are in line with the general notion that the effects of random drift decrease with population size.

Considering these expectations, it might be interesting to look at a situation where the total population size N is kept constant, while changing both the number of groups m and maximum number of individuals per group n. Specifically, we want to study how the fixation probability of a mutant changes for differing values of m and n and whether we can explain this trend using the calculated among- and within-group terms.

Mathematical results for the fixation probability

We can actually determine the fixation probability for a mutant in our model, following calculations proposed by Traulsen and Nowak (2006). However, in order to perform these calculations, some assumptions have to be made.

Firstly, the assumption is made that collectives have a low probability of dividing when full ($q \ll 1$). In this limit, two approximations can be made: i) groups will often be full and thus have size n and ii) most groups are homogeneous, meaning they often only consist of either cooperators or defectors, or in our model, wildtypes or mutants. Following these approximations, the fixation of a mutant in a population of wildtypes can be divided into two phases. The first phase consists of the mutant fixing in their respective group. The second phase consists of this group of mutants fixing in the population of groups. All groups are homogeneous again when the mutant has fixed in its group, meaning there are no within-group dynamics anymore. The mutant then fixes in the population by its group dividing and taking over other groups. The fixation probability then is simply the product of the probability of the mutant fixing in their group and the probability of a mutant group fixing in a population of wildtype groups. Coincidentally, in this limit, the fixation probability is a combination of two simple Moran processes (Moran, 1958), since the group of mutants fixing in the population of groups, is the same as a mutant individual fixing in a population of other individuals. Secondly, to simplify the equations, the assumption of weak selection is made ($w \ll 1$).

For this study, we are interested in changing the number of groups m, while keeping the total number of individuals N constant. Therefore, we want the equation for fixation probability to be a function of m. In our model, the critical group size $n = N/m$. Considering this definition of n and $b = o$, while $c > 0$, we get the following equation for the fixation probability of a mutant, ρ_{M}:

$$\rho_{\mathrm{M}} = \frac{1}{N} + \frac{wc}{2N} \cdot \frac{m^2 - 2m + N}{m}. \tag{11}$$

For a full derivation, see the appendix.

Eq. 11 shows that the fixation probability of a mutant with a fitness advantage is the fixation probability under neutral evolution, $1/N$, plus the factor $\frac{m^2 - 2m + N}{m}$ multiplied by the constant $\frac{wc}{2N}$. In the domain of $m = 1$ to $m = N$, this equation creates a convex function with a single minimum at $m = \sqrt{N}$ (see fig. 3). This means that fixation probability is lowest when the population is divided perfectly, 10 groups of 10 individuals in the case of fig. 3. Since we are looking at a mutant with a fitness advantage, a smaller effective population size would decrease its fixation probability, where for a mutant with a disadvantage, the reverse would be true. Therefore, from this minimum we can interpret that the effective population size is decreased due to the group structure and that this effect is strongest for $m = \sqrt{N}$. Additionally, the values for fixation probability are symmetrical around this point, $i.e.$ the fixation probability is the same value for 4 groups of 25 individuals and 25 groups of 4 individuals. This symmetry is present because the probability of a group of mutants fixing in a population of m groups is equal to a mutant individual fixing in a group of similar size m, referring to the double Moran process in this limit. Therefore, the fixation probability of m groups is equal to the fixation probability of N/m groups. Proof of these results can be found in the appendix.

Fixation probability as derived from simulations

In addition to the mathematical analysis of the fixation probability, which was valid only in the limit of small q and w, we performed simulations with our model. In these simulations, we consider a population of wildtype individuals and a single mutant individual, focusing on the mutants ability to fix in the population. We allow the simulation to proceed until the population consists either of only wildtype individuals (unsuccessful fixation) or only mutant individuals (successful fixation).

Simulations were performed with a population of 100 individuals, $N = 100$, for multiple values of m. The values for m were chosen such that it would result in no fractional individuals:
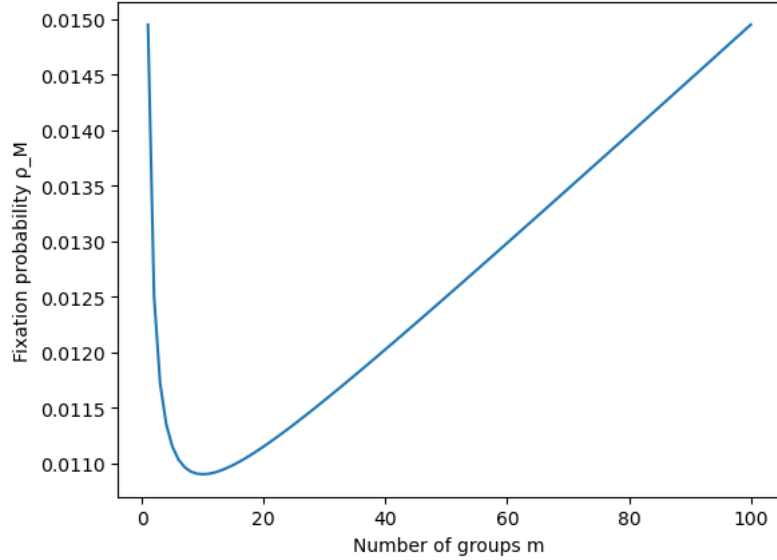
Figure 3: Fixation probability according to Eq. 11 for different m, with $N = 100, c = 1, b = 0$ and $w = 0.01$

$m = 2, 4, 5, 10, 20$, and 25. Unfortunately, due to computational limitations, no simulations were performed for $m = 50$. For every value of m, 10.000 simulation runs were performed, In these simulations $q = 0.01$ and $w = 0.01$ to adhere to the limit of small q and w. Furthermore, $b = 0$ and $c = 10$, giving the mutant a fitness advantage relative to the wildtype.

