The dynamical systems theory of natural selection



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I dedicate this thesis to my beautiful wife Sophia, who I am sure will take as much pleasure from reading it as I have from writing it.

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Abstract

Darwin's (1859) theory of evolution by natural selection accounts for the adaptations of organisms, but, as Fisher (1930) famously said, 'natural selection is not evolution.' Evolutionary theory has two major components: *i*) natural selection, which involves the underlying *dynamics* of populations; and *ii*) adaptive evolutionary change, which involves the *optimisation* of phenotypes for fitness maximisation. Many of the traditional theoretical frameworks in evolutionary theory have focussed on studying optimisation processes that generate biological adaptations. In recent years, however, a number of evolutionary theorists have turned to using frameworks such as the 'replicator dynamics' or 'eco-evolutionary dynamics', to explore the dynamics of natural selection. There has, however, been little attempt to explore how these dynamical systems frameworks relate to more traditional frameworks in evolutionary theory or how they incorporate the principles that embody the process of evolution by natural selection, namely, phenotypic variation, differential reproductive success, and heritability. In this thesis, I use these principles to provide the formal foundations of a general framework—a mathematical *synthesis*—in which the future state of an evolutionary system can be predicted from its present state; what I will call a 'dynamical systems theory of natural selection.' Given the state of an existing biological system, and a set of assumptions about how individuals within the system interact, the job of the dynamical systems theory of natural selection is no less than to predict the future in its entirety.

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Chapter 1

Introduction

1.1 Introduction

There are two major components of evolutionary theory: *i*) the *process* of natural selection, which involves the underlying *dynamics* of populations (Crow and Kimura, 1970; Nowak, 2006); and *ii*) the *product* of natural selection, which involves *adaptive* evolutionary change brought about through the *optimisation* of phenotypes for fitness maximisation (Maynard Smith, 1978c; Gardner, 2009). These two components have, for a long time, been formalised by evolutionary theorists using the language of mathematics. One might expect, therefore, that this formalisation would have led to a unifying mathematical theory of evolution by natural selection, but this has not been forthcoming. Instead there is a disconnect between major frameworks. Evolutionary theorists have therefore tended to exclusively utilise one framework or another, placing particular emphasis on the importance of understanding the dynamics of natural selection or the adaptive evolutionary changes brought about by natural selection, but rarely both simultaneously. In this thesis, I explore the extent to which a unification of these different approaches is possible.

1.1.1 Adaptation and natural selection

As Fisher (1930) famously said, 'natural selection is not evolution.' Darwin's (1859) theory of evolution by natural selection accounts for the adaptations of organisms (Gardner, 2009). Natural selection is not the only process that shapes evolutionary change—genetic drift, in particular, is also important (Kimura, 1985)—but it is the only known driver of *adaptive* evolutionary change. By favouring organisms with phenotypes that are better equipped to survive and reproduce, Darwin (1859) realised that natural selection can act

to *optimise* phenotypes in a population over time in a way that leads them to appear as if designed to maximise survival and reproduction.

The only major revision to Darwin's (1859) theory came about because of a realisation that certain classes of *social* trait often appear to be adaptations not for the focal individual expressing them, but for some other individual or group of individuals with whom the focal individual interacts (West et al., 2007b). For instance, it is not clear how Darwin's (1859) theory can explain the existence of sterile workers in eusocial insect societies. These are individuals displaying all the hallmarks of design that non-sterile individuals do, but clearly sterility and a lifelong commitment to working for the colony does not increase the direct, personal fitness of a worker and this type of trait therefore would seem to contradict Darwin's (1859) theory (Herbers, 2009).

Darwin (1859, pp. 236238) himself speculated that a solution to this problem could perhaps arise because of the indirect action of natural selection on the fitness consequences of traits on family members who share heritable tendencies for a trait. This idea was formalised decades later by Hamilton's (1963; 1964) insight that altruistic traits such as sterility can be viewed in population genetic, rather than individual, terms (Fisher, 1930). In these terms, altruistic behaviours can be the result of purely 'selfish' genes (Dawkins, 1976). The basis for this idea is that a gene promoting the expression of an altruistic trait by a focal actor might also be shared by the neighbours with whom the actor interacts Hamilton (1963). Thus an altruistic trait such as sterility could spread in a population, despite its obvious direct fitness cost, by providing sufficient indirect fitness benefits to neighbours that share the heritable basis for the trait. Thus Hamilton (1963, 1964) argued that the appearance of design in the natural world is shaped not by the optimisation of phenotypes for direct personal fitness maximisation, but for maximising the sum of the direct and overall indirect fitness effects which together form the 'inclusive fitness' of an individual. The selection *process* that acts on the indirect fitness effects of traits has come to be known as 'kin selection' (Maynard Smith, 1964). Kin selection theory paved the way for a whole new branch of evolutionary theory concerned with the adaptations organisms display to their *social* environment (Frank, 2007).

The social environment is quite unlike the abiotic environment because it introduces a strategic component into evolution (Lewontin, 1961; Maynard Smith and Price, 1973; Maynard Smith, 1974, 1982). The fitness of an individual depends on what other individuals in its environment are doing, and vice versa. In a strategic interaction, it is often not clear what a well-adapted phenotype even looks like. For instance, if a focal actor helps another individual, should the recipient individual reciprocate and return the favour at a later date or should it defect and be happy with the help it received (Trivers,

1971)? On the one hand, the formation of a partnership could be a successful lifetime strategy, but on the other, there is always the possibility of being cheated at some point by one's social partner.

Viewing evolution from this strategic perspective led to the development of the hugely successful framework of *evolutionary* game theory (Lewontin, 1961; Maynard Smith and Price, 1973; Maynard Smith, 1974, 1982). In a game theoretical model, biological entities are described as 'players', their phenotypes are termed 'strategies', and the effect interactions have on the success of players are termed 'pay-offs' (Maynard Smith, 1982). A population of socially interacting players is then represented as an evolutionary game, and the question is: 'which strategy accrues the greatest pay-off'? This pragmatic approach, known as the 'phenotypic gambit' (Grafen, 1984), places phenotypes at the centre of evolutionary theory by acknowledging that the underlying genetic details of traits are unlikely, if ever, to be known in completeness.

Although Hamilton's (1963; 1964) original work was grounded in population genetics, it was reinforced through the study of how social behaviours like altruism can ever be favoured in a strategic game (Axelrod and Hamilton, 1981; Axelrod, 1987). Importantly, both the original work and the game-theoretic form of kin selection models are grounded in optimisation theory (Maynard Smith, 1978c; Grafen, 2006a). A common form of the kin selection modelling approach is therefore to construct a model of some system of interest, assign a function of reproductive success to the entities under study, re-write the function in terms of its direct and indirect effects, and try to find a solution that maximises the measure of reproductive success (Taylor and Frank, 1996).

Importantly, this optimisation approach does not rest on any explicit description of dynamics of natural selection; the solution to the optimisation problem acts as a prediction for the types of adaptations one would expect to see in the natural world *given* the assumptions one puts in (Maynard Smith, 1978c). The approach follows from a direct extension of the logic Darwin (1859) used to formulate his theory. If the adaptations the model predicts are not seen in nature, this implies that the model is missing a key component of natural selection (or some other aspect of the real world that maybe acts against natural selection). In the case of altruistic traits like sterility, models that ignore the impact of fitness effects on related neighbours often lead to false conclusions about whether or not traits like altruism can evolve (West et al., 2007b; West and Gardner, 2010; Queller, 2011). When indirect fitness effects are accounted for, the predictions are much better (in the sense that altruistic traits are predicted to evolve if and only if there are sufficient indirect benefits for a trait that outweigh any direct costs). Thus, combining

kin selection theory with the phenotypic gambit and optimisation theory leads to a very simple but powerful explanatory tool (Maynard Smith, 1978c; Grafen, 1984).

1.1.2 Evolutionary dynamics

One of the earliest formal justifications for the idea that natural selection optimises phenotypes came from Fisher's (1930) Fundamental Theorem of Natural Selection. (Fisher, 1930) argued that his theorem proved that natural selection always leads to an increase in the mean fitness in the population, and interpreted this as evidence that organisms will appear increasingly well-adapted to their environments. Another form of optimisation argument was presented by Wright's (1932) who depicted a population moving toward peaks in fitness on an 'adaptive landscape'. A landmark paper by Moran (1963), however, cast doubt on the general applicability of Fisher's (1930) and Wright's (1932) results, and the optimisation hypothesis more generally, by showing that in simple models incorporating interactions among genetic loci a population's mean fitness will often not tend to increase under natural selection, but will often even decrease. There is a large literature on what Fisher really meant by the Fundamental Theorem (Li, 1967; Price, 1972b; Ewens, 1989; Frank and Slatkin, 1992; Lessard, 1997), and evolutionary theorists are now generally in agreement that Fisher's (1930) Fundamental Theorem does in fact hold true, providing one interprets mean population fitness as the mean of the *genetic component* of fitness in the population (Price, 1972b). Nevertheless, Moran's (1963) analysis paved the way for a separation between dynamical models in population genetics and optimisation models in the study of phenotypic change in a way that has never really been overturned (Gardner, 2009).

Another commonly perceived challenge with using the optimisation approach among evolutionary theorists is that a phenotype may optimise some measure of reproductive success under a given set of assumptions, but whether or not it can be expected to be observed in natural systems depends on whether or not the equilibrium point at which the optimum exists is a stable one or not, and whether or not the timescales over which selection acts permit its evolution. These ideas played an important role in the development of population ecology (Lotka, 1925; Volterra, 1926) and the study of gene frequency change in population genetics (Crow and Kimura, 1970), but were somewhat neglected in the development of the frameworks focussing on phenotypic evolution.

Around the same time that kin selection theory and evolutionary game theory were being unified (Axelrod and Hamilton, 1981; Axelrod, 1987), however, a number of evolutionary theorists interested in phenotypic evolution began to turn away from placing emphasis

on optimisation approaches and adaptation to return to the population genetic tradition of placing emphasis on dynamics. This new tradition began with the development of new dynamical analysis tools by Taylor and Jonker (1978), Hofbauer et al. (1979), Zeeman (1980) and others. These tools shared many of properties of the approaches originally developed in population genetics, but when applied to evolutionary game theory, they turned what were previously static games into dynamical systems by assuming that the rate of change in relative frequency of strategies being played in a game is proportional to the fitness of a strategy at each instant in time.

The conversion of static optimisation models into dynamical models allowed the power of dynamical systems theory to be brought to bear on the question of the existence of 'Nash equilibria' (Maynard Smith, 1974), the related concept of an 'unbeatable strategy' (Hamilton, 1967), and 'evolutionary stability' (Maynard Smith, 1982). As Maynard Smith (1978c) pointed out in a commentary on the (static) optimisation approach, 'there is an assumption, often tacit, about the mode of inheritance and the population structure; this will determine the type of equilibrium to which the population will move.' The dynamical systems approaches therefore made explicit the assumptions about population structure and inheritance that were otherwise implicit in static models. Moreover, the dynamical analysis paved the way for new perspectives on phenomena like evolutionary 'arms races'—the so-called 'Red Queen' effect—in which the optimum phenotype continually changes (Dawkins and Krebs, 1979; Ridley, 1994; Dieckmann et al., 1995). These approaches were also able to make predictions about systems that never reach an equilibrium point, for which an optimisation approach is clearly less-well suited. Indeed, the emphasis on dynamics led to the discovery of systems exhibiting endless regular or irregular oscillations and 'chaotic dynamics' (May, 1976; Nowak and May, 1992; Nowak and Sigmund, 1993; Sato et al., 2002).

One of the more striking findings from the study of these dynamical systems models was that there exists a general class of dynamical system, called 'replicator dynamics' (Schuster and Sigmund, 1983)[a], that connects evolutionary game theory with a wide range of other systems dating back to early work in population ecology (Lotka, 1925; Volterra, 1926) and population genetics (Fisher, 1930; Kimura, 1958). Further unification of the different classes of related equations led to the development of a more general framework simply known as 'evolutionary dynamics' (Page and Nowak, 2002; Nowak and Sigmund, 2004; Nowak, 2006).

With kin selection theory being studied under the guise of evolutionary game theory around the same time that evolutionary game theory was adopting an ever greater em-

[a]Named after the term introduced by Dawkins (1976, 1982).

phasis on dynamics, one might have expected that kin selection theory would soon follow, forming a truly unified mathematical theory of evolution by natural selection. Sadly, however, this never really took off, with the consequence that a major disconnect emerged between frameworks. This is all the more surprising given that both evolutionary dynamics and kin selection theory owe much of their modern-day form to Fisher's (1930) work on population genetics. Yet contemporary evolutionary theorists continue to tend to exclusively utilise one framework or another, placing particular emphasis on the importance of understanding the dynamics of natural selection or the adaptive evolutionary changes brought about by natural selection, but rarely both simultaneously. To understand why a synthesis never really emerged, it is important to understand the different responses these two frameworks had to another major development in evolutionary theory, namely, Price's (1970) theory of selection.

1.1.3 Relating traditions to one another

Price's (1970) theory captures the action of selection on any population in a succinct 'covariance' form. In particular, his theory suggests that the change in the average value of some measurable, but otherwise arbitrary, quantity, say the frequency of a gene in a population, is captured by the covariance between that quantity and reproductive success. What is remarkable about this discovery is its generality. In his own words, Price's (1970) covariance mathematics 'holds for any sort of dominance or epistasis, for sexual or asexual reproduction, for random or non-random mating, for diploid, haploid or polyploid species, and even for imaginary species with more than two sexes.' Designed to mirror similar developments in information theory, Price (1995) went a step further and even generalised his work from an evolutionary context to any context in which some form of selection occurs, to develop what he called a 'general' theory of selection. In reference to what circumstances Price's (1970) covariance mathematics can be applied to, Frank (2012a) has written that, 'it is important to realize that everything truly means every possible force that might arise and that is not accounted for by the particular expression for selection. Lightning may strike. New food sources may appear. The Price equation in its general and abstract form is a mathematical identity—what I previously called a mathematical tautology.'

Indeed, Price's (1970) covariance mathematics shows up across the spectrum of the more traditional theoretical frameworks in evolutionary theory. This should be no surprise, since the logic of evolution by natural selection is itself inherently general. The main requirements are that entities being selected meet the criteria of exhibiting phenotypic variation, differential survival and reproduction, and heritability (Lewontin, 1970; Godfrey-

Smith, 2007). When the quantity under selection is the 'genetic value' from quantitative genetics (Falconer and Mackay, 1995), Price's (1970) covariance mathematics leads to the famous 'breeder's equation' (Lush, 1937; Falconer and Mackay, 1995), which partitions evolutionary change into the product of a heritability measure and a selection differential, thereby formalising the distinction between natural selection and the evolutionary 'response to natural selection' (Fisher, 1930; Falconer and Mackay, 1995). When reproductive success is partitioned in terms of direct and indirect fitness effects using techniques from kin selection theory (Queller, 1992a,b; Frank, 1997; Gardner et al., 2011), Price's (1970) covariance mathematics leads to Hamilton's (1964; 1970) rule. When reproductive success is partitioned in terms of within-group and between-group fitness effects using techniques from multi-level selection theory, Price's (1970) covariance mathematics leads to a description of group selection (Okasha, 2006).

Whilst some of the more traditional frameworks in evolutionary theory have therefore embraced Price's (1970; 1972a) covariance mathematics, the same cannot be said of the evolutionary dynamics framework. Although Page and Nowak (2002) derived a form of Price equation for the replicator dynamics, and Nowak and Sigmund (2004) later claimed that this version of Price's equation *unifies* evolutionary dynamics, there has been little mention of the Price's (1970; 1972a) covariance mathematics in most of the evolutionary dynamics literature since. Those that have discussed Price's (1970; 1972a) covariance mathematics in the context of this tradition have tended to be critical of its use (van Veelen, 2005). Much of this criticism stems from questions about what Price's (1970) theory of selection really achieves. In some of the more traditional frameworks in evolutionary theory, the theory is used to identify the components of change in a population between generations that can be attributed to the action of natural selection. But since this approach isn't strictly needed for solving a dynamical system, some evolutionary theorists have recently questioned what good it could be (Traulsen, 2010; Van Veelen et al., 2012; Simon et al., 2013; Allen et al., 2013)?

Frank (1995) answered part of this question long ago: 'I have sometimes heard the question: 'What problems can the Price equation solve that cannot be solved by other methods? The answer is, of course, none, because the Price equation is derived from, and is no more than, a set of notational conventions. It is a mathematical tautology... the Price equation works well because it provides nothing more than a way to relate a problem to the fundamental properties of evolutionary change.' In the context of this thesis, however, the main utility of Price's (1970; 1972a) covariance mathematics is really its ability to transcend modelling assumptions to be able relate seemingly disparate frameworks to one another. As Gardner (2008) has written, 'because of its generality and simplicity,

Price's equation has been used to uncover fundamental processes in evolution and, as a meta-model, it allows comparisons and contrasts to be drawn between different models and methodologies. As such, it is an important conceptual aid that has led to the discovery of unexpected connections between different bodies of theory, has settled long running controversies, and has helped to resolve semantic confusion.'

A key question at this stage is why Price's (1970; 1972a) covariance mathematics does not connect frameworks like population genetics, quantitative genetics, kin selection theory and multi-level selection theory with evolutionary dynamics. Perhaps one of the most important differences between these theoretical frameworks that has prevented this translation is the timescales they operate on. The former are usually described in terms of discrete-time generational change, whereas the latter is usually described using continuous-time instantaneous change. In many parts of science, one can typically convert between discrete-time and continuous-time models by scaling time appropriately. In evolutionary theory, however, it is far from clear whether or not this is possible (Ariew and Lewontin, 2004). To understand why, let us briefly explore two alternative definitions of perhaps the most important concept in evolutionary theory: fitness.

1.1.4 Timescales and the confusions of fitness

Given its central role in evolutionary theory, one might expect that a definition of fitness would be one of the few concepts to remain invariant across theoretical frameworks, but this is not so (Day and Otto, 2001; Orr, 2009). Of the many different definitions of fitness, there are two main types: *i*) a discrete-time measure called 'absolute' fitness[b], w; and *ii*) a continuous-time measure known as 'Malthusian' fitness, m. It will be important to define these measures rigorously, and to do so we can use a derivation based on Price's (1995) general theory of selection (see also Frank (1995, 2009)).

Following Price (1995), we start by thinking of an abstract mapping between two populations: an ancestral population at time t, and a descendant population at some later time t' (Fig. 1.1). The length of time separating these two time periods is given by $\Delta t = t' - t$. We assume that between the two time periods, selection and other processes may act on the ancestral population giving rise to changes in the composition of types in the population over time, eventually leading to the composition we see in the descendant population.

[b]Also sometimes called 'Darwinian' fitness (Day and Otto, 2001).

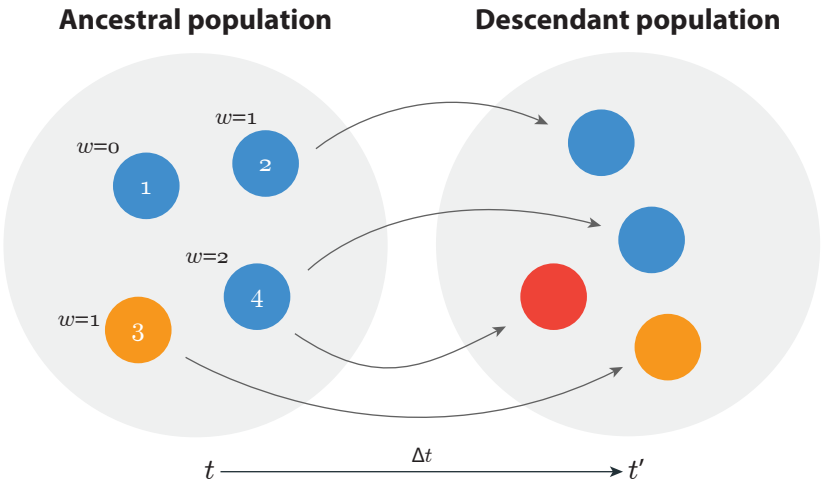


Figure 1.1: Defining fitness. To define fitness, we follow Price (1995) and think of two populations separated by a period of time. The individuals in each population are shown as small coloured circles, where the colour represents a specific type. The absolute fitness of each individual in the earlier ancestral population is given by its contribution to individuals in the later descendant generation, independent of whether or not those individuals are of the same type. Thus individual 3 in the ancestral population has an absolute fitness of $w = 2$ despite it giving rise to a descendant of a different type to itself.

In the ancestral population at time t (Fig. 1.1; left), we denote the number of type i individuals by $n_i := n_i(t)$, the total number of individuals of all types by $N = \sum n_i$, and the *relative* frequency of type i individuals by $x_i = n_i/N$. Note that we have not defined what a 'type' is here. One possibility is that each individual is its own separate type (so that $n_i = 1\ \forall i$). Another possibility is that individuals that share some *intrinsic* quality (such as the same genetic information) are grouped together into types (for instance, genotypes). The definition of a type is important for our interpretation of the processes that give rise to the descendant population, but is does not affect our interpretation of the composition of the descendant population because we are, in some sense, performing a retrospective analysis here such that the descendent composition is known from the outset. In the descendent population at time t' (Fig. 1.1; right), we denote the number of type i individuals *descended from* type i individuals at time t be denoted by $n'_i := n'_i(t')$, the total number of individuals of all types by $N' = \sum n'_i$, and the *relative* frequency of individuals *descended from* type i individuals at time t by $x'_i = n'_i/N'$. It is important to be aware of the unusual notation here: the subscript i in the descendant population references an individual of a particular type in the ancestral population (Price, 1995; Frank, 1995, 2009). That is, n'_i is *not* equal to the number of type i individuals at time t'.

1.1.4.1 Absolute fitness

The standard definition of fitness in evolutionary theory is absolute fitness, which we denote w_i for a type i individual in the descendant population. The definition of absolute fitness is given in terms of the number of descendants derived from each type after a discrete-period of time:

$$w_i = \frac{n_i'}{n_i}. \tag{1.1}$$

It is important to stress that w_i does not measure the relative number of type i individuals in the population at time t' compared to t, but the relative contribution to the total number of individuals at time t' descended from type i individuals at time t, regardless of their type (Price, 1995; Frank, 1995, 2009). Thus, an individual who produces only 'mutant' offspring of different types to itself will have the same absolute fitness as an individual who produces the same number of clonal offspring of the same type to itself. Rearranging equation (1.1), the definition of absolute fitness gives rise to the equation

$$x_i' = x_i \frac{w_i}{\bar{w}} = x_i \omega_i, \tag{1.2}$$

where $\bar{w} = \sum x_i w_i$ is the average absolute fitness in the ancestral population, and $\omega_i = w_i/\bar{w}$ is a quantity known as *relative* fitness. Note that the average relative fitness in the ancestral population is given by $\sum x_i \omega_i = \sum x_i w_i/\bar{w} = \bar{w}/\bar{w} = 1$. Alternatively, re-writing equation (1.1) as $n_i' = n_i w_i$ and taking the sum over all ancestral types of both sides, we obtain

$$N' = \sum n_i w_i = N \sum x_i w_i = N\bar{w}. \tag{1.3}$$

Thus, we have two interpretations for absolute fitness, w_i, which are: *i*) the per capita contribution of the number of type i individuals to the next generation, defined by equations (1.1) and (1.2); and *ii*) the per capita contribution of type i individuals to the overall change in size of the population, $\bar{w}$, defined by equation (1.3).