Moreover, additional simulations were performed where $q = 1$. Where for the previous simulations full homogeneous groups as initial conditions are taken, due to the low value of q, these initial conditions are not suited for the simulations for $q = 1$. Since the initial conditions might have a significant impact on the course of a simulation run, we try to average over its impact by allowing for a initiation period. Therefore, for these simulations, every simulation run would start with an initiation period of 3000 steps. Again note that the initiation period is not implemented for the simulations where $q = 0.01$, since a low q would result in all groups being full and homogeneous and this situation can just be taken as the initial condition.
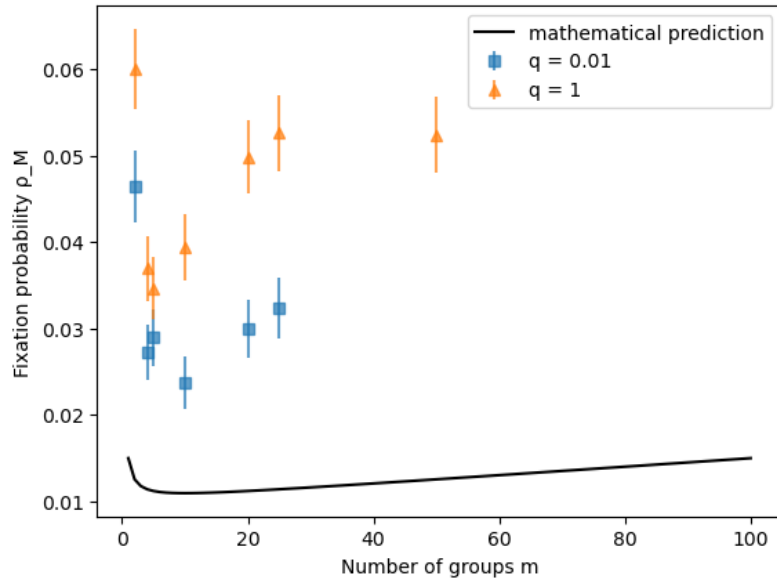

Figure 4: Fixation probability found in simulations for both $q = 0.01$ and $q = 1$ for multiple values of m. In these simulations, $N = 100$, $b = 0$, $c = 10$ and $w = 0.01$. The 95% Confidence interval of the proportions is shown, according to the Agresti-Coull method. Additionally, the mathematical prediction of fixation probability according to Eq. 11 is shown.

In Figure 4, the results of these simulations are shown. Interestingly, all simulated fixation

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probabilities are much higher than what was expected following the mathematical analysis based on Traulsen and Nowak (2006). This is probably due to the factor wc not being small enough in our simulations, compared to the approximation from Traulsen and Nowak (2006). However, the points of the simulation with a low q still roughly seem to follow a convex function with its minimum around $\sqrt{N}$. The simulations for $q = 1$ seem to show a similar trend, although having even higher values for the fixation probability. This might be a result of the mutants being able to spread to other groups easier as well as the mutants advancement not being stopped by groups being full, due to the high value of q.

In addition to the fixation probability, the cumulative values of the selection and drift terms on both levels were collected in all runs. As expected, over all runs, the within-group selection always worked in favour of the mutant (figure S2-14). Remarkably, the among-group selection term would not always be in favour of the mutant, which is surprising, considering the fitness of groups is simply the mean fitness of all its individuals (figure S2-14). We hypothesise that this is due to individuals in full groups having a very low expected fitness, since the probability of a group dividing is very low. Therefore, individuals in a group that is not yet full, have a much higher expected fitness. When the condition arises that wildtype individuals are situated in a group that is not yet full (for example following a group division), while mutant individuals are situated in full groups, group selection might favour the group with wildtype individuals and the among-group selection term will be in favour of the wildtype individuals. Both drift terms worked in favour of the mutant in some runs, as well as against the mutant in other runs, as is expected (figure S2-14). However, for lower values of m, more extreme values are found for the cumulative terms, where, especially, extreme values were found for $m = 2$. These results were found for simulations where $q = 0.01$ as well as $q = 1$.

Furthermore, in the case of $q = 0.01$ we found that both drift terms generally worked in favour of the mutant in simulation runs where the mutant achieved fixation (figure S2-7). Naturally, this is not a surprising result. For the simulation of $q = 1$, however, this effect was seen less distinctly, especially for the within-group drift term (figure S8-14).

Finally, for understanding the effects of group structure on fixation probability, we would like to know whether for multiple values of m either among-group or within-group drift, played a larger part in fixation or non-fixation.

We can take a look at all simulation runs and see the cumulative value of both among- and within-group drift. Based on which of these terms are positive or negative, we can somewhat determine which of these terms was most important for the result (fixation or non-fixation of the mutant) of that run.

We can plot the cumulative within-group drift term against the cumulative among-group drift term, and divide the plot into regions where the terms are either negative or positive. Additionally, in these plots we can draw a line where the cumulative within-group drift term (referred to as D_{w}) and the cumulative among-group drift term (referred to as D_{a}) are equal ($D_{\mathrm{a}} = D_{\mathrm{w}}$), dividing the region into two parts: one where $D_{\mathrm{w}} > D_{\mathrm{a}}$ and one where $D_{\mathrm{w}} < D_{\mathrm{a}}$. Moreover, since we know what the result of a simulation run will be (fixation or non-fixation), we can infer the relationship between the selection terms and the drift terms. For example, if a run resulted in the extinction of the mutant, we know that the change in the proportion of the wildtypes over the course of the simulation is $\frac{1}{N}$. Annotating the cumulative within-group and among-group drift terms as D_{w} and D_{a}, while annotating the selection term as S, we can conclude that

$$
\begin{aligned}
S + D_{\mathrm{w}} + D_{\mathrm{a}} &= \frac{1}{N}, \\
D_{\mathrm{a}} &= \frac{1}{N} - D_{\mathrm{w}} - S.
\end{aligned}
\tag{12}
$$

We plot this relationship between D_{w} and D_{a} for $S = 0$ in all panels of figure 5. For all data points above this line, the cumulative selection was negative, *i.e.* selection decreased the proportion of wildtype individuals and thus worked in favour of the mutant. For all data points below this line, the cumulative selection was positive, *i.e.* selection increased the proportion of wildtype individuals and thus worked against the mutant.

Similarly, for runs where the mutant was able to fix in the population, we can say that the change in proportion of wildtype is $-\frac{N-1}{N}$, therefore

$$
\begin{aligned}
S + D_{\mathrm{w}} + D_{\mathrm{a}} &= -\frac{N-1}{N}, \\
D_{\mathrm{a}} &= -\left(\frac{N-1}{N} + S + D_{\mathrm{w}}\right).
\end{aligned}
\tag{13}
$$

We plot this relationship between D_w and D_a for $S = 0$ in all panels of figure 6. Again, for all data points above this line, the cumulative selection was negative, *i.e.* selection decreased the proportion of wildtype individuals and thus worked in favour of the mutant. And similarly, for all data points below this line, the cumulative selection was positive, *i.e.* selection increased the proportion of wildtype individuals and thus worked against the mutant.

Figure 5 shows the cumulative among-group and within-group drift terms for all simulation runs for multiple values of m where the mutant was not able to fix in the population, where $q = 0.01$. Firstly, it becomes obvious that many data points are situated at the origin, exemplified by the colour of the data points, which shows the density of these data points. For these data points neither cumulative terms have extreme values, nor has the selection term. This indicates that in most runs, the mutant has become extinct quickly, which is not surprising, considering that in the early stage of fixation, when there are just a few mutants, it is easiest to die out. Secondly, a change in pattern can be observed from a low to a higher value of m. For lower values, points are clustered along the blue zero-selection-line. For higher values of m, data points seem to cluster along a vertical line left of the y-axis. This is a result of mutants being able to fix in their group aided by the within-group drift. Indeed, these data points are clustered around $D_\mathrm{w} = -\frac{n-1}{N}$, which is similar to the change in proportion of the wildtype individuals when a mutant takes over an entire group (indicated by the red dotted line in figure 5). When a mutant has fixed in its group, the within-group drift generally does not play a role anymore and the among-group drift starts having an impact. It is not surprising we see this effect more distinctly for higher values of m, since smaller groups are easier to fix in. Finally, again, it can be observed that there is a significant number of runs that have a positive cumulative selection, *i.e.* selection worked against the mutant.
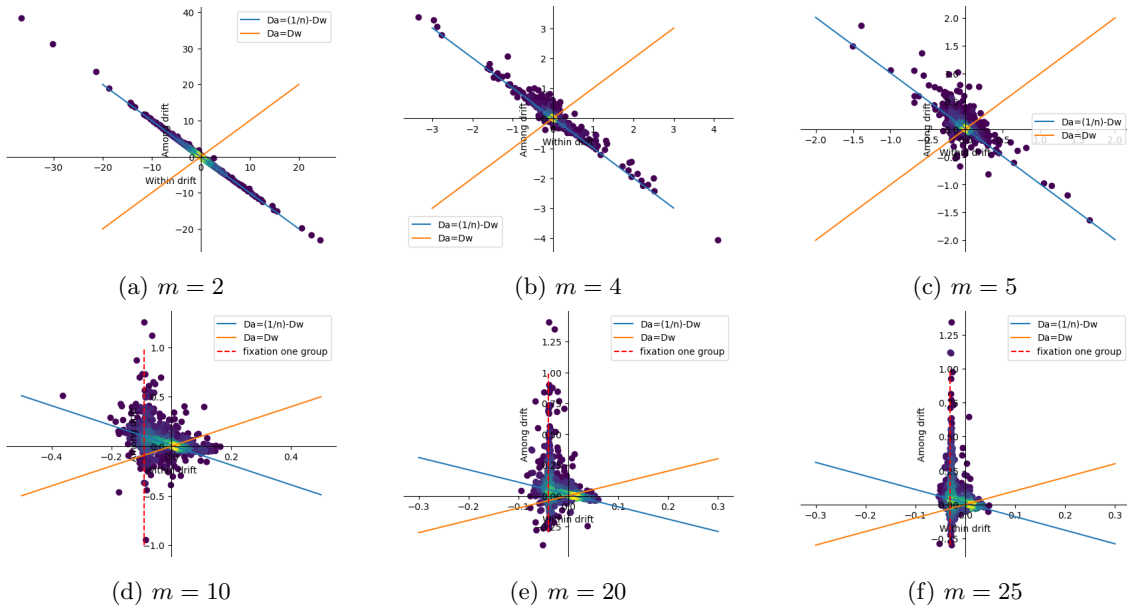

(a) $m = 2$ (b) $m = 4$ (c) $m = 5$

(d) $m = 10$ (e) $m = 20$ (f) $m = 25$

Figure 5: Plots of the cumulative within- and among-group drift terms for all runs where the mutant did not fix int he population and went extinct. The colour of the data points marks the density of these data points. Additionally, the orange line indicates where the drift terms are equal, where the blue line indicates where selection is zero. Points above the blue line, are simulation runs where selection worked in favour of the mutant and thus was negative. The opposite is true for points to the bottom of the line. Finally, the red dotted line, indicates where a point would be when within-group drift worked to make the mutant fix in its group. In these simulations, $q = 0.01, N = 100, b = 0, c = 10$ and $w = 0.01$

Figure 6 shows the cumulative values of the among- and within-group drift terms for simulation runs where the mutant was able to fix in the population for multiple values of m where $q = 0.01$ Again, a similar change in pattern is visible, for multiple values of m. Furthermore, most of the points are situated in the region where both drift terms are negative, *i.e.* both drift terms decreased the proportion of wildtype individuals and thus helped the mutant to fix in the population. Moreover, these data points are mostly situated in the region where selection was negative, i.e. selection decreased the proportion of wildtype individuals and thus helped the mutant fix in the population, as well. This is not a surprising result either, since we would expect the runs where a mutant succeeded in fixing in the population, to have been supported by both drift terms as

well as selection. Finally, in these runs, almost no points are situated in the area where selection was positive. Considering again that these are runs where the mutant succeeded in fixing in the population, we would expect that selection helped. Note, however, that still there are some runs where selection was positive, meaning that in these runs, drift was able to overcome the selection.
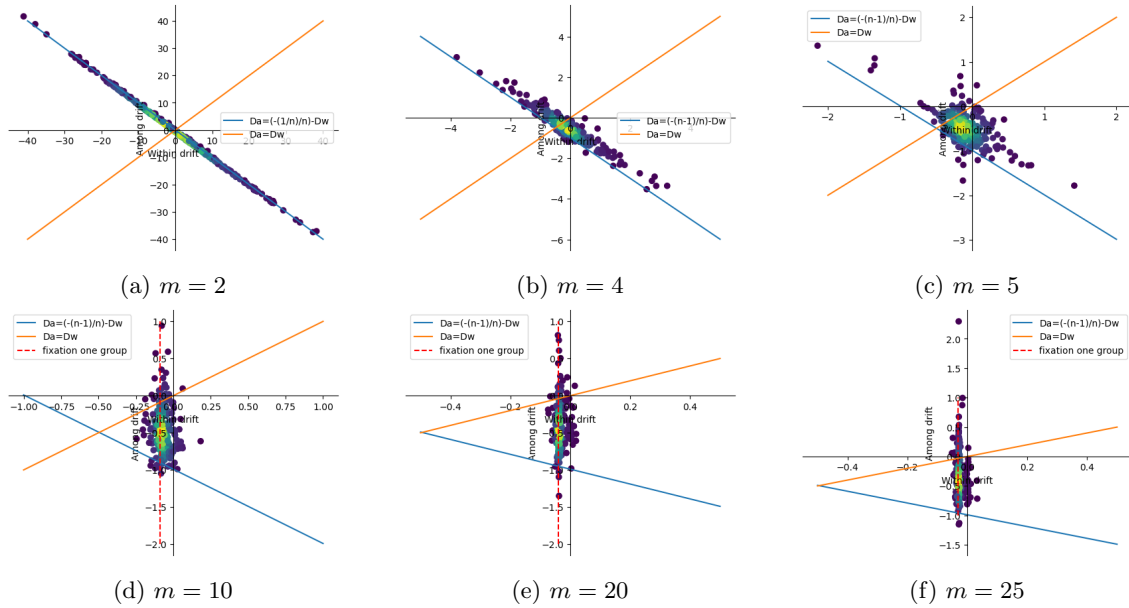