1.1.4.2 Malthusian fitness

The other major definition of fitness in evolutionary theory is Malthusian fitness, which we denote m_i for a type i individual in the descendant population. To be able to define

Malthusian fitness as a continuous-time measure we need to be able to allow the time difference between our two populations, Δt, to become arbitrarily small. To achieve this, let us first write

$$n_i' = n_i + \Delta n_i', \tag{1.4}$$

where $\Delta n_i' := \Delta n_i'(n,t) \in \mathbb{R}$ is a arbitrarily complex mapping function of the entire population, n, at time, t, with the property that $\Delta n_i' \to 0$ as $\Delta t \to 0$ (such that $\lim_{\Delta t \to 0} \Delta n_i'/\Delta t = 0$ is well defined). The mapping function, $\Delta n_i'$, is a function that takes into account events acting on the population including births, deaths, mutations and such like that alter the *composition* of types in the population.

Price (1972a) showed that if we subtract n_i' from both sides of equation (1.4), divide by Δt, and take the limit as $\Delta t \to 0$, we get $\dot{n}_i \equiv dn_i/dt$ on the LHS. This result then allows us to write a definition of Malthusian fitness given in terms of the number of descendants derived from each type at an *instantaneous* point in time:

$$m_i = \frac{\dot{n}_i}{n_i}. \tag{1.5}$$

Rearranging equation (1.5), the definition of Malthusian fitness gives rise to the equation

$$\dot{x}_i = x_i(m_i - \bar{m}), \tag{1.6}$$

where $\dot{x}_i \equiv dx_i/dt$ is the time derivative of the relative frequency of type i individuals in the ancestral population, $\bar{m} = \sum x_i m_i$ is the average Malthusian fitness in the ancestral population. This form of equation appears in many different contexts in evolutionary theory as we will see throughout this thesis (Fisher, 1941; Crow and Kimura, 1970; Nowak, 2006). Of particular note here is that it is a type of 'replicator equation' (Schuster and Sigmund, 1983), central to the evolutionary dynamics framework (Page and Nowak, 2002; Nowak and Sigmund, 2004; Nowak, 2006). Alternatively, re-writing equation (1.5) as $\dot{n}_i = n_i m_i$ and taking the sum of both sides, we obtain

$$\dot{N} = \sum n_i m_i = N \sum x_i m_i = N\bar{m}, \tag{1.7}$$

Thus we see that Malthusian fitness, m_i, just like absolute fitness, w_i, has two alternative interpretations: *i*) the per capita growth-rate of type i individuals, defined by equations (1.5) and (1.6); and *ii*) the per capita contribution of type i individuals to the overall growth-rate of the population, $\bar{m}$, defined by equation (1.3).

1.1.4.3 Incommensurate fitness measures

The use of Price's (1995) approach to define fitness seems simple and elegant (Frank, 1995, 2009), but there is conceptual problem that lies at the heart of the challenges in unifying discrete-time and continuous-time frameworks in evolutionary theory (Ariew and Lewontin, 2004). In taking the limit as $\Delta t \to 0$, we find that Malthusian fitness, m_i, is defined in terms of the rate of change of the number of type i individuals at time t (note the subtle different between the equalities in $\dot{n}_i = \lim_{\Delta t \to 0}(n_i'(t') - n_i(t))/\Delta t = \lim_{\Delta t \to 0}(n_i(t') - n_i(t))/\Delta t$). Thus by taking a limit we appear to have rendered our unusual notation system meaningless, since we end up focussing entirely on the properties of individuals defined at time t rather than the descendants at time t'.

The proof that these two limits are the same is not provided by Price (1972a). Intuitively, however, this makes sense, because if the time between the two populations is very small the ancestral population should just map back to itself so that $n_i' \to n_i$ as $\Delta t \to 0$. The big problem, however, is that our definitions of absolute fitness, w_i, and Malthusian fitness, m_i, no longer seem commensurate. They seem to refer to very different 'explanatory schemes', as Ariew and Lewontin (2004) have put it.

The problem arises because in many (if not all) biological contexts the rate of reproduction *by* a type is not equal to the rate of production *of* that type, but equation (1.5) appears to give rise to a world in which we can only explore the exponential growth of types. Thus Malthusian fitness, m_i, might be useful for capturing the essence of clonal reproduction in microbial systems, but possibly little else. It certainly does not seem to afford Malthusian fitness the same generality as Price's (1970) covariance mathematics, which we recall Price claimed 'holds for any sort of dominance or epistasis, for sexual or asexual reproduction, for random or non-random mating, for diploid, haploid or polyploid species, and even for imaginary species with more than two sexes.'

This problem with Malthusian fitness has long been known (Kempthorne and Pollak, 1970), and is probably one of the reasons why the majority of evolutionary theory is concerned instead with absolute fitness, w_i. Based on these perceived limitations of Malthusian fitness, Ariew and Lewontin (2004) have argued that 'we require the abandonment of the attempt to make a general quantitative dynamical theory of evolutionary change.'

Without a general quantitative dynamical theory of natural selection and evolutionary change, however, it will be very difficult to unify the conflicting streams of evolutionary theory that we have discussed. This is unfortunate, because different evolutionary frameworks seem to offer their own distinct advantages and disadvantages to the study of the evolutionary process.

1.1.5 The benefits and costs of alternative traditions

One of the key advantages of the frameworks of kin selection theory, quantitative genetics, and to some extent multi-level selection theory, is that the principles of evolution by natural selection are encoded in their very foundations (Hamilton, 1964, 1970, 1975; Queller, 1992a,b; Frank, 1997; Lande, 1979; Lande and Arnold, 1983; Arnold et al., 2008; Okasha, 2006). Thus it is always possible in those frameworks to isolate the components of change that have a heritable basis and may therefore be subject to adaptive evolutionary change (Frank, 1998).

In contrast, in the framework of evolutionary dynamics these principles are not truly embraced. For instance, in his book *Evolutionary Dynamics*, Nowak (2006) does not mention heritability, and does not distinguish between natural selection and the evolutionary response to natural selection. Indeed many dynamical systems theorists tend to focus on the *overall* outcomes of selection as they are described by changes in the frequencies of pre-specified types (Hofbauer, 1985; Stadler and Schuster, 1992; Bomze and Burger, 1995; Komarova, 2004; Hairston et al., 2005; Nowak, 2006; Ezard et al., 2009; Schoener, 2011). The trouble with this approach is that a dynamical system might exhibit all sorts of change, without saying anything at all about *adaptive* evolutionary change (Gardner, 2009).

One of the main advantages of a dynamical systems approach, however, is that through the solution, either analytical or numerical, of differential equations it is possible to gain a better understanding of the the impact of the dynamics of natural selection on a population over *arbitrarily* long timescales. If everything is known about a system at some instant in time, and there are transition equations describing how the system changes, it is possible to predict the future in its entirety. These tools provide powerful methods for studying populations that remain in unsteady states for a long period of time, as well as populations that have fluctuating gene frequencies, and even those that are subject to cyclical or chaotic dynamics (Nowak and May, 1992; Nowak and Sigmund, 1993; Sato et al., 2002). Dynamical models allow predictions about the strength of selective forces

to be made. They can be used to answer questions about the pace of evolutionary change (Traulsen et al., 2007; Gokhale et al., 2009; Park et al., 2010).

In contrast, frameworks like quantitative genetics, kin selection theory, and multi-level selection theory do not particularly lend themselves to the study of the dynamics of populations (Queller, 1992b, 2011; Steppan et al., 2002; Arnold et al., 2008; Okasha, 2006) (but see Liao et al. (2015)). The reason is that although Price's (1970; 1972a) covariance mathematics describes change between generations, the resulting equations cannot typically be iterated recursively through time in the same way that a differential equation can (Grafen, 1985; Falconer and Mackay, 1995; Frank, 1995, 1998, 2012a; Steppan et al., 2002; Arnold et al., 2008). To described recursive change one would need knowledge about change in (potentially infinitely many) higher-moments (Barton and Turelli, 1987). Only in cases in which 'moment closure' can be obtained from Price's (1970; 1972a) covariance mathematics can the resulting equations be iterated indefinitely.Thus any framework whose foundations rest upon the general form of Price's (1970; 1972a) covariance mathematics will tend to be 'dynamically insufficient' (Frank, 1995).

Another key strength of quantitative genetics and kin selection theory, however, is that they readily connect selection on phenotypes with underlying gene-frequency change. Thus Gardner et al. (2007) has explored a multi-locus genetic approach that reconnects kin selection theory with its population-genetic roots. In quantitative genetics, a particular strength is that it is possible to summarise the statistical effects of genetic constraints in adaptive evolution that might arise because of associations between traits brought about by pleiotropy, epistasis, linkage disequilibrium, and so on (Lande, 1979; Lande and Arnold, 1983). As Nowak and Sigmund (2004) acknowledge, these kind of molecular-level details simply cannot be captured in the framework of evolutionary dynamics, which is a purely phenotypic approach to studying evolutionary change.

1.1.6 Cooperation and conflict among evolutionary theorists

Despite the benefits and costs associated with different theoretical frameworks, it is very rare to see kin selection theory or quantitative genetics discussed in evolutionary dynamics, and vice versa. To gain the benefits of both worlds, it would seem the natural solution would be for evolutionary theorists to cooperate and either pick the framework best suited to a particular job or use both approaches and allow them to complement one another (Foster, 2009). Instead, however, evolutionary theorists have tended to engage in conflict with one another about the superiority of one framework or another. These are not minor quibbles. To quote Foster (2011): 'Some of these attacks are so spirited

that they can give the impression that sociobiology is in disarray.' Okasha (2010) warns that these attacks have the potential to do serious damage to the field, as the following quotes affirm. On the one hand we have theorists claiming 'Hamiltons rule almost never holds' (Nowak et al., 2010). On the other we have the opinion that kin selection theory is 'as general as the genetical theory of natural selection itself' (Gardner et al., 2011). Clearly these are incommensurate points of view.

An impasse appears to have been reached that shows no sign of easing. Evolutionary biologists working on the same problem draw orthogonal conclusions from the same results (Liao et al., 2015; Nowak and Allen, 2015; Queller et al., 2015). On this issue Okasha (2010) has recently stated, 'The root of the problem is the existence of several different frameworks for modelling the evolution of social behaviour. These include numerous variants of kin selection theory; multi-level selection; evolutionary game theory; and an approach from quantitative genetics based on the notion of 'indirect genetic effects'. The relationships between these frameworks are sometimes ambiguous, and biologists disagree about which is most fundamental and which most useful empirically.' Motivated by these issues, in this thesis, I will use the abstract principles that embody evolution by natural selection to formally link several presently disconnected frameworks in evolutionary theory.

1.2 This thesis

My goal in this thesis, is therefore to provide the formal foundations of a general framework—a mathematical *synthesis*—in which the future state of an evolutionary system can be predicted from its present state; what I will call a 'dynamical systems theory of natural selection.' To achieve this, I will use deterministic ordinary (ODE) and partial (PDE) differential equations to describe the time evolution of systems in which the principles that embody evolution by natural selection are realised at every instantaneous moment in continuous time. One of the virtues of this approach is that if one can show that any two frameworks are mathematically equivalent at a particular instant in time (the 'base case'), the solution of differential equations may be used to demonstrate that frameworks are equivalent for all of time.

It will not be my goal to advocate any particular type of selective process as the primary force or explanatory principle for evolutionary change, but rather to describe natural selection as a *process* that can be viewed from several different mathematically equivalent *perspectives*. For the purposes of unifying existing frameworks, I focus the development of the dynamical systems theory on several key areas: population dynamics and natural

selection, the dynamics of the evolutionary response to natural selection, kin selection, and group selection. It is also important to emphasise up-front that my goal here is not the generation of a model of some specific biological process, although I provide worked 'toy' examples at the end of the thesis to illustrate some potential applications of the general theory. The explanatory power of ecological theory, population genetics, evolutionary genetics, kin selection theory, evolutionary dynamics, multi-level selection theory, and so on have been demonstrated clearly by many others in both empirical and theoretical settings.

As Gardner et al. (2011) recently pointed out, 'evolutionary theory falls into two broad categories: that which aims for generality, and that which aims for applicability to specific problems.' The work in this thesis is very much intended to represent an example of the former. The mathematics I will explore in this thesis are therefore purposefully abstract; the general formulation of the framework itself is not expected to be analytically tractable[c]. Applications to specific biological problems can be made tractable only by specifying modelling assumptions that reduce the inherent complexity of the framework to something simpler; solutions can then be obtained analytically or numerically that can be used to test hypotheses or make further conjectures (May, 2004)[d]. The virtue of a synthesis is that it can be used not only to develop new ideas, but also to derive abstract relations among existing frameworks, to generalise theoretical concepts, and make conjectures. I hope to convey this virtue here.

1.2.1 Chapters

In Chapter 2, we consider the principles that embody evolution by natural selection and explore how they might come to be exhibited in a dynamical system consisting of a generic population of arbitrary individuals. Toward the goal of formulating a unifying dynamical systems theory of natural selection, we will derive several related dynamical selection equations and show that they not only generalise several important equations from population ecology, population genetics, and evolutionary dynamics, but are also amenable to analysis using Price's (1970; 1972a) covariance mathematics. We will consider how these equations provide three complementary perspectives—ecological, genotypic, and phenotypic—on which the dynamics of natural selection can be studied. Moreover, we will better understand how the problem associated with Malthusian fitness outlined above can be resolved.

[c]It is not yet possible to solve for the motion of three bodies in Newton's theory of gravity, but this does not detract from the power or generality of the theory itself.

[d]I will describe simple motivating examples of this form in Chapter 6.

In Chapter 3, we will extend the dynamical systems theory to incorporate the key principles of evolutionary genetics and study the *evolutionary response* to natural selection. We will derive a method of population-weighted least-squares linear regression that can be applied to the generic population introduced in Chapter 2—or indeed, a dynamical system describing any population—and show that it can be used to calculate key quantities of interest in evolutionary genetics at every instantaneous moment in time.

In Chapter 4, we will extend the framework to incorporate the key principles of kin selection theory and study the dynamics of social evolution. By building on the approaches from Chapters 2 and 3, we formulate a partition of the Malthusian fitness of individuals into a 'neighbour-modulated' fitness form (Queller, 1992a,b; Frank, 1997; Gardner et al., 2011). I then derive a univariate and multivariate form of Hamilton's rule that holds for any instantaneous moment in time. The multivariate form of the rule allows for the study of correlated interactions between traits in *unrelated* social partners (Frank, 1994; Doebeli and Knowlton, 1998; Foster and Wenseleers, 2006).

In Chapter 5, I extend the framework to study the dynamics of *group selection* (I focus on 'interdemic' group selection from the 'MLS2' tradition (Mayo and Gilinsky, 1987; Damuth and Heisler, 1988; Okasha, 2006)), by extending the selection equations obtained in earlier chapters to describe between-group selection (Maynard Smith, 1976). I show that contrary to recent claims (Simon et al., 2013), dynamical models of group selection are *also* amenable to analysis using Price's (1970; 1972a) covariance mathematics.

In Chapter 6, I present perspectives on applications of the theory presented herein using several motivating examples. I focus examples on the context of a population of asexually reproducing microbes undergoing logistic growth. These simple 'toy' models are intended to highlight some of the main components of the theory introduced in Chapters 2 and 3, but may also be useful in modelling the population dynamics of bacteria in empirical settings, including experimental evolution assays.

Finally, in the Discussion, I conclude with a short summary of the work herein, place the main results of this thesis in a wider context, and offer perspectives on future work and applications. In particular, I highlight relations between the theory presented herein and 'intrademic' group selection (group selection from the 'MLS1' tradition (Mayo and Gilinsky, 1987; Damuth and Heisler, 1988; Okasha, 2006)), evolution in age-structured populations Charlesworth (1970, 1994), spatially structured populations (Rousset, 2013), drift (Kimura, 1962), and stochastic dynamics (Traulsen et al., 2006).

Chapter 2

The dynamics of natural selection

2.1 Introduction

As Lewontin (1970) famously pointed out, the requirements for evolution by natural selection are phenotypic variation, differential survival and reproduction, and heritability. For all of these requirements to be satisfied, however, we need two more things: *i*) a *population*—there can be no variation or differential fitness without one; and *ii*) a period of *time*—evolution is about change, and change requires time. Thus population *dynamics* are central to any description of evolutionary change. The two main branches of the contemporary study of population biology are population ecology and population genetics (Singh and Uyenoyama, 2004).

In population ecology, ecological change is usually studied of in terms of changes in the attributes of ecosystems, communities, and populations (Lotka, 1925; Volterra, 1926; Maynard Smith, 1978a)[a]. The relevant variables of interest to theorists are the *absolute numbers* of different types of biological entity (usually species); phenotypes are usually represented implicitly, and genetic heterogeneity within species is usually not considered. The aim is to describe changes in the size and composition of a population through time (Box 2.1; Maynard Smith, 1978a; Singh & Uyenoyama, 2004). Ignoring genetic heterogeneity within-species is usually assumed to be a safe approximation because evolutionary changes in the genetic composition of a population are assumed to operate on a much longer timescale than the demographic processes ecologists are typically interested in (Slobodkin, 1961).

[a]In Chapter 5 on interdemic group selection I will discuss how many of the attributes of populations can be described as group 'traits' and subject to selection in their own right.

Box 2.1 | Population ecology

At the heart of population ecology is the 'exponential growth equation' (Maynard Smith, 1978a; Turchin, 2001), also known as the 'Malthusian growth equation', which describes changes in the size of a population. Suppose that we have a population of entities. Denote by $N := N(t) \in \mathbb{R}_+$ the population size at some time t. Let us assume that all the entities in this population reproduce at a constant rate $b \in \mathbb{R}_+$ and die at a constant rate $d \in \mathbb{R}_+$. The Malthusian growth equation describes the rate of change of the size of the population, $\dot{N} \equiv dN/dt$, as

$$\dot{N} = N(b - d) = Nm, \tag{2.1}$$

where the scalar $m = b - d$ is known as the 'Malthusian parameter' or the 'intrinsic growth rate' of the population (Fisher, 1930; Maynard Smith, 1978a; Turchin, 2001). Providing b and d are independent of n, which we assume here, the Malthusian growth equation is a very simple linear ODE that describes the growth dynamics of the population. The solution to the Malthusian growth equation (2.1) is given by the exponential function $N(t) = N(0)e^{(b-d)t} = N(0)e^{mt}$ where $N(0)$ denotes the abundance of entities at time $t = 0$. When $b > d$, the population grows exponentially, when $d > b$, the population size decays exponentially before converging to zero. If the reproduction rate and death rate are equal, $b = d$, then the population size is at steady-state and the population neither grows nor shrinks unless these rates are perturbed. The expected time until reproduction occurs for any particular entity is described by an exponential distribution with average $1/b$, and the lifespan for each entity is described by an exponential distribution with average $1/d$. The ratio, $b/d \in \mathbb{R}_+$, is known as the 'reproductive ratio' (Nowak, 2006), and represents the expected number of offspring that any one entity gives rise to in its lifetime.

The Malthusian growth equation (2.1) forms the foundation of many more complex and realistic models of growth in population ecology. By allowing the reproduction rate, $b := b(N) \in \mathbb{R}_+$, and the death rate, $d := d(N) \in \mathbb{R}_+$, to be functions of the population rather than parameters, virtually any kind of growth dynamics can be described. For instance by using $b = r$ and $d = rN/K$, after substituting into equation (2.1) and rearranging, we arrive at the logistic growth equation

$$\dot{N} = rN\left(1 - \frac{N}{K}\right), \tag{2.2}$$

where $r \in \mathbb{R}_+$ is a parameter specifying the intrinsic growth rate of entities, and $K \in \mathbb{R}_+$ is a parameter specifying the carrying capacity of the population (its maximum size). The logistic growth equation (2.2) incorporates more realistic assumptions about the growth dynamics of the population since it allows for *density-dependent* growth.

In population genetics, genotypic change is usually studied in terms of changes in the composition of genotypes and alleles in a population (Fisher, 1930; Crow and Kimura, 1970). The relevant variables of interest to theorists are the *relative frequencies* of different genotypes; phenotypes are again usually represented implicitly, and the population size, N, is often considered to be a fixed parameter or a variable that grows to be infinitely large. The aim is to describe changes in the relative frequency of genotypes through time (Box 2.2; Crow & Kimura, 1970; Rice, 2004). Ignoring the relevant variables of interest to population ecologists (absolute abundances) is usually justified on the grounds that the equations for changes in the relative frequencies of genotypes are similar no matter what ecological changes are occurring (Crow and Kimura, 1970, pg. 30)[b].

Box 2.2 | Population genetics

Suppose we have a population of entities each defined by a genotype, i, from a set $\mathbb{G}$. Let x_i denote the relative frequency of the ith genotype. The equation describing the rate of change of the relative frequency of genotypes over time as

$$\dot{x}_i = x_i(\phi_i - \bar{\phi}), \tag{2.3}$$

where $\phi_i \in \mathbb{R}_+$ denotes the fitness of the ith genotype, $\bar{\phi} = \sum_{i=1}^{|\mathbb{G}|} x_i\phi_i$ defines the average fitness of the population, and the quantity $\phi_i - \bar{\phi}$ defines the 'average excess' in the fitness of the ith genotype (see Crow and Kimura (1970, pg. 179)). When $\phi_i > \bar{\phi}$, the relative frequency of the ith genotype increases, and when $\phi_i < \bar{\phi}$, it decreases. If the fitness of the ith genotype is equal to the average fitness, $\phi_i = \bar{\phi}$, then the relative frequency of the ith genotype is at *steady-state*.
Equations of this form appear throughout population genetics (see Crow and Kimura (1970, pg. 26, pg. 179)) as well as the framework of evolutionary dynamics (Page and Nowak, 2002; Nowak, 2006) where they describe changes in frequency of phenotypes rather than genotypes. For this reason, equations of the form of equation (2.3) have been called 'replicator equations' (named by Schuster and Sigmund (1983) after the term introduced by Dawkins (1976, 1982)).

A generalisation of equation (2.3) to account for mutation between types during reproduction, for instance, is given by the 'quasispecies' equation or 'replicator-

[b]Crow and Kimura (1970, pg. 30) have written on this point that: 'the total population may be growing, or static, or decreasing and the different genotypes may differ in intrinsic birth rates, death rates, or their response to the environment; yet the equations for changes in proportions may be basically similar. For these reasons, population genetics has usually ignored the total numbers and concentrated on the proportions.' A useful property of this approach is that it often depicts evolutionary change in a more intuitive way. For instance, consider for a moment a genotype that happens to be increasing in absolute abundance over time in a population. Whilst this may be of interest to population ecologists for lots of reasons, it tells a population geneticist little about evolutionary change at a genetic level, because if the population as a whole is also growing, the genotype could becoming less and less common in the population relative to all other genotypes.

mutator' equation (Page and Nowak, 2002; Nowak and Sigmund, 2004; Nowak, 2006):

$$\dot{x}_i = \sum_{j=1}^{|\mathbb{G}|} x_j \phi_j q_{ji} - x_i \bar{\phi}, \tag{2.4}$$

where $q_{ij} \in [0, 1]$ is the probability that the offspring of the ith genotype 'mutates' to a different genotype j following reproduction. In the limiting case in which the rate of mutation is negligible, the mutation matrix $\mathbf{Q} = [q_{ij}]$ becomes the identity matrix and this equation reduces back to the the replicator equation (2.3).