(a) $m = 2$　　　　　(b) $m = 4$　　　　　(c) $m = 5$

(d) $m = 10$　　　　　(e) $m = 20$　　　　　(f) $m = 25$

Figure 6: Plots similar to those in figure 5, however, these plots show all runs where fixation by the mutant was achieved. In these simulations, again, $q = 0.01, N = 100, b = 0, c = 10$ and $w = 0.01$.

In figure 7, again simulations for runs where the mutant failed to fix in the population are shown, however, in these runs $q = 1$. In these simulations, it becomes apparent that runs are clustered around the blue zero-selection-line, even for some higher values of m, in contrast to the simulations of $q = 0.01$. This is because a high division probability leads to quick extinction of the mutant before it is able to fix in its group, even for higher values of m. Additionally, in these simulations, no runs can be seen where selection had a net positive effect and thus worked against the mutant. This is in contrast to the simulations for a lower q, where such runs were quite apparent. This accentuates that selection can be working against the mutant with a fitness advantage due to a low division probability leading to unfavourable among-group selection.

Finally, in figure 8, the simulations for runs where the mutant was able to achieve fixation, for $q = 1$, are shown. We can see a similar change in pattern for an increasing value of m, as was seen for the simulations where fixation did not occur. Additionally, the region where most runs are situated is where within-group drift is zero and the among-group drift is negative. This implies that in these simulations, mostly among-group drift was important, as opposed to within-group drift.

Adding mutation to the multi-level selection model

Random drift can create noise in any evolutionary process. Quantifying fluctuations around the proportion of wildtypes in our simulation, can tell us more about this effect of random drift. Specifically, we are interested in how much the within-group and the among-group drift contribute to these fluctuations and how the contribution changes for multiple values of m.

In our previous simulations, it is difficult to examine the long term fluctuations since a simulation was stopped when either the mutant or the wildtype went extinct. Moreover, if we would let the simulation continue after extinction, the proportion would not change anymore. Therefore, we will expand our model from the previous simulations by adding mutation. This way, the proportion of mutants will fluctuate around a certain mutation-selection equilibrium.

We will perform 7 simulations of 4.000.000 time steps, for multiple values of $m(m = 2, 4, 5, 10, 20, 25, 50)$. Every run, however, will start with an equilibration period of 10.000 time steps, such that the proportion of mutants is able to reach the mutation-selection equilibrium. After the proportion of wildtype was able to reach the equilibrium approximately during this equilibration period, we will monitor the fluctuations around the equilibrium. Mutation in these simulations is added by allowing offspring to mutate at rate μ. Finally, we used $q = 0.01, N = 100, b = 0$,

(a) $m = 2$

(b) $m = 4$

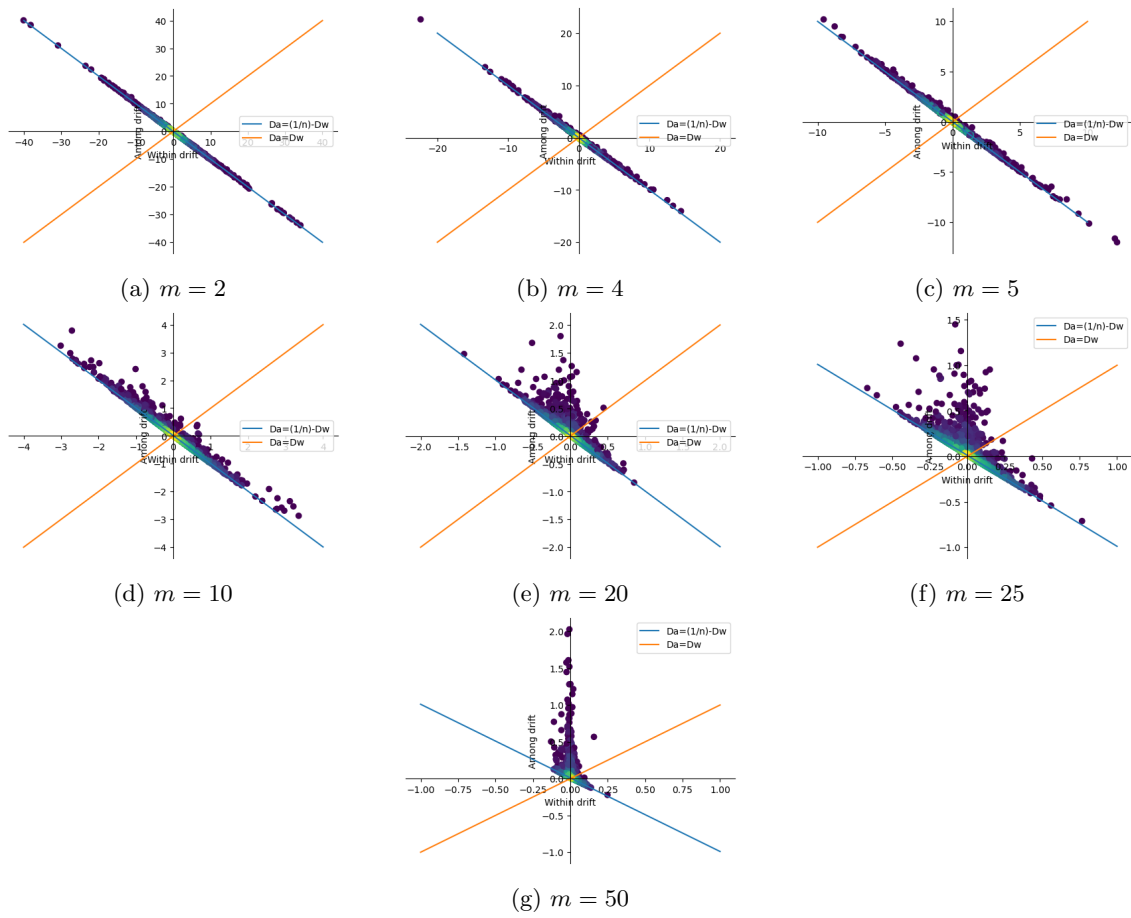(c) $m = 5$

(d) $m = 10$

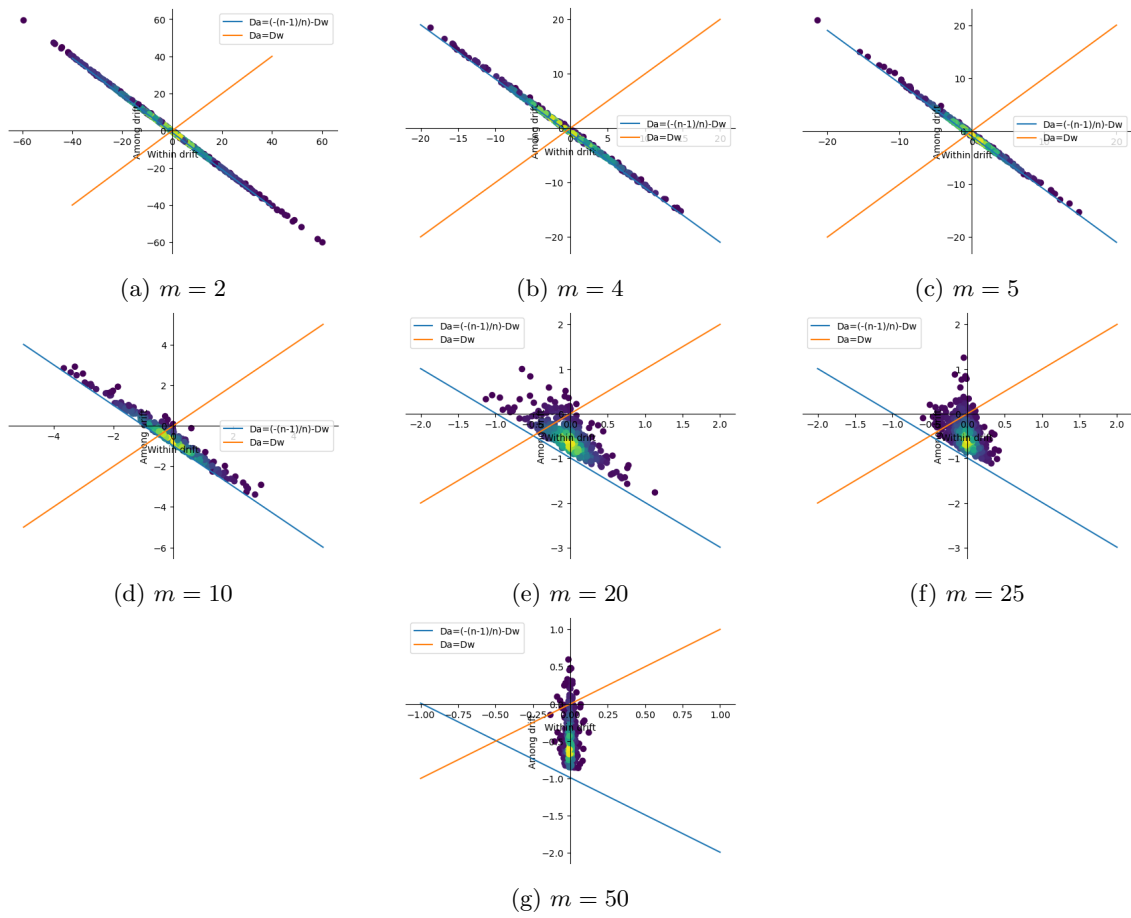(e) $m = 20$

(f) $m = 25$

(g) $m = 50$

Figure 7: Plots similar to those in figure 5, however, for these simulations, $q = 1$. Additionally, in these simulation $N = 100, b = 0, c = 10$ and $w = 0.01$.

(a) $m = 2$

(b) $m = 4$

(c) $m = 5$

(d) $m = 10$

(e) $m = 20$

(f) $m = 25$

(g) $m = 50$

Figure 8: Plots similar to those in figure 6, however, for these simulations, $q = 1$. Additionally, in these simulation $N = 100, b = 0, c = 10$ and $w = 0.01$.
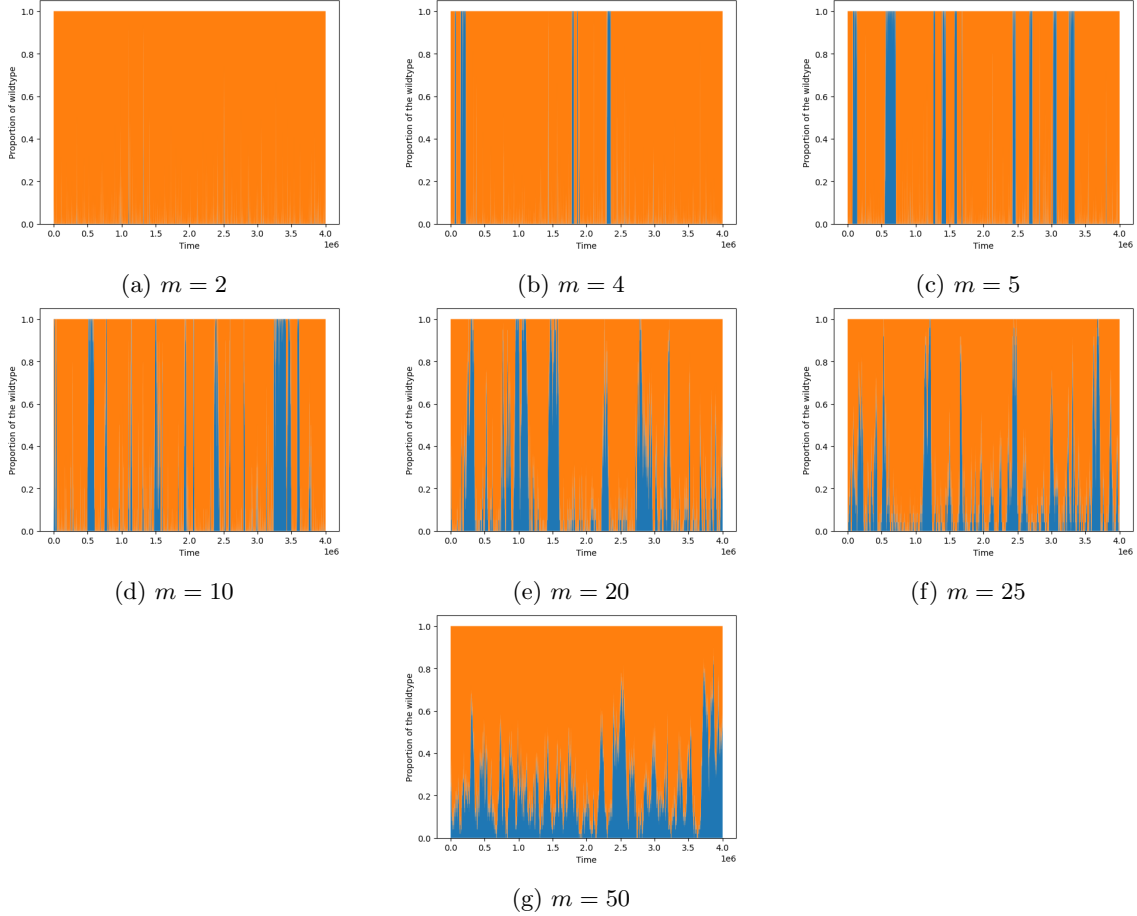
$c = 10$ and $\mu = 0.001$.