When fitness is constant, the replicator equation (2.3) and replicator-mutator equation (2.4) represent systems of linear ordinary differential equations (ODEs). In the special case in which the fitness of genotypes depends on the frequency of other genotypes in the population, so that $\phi_i := \phi_i(\boldsymbol{x})$, where the vector $\boldsymbol{x} = (x_1, ..., x_{|\mathbb{G}|})^{\mathrm{T}} \in [0, 1]^{|\mathbb{G}|}$ defines the composition of the population in terms of relative genotype frequencies, the equations represent a system of *non-linear* ODEs. In these cases the replicator equation (2.3) and replicator-mutator equation (2.4) incorporate more realistic assumptions about competition between genotypes since they allow for *frequency-dependent* selection.

Although replicator equations first appeared in the study of population genetics (Fisher, 1930; Crow and Kimura, 1970), they now play an important role in the study of the dynamics of evolutionary games (Page and Nowak, 2002; Nowak and Sigmund, 2004; Nowak, 2006). In these applications, however, the equations describe changes in relative frequency of phenotypes ('strategies') in an evolutionary game (Maynard Smith, 1982), rather than genotypes in a population.

Since Darwin (1859) conceived of his theory by integrating ecology and evolution—his argument was famously based on an essay by Thomas Malthus about overpopulation—one might have hoped that population ecology and population genetics would have have come together to help form a unified mathematical theory of evolution by natural selection. Sadly, however, these two frameworks have largely become separate enterprises since their foundations were described by Lotka (1925), Volterra (1926) and Fisher (1930) almost a century ago (Singh and Uyenoyama, 2004). Moreover, neither framework has ever really engaged explicitly with phenotypic dynamics in populations either brought about by *phenotypic plasticity* on relatively short ecological timescales or brought about by *natural selection* on relatively much longer evolutionary timescales.

Instead, phenotypic change has largely been studied using a suite of alternative frameworks including Fisher's (1930) other major framework, quantitative genetics (Falconer

and Mackay, 1995), as well as kin (Hamilton, 1963, 1964) and multi-level (Price, 1972a) selection theory, evolutionary game theory (Maynard Smith and Price, 1973), evolutionary dynamics (Nowak, 2006) and adaptive dynamics (Hofbauer and Sigmund, 1990). A general treatment of phenotypic change that unifies all of these frameworks is given by the Price equation (2.5) (Box 2.3; Price, 1970; 1972a). The relevant variables of interest to theorists using these frameworks are usually the summary statistics of phenotypes at the population level; genetic details are often disregarded, and population dynamics are often simplified to consider a single generation of change only[c] or more generally neglected in favour of an 'optimisation' perspective (Maynard Smith, 1978c; Parker and Maynard Smith, 1990). Most draw heavily from an assumption known as the 'phenotypic gambit', which is, in the words of Grafen (1984), 'to examine the evolutionary basis of a character as if the very simplest genetic system controlled it.' Those that don't use the phenotypic gambit tend to rely on statistical summaries of the genotype-phenotype relationship (Fisher, 1930; Falconer and Mackay, 1995), rather than articulating it in any detail (Orgogozo et al., 2015). Ignoring population dynamics and genetic details is usually justified on the basis that a simpler model without these features will often have as much explanatory power as a more complex model in which assumptions about these processes are incorporated (Maynard Smith, 1978c; Grafen, 1984; Parker and Maynard Smith, 1990).

Box 2.3 | The Price equation

A general treatment of phenotypic change of any kind is given the Price equation (2.5). The aim in studying phenotypic change using Price's (1970; 1972a) framework is typically to partition the total phenotypic change into meaningful components that can be understood in terms of *natural selection* or *transmission fidelity*.

Consider a population of individuals (the 'ancestral' generation) at some time t and a the same population at some time discrete period of time later at $t + \Delta t$ (the 'descendant' generation). Each individual at time t is index by $i \in \mathbb{I}$, where $\mathbb{I}$ is the index set of ancestors. Let z_i denote the trait value associated with the ith ancestor, w_i its number of descendants in the next generation (its 'Darwinian' or 'absolute' fitness (Day and Otto, 2001; Orr, 2009)), and $\Delta z_i = z_i' - z_i$ the discrepancy between the average trait value held by its descendants, z_i', and itself. Price (1970, 1972a) showed that the change between generations in the average trait value in the population, $\Delta \bar{z}$, weighted by the average fitness, $\bar{w}$, can be written as

$$\bar{w}\Delta\bar{z} = \mathrm{Cov}_{i\in\mathbb{I}}(z_i, w_i) + \mathrm{E}_{i\in\mathbb{I}}(w_i \Delta z_i). \tag{2.5}$$

[c]The exception to this possibly being evolutionary dynamics (see (Page and Nowak, 2002; Nowak, 2006)).

This equation separates the total change, $\Delta\bar{z}$, into two components. The first term, $\mathrm{Cov}_{\in\mathbb{I}}(z_i, w_i)$, describes the statistical association ('covariance') between a trait held by ancestors and the number of descendants they contribute. It is often interpreted as pertaining to the component of change due to *natural selection* (Frank, 1995; Gardner, 2008). For example, if the trait represents height, and taller individuals have more descendants on average, then $\mathrm{Cov}_{\in\mathbb{I}}(z_i, w_i) > 0$, and this is interpreted as positive selection on height. The second term, $\mathrm{E}_{i\in\mathbb{I}}(w_i\Delta z_i)$, describes the average ('expected value') of the difference between the trait held by descendants and their parents, weighted by the how many descendants each ancestor has. It is often interpreted as the component of change due to *transmission fidelity* (Frank, 1995; Gardner, 2008). For example, if the height of descendants and their parents is always the same, this term will be zero. If, however, descendants differ from their ancestors due to segregation and recombination, mutation, or systematic environmental changes, this term will be non-zero (positive if descendants are taller on average, negative if they are shorter). The Price equation (2.5) is a foundational result in evolutionary theory that helps to unify otherwise seemingly disparate frameworks (Frank, 1995; Page and Nowak, 2002; Gardner, 2008).

Despite the practical aspects of each of these streamlined frameworks for studying population ecology, population genetics, and phenotypic evolution independently, Maynard Smith (1978a, pg. 4) recognised long ago that there is a strong argument for adding 'additional complexity into a system already too complex for us to analyse.' In particular, the integration of population ecology, population genetics and phenotypic evolution might help bring about a general theory of eco-evolutionary dynamics (Maynard Smith, 1978a; Hairston et al., 2005; Fussmann et al., 2007; Ezard et al., 2009; Pelletier et al., 2009), a better understanding of the role of ecological processes involving phenotypic plasticity and niche construction in driving evolutionary change (Laland et al., 2014; Forsman, 2015), and the extent to which gene-frequency change brought about by ecological and evolutionary processes contributes to the evolution of phenotypic *adaptations* (Gardner, 2009). More generally, it would help us to see how different frameworks are related to one another, which might help resolve disagreements among evolutionary theorists about which framework is 'most fundamental or useful empirically' (Okasha, 2010).

In this chapter, we develop the concepts and underlying mathematical expressions for a general dynamical systems theory of natural selection. First, we return to the foundations of population ecology and population genetics and attempt to reinterpret these frameworks in terms of the abstract principles of natural selection. In order to circumvent issues regarding the mechanisms of inheritance, we argue for a return to an abstract information-theoretic notion of the genotype and phenotype. We describe a multivariate genotype-phenotype map, and an approach that generalises the notion of asexual birth

and death rates used in Fisher's (1930) description of population genetics to any mode of reproduction. Second, we show that a population embodying the abstract principles of natural selection can be viewed as a system whose dynamics can be described from three complementary perspectives: *i*) *ecological*—in terms of changes in the population composition and the population size; *ii*) *genotypic*—in terms of changes in the relative frequency of genotypes in the population; *iii*) *phenotypic*—in terms of changes in the summary statistics of phenotypic traits in the population. In doing so, we unify the dynamical systems theory with the Malthusian growth equation (2.1) and logistic growth equation (2.2) from the foundations of population ecology (Box 2.1; Maynard Smith, 1978a; Singh & Uyenoyama, 2004), the replicator equation (2.3) and replicator-mutator equation (2.4) from the foundations of population genetics and evolutionary dynamics (Box 2.2; Crow & Kimura, 1970; Rice, 2004; Page & Nowak 2002; Nowak & Sigmund, 2004; Nowak, 2006), and the covariance mathematics of Price (1970, 1972a) (Box 2.3).

2.2 The principles of natural selection

In this section, we develop a general model for an arbitrary population of entities undergoing evolution by natural selection. We start by considering the characteristics the population must embody to enable it to be acted on by natural selection, namely, phenotypic variation, differential survival and reproduction, and heritability (Lewontin, 1970; Godfrey-Smith, 2007). We take an abstract perspective on these characteristics in order to preserve the generality of the dynamical systems theory. The advantages of this approach will become apparent in later sections of this chapter and indeed throughout the remainder of the thesis. In subsequent sections, we then explore how best to describe the dynamics of natural selection in the model, concluding that there are three complementary perspectives that illuminate the impact of ecological and evolutionary forces on the population.

2.2.1 Units of selection

Entities on which natural selection can act are known formally as 'units of selection' (Lewontin, 1970). Units of selection are members of a population that exhibits phenotypic variation, differential survival and reproduction, and heritability (Lewontin, 1970; Godfrey-Smith, 2007). Candidate units of selection in evolutionary theory include genes, organelles, cells, organisms, populations, species, and so on (Lewontin, 1970; Mayr, 1997;

Okasha, 2006). For simplicity, we will refer to the units of selection in this chapter as simply 'individuals'. But it doesn't really matter what the units of selection are, providing they exhibit the properties just described.

We will think of the individuals as entities comprising *information*. At its core, information corresponds to physical *order*. Individuals consist of the *intrinsic* information they inherit from their ancestors, and the *extrinsic* information they obtain from their environment. Through its *interpretation* by the environment at any time t, information obtains 'meaning' by imbuing individuals with certain properties, such as the expression of an otherwise improbable phenotype that emerges in a predictable way in spite of the tendency of the environment to create disorder, and the ability to transmit copies of information to other individuals.

Thinking about individuals in terms of information is useful for two main reasons: *i*) information is incorporeal in the sense that it can be embodied by any type of physical system, which means that the same information can, in principle, be embodied by a collection of atoms, a computer generated code, a waveform, and so on; *ii*) information is scale independent, which means that the same information can be embodied just as easily by a microscopic string of DNA or a macroscopic collection of clay tablets. By defining individuals in terms of information, we will therefore not restrict our analyses to any particular type of unit of selection, or any specific mechanism of inheritance[d].

We will, however, use the convenient terminology 'gene' to refer to a unit of information that can be stored and transmitted by an individual, and 'genotype' to refer to any unique configuration of one or more units of information that defines an individual[e]. Since we use terminology that is fairly consistent with that found elsewhere in biology, the definition of gene we have used might seem excessively 'inclusive' (Danchin and Wagner, 2010), and the information theoretic approach we have decided to take might generally seem unnecessarily abstract. In light of the discovery that information in the natural world is stored, transmitted, and interpreted in a multitude of ways (through RNA, DNA, proteins, epigenetic marks, behaviour, culture, and so on), however, the generality afforded by the information theoretic approach seems necessary for any general theory of natural selection.

[d]That is, the dynamics of natural selection we consider do not *a priori* rule out a role for Lamarckian and saltational processes (Jablonka and Lamb, 2008)

[e]In classical information theory, each discrete unit of information must be defined by some physical state that can be measured in terms of 'bits' (Shannon and Weaver, 1949). In quantum information theory, on the other hand, an indivisible continuous form of information can be obtained called the 'qubit': a unit of *quantum* information (Bennett and DiVincenzo, 2000). The more conventional bits of discrete information emerge from a physical arrangement comprising two or more qubits.

Moreover, there is an historical precedent for using information theory in evolutionary biology (Maynard Smith, 2000; Frank, 2009). Indeed, for many contemporary biologists the term 'gene' is already used as a 'black box' definition for a more abstract concept pertaining to an inherited component of a phenotype that is passed on between generations (Gorelick and Laubichler, 2008). Although information theory had not been developed when Fisher (1930) wrote *The Genetical Theory of Natural Selection*, the notion of a gene he was using was really an information theoretic one. In some sense it must have been, since virtually nothing was known at that time about the chemical or biological make-up of genes. Dawkins' (1976) notion of a 'replicator', as an entity from which accurate copies can be made, also hints at the existence of some discrete package of information[f].

2.2.2 Population

To study the dynamics of natural selection we require a population. The population we consider here is one of individuals, where each individual is defined by a particular genotype. Each genotype has an index $i \in \mathbb{G}$, where $\mathbb{G}$ is the index set of all possible genotypes. The number of genotypes considered is given by the size of the set, $|\mathbb{G}|$. The number of possible genotypes is certainly a large number. The size of the set grows exponentially with the number of separate genes under consideration. For instance, even if our genotypes represent simple binary strings of length L, there are at least 2^L different genotypes in the set $\mathbb{G}$. This is one of the main reasons why population geneticists typically work with gene frequencies rather than genotype frequencies in their calculations (see Crow and Kimura (1970, pg. 32)).

A key advantage of the simplified approach is that the complexity of the system scales linearly with the number of loci under consideration (whereas the number of genotypes increases exponentially) making analysis tractable[g]. Moreover, in a randomly mating population in which there is negligible selection, genetic drift, epistasis, mutation and so on, gene frequencies will tend to be in so-called 'Hardy-Weinberg' equilibrium, such that they do not change from one generation to the next. One can then work backwards to calculate the genotype frequencies from the allele frequencies or to calculate the estimated

[f] A genotype can exist for a very short or very long period of time. Dawkins' (1976) famously emphasised that good replicators have the characteristics of fidelity, fecundity, and longevity. These time-dependent characteristics may be necessary for natural selection to bring about evolutionary adaptations and the appearance of 'design' in the natural world, but it is important to realise that natural selection can in principle act at any instant in time on any configuration of information.

[g] The same basic approach formed the basis for the development of classical mechanics in physics, where the number of distinct particles in a small volume of gas must be tracked through time. Yet this number is in the intractable order of 10^{23}. Hence, classical mechanics gave rise to the study of the more tractable *statistical* mechanics.

'average effects' of alleles on phenotypic traits. These are fairly restrictive assumptions for most (but not all) purposes, but they may provide good *approximations* to the state of real systems. For instance, in systems with weak selection and little epistasis a population will often converge on a 'quasi-linkage equilibrium' state, allowing theorists to understand the dynamics of selection on multi-locus trait evolution (Kimura, 1965; Kirkpatrick et al., 2002).

Whilst it is always possible to go from absolute numbers to relative frequencies, however, the reverse is not always true, particularly when information about which alleles belong to which genotype has been lost. In some cases we will also be interested in the dynamics of natural selection in out-of-equilibria populations where common simplifying assumptions are violated. As we discussed in Chapter 1, our goal here is not the development of some specific model that is tractable to solve, and so let us allow ourselves to work with large numbers like 2^L for now on the understanding that in order to solve a real-world problem, the solution space would need to be greatly simplified to make the general theory presented herein useful.

We refer to any individual defined by the ith genotype in the population as an 'i-genotype' individual. We then use the approach of population ecology and follow the *absolute* abundance of individuals defined by different genotypes in the population (Maynard Smith, 1978a). Let $n_i := n_i(t) \in \mathbb{R}_+$ denote the abundance of i-genotype entities in the population at some time t. The composition of the population as a whole is given by the vector $\boldsymbol{n} = (n_1, ..., n_{|\mathbb{G}|})^{\mathrm{T}} \in \mathbb{R}_+^{|\mathbb{G}|}$. We denote the finite size of the population by using vector notation as $N = \mathbf{1}^{\mathrm{T}}\boldsymbol{n} = \boldsymbol{n}^{\mathrm{T}}\mathbf{1} = \sum_{i=1}^{|\mathbb{G}|} n_i$, where $\mathbf{1} = (1_1, \ldots, 1_{|\mathbb{G}|})^{\mathrm{T}} \in \mathbb{R}^{|\mathbb{G}|}$ is the 'summation' vector.

As we have discussed, in population genetics it is more common to focus on the *relative* frequencies of genotypes rather than their absolute abundances. This approach serves to simplify the analysis of evolving systems to some extent, but it also provides a complementary perspective on the nature of evolutionary change (Crow and Kimura, 1970). The relative frequency of i-genotype individuals in our population at any time t is simply given by $x_i = n_i/N$. The relative composition of the population as a whole is given by the vector $\boldsymbol{x} = (x_1, ..., x_{|\mathbb{G}|})^{\mathrm{T}} \in [0, 1]^{|\mathbb{G}|}$. Note that the sum of all relative frequencies is simply unity, $\mathbf{1}^{\mathrm{T}}\boldsymbol{x} = \boldsymbol{x}^{\mathrm{T}}\mathbf{1} = \sum_{i=1}^{|\mathbb{G}|} x_i = 1$.

2.2.3 Phenotypes

For natural selection to act on our population, there must be variation among the phenotypes expressed by individuals (Lewontin, 1970; Godfrey-Smith, 2007). Whereas pheno-

types are often implicitly defined in frameworks such as population ecology, population genetics, and evolutionary dynamics, we define them explicitly, as they do in quantitative genetics, as a set of observable characteristics or 'quantitative traits' (Falconer and Mackay, 1995).

We index each trait of interest by $k \in \mathbb{P}$, where $\mathbb{P}$ is the index set of all traits. The total number of traits is given by the size of the set, $|\mathbb{P}|$. For the kth trait, we let $z_{ik} := z_{ik}(t, \boldsymbol{n}) \in \mathbb{R}$ denote the 'phenotypic trait value' of the trait expressed by i-genotype individuals at time t. The value of traits varies among genotypes because the unique information held by i-genotype individuals resolves uncertainty about what values traits held by individuals can take in a given context. In this way, the information held by an individual does not determine its phenotype directly, but rather influences the functional form of the mapping function, z_{ik}, that *does* determine its phenotype. The phenotype of an individual therefore emerges from the *interpretation* of the information it holds, *given* the 'environment' it experiences. The environment here refers to the entire state of the system the individual occupies at time t. That is, *anything* in the system can be viewed as an environmental or ecological variable. Phenotypic trait values can therefore be specified as arbitrary functions of the genotype and the environment, that may or may not vary through time. We will discuss the causes and implications of time-dependent phenotypes in a later section when we consider phenotypic *dynamics*.

We do not account for age-structure or environmental stochasticity in the present model, and so for now all i-genotype individuals are assumed to express the same value for a trait (we can think of the trait value as the average value of a trait held by all individuals of a given genotype). The values of all $|\mathbb{P}|$ traits expressed by i-genotype individuals at time t define their phenotype at that time. The phenotypes expressed by all genotypes are given by a $|\mathbb{G}| \times |\mathbb{P}|$ matrix

$$\mathbf{Z} = \begin{array}{c} \\ \mathbb{G}_1 \\ \mathbb{G}_2 \\ \vdots \\ \mathbb{G}_{|\mathbb{G}|} \end{array} \begin{array}{c} \begin{array}{cccc} \mathbb{P}_1 & \mathbb{P}_2 & \cdots & \mathbb{P}_{|\mathbb{P}|} \end{array} \\ \begin{bmatrix} z_{11} & z_{12} & \cdots & z_{1|\mathbb{P}|} \\ z_{21} & z_{22} & \cdots & z_{2|\mathbb{P}|} \\ \vdots & \vdots & \ddots & \vdots \\ z_{|\mathbb{G}|1} & z_{|\mathbb{G}|2} & \cdots & z_{|\mathbb{G}||\mathbb{P}|} \end{bmatrix} \end{array}. \tag{2.6}$$

We refer to this matrix as the 'genotype-phenotype map'. For any time t, the ith row vector $\boldsymbol{z}_{i\bullet} \in \mathbb{R}^{|\mathbb{P}|}$ denotes the overall phenotype of an i-genotype individual, and the

kth column vector $\boldsymbol{z}_{\bullet k} \in \mathbb{R}^{|\mathbb{G}|}$ gives the distribution of the values of the kth trait for all genotypes.

An important implication of the way we have defined $\mathbf{Z}$ is that whether or not a genotype holds a particular unit of information is technically *also* part of its phenotype, blurring the distinction between genotype and phenotype. Although it is common to think of phenotypic traits as being externally visible features of an individual whose values can be measured in specified units, such as height or weight (whose values can be measured units of length^{-1} or mass^{-1}, respectively), genetic features like alleles, epigenetic marks, chromosomes, and so on, represent packets of information that can also tangibly be measured and are therefore certainly also part of the genotype-phenotype map, $\mathbf{Z}$. This idea will be important in Chapter 3 when we study the principles of evolutionary genetics.

It is important to note that whilst phenotypes are measured on individuals, it is phenotypic variation at the level of the *population* that defines whether or not selection can take place (Lewontin, 1970; Godfrey-Smith, 2007). Thus, in many circumstances we will typically be interested not in individual phenotypes *per se*, but rather in their summary statistics in the population. The average values of all traits in the population at time t are held by a vector $\bar{\boldsymbol{z}} := \bar{\boldsymbol{z}}(t, \boldsymbol{n}, \mathbf{Z}) \in \mathbb{R}^{|\mathbb{P}|}$. In vector-matrix notation, this is given by

$$\bar{\boldsymbol{z}} = \frac{1}{N}\mathbf{Z}^{\mathrm{T}}\boldsymbol{n} = \mathbf{Z}^{\mathrm{T}}\boldsymbol{x}. \tag{2.7}$$

where we have simply taken the product of the genotype-phenotype map, $\mathbf{Z}$, with the relative composition vector, $\boldsymbol{x}$. An alternative 'moment' notation for statistical summaries of populations popularised by Price (1970, 1972a) is also often used in evolutionary theory to describe the average or 'expected value' of a trait. A summary of this notation is given in Box 2.4.