(a) $m = 2$ (b) $m = 4$ (c) $m = 5$

(d) $m = 10$ (e) $m = 20$ (f) $m = 25$

(g) $m = 50$

Figure 9: This figure shows all runs of the simulations including mutation for multiple values of m. Specifically, the proportion of the wildtype (blue) is shown over time. For these simulations, $N = 100, q = 0.01, b = 0, c = 10, w = 0.01$ and $\mu = 0.001$
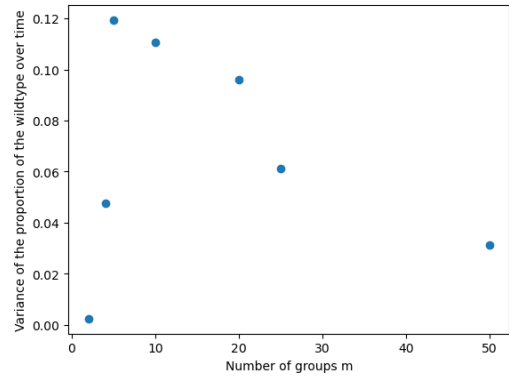
In figure 9, the proportion of the wildtype (blue) is shown over time. For lower values of m, the proportion of the wildtypes is often zero, with short bursts of increase of this proportion. Remarkably, these short burst in proportion are able to reach the maximum value, meaning that the mutant goes extinct for a short while. These burst of increase in wildtype proportion become more prominent and frequent for an increasing value of m. However, for the highest values of m the wildtype is almost always present and fluctuations are not as extreme. This might be the case because for a low number of groups, the group events are more significant and a few divisions allow for the wildtype to become dominant in the population, after which the wildtypes quickly die out again due to mutation as well as selection. For a high number of groups, it is easier for the wildtype to remain present in some groups, however it is unable to take over the entire populations since that takes many group events during which the wildtype needs to persist in the population.

Furthermore, in figure 10a, it is shown that the mean proportion of the wildtype increases for higher values of m. This represents that for higher values of m, the wildtype is able to almost constantly exist in the population. Moreover, in figure 10b, we can see that the variance is maximum for $m = 5$, decreasing for higher an lower values of m. This represents that the combination of number of bursts and size of these bursts is most significant for the intermediate values of m. For a lower number of groups, the number of bursts is not very high leading to a lower variance of the proportion over time, while for a higher number of groups, the bursts become less extreme, leading to a lower variance of the proportion over time.

We would expect the variance of the proportion to be explained by the drift in the system. Therefore, in figure 11a, the variance of the proportion of wildtypes over time is shown against the variance of the drift. Although a significant linear correlation can be found between the two variables ($p = 0.004$, $R^2 = 0.774$, F(1,6)), from the figure it becomes obvious that there is an additional pattern following the number of groups m. Especially the data points for $m = 2$ and $m = 4$ seem to be much lower compared to the other data points, which roughly follow a similar
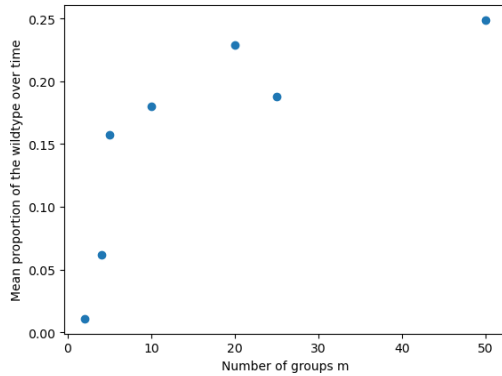
(a) Mean proportion for different m   (b) Variance of the proportion for different m

Figure 10: These plots show the mean of the proportion over time for multiple values of m (10a) and the variance of the proportion over time for multiple values of m (10b)

trend.

Furthermore, in figure 11b and 11c the variance of the drift is shown for multiple values of m. The variance of the drift is maximum for $m = 5$, similar to the variance of the proportion of wildtypes over time, and decreases for lower and higher values of m. Additionally, we would expect the variance of the among-group drift to increase for a higher number of groups m since we expect the among-group dynamics to play a bigger role for a higher number of groups. Simultaneously, we would expect the variance of the within-group drift to decrease for a higher number of groups m. Surprisingly, it can be seen that both drift terms decrease exponentially for a higher number of groups m. The covariance of within-group drift and among-group drift increased exponentially for number of groups m, which summed with the variance of within-group drift and the variance of the among-group drift is equal to the variance of the total drift. Because the covariance of within-group and among-group drift is very low for the lower values of m, the variance of the total drift takes on much lower values for a low number of groups m

Finally, in figure 11a it became apparent that the data points for the lowest values of m deviate from the trend that the other data points seem to follow. Therefore, we can conclude that the covariance of among-group and within-group drift results in the variance of the drift not properly predicting the variance of the proportion over time. This covariance makes it more difficult to draw conclusions on how drift affects the fluctuations around the mutation-selection equilibrium. Unfortunately we have not been able to find concrete evidence to why we see this covariance for lower values of m yet. Although, intuitively, we suspect it is connected to heterogeneous groups dividing and eliminating a homogeneous group. Consider the scenario where a mutant in a heterogeneous group reproduces, leading to a division of the group, while a homogeneous group of mutants is eliminated. We could then expect the within-group drift to be in favour of the mutants, since a mutant was able to reproduce, while the among-group drift worked against the mutants, since a group of mutants was eliminated. However, we have not yet found whether this scenario is occurring often enough or is significant enough to explain the strong covariance.

3   Discussion

Most importantly, we have found that we are able to extend Price's equation by adding multi-level selection as well as random drift to create a new framework for quantifying random drift in a multi-level selection model. We have shown this by applying this framework on a simple multi-level selection model, based on Traulsen and Nowak (2006).

Although Price's equation is one of the most important equations in the field of evolutionary theory, its use is not undisputed.

Firstly, Price's equation is often described as a mathematical tautology (Luque, 2017; Okasha, 2006), *i.e.* Price's equation is by definition true in the way its terms are defined. This feature of Price's equation has been noted as a flaw by multiple authors (Nowak & Highfield, 2011; van Veelen, 2005; van Veelen et al., 2012). However, Luque (2017) points out that the importance of Price's equation becomes apparent when using it in a certain framework or theory, not when it exists just on its own. To expand on this, Price's equation is not about how it is defined mathematically, but

(a) Variance of the drift vs. Variance of the proportion over time

(b) Variance of the drift terms as well as covariance of the within- and among-group drift

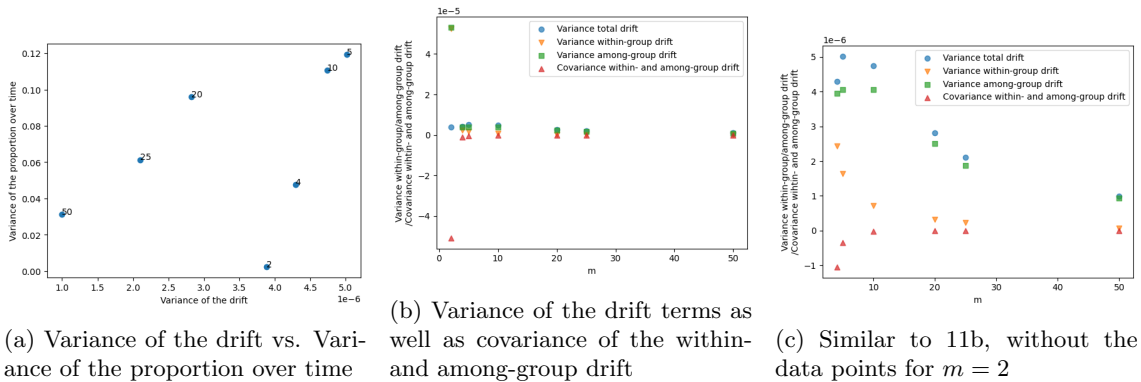(c) Similar to 11b, without the data points for $m = 2$

Figure 11: 11a shows the variance of the proportion over time plotted against the variance of the total drift. Additionally, for each data point the corresponding number of groups m is shown. 11b and 11c show the variance of the total drift (blue), the among-group drift (green) and the within-group drift (orange) as well as the covariance of the within-group and the among-group drift (red) for multiple values of m. However, 11c does not show the values for $m = 2$. This allows us to inspect the other data points in more detail.

about how its terms can be interpreted when applied to a certain model or theory (Luque, 2017). In our study, we present an extended version of Price's equation, which then can be applied to a model, for which we use a relatively simple multi-level selection model. In this way, our proposed framework can nevertheless be used in a convenient way to get new insights on the role of drift in a multi-level selection model.

Secondly, Price's equation is often criticised for not being 'dynamically sufficient' (Grafen, 2000; S. H. Rice, 2008). In other words, Price's equation is often criticised for not being able to predict the state of the system in the future. However, it has been noted on multiple occasions in literature that, although Price's equation itself might not be considered dynamically sufficient, a model on which the equation is used can be dynamically sufficient (Frank, 2012; Frank, 1995; Gardner et al., 2007). Furthermore, Luque (2017) points out that being able to predict is not the sole property of importance. Price's equation, as well as our extension of it, gets its value as a theoretical principle, under which multiple systems can be unified (Luque, 2017).

Finally, it is important to note that Price's equation is purely statistical and does not indicate causal relationships (Okasha, 2006). This notion can be extended to our own version of Price's equation. The covariance of fitness and a phenotypic character describes correlation and not causality of these two variables.

When applying the extended Price equation on our model, which was based on Traulsen and Nowak (2006), we found that the cumulative among-group selection term often disfavoured the mutant with a fitness advantage. This could be explained by individuals in a full group having a very low expected number of offspring compared to individuals in a non-full group due to a low division probability q. This hypothesis is underpinned by the fact that for $q = 1$, the cumulative among-group selection was never found to be unfavourable of the mutant. This phenomenon corresponds to the notion by Whitlock and Barton (1997) that the effective size of a population decreases with extinction and recolonisation events, due to 'colonists' having much more offspring than individuals in a full group. The among-group selection being in favour of the wildtype, which has a fitness disadvantage, at certain times, represents this decrease in effective population size.

For future research it might be interesting to find more connections between the terms from our framework and effective population size. Especially, since effective population size is a concept often used in the study of population genetics and the study of meta-populations. However, effective population size is not often used in terms of multi-level selection yet, even though it could bring us more insight on how multi-level selection models behave. Inversely, Price's equation and multi-level selection are concepts not often used in population genetics and meta-populations, even though these fields cover very similar notions.

Although we are able to explain patterns for multiple values of m using the terms from our extension of Price's equation, it remains difficult to make direct connections between the proposed drift terms and other quantities of drift, *e.g.* fixation probability. Specifically, we are able to see patterns of the within-group and among-group drift for multiple values of m in figures 5, 6, 7, 8

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and explain these. However, it still remains a trouble to explain how the change in patterns results in the convex function for fixation probability (figure 4). Additionally, we are able to explain the differences in fluctuations around the mutation-selection equilibrium for multiple values of m. However, it proved to be difficult to explain them in terms of within-group and among-group drift. For future research it might be useful to study how drift on a single level affects the fluctuations around such an equilibrium, since its findings might help us how to interpret this for multiple levels.