Box 2.4 | A note on statistical notation

We denote the average value or, in this context, 'expected value' of a particular trait k in the population at time t by $\bar{z}_k := \bar{\boldsymbol{z}}_k(t, \boldsymbol{n}, \mathbf{Z}) \in \mathbb{R}$. The expected value of a trait is a measure of the centre of its distribution in the population at time t. In this context, it follows from equation (2.7), that the expected value of the kth trait is given by

$$\mathrm{E}_{i\in\mathbb{G}}(z_{ik}) = \bar{z}_k = \frac{1}{N}\sum_{i=1}^{|\mathbb{G}|} n_i z_{ik} = \sum_{i=1}^{|\mathbb{G}|} x_i z_{ik} = \boldsymbol{z}_{\bullet k}^{\mathrm{T}}\boldsymbol{x}, \tag{2.8}$$

where the subscript notation $i \in \mathbb{G}$ indicates that the expectation is taken over

all genotypes from the index set $\mathbb{G}$. Writing the average in this notation is useful because we can easily see the relations to other summary statistics that may be of interest (Price, 1970, 1972a). For instance, the covariance between two traits, say the kth and lth traits, gives a measure of their statistical association in the population. We calculate the covariance as

$$\begin{aligned} \mathrm{Cov}_{i\in\mathbb{G}}(z_{ik}, z_{il}) &\equiv \mathrm{E}_{i\in\mathbb{G}}(z_{ik}z_{il}) - \mathrm{E}_{i\in\mathbb{G}}(z_{ik})\mathrm{E}_{i\in\mathbb{G}}(z_{il}) \\ &= \boldsymbol{z}_{\bullet k}^{\mathrm{T}}\mathbf{X}\boldsymbol{z}_{\bullet k} - (\boldsymbol{z}_{\bullet l}^{\mathrm{T}}\boldsymbol{x})(\boldsymbol{x}^{\mathrm{T}}\boldsymbol{z}_{\bullet l}) \\ &= \boldsymbol{z}_{\bullet k}^{\mathrm{T}}(\mathbf{X} - \boldsymbol{x}\boldsymbol{x}^{\mathrm{T}})\boldsymbol{z}_{\bullet l} \\ &= \boldsymbol{z}_{\bullet k}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{z}_{\bullet l} \end{aligned} \tag{2.9}$$

where $\mathbf{X} = \mathrm{diag}(\boldsymbol{x})$ is the diagonalised relative composition vector $\boldsymbol{x}$. The square symmetric $|\mathbb{G}| \times |\mathbb{G}|$ matrix

$$\boldsymbol{\Sigma} = \mathbf{X} - \boldsymbol{x}\boldsymbol{x}^{\mathrm{T}} \tag{2.10}$$

acts as a general covariance 'operator'. We can take the covariance of two or more traits at any time in the population by pre- and post-multiplying the covariance operator $\boldsymbol{\Sigma}$ by vectors (or matrices) of the required dimension(s). We will encounter $\boldsymbol{\Sigma}$ in later sections in this chapter and extensively in Chapter 3, when we explore the dynamics of the evolutionary response to natural selection. The variance of a trait k is a measure of its dispersal around the population average, $\bar{z}_k$. We calculate the variance as

$$\begin{aligned} \mathrm{Var}_{i\in\mathbb{G}}(z_{ik}) &\equiv \mathrm{Cov}_{i\in\mathbb{G}}(z_{ik}, z_{ik}) \\ &= \mathrm{E}_{i\in\mathbb{G}}(z_{ik}^2) - \mathrm{E}_{i\in\mathbb{G}}(z_{ik})^2 \\ &= \boldsymbol{z}_{\bullet k}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{z}_{\bullet k}, \end{aligned} \tag{2.11}$$

where we see it is simply given by the covariance between a trait and itself.

In a later section, when we explore a phenotypic perspective on the dynamics of natural selection, we will see that this notation plays an important role in succinctly summarising the instantaneous rate of change of the average trait values in the population, $\bar{\boldsymbol{z}}$, with respect to time. In particular, it is worth noting that an advantage of this notation is that it leads naturally to definitions for other statistical quantities, such as the variance of a trait and the covariance of one trait with another. For instance, if we use the the covariance operator, $\boldsymbol{\Sigma}$, given by equation (2.10) in conjunction with the entire genotype-phenotype map, $\mathbf{Z}$, we obtain a $|\mathbb{P}| \times |\mathbb{P}|$ square symmetric variance-covariance matrix

$$\mathbf{P} = \mathbf{Z}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{Z} = \begin{bmatrix} \mathrm{Var}_{i\in\mathbb{G}}(z_{i1}) & \mathrm{Cov}_{i\in\mathbb{G}}(z_{i1}, z_{i2}) & \cdots & \mathrm{Cov}_{i\in\mathbb{G}}(z_{i1}, z_{i|\mathbb{P}|}) \\ \mathrm{Cov}_{i\in\mathbb{G}}(z_{i2}, z_{i1}) & \mathrm{Var}_{i\in\mathbb{G}}(z_{i2}) & \cdots & \mathrm{Cov}_{i\in\mathbb{G}}(z_{i2}, z_{i|\mathbb{P}|}) \\ \vdots & \vdots & \ddots & \vdots \\ \mathrm{Cov}_{i\in\mathbb{G}}(z_{i|\mathbb{P}|}, z_{i1}) & \mathrm{Cov}_{i\in\mathbb{G}}(z_{i|\mathbb{P}|}, z_{i2}) & \cdots & \mathrm{Var}_{i\in\mathbb{G}}(z_{i|\mathbb{P}|}) \end{bmatrix}, \tag{2.12}$$

whose diagonal elements contain the phenotypic variances of every kth trait, $\mathrm{Var}_{i\in\mathbb{G}}(z_{ik})$, and whose off-diagonal elements contain the covariance of every trait kth trait with every lth trait, $\mathrm{Cov}_{i\in\mathbb{G}}(z_{ik}, z_{il})$. This matrix will appear again when we explore the dynamics of the *evolutionary response* to natural selection in Chapter 3.

2.2.4 Survival and reproduction

Now that we have a description of the phenotypes expressed by individuals in our population, let us consider how these phenotypes give rise to differential survival and reproduction among genotypes (Lewontin, 1970; Godfrey-Smith, 2007). In this section, we argue that just as the logic of natural selection does not depend on what the units of selection in question are, or how how we measure phenotypes, it also does not depend on the specific processes that influence the gain or loss of copies particular genotypes in the population.

The most obvious processes that lead to gain or loss of copies of particular genotypes are births and deaths of individuals, by which we mean the gain of a new individual following asexual or sexual reproduction and the loss of an individual due to an irreversible state change from living to dead. Yet there are other processes that influence the gain or loss of genotypes in a population. For instance, the transfer of information from one individual (the 'donor') to another (the 'recipient') also leads to a gain and loss of a genotype. The population loses a copy of whatever genotype defined the recipient, but gains a copy of whatever genotype defines the new 'transformed' recipient. Similarly, if an individual fissions (splits into two or more pieces), the population loses a copy of whatever genotype defined the fissioning individual, but gains a copy of whatever new genotype(s) define the resulting propagules. In a like manner, if two individuals fuse (aggregate to form a new individual), the population loses copies of two genotypes, but gains a copy of a new genotype corresponding to whatever information the newly fused individual holds.

Whatever processes are involved in the gain or loss of genotypes, we can describe them all using a conceptual generalisation of the scheme introduced by Charlesworth (1970). To describe this scheme, it is important to first give some context. In deriving the foundations

of population genetics, Fisher (1930) supposed that if the population is growing at a rate m (see the Malthusian growth equation (2.1) in Box 2.1), then each genotype is growing at a geometric rate of increase $m_i = b_i - d_i$, known as its 'Malthusian parameter' or 'Malthusian fitness' (Day and Otto, 2001; Orr, 2009). If there is variability in fitness, then the composition of genotypes within the population, Fisher (1930) reasoned, will change over time. As several authors subsequently pointed, however, this does not hold true when reproduction is sexual, owing to the segregation and recombination of genetic information during meiosis (Kempthorne and Pollak, 1970; Charlesworth, 1970)[h]. In a sexually reproducing population, when a genotype reproduces it therefore does not give rise to another copy of itself, but rather to a copy of another genotype that results from the recombination of two different sets of genetic information[i]. Recall our discussion of this problem in Chapter 1.

The solution to this problem was partially solved by both Kimura (1958) and Charlesworth (1970). Firstly, Kimura (1958) redefined Malthusian fitness to be the 'the net reproductive rate of [a] genotype m_i such that [its] contribution to the rate of increase of the population number N is $n_i m_i$' (where n_i is the number of i genotypes). Thus, from Kimura's (1958) perspective, the Malthusian parameter of the population is not really a direct property of the population m, but an emergent feature of the population dynamics determined by the average Malthusian fitness $\bar{m}$ of the population's constituent genotypes (reviewed in Crow and Kimura (1970, pg. 25)). Indeed, this definition is the same as the second definition of Malthusian fitness we derived in Chapter 1, that we described as, 'the per capita contribution of type i individuals to the overall growth-rate of the population, $\bar{m}$.' Secondly, Charlesworth (1970, pg. 356) formalised the contrast between reproduction *by* a genotype and production *of* a genotype (see Ariew and Lewontin (2004) for a discussion) by developing a model of sexual reproduction in which a distinction was made between rates affecting zygotes and gametes.

Here, we use the logic of Charlesworth (1970) to define an approach that holds for any arbitrary processes that lead to the gain and/or loss of a copy of a genotype from the population. We use the terminology[j] 'ancestor' to describe any individual alive at time t that contributes information to the creation of a new 'descendant' individual some

[h]For instance, Kempthorne and Pollak (1970) said, 'one can certainly envisage a function, d, for each genotype, but (sexual) reproduction involves two ancestors and it is obscure what Fisher meant the term b to convey. The treatment seems inadequate for genetic situations because the mathematical argument leading to this equation applies to the case of a population of genotypes with each individual producing descendant of its own genotype.'

[i]In actual fact, this is also true in an asexually reproducing population if there is, for instance, a non-negligible rate of mutation.

[j]Later in the thesis we will use the terms 'ancestor', and 'parent' interchangeably depending on the context. Similarly we will use 'offspring' as interchangeable with 'descendant'.

instant later at $t + \delta t$. Thus, an asexually or sexually reproducing parent is an ancestor. Both the donor and recipient engaging in the transfer of information are ancestors. An individual that fissions is an ancestor. All individuals that aggregate or fuse with one another are ancestors. A descendant is any individual alive at time $t + \delta t$ that was not alive at time t, whose creation depended on the receipt of information from an ancestor. That is, an offspring individual resulting from the asexual or sexual reproduction of an ancestor is a descendant. The transformed recipient created by the transfer of information between ancestors is a descendant. The emitted propagule individuals resulting from a fissioning ancestor are descendants. The new aggregate individual resulting from a fusion of ancestors is a descendant. We give a depiction of this abstract way of thinking about survival and reproduction in Figure 2.1.

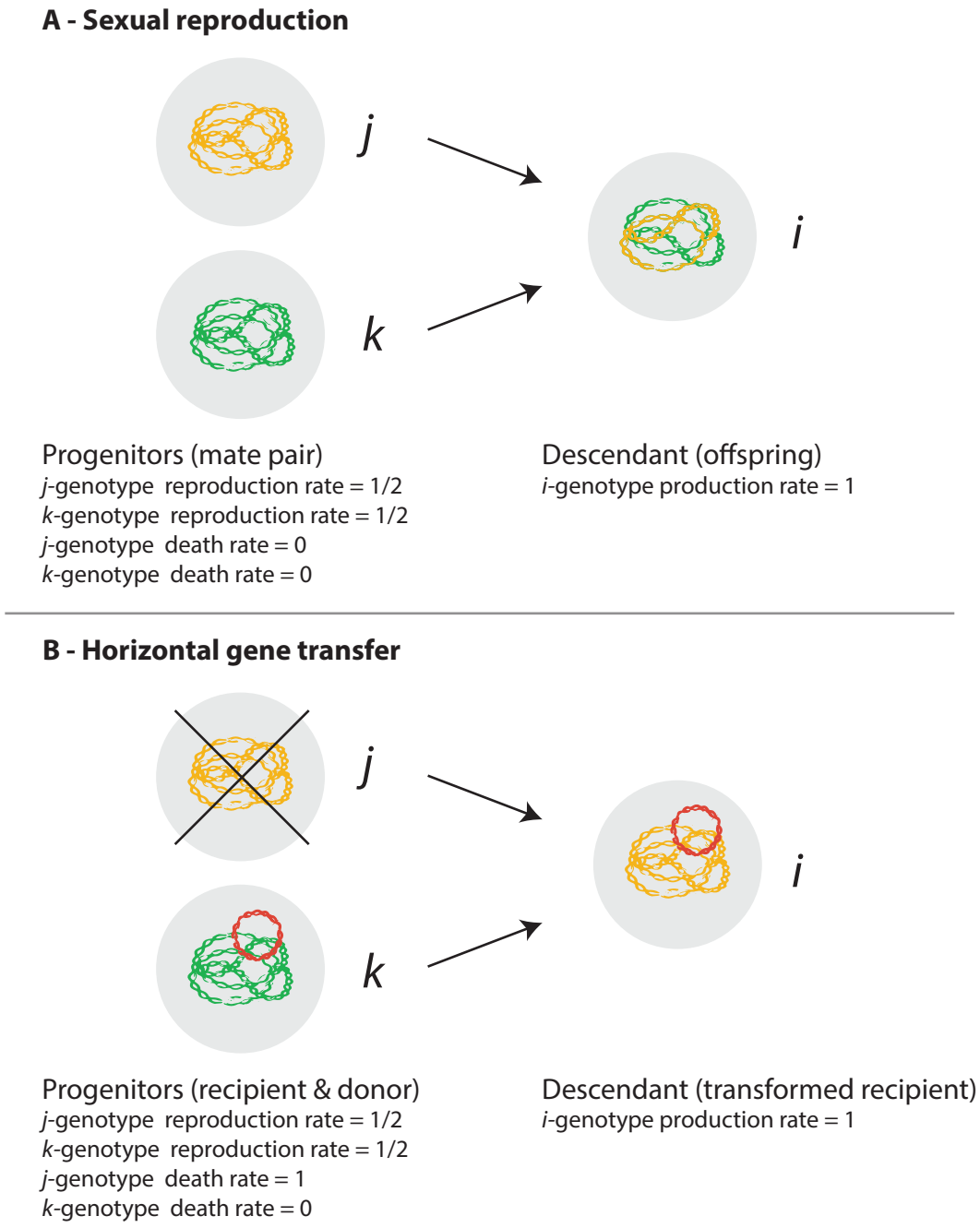


Figure 2.1: Survival and reproduction | We use an abstract notion of survival and reproduction by thinking about all processes that lead to changes in the composition of information in a population through the gain and loss of copies of different genotypes in the population. We say that ancestors (parents) *reproduce*, and descendants (offspring) are *produced*. That is, we emphasise that these are two different processes that are intimately related and happen to occur at the same time. We give two examples that have typically been thought to be difficult to describe in general terms, namely, sexual reproduction (Ariew and Lewontin, 2004), and horizontal gene transfer (Birch, 2014). In panel **A** we depict sexual reproduction between j-genotype and k-genotype ancestors giving rise to the production of an i-genotype descendant. In panel **B** we depict horizontal gene transfer between j-genotype and k-genotype ancestors giving rise to the production of an i-genotype descendant. Note that in both panels the reproduction rate of each ancestor is scaled so that the total rate of reproduction always equals the total rate of production.

The important point is this: whatever process we consider, the ancestors and descendants involved must always be in the set $\mathbb{G}$ since it is the set of *all* genotypes. It is therefore possible to assign rates—measurable in units of time^{-1}—to existing genotypes that account for the gain and loss of new genotypes. Beginning with processes that cause the loss of genotypes, let $d_i := d_i(\boldsymbol{n}, t) \in \mathbb{R}_+$ denote the 'death' rate of i-genotype individuals at time t. We use the term death for want of a better word; as we have just discussed, this rate is inclusive of the usual definition of death, but also pertains to other processes that lead to the loss of an i-genotype individual, including transfer, fission, fusion, and so on. The death rates of genotypes are given by the vector $\boldsymbol{d} = (d_1, ..., d_{|\mathbb{G}|})^{\mathrm{T}} \in \mathbb{R}_+^{|\mathbb{G}|}$. Combining the death rate vector with the composition vector $\boldsymbol{n}$, we can obtain the average death rate in the population at time t, which we denote by

$$\bar{d} = \frac{1}{N} \sum_{i=1}^{|\mathbb{G}|} n_i d_i = \sum_{i=1}^{|\mathbb{G}|} x_i d_i = \boldsymbol{d}^{\mathrm{T}} \boldsymbol{x}. \tag{2.13}$$

We can always think of the death rate as being part of the phenotype of an individual since it is a measurable property of individuals. Just like other traits in the genotype-phenotype map, $\mathbf{Z}$, the death rate is potentially dependent on the state of the entire system, including the composition of the population, $\boldsymbol{n}$, and time, t. It is therefore not necessarily a static trait, but may change through time. For example, if resources are limited in a population, then individuals might become increasingly aggressive with one another, leading to a density-dependent death rate that scales proportionately with the population size, N.

Moving on to processes that cause the gain of a copy of a particular genotype, things get a little more complicated (for the reasons why we described above associated with sexual reproduction). It would initially seem natural to simply define another function, say b, denoting the 'birth' rate of i-genotype ancestors at time t and continue from there (this was seemingly the approach Fisher (1930) took). The problem, as we have discussed, is that the rate of reproduction *by* an ancestor of a specified genotype is not the same as the rate of increase of that genotype in the population at that time. If our individuals reproduce by any other process than purely clonal reproduction they will typically give rise to descendants of a different genotype to themselves (at least some of the time). Also of interest to us, therefore, is the rate of 'production' of descendants of a specified genotype.

The solution to obtaining both the rates of reproduction and production in the population rests on defining pairwise rates. To be more specific, we let $f_{ij} := f_{ij}(\boldsymbol{n}, t) \in \mathbb{R}_+$ denote

a *compound* fidelity rate, giving the rate at which i-genotype ancestors reproduce *and* give rise to the production of j-genotype descendants (these rates are similar to rate of 'gamete' production K_{ij} described by Charlesworth (1970, pg. 356). The fidelity rates expressed by all genotypes are given by a $|\mathbb{G}| \times |\mathbb{G}|$ matrix

$$\mathbf{F} = \begin{array}{c} \\ \mathbb{G}_1 \\ \mathbb{G}_2 \\ \vdots \\ \mathbb{G}_{|\mathbb{G}|} \end{array} \begin{array}{c} \begin{array}{cccc} \mathbb{G}_1 & \mathbb{G}_2 & \cdots & \mathbb{G}_{|\mathbb{P}|} \end{array} \\ \begin{bmatrix} f_{11} & f_{12} & \cdots & f_{1|\mathbb{G}|} \\ f_{21} & f_{22} & \cdots & f_{2|\mathbb{G}|} \\ \vdots & \vdots & \ddots & \vdots \\ f_{|\mathbb{G}|1} & f_{|\mathbb{G}|2} & \cdots & f_{|\mathbb{G}||\mathbb{G}|} \end{bmatrix} \end{array}. \tag{2.14}$$

We refer to this matrix as the 'fidelity rate matrix'. For any time t, the ith row vector $\boldsymbol{f}_{i\bullet} \in \mathbb{R}^{|\mathbb{G}|}$ denotes the mapping between an i-genotype ancestor individual and the genotype of descendants it gives rise to, and the jth column vector $\boldsymbol{f}_{\bullet j} \in \mathbb{R}^{|\mathbb{G}|}$ gives the mapping between a j-genotype descendant individual and the genotype of ancestors it may be produced by. It is important to note that to specify the fidelity rate matrix we need to know specific details about the mode of reproduction and the mechanisms of inheritance. We will return to this point shortly.

For now we can return to the goal we started with and let $b_i := b_i(\boldsymbol{n}, t) \in \mathbb{R}_+$ denote the rate of reproduction of i-genotype ancestor individuals. From the fidelity rate matrix $\mathbf{F}$ we can now see that the reproduction rate is simply given by the sum over the rates at which i-genotype ancestors reproduce and give rise to descendants of *any* genotype:

$$b_i = \sum_{j=1}^{|\mathbb{G}|} f_{ij}. \tag{2.15}$$

The reproduction rates of the population as a whole are given by the vector $\boldsymbol{b} = \left(b_1, ..., b_{|\mathbb{G}|}\right)^{\mathrm{T}} \in \mathbb{R}_+^{|\mathbb{G}|}$, which we can describe in matrix notation as $\boldsymbol{b} = \mathbf{F}\mathbf{1}$, where $\mathbf{1}$ is the summation vector. Just like the death rate, we can always think of the birth rate as being a phenotypic trait, since it is also a measurable property of individuals. Just like other traits in the genotype-phenotype map, $\mathbf{Z}$, the reproduction rate is also dependent on the composition of the population $\boldsymbol{n}$ and time t. It is also therefore not necessarily a static trait, but may change through time. For example, if individuals reproduce sexually, then the rate of reproduction will depend on the abundance of potential sexual partners in the population, as well as the abundance of competing conspecifics. Thus, the reproduction rate

for individuals might scale proportionately with the abundance of the genotype corresponding to potential sexual partners, but with the reciprocal abundance of the genotype corresponding to potential competitors, leading to a frequency-dependent reproduction rate.

Now let us turn to the rate at which new copies of genotypes are created in the population. Let $p_i := p_i(\boldsymbol{n}, t) \in \mathbb{R}_+$ denote the rate of production of i-genotype descendant individuals. This is simply given by summing over the rate at which j-genotype ancestors (weighted by their abundance) reproduce and give rise to i-genotype descendants:

$$p_i = \sum_{j=1}^{|\mathbb{G}|} n_j f_{ji}. \tag{2.16}$$

The production rates of all genotypes are given by the vector $\boldsymbol{p} = (p_1, ..., p_{|\mathbb{G}|})^{\mathrm{T}} \in \mathbb{R}_+^{|\mathbb{G}|}$. In matrix notation we can write $\boldsymbol{p} = \mathbf{F}^{\mathrm{T}}\boldsymbol{n}$. Unlike the *per capita* reproduction rate and death rate, we cannot think of the production rate as a phenotypic trait, since it is *not* a *per capita* rate or a measurable property of any particular individual, but instead a measurable property of the population. In this respect, the rate of production is more like a demographic rate from population ecology (it corresponds to what Maynard Smith (1978a) has referred to as a 'macroscopic variable').

Although the rate of reproduction and production of any given genotype are not equivalent, it *is* logically the case that the total, and hence the average, reproduction and production rates of all genotypes are the same at any time t, since the production of an individual implies that another individual reproduced and vice versa. To prove that this is indeed the case, let us start by denoting the average rate of reproduction in the population by

$$\bar{b} = \frac{1}{N}\sum_{i=1}^{|\mathbb{G}|} n_i b_i = \sum_{i=1}^{|\mathbb{G}|} x_i b_i = \boldsymbol{b}^{\mathrm{T}}\boldsymbol{x}. \tag{2.17}$$

Similarly, the average rate of production of all genotypes is given by

$$\bar{p} = \frac{1}{N}\sum_{i=1}^{|\mathbb{G}|} p_i = \frac{1}{N}\sum_{i=1}^{|\mathbb{G}|}\sum_{j=1}^{|\mathbb{G}|} n_j f_{ji} = \sum_{i=1}^{|\mathbb{G}|}\sum_{j=1}^{|\mathbb{G}|} x_j f_{ji}. \tag{2.18}$$

where we have substituted for p_i from equation (2.16). If we now take the sum over i inside the sum over j, and then switch the order of summation (which has no effect on the equality), we obtain

$$\bar{p} = \sum_{j=1}^{|\mathbb{G}|} x_j \sum_{i=1}^{|\mathbb{G}|} f_{ji} = \sum_{i=1}^{|\mathbb{G}|} x_i \sum_{j=1}^{|\mathbb{G}|} f_{ij} = \sum_{i=1}^{|\mathbb{G}|} x_i b_i = \bar{b}. \tag{2.19}$$

where we have substituted for $b_i = \sum_{j=1}^{|\mathbb{G}|} f_{ij}$ from equation (2.15) and $\bar{b} = \sum_{i=1}^{|\mathbb{G}|} x_i b_i$ from equation (2.17). Hence, we have proved that average rate of reproduction, given by equation (2.17), is equivalent to the average rate of production, given by equation (2.18). An important consequence of this equality is that the fidelity rate of an i-genotype ancestors, f_{ij}, should be weighted by the ratio of the average number of descendants produced to the average number of reproducing ancestors involved in reproduction, #avg. descendants/#avg. ancestors. For instance, if an individual reproduces sexually, the rate of reproduction of both ancestors must be weighted by #descendants/#ancestors = 1/2. This recapitulates the famous 'two-fold cost of sex' described by Maynard Smith (1978b). It says that sex is costly because all else being equal, a sexually reproducing population must reproduce twice as fast as an asexually reproducing population to have the same growth rate.

The cost of describing survival and reproduction related processes in the abstract way we have defined in this section is that it inevitably obscures the biology behind the process we are interested in. The virtue of this approach, however, is its generality (Price, 1995). Any process can be depicted in this way, no matter how unnatural it might seem from a biological perspective. As Okasha (2006) notes, when we are describing a process in mathematical terms, 'naturalness is not logical necessity'. Moreover, the abstract approach can enable us to see and quantify the relations among processes that might seem entirely unrelated from a biological perspective (May, 2004). For instance, mathematics tells us that the processes of kin selection and multi-level selection are equivalent (Wade, 1985; Queller, 1992b; Lehmann et al., 2007; Marshall, 2011), even though they seem to be conceptually very different. Similarly, from Figure 2.1, we can see that the description we have given of sexual reproduction and horizontal gene transfer highlights a similarity between these two processes. This similarity has been noted previously (Redfield et al., 1997; Shapiro et al., 2012; Papke and Gogarten, 2012; Cohan and Aracena, 2012), but the abstract approach we have described formalises this idea, and allows us to quantify what the similarity is and why it matters for evolutionary change. A simplified example model of horizontal gene transfer is given in Chapter 6.

2.2.5 Inheritance

Now that we have a description of the ways in which individuals 'reproduce', the third principle of evolution by natural selection that our population must meet is that there is heritability (Lewontin, 1970; Godfrey-Smith, 2007). In quantitative genetics 'heritability' is understood to be a quantitative statistical measure of the similarities between parents and their offspring. We will turn to this definition of heritability in Chapter 3. As Godfrey-Smith (2007) points out, however, this was not what Lewontin (1970) was referring to in his definition. Lewontin (1970) was talking about the vaguer notion of there being something inherited by offspring from their parents. Similarly in an alternative definition of the requirements for natural selection, Endler (1986) stated that there must be 'a consistent relationship ... between parents and their offspring, which is at least partially independent of common environmental effects: inheritance.' Whilst this condition is therefore often stated as if the phenotype of individuals is transmitted across generations, this is not quite true.

What is *really* transmitted between parents and the offspring they give rise to is biological information. It is the correlation between the information received and the conception of a particular phenotype that gives rise to similarity between parents and their offspring. The phenotype expressed by descendants depends on the information it received from its parents, and how this information then gets interpreted by the environment. We have actually already made the assumption of information transfer between ancestors and descendants in the last section, in our description of the fidelity rate matrix, $\mathbf{F}$, we described in the previous section. Clearly, to know the rate at which j-genotype descendants are produced when an i-genotype ancestor reproduces, we need to know how it reproduced, who it reproduced with, what kind of information it passed to its descendants *given* that it reproduced in that way, and so on.

To give a couple of concrete examples, suppose that our individuals represent bacteria reproducing asexually. In this case the fidelity rate f_{ij} must account for the rate at which i-genotype bacteria divide per unit time as well as the *conditional* probability that, *given* that they reproduced, specific mutation(s) did or did not occur, causing them to produce j-genotype descendants. Indeed, we have already seen a dynamical equation describing mutations in this way in our description of the replicator-mutator equation (2.4) (Box 2.2). The mutation rate represents the conditional probability that an i-genotype ancestor produces j-genotype descendants, given that it reproduced, q_{ij}.

If instead we suppose that our individuals represent multicellular organisms reproducing sexually, then things become even more complex. The fidelity rate f_{ij} must now account

for the rate at which i-genotype organisms reproduce sexually per unit time, which depends on the conditional probability that, *given* that they reproduced, reproduction took place with a particular partner. It then depends on the the conditional probability that, given reproduction took place with that particular sexual partner, it led to the production of j-genotype descendants due to the particular features of segregation and recombination associated with those genotypes. Putting this altogether, we might have something like $f_{ji} = x_j s_{jk} q_{jki}$. That is, the rate depends on some probability that a j-genotype ancestor meets an k-genotype partner, x_j, the rate at which sex takes place, given that they met, s_{jk}, and the probability that their descendant offspring are of genotype i, given that their their biological information segregated and recombined in a particular way, q_{jki}.

2.2.5.1 Expected genotypic distribution of descendants

By analogy with the approach in population genetics of studying relative genotype frequencies rather than absolute numbers (Crow and Kimura, 1970), we can gain a clearer perspective on the mechanisms of inheritance in our framework by exploring the question: on average, what genotype do we expect j-genotype descendants to inherit from i-genotype ancestors, assuming that they have just reproduced? To give an example of why we might want to ask this, suppose our individuals represent bacteria of the species *Pseudomonas aeruginosa*, which is implicated in the development of cystic fibrosis in humans. Some bacteria of this species, known as *mutS* mutants, lack a functional DNA mismatch repair system and exhibit a hypermutable phenotype (Oliver and Mena, 2010). Since mutants vary in their propensity to be resistant to antibiotics, in this context, we might therefore be interested in the expected genotypic distribution of descendants *mutS* mutants produce as compared wild-type cells. That is, what is the probability they reproduce and give rise to an antibiotic resistant descendant given the current population density and the rate of growth.

To answer this question, let $h_{ij} := h_{ij}(\boldsymbol{n}, t) \in [0, 1]$ denote the *conditional* 'inheritance probability' that an i-genotype ancestor produces j-genotype descendants, *given* that it is has reproduced. We calculate the inheritance probability by simply dividing the fidelity rate by the overall reproduction rate to give $h_{ij} = f_{ij}/b_i$. The conditional inheritance probability follows straight from basic probability theory: the conditional probability of an event A given an event B is given by $\mathbb{P}(A|B) = \mathbb{P}(A \cap B)/\mathbb{P}(A)$, where $\cap$ denotes the intersection of two events (i.e. a compound event). The event A represents the reproduction of an i-genotype ancestor, and the event B represents the production of j-genotype descendant. The inheritance probabilities for all genotypes are given by a square 'inheritance matrix', $\mathbf{H} = [h_{ij}] \in \mathbb{R}^{|\mathbb{G}|\times|\mathbb{G}|}$. In matrix notation we have

$$\mathbf{H} = \mathbf{B}^{-1}\mathbf{F}, \tag{2.20}$$

where $\mathbf{B} = \text{diag}(\boldsymbol{b})$ is the diagonalised vector $\boldsymbol{b}$. The inheritance matrix is a right-stochastic $|\mathbb{G}| \times |\mathbb{G}|$ matrix. We can think of its rows as a probability mass functions describing the expected genotypic distribution of descendants for each ancestor. An important property of a stochastic matrix is that the sum of each row is 1, that is, we have $\sum_{j=1}^{|\mathbb{G}|} h_{ij} = 1$. The equivalent statement in matrix notation is, $\mathbf{H1} = \mathbf{1}$. In the special limiting case where the reproduction is perfectly clonal, the inheritance matrix simply becomes the identity matrix, $\mathbf{H} = \mathbf{I}$.

When the matrix largely consists of zeros (a 'sparse' matrix), we can infer that reproduction gives rise to predictable types of offspring and there is little potential for diversity to be generated (which will be the case if reproduction is largely clonal, for instance). When the matrix largely consists of non-zero values (a 'dense' matrix), however, it indicates that reproduction generates diversity, which might occur because reproduction is sexual or because there is a high rate of mutation. If the element of the inheritance matrix $h_{ii} = 0$, then we expect that i-genotype descendants will inherit the information they hold from ancestors with less than perfect fidelity. For instance, in our hypermutability example (Oliver and Mena, 2010), it would indicate that *every* time a *mutS* bacterium reproduced, it gave rise to another mutant strain different to itself. If, however, the element $h_{ii} = 1$, then we expect i-genotype descendant individuals to inherit the information they hold with perfect fidelity. Reproduction in this scenario *must be* clonal. For instance, the wild-type bacterium in our example might have $h_{ii} \approx 1$. In the special case when the inheritance probabilities are constants rather than time-dependent functions, they are equivalent to mutation probabilities from the mutation matrix, $\mathbf{Q} = [q_{ij}]$, used in quasispecies theory (Nowak, 1992).

So far we have focussed on the rows of the inheritance matrix, but if we look at its columns, we can infer something about the predisposition of the *population* to give rise to individuals of a particular genotype. If the sum of the entries of a particular column j is greater than 1, this indicates that many ancestor genotypes are in some sense 'naturally predisposed' to give rise to descendants of genotype j. Thus, we can think of genotype j as a 'sink genotype', since it has the potential to be easily 'reached' by the population. Conversely, if the sum of the entries of column j is less than 1, we can think of genotype j as a 'source genotype' at time t, since it has the potential to be easily 'exited' by the population. In some sense, the columns of the inheritance therefore measure the ability

of a genotype to evolve (Wagner and Altenberg, 1996; Kirschner and Gerhart, 1998; Pigliucci, 2008)[k].

2.2.5.2 Expected phenotypic values of descendants

Since the inheritance matrix tells us the expected distribution of descendants produced by a given genotype, we can also use it to calculate a measure of the expected phenotypic values expressed by future descendants. That is, we can use it get the phenotypic value of an i-genotype individual as measured by the expected value of its progeny. In quantitative genetics the average phenotypic value of an individual's progeny (calculated retrospectively) is known as it's a 'breeding value' (Falconer and Mackay, 1995)[l]. The value we seek to calculate here is therefore equivalent to a *prospective* breeding value—the breeding value of an individual if it were to produce the progeny predicted by the inheritance matrix. Taking a product of the ith row of the inheritance matrix with an arbitrary column vector of trait values from the genotype-phenotype map, say $\boldsymbol{z}_{\bullet k}$, represents an expected value of trait k in the descendants of an i-genotype ancestor at time t (assuming that it has reproduced):

$$\mathrm{E}'_{i\in\mathbb{G}}(z_{ik}) \equiv \sum_{j=1}^{|\mathbb{G}|} h_{ij} z_{jk} = \boldsymbol{h}_{i\bullet}\boldsymbol{z}_{\bullet k} = z'_{ik}, \tag{2.21}$$

where the notation $\mathrm{E}'_{i\in\mathbb{G}}(\cdot)$ indicates that we have taken the expectation using the probability mass function given by the ith row of the inheritance matrix $\mathbf{H}$. The notation $z'_{ik} := z'_{ik}(\mathbf{Z}, \boldsymbol{n}) \in \mathbb{R}$ is an alternative short-hand notation we use for the expected trait values in an descendants. It is important to note that these quantities are prospective or *conditional* values that descendants will express, on the assumption that they have been produced. That is, these values exist independently of whether or not a particular ancestor actually reproduces or not (we can always predict what the phenotypic trait values its descendants would express if they *were* produced). The expected trait values for all ancestor genotypes over all traits are given by the matrix $\mathbf{Z}' = [z'_{ik}] \in \mathbb{R}^{|\mathbb{G}|\times|\mathbb{P}|}$. We can express equation (2.21) in matrix notation by simply taking the product of the inheritance matrix, $\mathbf{H}$, and the genotype-phenotype map, $\mathbf{Z}$, to get

[k] One way to formalise this concept could be to compute the eigen-decomposition of the inheritance matrix, $\mathbf{H}$. This would give us its stationary distribution at time t, and hence a prediction of what the future composition of the population, $\boldsymbol{n}$, would be if the inheritance matrix remained constant and there were no differences in fitness between genotypes.

[l] The definition Falconer and Mackay (1995) give is: 'the value of an individual, judged by the mean value of its progeny, is called the *breeding value* of the individual.'

$$\mathbf{Z}' = \mathbf{H}\mathbf{Z}. \tag{2.22}$$

Note that in the special limiting case where the fidelity of transmission of information is perfect, the inheritance matrix becomes the $|\mathbb{G}| \times |\mathbb{G}|$ identity matrix, $\mathbf{H} = \mathbf{I}$, so that $\mathbf{Z}' = \mathbf{I}\mathbf{Z} = \mathbf{Z}$, and we find that the expected trait values of descendants are identical to the values of their ancestors, as we would expect. In the more general case where the fidelity of transmission of information is imperfect, there will be differences between the trait values of ancestors and the expected trait values of descendants. Let us therefore define another matrix

$$\Delta\mathbf{Z} = \mathbf{Z}' - \mathbf{Z}. \tag{2.23}$$

to hold these differences. Since the entries of the inheritance matrix, $\mathbf{H}$, depend on the composition of the population, $\boldsymbol{n}$, and time, t, it is clearly the case that $\mathbf{Z}'$ and $\Delta\mathbf{Z}$ will also have this dependence and consequently may vary continuously through time.

2.3 The dynamics of natural selection

We now have a system describing a population of individuals, defined at any time t by the composition vector, $\boldsymbol{n}$, and the genotype-phenotype map, $\mathbf{Z}$. Under certain conditions our population may exhibit phenotypic variation, differential survival and reproduction, and heritability, and therefore satisfy the principles required for evolution by natural selection (Lewontin, 1970; Godfrey-Smith, 2007). When these principles are satisfied, and even in some cases when they are not, we should expect changes in the population to occur over time. That is, our population not only represents a system, but a *dynamical* system. To describe the dynamics of the system we will need calculus. In Box 2.5, we introduce some notation for the different types of derivatives that will be of interest to us here and in later chapters.

Box 2.5 | A note on derivative notation

To keep things concise, we define the (total) derivative of, for example, the composition vector, $\boldsymbol{n}$, with respect to time, t, using the notation

$$\dot{\boldsymbol{n}} \equiv \frac{d\boldsymbol{n}}{dt}. \tag{2.24}$$

To take the *partial* derivative of the composition vector, $\boldsymbol{n}$, with respect to time, t, we use the notation

$$\partial_t \boldsymbol{n} \equiv \frac{\partial \boldsymbol{n}}{\partial t}. \tag{2.25}$$

Finally, to take the partial derivative of, for example, the relative composition vector, $\boldsymbol{x}$, with respect to the composition vector, $\boldsymbol{n}$, we define the *gradient* operator using the notation

$$\nabla_{\boldsymbol{n}}[\boldsymbol{x}] \equiv \frac{\partial \boldsymbol{x}}{\partial \boldsymbol{n}^{\mathrm{T}}} = (\partial_{n_1} x_1, \ldots, \partial_{n_{|\mathbb{G}|}} x_{|\mathbb{G}|}). \tag{2.26}$$

Note: strictly speaking we cannot take the derivative with respect to a vector or matrix, but this notation will act as a useful heuristic for such an operation. This abuse of notation is common in the field of *matrix calculus*, a relatively new field of mathematical theory that has been given an introductory treatment in a recent book by Bodewig (2014). A more rigorous approach to defining this type of operation requires the introduction of the concept of linear maps, which is beyond the scope of the work in this thesis.

The state of the system at any instant in time t is defined by the composition of the population, $\boldsymbol{n}$, and the trait values in the genotype-phenotype map, $\mathbf{Z}$. The state can be thought of in the following way: the composition vector $\boldsymbol{n}$ and each of the $|\mathbb{P}|$ column vectors, $\boldsymbol{z}_{\bullet k}$, from the genotype-phenotype map, $\mathbf{Z}$, represent points in $|\mathbb{G}|$-dimensional space. Altogether we have $|\mathbb{P}| + 1$ points. The composition vector, $\boldsymbol{n}$, occupies what we call the 'composition space' $\Omega = \mathbb{R}_+^{|\mathbb{G}|}$ (with a boundary $\partial\Omega$). Each trait vector, $\boldsymbol{z}_{\bullet k}$, occupies a phenotypic space in $\mathbb{R}^{|\mathbb{G}|}$.

For each point in each of the spaces, we attach a vector that tells us the direction in which the point is moving. If we join these vectors together, we obtain trajectories for the composition of the population and each of the $|\mathbb{P}|$ traits. To be able to do this, we need to write a velocity function—a 'dynamical law' or 'evolution rule'—describing the local behaviour of each of the points. In this section, we show that the formulation of such rules naturally leads us to consider the dynamics of natural selection in our population from three complementary perspectives: *i*) *ecological*—in terms of changes in the population composition and the population size; *ii*) *genotypic*—in terms of changes in the relative frequency of genotypes in the population; *iii*) *phenotypic*—in terms of changes in the summary statistics of phenotypic traits in the population.

2.3.1 Ecological perspective

Ecological change is about changes in the attributes of ecosystems, communities, and populations (Hairston et al., 2005). In population ecology the relevant variables are the *absolute* abundances of different types, and the aim is to describe changes in the size and composition of a population through time (Box 2.1; Maynard Smith, 1978a; Singh & Uyenoyama, 2004).

In our population, as we have said, change in the population composition over time can be pictured as a trajectory of the population across the composition space, Ω. To describe this trajectory, we need a *dynamical law*. That is, we need a rule for predicting the future composition of the population given its current composition, $\boldsymbol{n}$. Let the vector $\dot{\boldsymbol{n}} \equiv d\boldsymbol{n}/dt$ denote the rate of change of the composition of the population, $\boldsymbol{n}$, with respect to time, t. If we think of the population as occupying a point in the composition space, Ω, the vector $\dot{\boldsymbol{n}}$ represents the population *velocity*. Clearly, the change in the absolute abundance of each genotype depends upon the rates at which they are being produced and dying. Thus we can define the dynamical law for the rate of change of the composition vector, $\boldsymbol{n}$, with respect to time to be

$$\dot{\boldsymbol{n}} = \boldsymbol{p} - \mathbf{N}\boldsymbol{d} = \mathbf{F}^{\mathrm{T}}\boldsymbol{n} - \mathbf{N}\boldsymbol{d} = \mathbf{H}^{\mathrm{T}}\mathbf{N}\boldsymbol{b} - \mathbf{N}\boldsymbol{d}, \tag{2.27}$$

where $\boldsymbol{p} = \mathbf{F}^{\mathrm{T}}\boldsymbol{n} = \mathbf{H}^{\mathrm{T}}\mathbf{N}\boldsymbol{b}$ is the rate of production of all genotypes, and $\mathbf{N}\boldsymbol{d}$ is the rate of 'death' for all genotypes. The square matrix $\mathbf{N} = \mathrm{diag}(\boldsymbol{n})$ is the diagonalised composition vector. We multiply the birth-rate and death-rate vectors, $\boldsymbol{b}$ and $\boldsymbol{d}$, by this, but not the production-rate vector, $\boldsymbol{p}$, because birth and death rates are measured on individuals (they are *per capita* rates), whereas production rates are population measures. We can re-write the vector-matrix equation (2.27) in a scalar form defining the dynamical law for the rate of change of i-genotype individuals with respect to time as

$$\dot{n}_i = p_i - n_i d_i = \sum_{j=1}^{|\mathbb{G}|} n_j f_{ji} - n_i d_i = \sum_{j=1}^{|\mathbb{G}|} n_j b_j h_{ji} - n_i d_i, \tag{2.28}$$

where $p_i = \sum_{j=1}^{|\mathbb{G}|} n_j f_{ji} = \sum_{j=1}^{|\mathbb{G}|} n_j b_j h_{ji}$ is just the rate at which i-genotype descendants are being produced following the reproduction of j-genotype ancestors, and $n_i d_i$ is just the rate at which i-genotype individuals are 'dying'. We call this the 'Malthusian selection equation'. By solving the Malthusian selection equation (2.28) we obtain the complete

trajectory of the population through the composition space Ω. The equation represents a system of non-linear ODEs that describe the rate of change of the abundances of genotypes in the population with respect to time.

The utility of re-writing the first term of the Malthusian selection equation (2.28) as $\sum_{j=1}^{|\mathbb{G}|} n_j b_j h_{ji}$ is that it emphasises the role that ancestors play in giving rise to descendants through their reproductive rate, b_j, but also the important role that inheritance plays, h_{ji}, in shaping which descendants are produced. A slight problem with the definition of $h_{ji} = f_{ji}/b_j$ arises when $b_j = 0$, but from a practical perspective we can just treat this as $h_{ji} = 0$. Clearly, if a j-genotype individual does not reproduce then we are not likely to be interested in accounting for the genotypes or phenotypes of its descendants.

In the special case in which reproduction is entirely clonal, the inheritance matrix becomes the identity matrix, $\mathbf{H} = \mathbf{I}$, and the Malthusian selection equation (2.27) simplifies to

$$\dot{\boldsymbol{n}} = \mathbf{N}\boldsymbol{b} - \mathbf{N}\boldsymbol{d} = \mathbf{N}(\boldsymbol{b} - \boldsymbol{d}), \tag{2.29}$$

so that the scalar equation (2.28) simplifies to

$$\dot{n}_i = n_i(b_i - d_i). \tag{2.30}$$

These equations show that when reproduction is clonal, the change in abundance of each genotype is proportional to the difference in the birth and death rates of that type in the population at time t.