References

Beatty, J. (1984). Chance and natural selection [Publisher: [The University of Chicago Press, Philosophy of Science Association]]. *Philosophy of Science*, *51*(2), 183–211. Retrieved March 20, 2023, from https://www.jstor.org/stable/187421

Damuth, J., & Heisler, I. L. (1988). Alternative formulations of multilevel selection. *Biology and Philosophy*, *3*(4), 407–430. https://doi.org/10.1007/BF00647962

Fisher, R. (1922). On the dominance ratio. *Proceedings of the Royal Society of Edinburgh*, 321–341.

Frank, S. A. (2012). Natural selection. IV. the price equation* [_eprint: https://onlinelibrary.wiley.com/doi/pdf/10.1111/9101.2012.02498.x]. *Journal of Evolutionary Biology*, *25*(6), 1002–1019. https://doi.org/10.1111/j.1420-9101.2012.02498.x

Frank, S. A. (1995). George price's contributions to evolutionary genetics. *Journal of Theoretical Biology*, *175*(3), 373–388. https://doi.org/10.1006/jtbi.1995.0148

Frank, S. A. (1998, July 21). *Foundations of social evolution* [Google-Books-ID: vVc7ihV9wwcC]. Princeton University Press.

Gardner, A., West, S. A., & Barton, N. H. (2007). The relation between multilocus population genetics and social evolution theory. [Publisher: The University of Chicago Press]. *The American Naturalist*, *169*(2), 207–226. https://doi.org/10.1086/510602

Gillespie, J. H. (1998). *Population genetics: A concise guide*. JHU Press.

Grafen, A. (2000). Developments of the price equation and natural selection under uncertainty [Publisher: Royal Society]. *Proceedings of the Royal Society of London. Series B: Biological Sciences*, *267*(1449), 1223–1227. https://doi.org/10.1098/rspb.2000.1131

Grantham, T. A. (1995). HIERARCHICAL APPROACHES TO MACROEVOLUTION: Recent work on species selection and the "effect hypothesis" [_eprint: https://doi.org/10.1146/annurev.es.26.110195.00 *Annual Review of Ecology and Systematics*, *26*(1), 301–321. https://doi.org/10.1146/annurev.es.26.110195.001505

Hamilton, W. (1975). Innate social aptitudes in man: An approach from evolutionary genetics.

Hermsen, R. (2022). Emergent multilevel selection in a simple spatial model of the evolution of altruism [Publisher: Public Library of Science]. *PLOS Computational Biology*, *18*(10), e1010612. https://doi.org/10.1371/journal.pcbi.1010612

Kerr, B., & Godfrey-Smith, P. (2002). Individualist and multi-level perspectives on selection in structured populations. *Biology and Philosophy*, *17*(4), 477–517. https://doi.org/10.1023/A:1020504900646

Lloyd, E. A. (1988). The semantic approach and its application to evolutionary theory [Publisher: Cambridge University Press]. *PSA: Proceedings of the Biennial Meeting of the Philosophy of Science Association*, *1988*(2), 278–285. https://doi.org/10.1086/psaprocbienmeetp.1988.2.192890

Luque, V. J. (2017). One equation to rule them all: A philosophical analysis of the price equation. *Biology & Philosophy*, *32*(1), 97–125. https://doi.org/10.1007/s10539-016-9538-y

Moran, P. a. P. (1958). Random processes in genetics [Publisher: Cambridge University Press]. *Mathematical Proceedings of the Cambridge Philosophical Society*, *54*(1), 60–71. https://doi.org/10.1017/S0305004100033193

Nowak, M., & Highfield, R. (2011, March 22). *SuperCooperators: Altruism, evolution, and why we need each other to succeed* [Google-Books-ID: icuUApNfFrMC]. Simon; Schuster.

Okasha, S. (2006). *Evolution and the levels of selection*. Oxford University Press.

Pannell, J. R., & Charlesworth, B. (2000). Effects of metapopulation processes on measures of genetic diversity [Publisher: Royal Society]. *Philosophical Transactions of the Royal Society of London. Series B: Biological Sciences*, *355*(1404), 1851–1864. https://doi.org/10.1098/rstb.2000.0740

Price, G. R. (1972). Extension of covariance selection mathematics. *Annals of Human Genetics*, *35*(4), 485–490. https://doi.org/10.1111/j.1469-1809.1957.tb01874.x

Rice, S. (2004). Evolutionary theory: Mathematical and conceptual foundations [Publisher: Sinauer Associates]. Retrieved September 22, 2023, from https://scholars.ttu.edu/en/publications/evolutionary-theory-mathematical-and-conceptual-foundations-5

Rice, S. H. (2008). A stochastic version of the price equation reveals the interplay of deterministic and stochastic processes in evolution. *BMC Evolutionary Biology*, *8*(1), 262. https://doi.org/10.1186/1471-2148-8-262

Slatkin, M. (1977). Gene flow and genetic drift in a species subject to frequent local extinctions. *Theoretical Population Biology*, *12*(3), 253–262. https://doi.org/10.1016/0040-5809(77)90045-4

Traulsen, A., & Nowak, M. A. (2006). Evolution of cooperation by multilevel selection. *Proceedings of the National Academy of Sciences*, *103*(29), 10952–10955. https://doi.org/10.1073/pnas.0602530103

van Veelen, M. (2005). On the use of the price equation. *Journal of Theoretical Biology*, *237*(4), 412–426. https://doi.org/10.1016/j.jtbi.2005.04.026

van Veelen, M., García, J., Sabelis, M. W., & Egas, M. (2012). Group selection and inclusive fitness are not equivalent; the price equation vs. models and statistics. *Journal of Theoretical Biology*, *299*, 64–80. https://doi.org/10.1016/j.jtbi.2011.07.025

Wang, J., & Caballero, A. (1999). Developments in predicting the effective size of subdivided populations [_eprint: https://onlinelibrary.wiley.com/doi/pdf/10.1046/j.1365-2540.1999.00467.x]. *Heredity*, *82*(2), 212–226. https://doi.org/10.1046/j.1365-2540.1999.00467.x

Whitlock, M. C., & Barton, N. H. (1997). The effective size of a subdivided population. *Genetics*, *146*(1), 427–441. https://doi.org/10.1093/genetics/146.1.427

Wright, S. (1931). Evolution in mendelian populations. *Genetics*, *16*(2), 97–159. Retrieved October 17, 2023, from https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1201091/