2.3.1.1 Population growth

The Malthusian selection equation (2.28) provides an ecological perspective on how the dynamics of natural selection shape the *composition* of the population over time. It is not immediately obvious, however, how the population size as a whole, N, varies through time. Therefore let us now consider the rate of change of the size of the population. Recall that the total population size is given by $N = \sum_{i=1}^{|\mathbb{G}|} n_i = \mathbf{1}^{\mathrm{T}}\boldsymbol{n}$. Let $\dot{N} \equiv dN/dt$ denote the derivative of the population size, N, with respect to time. We have

$$\dot{N} = \frac{d}{dt}\left[\mathbf{1}^{\mathrm{T}}\boldsymbol{n}\right] = \mathbf{1}^{\mathrm{T}}\dot{\boldsymbol{n}}, \tag{2.31}$$

where we have simply taken the summation vector $\mathbf{1}^{\mathrm{T}}$ outside of the derivative operator since it is a vector of constants. Now substituting for $\dot{\boldsymbol{n}}$ from the Malthusian selection equation (2.28) and simplifying using a standard transpose identity, we obtain

$$\begin{aligned}\dot{N} &= \mathbf{1}^{\mathrm{T}}(\mathbf{H}^{\mathrm{T}}\mathbf{N}\boldsymbol{b} - \mathbf{N}\boldsymbol{d}) \\ &= \mathbf{1}^{\mathrm{T}}\mathbf{H}^{\mathrm{T}}\mathbf{N}\boldsymbol{b} - \mathbf{1}^{\mathrm{T}}\mathbf{N}\boldsymbol{d} \\ &= (\mathbf{H}\mathbf{1})^{\mathrm{T}}\mathbf{N}\boldsymbol{b} - \mathbf{1}^{\mathrm{T}}\mathbf{N}\boldsymbol{d}.\end{aligned} \tag{2.32}$$

We can now simplify using the property of the inheritance matrix, $\mathbf{H}$, that the sum over its columns is equal to 1 (see description of equation (2.20)), which implies that $\mathbf{H}\mathbf{1} = \mathbf{1}$. We are left with

$$\begin{aligned}\dot{N} &= \mathbf{1}^{\mathrm{T}}\mathbf{N}\boldsymbol{b} - \mathbf{1}^{\mathrm{T}}\mathbf{N}\boldsymbol{d} \\ &= \mathbf{1}^{\mathrm{T}}\mathbf{N}(\boldsymbol{b} - \boldsymbol{d}) \\ &= \boldsymbol{n}^{\mathrm{T}}(\boldsymbol{b} - \boldsymbol{d}) \\ &= N\boldsymbol{x}^{\mathrm{T}}(\boldsymbol{b} - \boldsymbol{d}),\end{aligned} \tag{2.33}$$

where $\mathbf{N} = \mathrm{diag}(\boldsymbol{n})$ is the diagonalised composition vector, and we have substituted for the individual $\mathbf{1}^{\mathrm{T}}\mathbf{N} = \boldsymbol{n}^{\mathrm{T}}$, followed by $\boldsymbol{n}^{\mathrm{T}} = N\boldsymbol{x}^{\mathrm{T}}$. Now substituting for the definition of the average reproduction rate, $\bar{b} = \boldsymbol{x}^{\mathrm{T}}\boldsymbol{b}$ from equation (2.17), and the average death rate, $\bar{d} = \boldsymbol{x}^{\mathrm{T}}\boldsymbol{d}$ from equation (2.13), we can re-write this equation as

$$\dot{N} = N\sum_{i=1}^{|\mathbb{G}|} x_i(b_i - d_i) = N(\bar{b} - \bar{d}). \tag{2.34}$$

This equation tells us that the rate of change of the population size with respect to time, $\dot{N}$, at any particular instant is simply proportional to the difference between the average birth rate and average death rate of individuals in the population, $\bar{b} - \bar{d}$.

2.3.1.2 Malthusian fitness

As we have mentioned previously, the quantity determining the growth-rate of the overall population has a special role in evolutionary theory. In particular, recall that Kimura

(1958) redefined the Malthusian fitness of a genotype, m_i, to be the net *relative contribution* it makes to the growth-rate of a population[m]. We can see by inspection from equation (2.34) that Kimura's (1958) definition of Malthusian fitness in the context of our population is given by

$$m_i = b_i - d_i, \tag{2.35}$$

which is just the difference between the rate at which i-genotype individuals reproduce and the rate at which they die, d_i. The Malthusian fitness values of every genotype are given by the vector $\boldsymbol{m} = \boldsymbol{b} - \boldsymbol{d}$. Identifying the difference in the rate at which individuals reproduce and die as measure of Malthusian fitness might seem somewhat trivial and/or unsurprising in this context, yet it has a profound effect on how we interpret the action of natural selection on populations.

Moreover, it does not correspond to the definition of Malthusian fitness arising from the Price's (1995) approach that we discussed in Chapter 1. In Chapter 1, we saw that the definition of Malthusian fitness emerging from Price's (1995) analysis is defined naturally by $m_i = \dot{n}_i/n_i$, which is clearly not equal to the definition of fitness Kimura (1958) had in mind i.e. it is generally the case that $\dot{n}_i/n_i \neq b_i - d_i$.

We might ask what the relationship is between the two definitions? Firstly, we can see that the two definitions are equal in the special case in which the inheritance matrix is the identity matrix, $\mathbf{H} = \mathbf{I}$, so that the Malthusian selection equation (2.28) simplifies to equation (2.30), and we have $\dot{n}_i = n_i(b_i - d_i)$, with $\dot{n}_i/n_i = (b_i - d_i)$. Secondly, we can see that the two definitions are related by virtue of the fact that they predict the same population growth-rate. Using Kimura's (1958) definition we have already seen via equation (2.34) that $\dot{N}$ can be written as

$$\dot{N} = \sum_{i=1}^{|\mathbb{G}|} \dot{n}_i = N \sum_{i=1}^{|\mathbb{G}|} x_i(b_i - d_i), \tag{2.36}$$

but we can also use Price's (1995) definition to re-write $\dot{N}$ in the form

$$\dot{N} = \sum_{i=1}^{|\mathbb{G}|} \dot{n}_i = \sum_{i=1}^{|\mathbb{G}|} n_i \frac{\dot{n}_i}{n_i} = N \sum_{i=1}^{|\mathbb{G}|} x_i \frac{\dot{n}_i}{n_i}. \tag{2.37}$$

[m]See Charlesworth (1970) for a description of the difference between Kimura's (1958) definition and the definition of Malthusian fitness given by Fisher (1930).

If both definitions of Malthusian fitness predict the same overall growth-rate for the population, we might question why Kimura's (1958) definition is therefore preferable? The reason is that Malthusian fitness defined by $m_i = b_i - d_i$ is a quantity measurable on an individual (which can be thought of as a phenotypic trait in its own right), and is therefore something under an individual's 'control' that natural selection may act upon. If we were to define $m_i = \dot{n}_i/n_i$ on the other hand, Malthusian fitness would depend on the rates of reproduction and death of other individuals and therefore not be a quantity measurable on an individual, but a quantity measurable on the population. Conceptual issues of a similar nature arise in kin selection theory in discussions about so-called 'neighbour-modulated fitness' and 'inclusive fitness' (Taylor et al., 2007).

We will discuss at the end of this thesis how the Malthusian fitness of an individual is not always such an 'obvious' quantity as $m_i = b_i - d_i$. Combining the Malthusian fitness vector with the composition vector $\boldsymbol{n}$, we can obtain the average Malthusian fitness in the population at time t, which we denote by

$$\bar{m} = \frac{1}{N}\sum_{i=1}^{|\mathbb{G}|} n_i m_i = \sum_{i=1}^{|\mathbb{G}|} x_i m_i = \boldsymbol{m}^{\mathrm{T}}\boldsymbol{x}. \tag{2.38}$$

Since Malthusian fitness is a quantitative trait, measurable in units of $(\text{time})^{-1}$, it is part of the phenotype of an i-genotype individual. Moreover, like all other traits in the genotype-phenotype map, $\mathbf{Z}$, it is not necessarily constant, but may change through time as the environment changes. In some sense Malthusian fitness is the most important trait of all, since it is through fitness that all other traits become 'visible' to selection (Mayr, 1997). That is, if a trait does not affect fitness, it cannot be favoured by natural selection. We will see a formal proof of this when we come to the covariance mathematics of Price (1970) in a later section.

By substituting for the definition of Malthusian fitness given by equation (2.35) it is easy to see that the average Malthusian fitness is equal to the difference between the average rate of reproduction and the average rate of death, $\bar{m} = \bar{b} - \bar{d}$. Hence, returning to the dynamics of population growth, we may re-write equation (2.34) as

$$\dot{N} = N\bar{m}, \tag{2.39}$$

This equation tells us that at any instant in time the population is growing exponentially with rate, $\bar{m}$. Yet since $\bar{m}$ itself is changing through time, the population dynamics

may be very complicated. Importantly, we can see that the Malthusian growth equation (2.1) from population ecology can therefore be obtained as special case of the Malthusian selection equation (2.28) when the Malthusian fitness of individuals is a constant, m, so that $\bar{m} = m$. Indeed, it tells us that the Malthusian selection equation (2.28) leads to a *generalised* version of the Malthusian growth equation (2.1) that we call the 'Malthusian growth-selection equation'.

Since the Malthusian growth equation (2.1) forms the foundation of many more complex and realistic models of growth in population ecology (Box 2.1), it follows that this Malthusian growth-selection equation (2.39) also forms the foundation of various models in population ecology. For instance, we previously showed that by substituting $b = r$ and $d = rN/K$ into the Malthusian growth equation (2.1) that we could arrive at the logistic growth equation (2.2) (Box 2.1). Logistic population growth may therefore also emerge from the Malthusian selection equation (2.28). One of many potential ways this might happen is if the average reproduction rate and death rate of individuals satisfy $\bar{b} = r$ and $\bar{d} = rN/K$, respectively, for all times t. In this case, the population size N would eventually reach its carrying capacity, K, so that the growth dynamics would arrive at a steady-state. Even at steady-state, however, there could be interesting selection dynamics taking place among individuals within the population, because the conditions for logistic growth only specify the average rates of reproduction and death, and say nothing about the variance of these rates in the population. This equation might therefore be useful for studying, for instance, the competitive dynamics of bacteria that grow logistically, but continue to compete when the population reaches stationary phase.

2.3.2 Genotypic perspective

Evolutionary change is usually though of in terms of changes in the mean (and/or variance) of the heritable component of a phenotype (attribute of an entitity *within* the population) or more directly in terms of changes in gene frequencies in a population (Fisher, 1930; Falconer and Mackay, 1995). In population genetics the relevant variables are the *relative* frequencies of different genotypes, and the aim is to describe changes in the relative frequency of genotypes through time (Box 2.2; Crow & Kimura, 1970; Rice, 2004).

Let us therefore now consider the rate of change of the relative composition vector $\boldsymbol{x} = \boldsymbol{n}/N$. Taking the derivative with respect to time of this vector using the chain rule, we obtain

$$\dot{\boldsymbol{x}} = \nabla_{\boldsymbol{n}}[\boldsymbol{x}]\dot{\boldsymbol{n}}, \tag{2.40}$$

where $\nabla_{\boldsymbol{n}}$ denotes the gradient taken with respect to the composition vector $\boldsymbol{n}$ as defined in equation (2.26). The gradient of the relative composition vector, $\nabla_{\boldsymbol{n}}[\boldsymbol{x}] = \nabla_{\boldsymbol{n}}[\boldsymbol{n}/N]$, gives the *Jacobian matrix* of $\boldsymbol{x}$. Since $\boldsymbol{x} = \boldsymbol{n}/N$, we can expand $\nabla_{\boldsymbol{n}}[\boldsymbol{x}]$ using the quotient rule to give

$$\nabla_{\boldsymbol{n}}[\boldsymbol{x}] = \frac{\nabla_{\boldsymbol{n}}[\boldsymbol{n}]N - \boldsymbol{n}\nabla_{\boldsymbol{n}}[N]}{N^2} = \frac{\nabla_{\boldsymbol{n}}[\boldsymbol{n}]}{N} - \frac{\boldsymbol{n}}{N}\frac{\nabla_{\boldsymbol{n}}[N]}{N}. \tag{2.41}$$

The derivative of the composition vector $\boldsymbol{n}$ with respect to itself, is simply the $|\mathbb{G}| \times |\mathbb{G}|$ identity matrix, $\nabla_{\boldsymbol{n}}\boldsymbol{n} = \mathbf{I}$. The gradient of the population size N is given by $\nabla_{\boldsymbol{n}}N = \nabla_{\boldsymbol{n}}(\mathbf{1}^{\mathrm{T}}\boldsymbol{n}) = \mathbf{1}^{\mathrm{T}}\nabla_{\boldsymbol{n}}\boldsymbol{n} = \mathbf{1}^{\mathrm{T}}$. Hence, we have

$$\nabla_{\boldsymbol{n}}[\boldsymbol{x}] = \frac{\mathbf{I}}{N} - \boldsymbol{x}\frac{\mathbf{1}^{\mathrm{T}}}{N}. \tag{2.42}$$

Now substituting $\nabla_{\boldsymbol{n}}[\boldsymbol{x}]$ back into equation (2.40), we obtain

$$\dot{\boldsymbol{x}} = \left(\frac{\mathbf{I}}{N} - \boldsymbol{x}\frac{\mathbf{1}^{\mathrm{T}}}{N}\right)\dot{\boldsymbol{n}} = \frac{\dot{\boldsymbol{n}}}{N} - \boldsymbol{x}\frac{\mathbf{1}^{\mathrm{T}}\dot{\boldsymbol{n}}}{N}. \tag{2.43}$$

We again substitute for $\dot{\boldsymbol{n}}$ from the Malthusian selection equation (2.28) and for $\mathbf{1}^{\mathrm{T}}\dot{\boldsymbol{n}} = N\boldsymbol{x}^{\mathrm{T}}\boldsymbol{m}$ from the Malthusian growth-selection equation (2.39), and simplify, to arrive at

$$\dot{\boldsymbol{x}} = \mathbf{H}^{\mathrm{T}}\mathbf{X}\boldsymbol{b} - \mathbf{X}\boldsymbol{d} - \boldsymbol{x}\boldsymbol{x}^{\mathrm{T}}\boldsymbol{m}. \tag{2.44}$$

where $\mathbf{X} = \mathrm{diag}(\boldsymbol{x})$ is the diagonalised relative composition vector. In scalar notation, the vector-matrix equation (2.44) reads

$$\dot{x}_i = \sum_{j=1}^{|\mathbb{G}|} x_j b_j h_{ji} - x_i d_i - x_i \bar{m}, \tag{2.45}$$

which is remarkably similar to the replicator-mutator equation (2.4), except that the constant mutation rate, q_{ji}, has been replaced by a time-varying inheritance probability, h_{ji}, and we now have an additional term, $x_i d_i$, that accounts for the death of individuals. Thus, we can see that the replicator-mutator equation (2.4) is a special case of the Malthusian selection equation (2.28) when the population undergoes continuous growth (i.e. when the death-rate of individuals, d_i, is zero) and the inheritance matrix is constant (i.e. when there is no sexual reproduction). Indeed, it tells us that the Malthusian selection equation (2.28) leads to a *generalised* version of the replicator-mutator equation (2.4), and by extension the replicator equation (2.3). We therefore refer to equation (2.45) as the 'Malthusian replicator equation'.

One of the key differences between this new equation and the original replicator-mutator equation (2.4) is that the former utilises a time-varying genotype-phenotype map, $\mathbf{Z}$, whereas the latter utilises the assumption that the phenotype of players is represented by a fixed strategy from some strategy set (Maynard Smith, 1982). A consequence of this game-theoretic approach is that the field of replicator dynamics has been slow to incorporate assumptions about the underlying molecular mechanisms of phenotypes (Nowak and Sigmund, 2004). By switching to the use of a time-varying genotype-phenotype map, $\mathbf{Z}$, however, it becomes possible to incorporate more realistic biological assumptions about the individuals represented by a particular model. For instance, one limitation of the fixed strategy approach is that it ignores the problem of correlations between traits, whereas we know that in nature directional selection can act on multiple traits simultaneously leading to constraints in phenotypic evolution (Lande, 1979; Lande and Arnold, 1983). We will study various means to explore the dynamics of natural selection on multiple traits simultaneously in Chapter 3.

2.3.3 Phenotypic perspective

So far we have shown that the Malthusian selection equation (2.28) leads to a simultaneous generalisation of the Malthusian growth equation from population ecology (2.1) (Box 2.1) and the replicator-mutator equation (2.4) from population genetics (Box 2.2). On the face of it, however, the Malthusian selection equation (2.28) seems to say little about the dynamics of *phenotypic* change. This can be considered on two different levels: *i*) an *individual* perspective on change in the values of traits themselves due to phenotypic plasticity; and *ii*) a *population* perspective on change in the summary statistics of traits due to the effects of natural selection on the genotypic and phenotypic composition of the population.

2.3.3.1 Individual-level

Let us first return to the genotype-phenotype map, $\mathbf{Z}$, and explore reasons why it is may not be constant, but instead vary through time. As we have said, change in the phenotypic values expressed by individuals over time can be pictured as a trajectory of the point specified by a column vector of $\mathbf{Z}$ over the space $\mathbb{R}^{|\mathbb{G}|}$. To describe the trajectories of all points corresponding to all $|\mathbb{P}|$ traits, we need an dynamical law for each of them. These dynamical laws are given by the column vectors of derivative of the genotype-phenotype map, $\mathbf{Z}$, with respect to time. Since each phenotypic trait is an explicit function of the composition vector, $\boldsymbol{n}$, and time, t, the total derivative is found, by the chain rule, to be given by

$$\dot{\mathbf{Z}} = \nabla_{\boldsymbol{n}}[\mathbf{Z}]\dot{\boldsymbol{n}} + \partial_t \mathbf{Z}. \tag{2.46}$$

This equation indicates that the dynamical law describing phenotypic change must specify two reasons why the trait values change. Firstly, if a phenotypic trait is dependent on the composition of the population, $\boldsymbol{n}$, then if the composition changes, so too will the trait values[n]. This corresponds to *phenotypic plasticity* in trait expression (Via and Lande, 1985; Stearns, 1989; Miner et al., 2005). Secondly, if a trait is dependent on time, t, the trait values may be functions of the values held by the ancestors that gave rise to them in the past. This corresponds to a non-genetic mechanism of inheritance, that is sometimes called 'ecological inheritance' (Danchin and Wagner, 2010; Danchin et al., 2011).

Phenotypic plasticity

Plasticity might arise, for instance, because of a response to some ecological variable such as the population size, N. This would correspond to density-dependent expression of traits. These kind of traits are expressed across a wide range of taxa (Arendt, 1997), but one of the most striking instances of a density-dependent trait derives from the study of the locust *Schistocerca gregaria* (Gotham and Song, 2013). When the locust population is at low density, locust nymphs exhibit cryptic colouring patterns and shy behaviour. At high population densities, however, the grasshoppers undergo a dramatic transformation, exhibiting conspicuous colour patterns and swarming behaviours. Alternatively, plasticity might arise because of social interactions with others, which depends on the composition of the population, $\boldsymbol{n}$. Phenotypically plastic traits are common in social signalling in many organisms (Maynard Smith and Harper, 2003). A good example is the expression

[n]Note that when phenotypes are constant through time they closely resemble the notion of a fixed 'strategy' from evolutionary game theory (Maynard Smith, 1982).

of conspicuous colour pigments in birds, which are driven by differences in diets of birds when in the presence of mates and/or conspecific competitors (Price, 2006). Healthy birds can display their health through a conspicuous signal to potential mates, whereas less healthy mates cannot afford to do so. Importantly, whilst social interactions can be viewed as just another part of the environment an individual experiences, the social environment is different because it can represent a *heritable* component of the environment. This appreciation has led to a new field of study in quantitative genetics known as 'indirect genetic effects' (Moore et al., 1997; Wolf et al., 1998; Bijma, 2014).

Ecological inheritance

Ecological inheritance might play a role, for instance, if some of the traits represent a kind of 'extended phenotype' that can be passed vertically between generations (Dawkins, 1982; Laland et al., 2001; Odling-Smee et al., 2003; Danchin et al., 2011). The best known example of this kind of trait is a beaver's dam[o]. As Dawkins (2004) says, a 'beaver's dam is as much an adaptation as the beaver's tail.' A key difference, however, is that a beaver's tail ceases to exist when the beaver dies, but the beaver's dam may remain for many generations, benefiting relatives in the future (probably even more so than the founding beaver(s) that does all the work). Thus, these kind of traits can have a heritable component in the genetic sense, because they can lead to indirect fitness benefits to relatives in the future.

2.3.3.2 Population-level

If the traits in the genotype-phenotype map, $\mathbf{Z}$, are selectively significant, we might expect their population averages, given by the $|\mathbb{P}| \times 1$ vector $\bar{\boldsymbol{z}}$, to change over time due owing to the impact of *natural selection*. The population average trait values depend on the trait values in the genotype-phenotype map, $\mathbf{Z}$, and the relative composition, $\boldsymbol{x}$. Taking the derivative with respect to time t, using the product rule, we obtain

$$\dot{\bar{\boldsymbol{z}}} = \mathbf{Z}^{\mathrm{T}}\dot{\boldsymbol{x}} + \dot{\mathbf{Z}}^{\mathrm{T}}\boldsymbol{x}, \tag{2.47}$$

where $\dot{\boldsymbol{x}}$ is the rate of change of the vector relative genotype frequencies with respect to time, given by the Malthusian replicator equation (2.45), and $\dot{\mathbf{Z}}$ is the derivative of the genotype-phenotype map with respect to time given by equation (2.46). This equation

[o]In addition to being an extended phenotype, a beaver's dam is also an example of an adaptive trait based on Lamarckian inheritance, since it is passed on each generation with the characteristics acquired by the previous generation (Jablonka et al., 1998).

doesn't yield much insight into the action of natural selection in our population. Yet, by substituting for $\dot{\boldsymbol{x}}$ from the Malthusian replicator equation (2.45), and by performing some algebraic manipulation, we show in Box 2.6, that equation (2.47) can be re-written as

$$\dot{\bar{\boldsymbol{z}}} = \mathbf{Z}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m} + (\Delta\mathbf{Z})^{\mathrm{T}}\mathbf{X}\boldsymbol{b} + \dot{\mathbf{Z}}^{\mathrm{T}}\boldsymbol{x}, \tag{2.48}$$

where $\Delta\mathbf{Z}$ is the difference between the expected trait values in descendants and their ancestors, and $\dot{\mathbf{Z}}$ is the derivative of the genotype-phenotype map with respect to time, from equation (2.46) that we discussed in the last section. In fact, this equation is now written in a similar form to the Price equation (2.5) (Box 2.3; Price, 1970; 1972a), but the matrix notation we have used obscures its similarity to Price's (1970; 1972a) original work. Switching to the more traditional 'moment' notation Price (1970, 1972a) used, which corresponds to the notation that we introduced in Box 2.4, equation (2.48) can be re-written as

$$\begin{bmatrix} \dot{\mathrm{E}}_{i\in\mathbb{G}}(z_{i1}) \\ \vdots \\ \dot{\mathrm{E}}_{i\in\mathbb{G}}(z_{i|\mathbb{P}|}) \end{bmatrix} = \begin{bmatrix} \mathrm{Cov}_{i\in\mathbb{G}}(z_{i1}, m_i) \\ \vdots \\ \mathrm{Cov}_{i\in\mathbb{G}}(z_{i|\mathbb{P}|}, m_i) \end{bmatrix} + \begin{bmatrix} \mathrm{E}_{i\in\mathbb{G}}(b_i\Delta z_{i1}) \\ \vdots \\ \mathrm{E}_{i\in\mathbb{G}}(b_i\Delta z_{i|\mathbb{P}|}) \end{bmatrix} + \begin{bmatrix} \mathrm{E}_{i\in\mathbb{G}}(\dot{z}_{i1}) \\ \vdots \\ \mathrm{E}_{i\in\mathbb{G}}(\dot{z}_{i|\mathbb{P}|}) \end{bmatrix}. \tag{2.49}$$

Like Price's (1970) original equation (2.5), this equation separates the total change in the average trait values in the population, $\dot{\bar{\boldsymbol{z}}}$, into separate components that we may interpret as resulting from distinct causal processes. Whilst the Price equation describes change over any arbitrary period of discrete time, however, this equation describes the total *instantaneous* rate of change in average trait values. We therefore refer to this equation as the 'Malthusian Price equation'.

Box 2.6 | Derivation of a Malthusian form of the Price equation

We start by taking the derivative with respect to time of the vector of average trait values, $\boldsymbol{z}$, using the product rule, to obtain

$$\dot{\bar{\boldsymbol{z}}} = \mathbf{Z}^{\mathrm{T}}\dot{\boldsymbol{x}} + \dot{\mathbf{Z}}^{\mathrm{T}}\boldsymbol{x}. \tag{2.50}$$

Next, substituting for $\dot{\boldsymbol{x}}$ from the Malthusian replicator equation (2.45), and simplifying using a standard transpose identity, we arrive at

$$\begin{aligned}\dot{\bar{\boldsymbol{z}}} &= \mathbf{Z}^{\mathrm{T}}\left(\mathbf{H}^{\mathrm{T}}\mathbf{X}\boldsymbol{b} - \mathbf{X}\boldsymbol{d} - \boldsymbol{x}\boldsymbol{x}^{\mathrm{T}}\boldsymbol{m}\right) + \dot{\mathbf{Z}}^{\mathrm{T}}\boldsymbol{x} \\ &= \mathbf{Z}^{\mathrm{T}}\mathbf{H}^{\mathrm{T}}\mathbf{X}\boldsymbol{b} - \mathbf{Z}^{\mathrm{T}}\mathbf{X}\boldsymbol{d} - \mathbf{Z}^{\mathrm{T}}\boldsymbol{x}\boldsymbol{x}^{\mathrm{T}}\boldsymbol{m} + \dot{\mathbf{Z}}^{\mathrm{T}}\boldsymbol{x} \\ &= (\mathbf{H}\mathbf{Z})^{\mathrm{T}}\mathbf{X}\boldsymbol{b} - \mathbf{Z}^{\mathrm{T}}\mathbf{X}\boldsymbol{d} - \mathbf{Z}^{\mathrm{T}}\boldsymbol{x}\boldsymbol{x}^{\mathrm{T}}\boldsymbol{m} + \dot{\mathbf{Z}}^{\mathrm{T}}\boldsymbol{x}.\end{aligned} \tag{2.51}$$

In the first term on the RHS we now substitute for the definition of the expected trait values in descendants, $\mathbf{Z}' = \mathbf{H}\mathbf{Z}$, from equation (2.22), to obtain

$$\dot{\bar{\boldsymbol{z}}} = (\mathbf{Z}')^{\mathrm{T}}\mathbf{X}\boldsymbol{b} - \mathbf{Z}^{\mathrm{T}}\mathbf{X}\boldsymbol{d} - \mathbf{Z}^{\mathrm{T}}\boldsymbol{x}\boldsymbol{x}^{\mathrm{T}}\boldsymbol{m} + \dot{\mathbf{Z}}^{\mathrm{T}}\boldsymbol{x}. \tag{2.52}$$

We then simultaneously subtract and add (thereby not altering the equality) the expression $\mathbf{Z}^{\mathrm{T}}\mathbf{X}\boldsymbol{b}$ after the first term on the RHS, and rearrange, to get

$$\begin{aligned}\dot{\bar{\boldsymbol{z}}} &= (\mathbf{Z}')^{\mathrm{T}}\mathbf{X}\boldsymbol{b} - \mathbf{Z}^{\mathrm{T}}\mathbf{X}\boldsymbol{b} + \mathbf{Z}^{\mathrm{T}}\mathbf{X}\boldsymbol{b} - \mathbf{Z}^{\mathrm{T}}\mathbf{X}\boldsymbol{d} - \mathbf{Z}^{\mathrm{T}}\boldsymbol{x}\boldsymbol{x}^{\mathrm{T}}\boldsymbol{m} + \dot{\mathbf{Z}}^{\mathrm{T}}\boldsymbol{x} \\ &= (\mathbf{Z}' - \mathbf{Z})^{\mathrm{T}}\mathbf{X}\boldsymbol{b} + \mathbf{Z}^{\mathrm{T}}\mathbf{X}(\boldsymbol{b} - \boldsymbol{d}) - \mathbf{Z}^{\mathrm{T}}\boldsymbol{x}\boldsymbol{x}^{\mathrm{T}}\boldsymbol{m} + \dot{\mathbf{Z}}^{\mathrm{T}}\boldsymbol{x}.\end{aligned} \tag{2.53}$$

Now substituting for the definition of the difference between the expected trait values in descendants and their ancestors, $\Delta\mathbf{Z} = \mathbf{Z}' - \mathbf{Z}$, from (2.23), and the definition of Malthusian fitness, $\boldsymbol{m} = \boldsymbol{b} - \boldsymbol{d}$, from equation (2.35), and simplifying, we have

$$\begin{aligned}\dot{\bar{\boldsymbol{z}}} &= (\Delta\mathbf{Z})^{\mathrm{T}}\mathbf{X}\boldsymbol{b} + \mathbf{Z}^{\mathrm{T}}\mathbf{X}\boldsymbol{m} - \mathbf{Z}^{\mathrm{T}}\boldsymbol{x}\boldsymbol{x}^{\mathrm{T}}\boldsymbol{m} + \dot{\mathbf{Z}}^{\mathrm{T}}\boldsymbol{x} \\ &= (\Delta\mathbf{Z})^{\mathrm{T}}\mathbf{X}\boldsymbol{b} + \mathbf{Z}^{\mathrm{T}}\left(\mathbf{X} - \boldsymbol{x}\boldsymbol{x}^{\mathrm{T}}\right)\boldsymbol{m} + \dot{\mathbf{Z}}^{\mathrm{T}}\boldsymbol{x}.\end{aligned} \tag{2.54}$$

Finally, we notice that the second term contains the expression for the covariance operator $\boldsymbol{\Sigma} = \mathbf{X} - \boldsymbol{x}\boldsymbol{x}^{\mathrm{T}}$ described by equation (2.9) from Box 2.4. After making the substitution and reordering the terms for convenience, we obtain

$$\dot{\bar{\boldsymbol{z}}} = \mathbf{Z}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m} + (\Delta\mathbf{Z})^{\mathrm{T}}\mathbf{X}\boldsymbol{b} + \dot{\mathbf{Z}}^{\mathrm{T}}\boldsymbol{x}. \tag{2.55}$$

This gives equation (2.48) in the main text.

The first term describes a vector of the statistical associations, $\mathrm{Cov}_{i\in\mathbb{G}}(z_{ik}, m_i)$, between the trait values held by individuals, z_{ik}, and their Malthusian fitness, m_i. Indeed, it is a Malthusian analogue of what is called the vector of 'directional selection differentials' in evolutionary genetics (Lush, 1937; Lande, 1979; Lande and Arnold, 1983; Falconer and Mackay, 1995)[p]. By analogy with the term $\mathrm{Cov}_{i\in\mathbb{I}}(z_i, w_i)$ from the Price equation (2.5)

[p]This vector will appear again when we explore the dynamics of the evolutionary response to natural selection in Chapter 3.

(Box 2.3; Price, 1970; 1972a), we can interpret each entry of this vector as pertaining to the component of change in average trait values in the population due to *natural selection* (Frank, 1995; Gardner, 2008). For example, if a particular trait k represents height, and taller individuals have a higher rate of reproduction and lower rate of death, on average, then we will have $\mathrm{Cov}_{i\in\mathbb{G}}(z_{ik}, m_i) > 0$, and we interpret this as positive selection on height.

The second term from the Malthusian Price equation (2.49) describes a vector of expected values of the form $\mathrm{E}_{i\in\mathbb{G}}(b_i\Delta z_{ik})$. These expected values represent the average differences between the trait values held by descendants, z'_{ik}, and the ancestors that gave rise to them, z_{ik}, weighted by the reproduction rate of the ancestors, b_i. By analogy with the term $\mathrm{E}_{i\in\mathbb{G}}(w_i\Delta z_i)$ from the Price equation (2.5), we may interpret this term as the component of change in average trait values due to *transmission fidelity* (Frank, 1995; Gardner, 2008). For example, if a particular trait k represents height, and the height of descendants and the ancestors that give rise to them is always the same, then we will have $\mathrm{E}_{i\in\mathbb{G}}(b_i\Delta z_{ik}) = 0$, and we interpret this zero transmission bias. If, however, descendants differ from the ancestors that gave rise to them due to segregation and recombination, mutation, or systematic environmental changes, this term will be non-zero (positive if descendants are taller on average, negative if they are shorter), and we say that there is a degree of transmission bias for traits.

Before moving on to the third term of the Malthusian Price equation (2.49), it is worth mentioning some important differences between the second term here, and that from the Price equation (2.5) (Box 2.3; Price, 1970; 1972a). Firstly, z'_{ik} in our framework and z'_i from the original Price equation (2.5) represent different currencies. The value z'_{ik} described by (2.21) in this thesis represents an *expected* trait value in descendants, assuming that descendants *will be* produced by ancestors at the next instant in time. It is therefore a prediction or *prospective* measure of a phenotypic trait. In contrast, z'_i, from the Price equation (2.5) (Box 2.3; Price, 1970; 1972a) represents an *average* trait value in descendants that were produced at some point between time t and $t + \Delta t$. It is therefore a *retrospective* measure of a phenotypic trait. This links closely with another important difference, which is that the quantity $b_i\Delta z_{ik}$ in our framework is a reproduction-rate-weighted difference in trait values, not a Malthusian-fitness-weighted difference, $m_i\Delta z_{ik}$, as we might have predicted by comparison with the term $w_i\Delta z_i$ from the Price equation (2.5) (Box 2.3; Price, 1970; 1972a). This difference arises because Darwinian fitness, w_i, which is synonymous with the Price equation (2.5) (indeed, defined by it (Price, 1995)), cannot distinguish between births, deaths, or anything else. It can only see the 'end product' after a discrete period of time has elapsed; it is a retrospective view of fitness.

The particular form of Malthusian fitness, m_i, that we use here on the other hand, is explicitly defined in terms of rates of birth and death (as given by equation (2.35)). It is a prospective, predictive measure of fitness. The reason the term is reproductive-rate weighted therefore is because it is strictly only production of descendants that can be measured in terms of transmission fidelity. Deaths, by definition, do not contribute to the transmission of traits between ancestors and their descendants.

The third and final term from the Malthusian Price equation (2.49) describes a vector of expected values of the form, $\mathrm{E}_{i\in\mathbb{G}}(\dot{z}_{ik})$. These expected values represent the the expected change in the values of the genotype-phenotype map, $\mathbf{Z}$, with respect to time. The third term in our equation has no analogue in the original Price equation (2.5). Since we know that the genotype-phenotype map, $\mathbf{Z}$, changes with respect to time from equation (2.46), however, it is easy to see that this term accounts for the component of change due to phenotypic plasticity and ecological inheritance we discussed in the previous section. To understand why this term is absent in the original Price equation (2.5), it is important to realise that the Price equation (2.5) in its general form is not strictly a model, but more of an identity that allows one to map between ancestral and descendant populations (Frank, 1995). Thus, the original Price equation (2.5) only 'sees' the differences between ancestors and their descendants and not the underlying *causes* of these differences.

For instance, suppose we return to the *S. gregaria* locust population example we described previously (Gotham and Song, 2013). If we use the Price equation (2.5) (Box 2.3; Price, 1970; 1972a) to census the colour patterns in locusts when the locust population is at low-density, and then again some time later when the population is at high-density, the Price equation (2.5) (Box 2.3; Price, 1970; 1972a) would identify a fidelity of transmission 'bias' in the transmission of the trait due to changes in the colouration of individuals in the population. In contrast, if we were to model the locust population using the framework described here, we would identify colouration as a plastic, density-dependent trait. Hence, the Malthusian Price equation (2.49) would not identify a fidelity of transmission bias, but instead an average change in the state of the genotype-phenotype map in the population.

2.4 Concluding remarks

To summarise, in this chapter we have derived a general dynamical systems framework that unifies the core principles of evolutionary theory (Lewontin, 1970; Godfrey-Smith, 2007), population ecology (Maynard Smith, 1978a; Singh and Uyenoyama, 2004) and population genetics (Fisher, 1930; Crow and Kimura, 1970), and better integrates them with frameworks for the description of phenotypic change, via a form of Price's (1970;

1972a) covariance matheamtics. The framework is not completely general. In particular, it neglects important sources of variation, such as environmental noise and genetic drift (Kimura, 1985; Lande, 1976), sources of non-randomness in interactions among individuals, such as spatial structure (Nowak and May, 1992), and sources of differences between between individuals with the same genotype, such as age-structure (Charlesworth, 1994). Yet it generalises important equations in population ecology (Maynard Smith, 1978a; Turchin, 2001), population genetics and evolutionary dynamics (Crow and Kimura, 1970; Schuster and Sigmund, 1983; Page and Nowak, 2002; Nowak and Sigmund, 2004; Nowak, 2006), and can describe the dynamics of natural selection in populations characterised by processes that have been thought of as difficult to capture in a general model, including arbitrary modes of reproduction among individuals (Ariew and Lewontin, 2004), phenotypic plasticity (Pigliucci, 2005), and inclusive inheritance mechanisms (Danchin and Wagner, 2010; Danchin et al., 2011). Moreover, we have shown that the Malthusian selection equation (2.28) provides three complementary perspectives from which the dynamics of natural selection can be described: *i*) *ecological*—in terms of changes in the growth of the population as a whole and the abundance of particular genotypes of individuals; *ii*) *genotypic*—in terms of changes in the relative frequency of genotypes in the population; *iii*) *phenotypic*—in terms of changes in the summary statistics of phenotypic traits in the population. Hence, in this chapter we have laid the foundations for a general dynamical systems theory of natural selection that we will use in the remaining chapters in this thesis as a stepping stone—via the covariance mathematics of Price (1970, 1972a)—for unifying connections to other areas of evolutionary theory.

Chapter 3

The dynamics of the evolutionary response to natural selection

3.1 Introduction

As Fisher (1930) famously wrote, 'natural selection is not evolution.' Natural selection can drive changes in the composition of phenotypes in a population regardless of whether or not the traits it acts on are heritable. The *evolutionary response* to natural selection, however, corresponds to the portion of the overall change in phenotypes that has a heritable basis (Fisher, 1930). Importantly, it is this portion of change alone that is able to explain the appearance of design in the natural world (Gardner, 2009).

The study of the evolutionary response to natural selection is the cornerstone of the theoretical framework of evolutionary genetics. This framework was borne out of the integration of Mendelian genetics with Darwin's (1859) theory of evolution by natural selection, in what came to be known as the 'modern synthesis' of evolutionary theory (Huxley, 1942). The key assumption of the modern synthesis is that the underlying mechanisms of inheritance are particulate and genetic. This idea followed from the discovery of Mendelian genetics and subsequent work by Fisher (1930), who showed that the phenotypic variability in populations on which natural selection acts can be partitioned into contributions coming from the environment and from the small additive effects of a large number of genetic factors.

Broadly speaking, contemporary evolutionary genetics can be subdivided into population genetics, in which the evolutionary response to natural selection concerns changes in genotype and gene frequencies brought about natural selection (Crow and Kimura, 1970), and quantitative genetics, in which the evolutionary response to natural selection concerns evolutionary changes in the heritable component of continuously varying phenotype

traits (like height or weight, for example) in a population (Falconer and Mackay, 1995). Whereas contemporary population genetic theory is a bottom-up approach to evolutionary theory (genotype → phenotype), contemporary quantitative genetics is more of a top-down approach (phenotype → genotype). It is somewhat of a pragmatic framework in evolutionary theory, which recognises the important role that genes play in inheritance and in 'causing' phenotypes to appear the way they do, but acknowledges that the true functional relationship between genotype and phenotype is unlikely to ever be truly knowable. As Steppan et al. (2002) say, 'quantitative genetics is useful for intermediate cases where genetics matters, but where genetic details do not.'

The central principle of quantitative genetics is that the evolutionary response to natural selection can be partitioned into two causal components (Falconer and Mackay, 1995): *i*) *heritabilities*, which statistically summarise the relationship between genes and phenotypes; and *ii*) *selection differentials*, which statistically summarise the relationship between phenotypic traits and fitness. The heritable portion of a phenotype is defined by an individual's 'genetic value', which Fisher (1918) defined as a quantity indicating the likely value of an individual's genes to its future descendants (who it is assumed inherit copies of those genes and their associated causal effects). The 'heritability' for a trait is then a measure of the fraction of the total phenotypic variance in a population that is attributable to variance in genetic values (Fisher, 1918; Falconer and Mackay, 1995). Selection differentials measure the extent to which traits are correlated with survival and reproduction, and are equivalent to the covariance components of the Price equation (2.5) (Box 2.3, Chapter 2; Price, 1970; 1972a).

With these definitions in place, the evolutionary response to natural selection for a single phenotypic trait in a population is then predicted by the well-known 'breeder's equation' (3.1) (Box 3.1; Lush, 1937; Falconer, 1995). When selection acts on multiple traits simultaneously, the evolutionary response is predicted by a multivariate generalisation of the breeder's equation (3.1) called the 'multivariate breeder's equation' (3.2), or sometimes 'Lande's equation' (Box 3.1; Lande, 1979; Lande & Arnold, 1983). The multivariate breeder's equation (3.2) formalises the idea that the evolutionary response to natural selection for traits can be affected not only by *direct* selection on a particular focal trait, but also by *indirect* selection on other traits with which the focal trait is correlated. Such indirect fitness effects can be 'removed' from the analysis by means of the directional selection gradient, $\boldsymbol{\beta}_{\omega z}$, which provides a measurement of directional selection on each trait when holding the effects of all other traits constant. The multivariate breeder's equation (3.2) also formalises the idea, through the matrix $\mathbf{G}$, that genetic correlations arising from phenomena such as epistasis (Hermisson et al., 2003; Jones et al., 2012),

pleiotropy (Turelli, 1985), and linkage disequilibrium (Lynch et al., 1998) in the genetic architectures of individuals can constrain the direction and speed of adaptive evolutionary change (Arnold, 1992; Pigliucci, 2006).

Box 3.1 | The evolutionary response to natural selection

At the heart of quantitative genetics is the 'breeder's equation' or 'univariate breeder's equation' (Lush, 1937; Falconer and Mackay, 1995), which describes changes in the average value of some trait in a population after selection on that trait has been applied. Consider an ancestral population at some time t and a population of descendants at some time $t' = t + \Delta t$. Each ancestral individual is indexed by $i \in \mathbb{I}$, where $\mathbb{I}$ is the index set of ancestors. Let z_i denote the trait value associated with the ith ancestor, w_i its absolute fitness as measured by the number of descendants it leaves in the next generation, and $\Delta z_i = z_i' - z_i$ the discrepancy between the average trait value held by its descendants and itself. These definitions are the same as those for the Price equation (2.5) (Box 2.3, Chapter 2; Price, 1970; Price, 1972a). The breeder's equation, however, is given by

$$\Delta \bar{z} = h^2 s_{z\omega} = \mathrm{Var}_{i\in\mathbb{I}}(a_i)\beta_{\omega z} = h^2 \mathrm{Var}_{i\in\mathbb{I}}(z_i)\beta_{\omega z}, \tag{3.1}$$

where $\Delta \bar{z} = \bar{z}' - \bar{z}$ is the 'evolutionary response to natural selection', $h^2 = \mathrm{Var}_{i\in\mathbb{I}}(a_i)/\mathrm{Var}_{i\in\mathbb{I}}(z_i)$, is the 'narrow-sense heritability' of the trait (Fisher, 1918), $s_{z\omega} = \mathrm{Cov}_{i\in\mathbb{I}}(z_i, \omega_i)$ is the 'selection differential', which is measured as the covariance between the trait value and *relative* fitness[a].
As confirmation that the breeder's equation (3.1) describes not only natural selection but its evolutionary consequences, we can see that it shows that if there is no heritability, so that $h^2 = 0$, or no phenotypic variation, so that $\mathrm{Var}_{i\in\mathbb{I}}(z_i) = 0$, then no amount of selection, as measured by $\beta_{\omega z}$, can drive an evolutionary response to natural selection (Lewontin, 1970; Godfrey-Smith, 2007). As Frank (1997) has pointed out, however, strictly speaking, the breeder's equation (3.1) concerns only a *partial* change in the average trait values due to natural selection, and should therefore not really be denoted by $\Delta \bar{z}$, which is the *total* change in average trait values.

Although the univariate breeder's equation (3.1) provides a conceptually elegant way to think about the evolutionary response to natural selection, it ignores the fact that natural selection often acts, directly or indirectly, on multiple traits simultaneously. When multiple traits are under consideration, the multivariate breeder's equation, derived by Lande (1979); Lande and Arnold (1983), is given by

$$\Delta \bar{\boldsymbol{z}} = \mathbf{G}\mathbf{P}^{-1}\boldsymbol{s}_{z\omega} = \mathbf{G}\boldsymbol{\beta}_{\omega z} = \boldsymbol{\beta}_{az}\mathbf{P}\boldsymbol{\beta}_{\omega z}, \tag{3.2}$$

where $\Delta \bar{\boldsymbol{z}} = \bar{\boldsymbol{z}}' - \bar{\boldsymbol{z}}$ is multivariate response to selection for each of a set of correlated traits, $\mathbf{G}$ is a square symmetric (additive) genetic variance-covariance matrix often called simply the '$\mathbf{G}$-matrix' (Steppan et al., 2002; Arnold et al., 2008), containing

the genetic variance for each trait along its main diagonal and the genetic covariances between traits in off-diagonal entries, $\mathbf{P}^{-1}$ is the inverse of a square symmetric phenotypic variance-covariance matrix, containing the total phenotypic variance for each trait along its main diagonal and the phenotypic covariances between traits in off-diagonal entries, $\boldsymbol{s}_{z\omega}$ is a vector containing the selection differentials for each trait, and $\boldsymbol{\beta}_{\omega z} = \mathbf{P}^{-1}\boldsymbol{s}_{z\omega}$, defines what is called the 'directional selection gradient' (Steppan et al., 2002; Arnold et al., 2008). Note that the product $\mathbf{GP}^{-1}$ is the multivariate equivalent to Fisher's (1918) definition of narrow-sense heritability, h^2.

[a]Recall from Chapter 1 that relative fitness, often denoted by the Greek letter ω is defined to be equal to the absolute fitness of an individual, w_i, divided by the average population fitness, $\bar{w}$, to give $\omega_i = w_i/\bar{w}$

The dynamics of the evolutionary response to selection can be visualised using an 'adaptive landscape' (Wright, 1932; Simpson, 1944; Phillips and Arnold, 1989; Arnold et al., 2001). The first adaptive landscape was conceived of by Wright (1932) in a population genetic context as a fitness landscape of gene frequencies. A phenotypic version of the adaptive landscape was then introduced in a quantitative genetic context by Simpson (1944) (Fig. 3.1). Simpson (1944) thought of a population as being represented as a point, $(\bar{\boldsymbol{z}}, \bar{w})$, on a high-dimensional surface of average phenotypic values, $\bar{\boldsymbol{z}}$, and, average fitness, $\bar{w}$. Lande (1979) and Lande and Arnold (1983) later formalised the relationship between this type of adaptive landscape and the multivariate breeder's equation (3.2) by showing that the evolutionary response to natural selection can be thought of as a hill-climbing optimisation process guided by the directional selection gradient $\boldsymbol{\beta}_{\omega z}$. Finally, Schluter (1996) clarified the role of the matrix $\mathbf{G}$ on the adaptive landscape by showing that the leading eigenvector of $\mathbf{G}$ provides an indication of the 'genetic line of least resistance' for a population—as measured by the direction in which there is greatest additive genetic variance (Arnold et al., 2008).

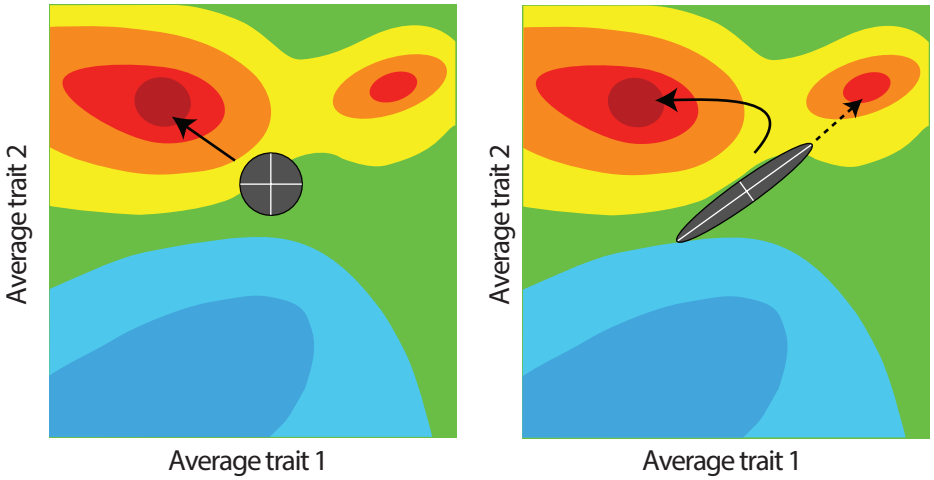


Figure 3.1: Simpson's (1944) phenotypic adaptive landscape. The relationship between Simpson's (1944) phenotypic adaptive landscape and the multivariate breeder's equation (3.2) (Lande, 1979; Lande and Arnold, 1983) is shown as follows: the vector of average phenotypic trait values, $\bar{\boldsymbol{z}}$, defines the location of the population on the horizontal axes (here represented by the centre of the grey ellipse), the average fitness, $\bar{w}$, defines the elevation of the population on the vertical axis (here represented by the contour map), the slope of the surface at that location and the direction of steepest ascent is given by the directional selection gradient, $\boldsymbol{\beta}_{z\omega}$, and the matrix $\mathbf{G}$ is represented by an ellipse[a] on the surface depicting direction in which there is greatest additive genetic variance—the 'genetic line of least resistance' (Schluter, 1996; Arnold et al., 2008). The evolutionary response to natural selection can be pictured as a trajectory of the population over time towards adaptive peaks on the surface (Phillips and Arnold, 1989; Arnold et al., 2001). On the left a population with genetic variance in two genetically *un*correlated traits is shown. Theory predicts that this population will traverse the adaptive landscape in the direction of the steepest ascent (black arrow), towards the global optimum (dark red peak). On the right a population with genetic variance in two genetically correlated traits is shown. This population has a dominant genetic line of least resistance corresponding to the line $\bar{z}_1 = \bar{z}_2$. Theory predicts that this population will preferentially move along the genetic line of least resistance (dashed arrow). This may lead it towards the local optimum (lighter red peak). If selection is strong enough, it may still go toward the global optimum, but it will a traverse a different longer trajectory (black arrow) than that shown in the landscape on the left. Adapted from Steppan et al. (2002).

The multivariate breeder's equation (3.2) and the adaptive landscape (Fig. 3.1) seem to provide an intuitive picture of the dynamics of the evolutionary response to natural selection, but in recent years both of these pillars of quantitative genetic theory have been criticised. Many of the concerns raised relate in some way to issues of dynamics. Much like the Price equation (2.5) (Box 2.3, Chapter 2; Price, 1970; 1972a), the problem is that both the univariate and multivariate breeder's equations (3.1) and (3.2) are 'dynamically insufficient', meaning that they can only be iterated over a single generation of change and therefore only provide a short-term perspective on the dynamics of the evolutionary response to natural selection (Frank, 1995). The criticisms arise because a short-term perspective is often not enough; many of the key quantities in quantitative genetics are liable to change over time rendering short-term predictions of limited use.

Narrow-sense heritability, h^2, and the matrix $\mathbf{G}$, for instance, are widely studied in the context of the evolutionary response to natural selection and the study of genetic constraints, but are valid measures only at the point in time in which they calculated (Steppan et al., 2002; Arnold et al., 2008). They cannot, therefore, be used to determine the likely constraints on the long-term evolutionary trajectories of populations that many evolutionary biologists would like to understand. As Pigliucci (2006) has argued, 'we do not have a theory of how $\mathbf{G}$ changes during long-term evolution, though we know that it does change... developing such theory has been an elusive goal of theoretical evolutionary biology for a long time, but at the moment at least there is no sign of anybody coming even close to it.' Even when narrow-sense heritability, h^2, and the matrix $\mathbf{G}$ are predicted to be relatively stable over time, there are many reasons why the adaptive landscape may not be.

The adaptive landscape (Fig. 3.1) is meant to represent the selective components of the environment in which a population evolves, but the population itself is *part of* that selective environment (Gillespie, 1994). As Nowak and Sigmund (2004) have said, the portrayal of evolutionary change on an adaptive landscape is often misleading, since it suggests 'some solid ground over which the population moves.' In many systems, evolutionary equilibrium points may not exist since peaks on the adaptive landscape might continually move as the population approaches them (Steppan et al., 2002; Nowak and Sigmund, 2004; Arnold et al., 2008). On this point Mustonen and Lässig (2009) have argued that although the 'static' adaptive landscape metaphor may be unhelpful in such 'non-equilibrium' cases, an 'adaptive seascape' might be.

In principle, these types of criticisms would not detract too much from the utility of quantitative genetics in evolutionary theory, if we could develop a better understanding of how the adaptive landscape and $\mathbf{G}$ matrix change through time. Indeed, a growing

number of theorists have turned to using comparative empirical approaches (Steppan et al., 2002; Calsbeek and Goodnight, 2009; Johansson et al., 2012; Björklund et al., 2013) or simulations studies (Reeve, 2000; Jones et al., 2003, 2004; Revell, 2007; Jones et al., 2012, 2014) to make progress on these issues. As Arnold et al. (2008) have said, however, the big challenge is that 'although the importance of these issues is both apparent and widely acknowledged, we have so far been unable to settle them with the analytical machinery of algebra and calculus.'

In this chapter, we address these challenges by developing the concepts and underlying mathematical expressions needed to unify the dynamical systems theory presented in Chapter 2 with the framework of quantitative genetics. We begin by exploring the core principles of evolutionary genetics and develop a theory of *population-weighted* least-squares that can be used in conjunction with the Malthusian selection equation (2.28) from Chapter 2 to obtain analogues of many of the standard mathematical expressions in quantitative genetics, including genetic values, heritability measures, selection differentials, and directional selection gradients. We then use these expressions in combination with the Malthusian Price equation (2.48) from Chapter 2 to study the dynamics of the evolutionary response to natural selection. We present Malthusian analogues of several important results in quantitative genetics, including Robertson's (1966) secondary theorem of natural selection, Fisher's (1930) fundamental theorem of natural selection, and several alternative perspectives on the multivariate breeder's equation (3.2) (Lande, 1979; Lande and Arnold, 1983) and Simpson's (1944) adaptive landscape: *i*) based on a '*phenotypic* version' of a 'Malthusian directional selection gradient'; *ii*) based on what we call a '*genic* version' of a 'Malthusian directional selection gradient'; and *iii*) based on a what we call a '*genetical* version' of a 'Malthusian directional selection gradient'.

3.2 The principles of evolutionary genetics

What is the relationship between an individual's genotype and its phenotype or the relationship between its phenotype and ability to survive and reproduce? These are key questions in any evolutionary analysis. In this section, our goal is to revisit the population we studied in Chapter 2 to investigate these questions using the central principles of evolutionary genetics (Fisher, 1930; Crow and Kimura, 1970; Falconer and Mackay, 1995). We start by deriving a theoretical toolkit with which some of these principles can be applied to our population. We then use this toolkit to explore the concept of the *genetic value* of traits as a measure of the heritable portion of an individual's phenotype, the concept of *heritability* as a measure of the fraction of the phenotypic variation in our

population that is attributable to variation in genetic values, the notion of a *selection differential* as a measure of the action of selection on a trait including direct and indirect effects, and the concept of a *directional selection gradient* as a measure of the direct effects of selection on a trait. In Section 3.3, we will then explore the dynamics of the evolutionary response to natural selection and, in doing so, unify the dynamical systems theory we are developing in this thesis with seminal work by Robertson (1968) and Price (1970), Fisher (1930), and Lande (1979); Lande and Arnold (1983).

3.2.1 Causal analysis

The relationship between genotype and phenotype is a complicated one. Following the integration of Mendelian genetics with Darwin's (1859) theory, Fisher (1918) reasoned that the overall phenotype of an individual is influenced by two distinct causal factors: *i*) the environment an individual resides in; and *ii*) the information held by an individual's genotype. He argued that if the environment is defined in such a way that it captures *all* influences on an individual's phenotype not directly due to the effects of its genes, the logical consequence of this assumption is that the trait values defining an individual's phenotype can be decomposed into a *genetic value* and a statistically uncorrelated *environmental deviation* from this value.

The appeal of Fisher's (1918) argument is that it provides a means for evolutionary theorists to focus on the component of the phenotype that is transmissible between generations—the value that can be attributed to the underlying heritable (causal) factors or what we will refer to as 'genetic factors'. In particular, Fisher's (1918) insight was that, given some knowledge about the presence or absence of a set of genetic factors that vary among individuals in a population, it is always the case that we can attribute some *average effect* to a particular genetic factor at a given locus at a particular moment in time. In mathematical terms, Fisher's (1918) reasoning derives from the ordinary least-squares linear regression of trait values on the genetic factors held by individuals.

This ordinary least-squares approach is often referred to as a 'causal analysis' (Frank, 1997), since it is based on an *assumption* about causal effects of the genetic factors present on the trait values held by an individual[b]. As Frank (1997) has put it, ordinary least-squares approach 'has the advantages of maximizing the use of information about

[b]Ordinary least-squares linear regression only provides a method of causal analysis if there is some knowledge about the true relationship between variables, otherwise its predictions about correlations cannot be interpreted causally. The formal approach for evaluating causal hypotheses using ordinary least-squares linear regression is known as 'path analysis' (Kingsolver and Schemske, 1991; Lynch et al., 1998). This approach advocates *identifying* 'causal paths' between variables of interest first, and then *quantifying* them using ordinary least-squares linear regression.

phenotype available in the data, and rendering additive the individual contributions of various factors.' The approach forms the foundations of quantitative genetics, as well as playing an important role in kin (Hamilton, 1964; Queller, 1992b; Gardner et al., 2011) and multi-level (Wade, 1985; Bijma et al., 2007; Goodnight, 2013a; Gardner, 2015) selection theory, and we therefore dedicate some time to understanding how we can go about using a form of least-squares theory in conjunction with the dynamical systems theory of natural selection we are developing in this thesis.

3.2.2 Genetic factors

To introduce the least-squares approach, we will study a linear regression model that regresses the genotype-phenotype map, $\mathbf{Z}$, on a matrix of 'genetic factors'. As in Chapter 2, we are using the term 'genetic' here in a very loose sense as pertaining to an inherited component of a phenotype that is passed on between generations (Gorelick and Laubichler, 2008; Danchin and Wagner, 2010). The types of genetic factors we will typically have in mind are characteristics of genotypes like alleles, epigenetic marks, chromosomes, and so on, that represent discrete 'packets' of information that can tangibly be measured as being either present or absent for each genotype. A model of inheritance of this kind is sufficiently general for a great number of evolutionary problems, although maybe not all (Jablonka and Lamb, 2008; Laland et al., 2014). Nevertheless, as both Goodnight et al. (1992) and Frank (1997, 1998) have emphasised, the least-squares approach we will come to shortly allows us to use *any* type of predictor if we wish, meaning that alternatives to genetic factors could be considered in principle. The main constraint we place on genetic factors is that they should be constant for a given genotype, because genotypes are defined as unique configurations of units of information, and genetic factors represent packets of such information[c].

Genetic factors are part of the phenotype of an individual: they are simply traits that are assigned values of zero or one. Let us therefore denote by $\mathbb{L} \subset \mathbb{P}$ an index set of loci to identify these genetic factors, where $l \in \mathbb{L}$ denotes the locus of a particular genetic factor. The total number of loci under consideration is given by the size of the index set, $|\mathbb{L}|$. For the lth locus, let $\lambda_{il} := \lambda_{il} \in \{0, 1\}$ denote an indicator variable for the presence of absence of a particular genetic factor. The presence or absence of a genetic factor at all loci for all i-genotype entities is given by a $|\mathbb{G}| \times |\mathbb{L}|$ matrix

[c]As we argued in Chapter 2, from our perspective, any change in the genetic factors held by an individual should be considered in terms of 'birth' and 'death' events, for it constitutes a change in the composition of the units of selection in the population.

$$\boldsymbol{\Lambda} = \begin{array}{c} \\ \mathbb{G}_1 \\ \mathbb{G}_2 \\ \vdots \\ \mathbb{G}_{|\mathbb{G}|} \end{array} \begin{array}{c} \begin{array}{cccc} \mathbb{L}_1 & \mathbb{L}_2 & \cdots & \mathbb{L}_{|\mathbb{L}|} \end{array} \\ \begin{bmatrix} \lambda_{11} & \lambda_{12} & \cdots & \lambda_{1|\mathbb{L}|} \\ \lambda_{21} & \lambda_{22} & \cdots & \lambda_{2|\mathbb{L}|} \\ \vdots & \vdots & \ddots & \vdots \\ \lambda_{|\mathbb{G}|1} & \lambda_{|\mathbb{G}|2} & \cdots & \lambda_{|\mathbb{G}||\mathbb{L}|} \end{bmatrix} \end{array}. \tag{3.3}$$

We refer to this as the 'matrix of genetic factors'. For the reason mentioned above, unlike other traits in genotype-phenotype map, $\mathbf{Z}$, the entries of this matrix are constant through time, that is, $\dot{\boldsymbol{\Lambda}} = \mathbf{0}$. The ith row vector $\boldsymbol{\lambda}_{i\bullet} \in \{0,1\}^{|\mathbb{L}|}$ denotes the genetic factors held by i-genotype individuals, and the lth column vector $\boldsymbol{\lambda}_{\bullet l} \in \{0,1\}^{|\mathbb{G}|}$ gives the distribution of the values of the lth genetic factor for all genotypes. Note here that we see a degree of formalisation of the idea that genotypes encode *information* that we discussed in Chapter 2, since each genotype is now defined by a binary string of length $|\mathbb{L}|$. It is important to note that each row vector of genetic factors held by each genotype is strictly unique, since two genotypes with the same genetic factors contain the same information, and are merely two instances of the same unit of selection.

The average values of all genetic factors in the population at time t corresponds to the *relative frequency* of each genetic factor in the population at that time. These relative frequencies are held by a vector $\bar{\boldsymbol{\lambda}} := \bar{\boldsymbol{\lambda}}(\boldsymbol{\Lambda}, \boldsymbol{n}, t) \in \mathbb{R}^{|\mathbb{L}|}$. In vector-matrix notation, this is given by

$$\bar{\boldsymbol{\lambda}} = \frac{1}{N}\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{n} = \boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{x}. \tag{3.4}$$

If we pre- and post-multiply the covariance operator, $\boldsymbol{\Sigma}$, given by equation (2.10) (Box 2.4, Chapter 2) by the matrix of genetic factors, $\boldsymbol{\Lambda}$, we obtain a $|\mathbb{L}| \times |\mathbb{L}|$ square symmetric variance-covariance matrix

$$\mathbf{L} = \boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{\Lambda}, \tag{3.5}$$

whose diagonal elements contain the phenotypic variances of every kth genetic factor, $\mathrm{Var}_{i\in\mathbb{G}}(\lambda_{ik})$, and whose off-diagonal elements contain the covariance of every kth genetic factor with every lth genetic factor, $\mathrm{Cov}_{i\in\mathbb{G}}(\lambda_{ik}, \lambda_{il})$.

Since genetic factors are measurable properties of individuals and part of their phenotype, we can write a 'genic' version of the Malthusian Price equation (2.48) to understand the total change in the relative frequency of genetic factors in the population, $\dot{\bar{\boldsymbol{\lambda}}}$. In vector-matrix notation the equation is given by

$$\dot{\bar{\boldsymbol{\lambda}}} = \boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m} + (\Delta\boldsymbol{\Lambda})^{\mathrm{T}}\mathbf{X}\boldsymbol{b}, \tag{3.6}$$

where all the references to the genotype-phenotype map, $\mathbf{Z}$, have simply been replaced by references to the matrix of genetic factors, $\boldsymbol{\Lambda}$. This equation provides us with a new 'genic' perspective on the dynamics of natural selection in our population, complementary to the ecological, genotypic, and phenotypic perspectives we explored in Chapter 2. We refer to equation (3.6) as the 'genic version' of the Malthusian Price equation, to emphasise that it refers to the specific part of the phenotype concerned with the genetic factors held by individuals.

The components of the genic version of the Malthusian Price equation (3.34) can be interpreted, with care, in a similar way to those from the phenotypic version of the Malthusian Price equation (2.48) from Chapter 2. Thus we have a component associated with natural selection represented by a vector of covariances of genetic factors with Malthusian fitness, $\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m}$, and a component associated with transmission fidelity represented by a vector of differences between the expected frequency of genetic factors in descendants and their ancestors, $(\Delta\boldsymbol{\Lambda})^{\mathrm{T}}\mathbf{X}\boldsymbol{b}$. There is no component associated with phenotypic plasticity or ecological inheritance, because the matrix of genetic values is constant, and neither of these processes have any meaning when considered from a genic perspective. Equation (3.6) provides us with a picture of the dynamics of natural selection in terms of gene-frequency change, which corresponds to the definition of evolutionary change in the theoretical framework of population genetics (Crow and Kimura, 1970; Price, 1970, 1972a).

3.2.3 Population-weighted least-squares linear regression

With our model of inheritance in place, let us return to the causal analysis approach we began the section with. In the context of the population we studied in Chapter 2, it may not be immediately obvious why we would want to use causal analysis to perform Fisher's (1918) decomposition, given that we already assumed that trait values are defined by a functional relationship between genotype and the environment (as defined by the

genotype-phenotype map, $\mathbf{Z}$, given by equation (2.6)) and there is, therefore, strictly no need for such a decomposition[d].

To understand why, it is important to first reiterate the main goal in this thesis, which is to develop a unifying framework from which we can view the dynamics of natural selection from multiple complementary perspectives. By making explicit the links between evolutionary genetics and our dynamical systems theory, we may expose the similarities, differences, advantages and disadvantages of both. Since quantitative genetics is typically studied using discrete-time models that cannot be iterated through time, the connections we establish here using a continuous-time approach may also help us to answer questions that have vexed those studying theoretical quantitative genetics for a number of years, such as questions pertaining to the dynamical properties of narrow-sense heritability and the stability and directionality of the $\mathbf{G}$-matrix (Steppan et al., 2002; Pigliucci, 2006; Arnold et al., 2008), or the extent to which the adaptive landscape provides us with a useful picture of the dynamics of the evolutionary response to natural selection (Nowak and Sigmund, 2004; Mustonen and Lässig, 2009).

To understand how we can go about performing the causal analysis approach in the context of the population we studied in Chapter 2, we need to develop a modified version of ordinary least-squares theory. The challenge we face is that our population is defined not by discrete population data at a single point in time (as would typically be available in an ordinary least-squares analysis), but by a dynamical system with continuous variables that may change at every instantaneous moment in time. There are two insights that will enable us to make progress: *i*) to account for the absence of discrete population data, we need to weight genotypes in the population by their abundance; and *ii*) an ordinary least-squares linear regression model is generally only guaranteed to provide a satisfactory model of the population dynamics for a single generation, but there is nothing stopping us from making the calculation at every *instantaneous* moment in time, t, in order to gain a different perspective on the dynamics of natural selection *at that time*.

We call the modified theory derived here a 'population-weighted' form of least-squares theory[e]. In a typical ordinary least-squares linear regression model the number of rows of the vectors and/or matrices holding the data is equal to the number of data points measured. In our case, the number of rows is equal to the number of genotypes in our

[d]By 'no need', we mean in terms of solving the equations defining the system.

[e]Weighted least-squares linear regression is already a well-known technique in statistical theory (Ruppert and Wand, 1994), but it is more typically used in circumstances where the confidence or accuracy of individual measurements are called into question—for instance, in the case of extreme outliers—whereas here we are interested in using weights to ensure that the composition of different units of selection in our population is properly accounted for.

dynamical system, $|\mathbb{G}|$ and the number of columns corresponds to the number of dependent or explanatory variables we wish to analyse. We will be interested in three types of model in this chapter: *i*) a model with a single dependent variable and single explanatory variable, which is known as a 'simple' linear regression; *ii*) a model with a single dependent variable, but multiple explanatory variables, which is known as a 'multiple' linear regression; and *iii*) a model with multiple dependent variables *and* multiple explanatory variables, which is known as a 'general' linear model (GLM).

The linear model we consider here is for the regression of the genotype-phenotype map, $\mathbf{Z}$, on the matrix of genetic factors, $\mathbf{\Lambda}$. This corresponds to a GLM[f] since we have $|\mathbb{P}|$ dependent variables (traits) being regressed on $|\mathbb{L}|$ explanatory variables (genetic factors). In the next section, we will see that this GLM provides us with a decomposition corresponding to a multivariate form of Fisher's (1918) causal analysis. The linear model takes the form

$$\mathbf{Z} = \mathbf{1}\boldsymbol{\alpha}_{z\lambda}^{\mathrm{T}} + \mathbf{\Lambda}\boldsymbol{\beta}_{z\lambda} + \boldsymbol{\varepsilon}_{z\lambda}, \tag{3.7}$$

where $\mathbf{1} = (1_1, ..., 1_{|\mathbb{G}|})^{\mathrm{T}} \in \mathbb{R}^{|\mathbb{G}|}$ is vector of all ones, $\boldsymbol{\alpha}_{z\lambda}^{\mathrm{T}} \in \mathbb{R}^{|\mathbb{P}|}$ is a vector of intercept coefficients, $\boldsymbol{\beta}_{z\lambda} \in \mathbb{R}^{|\mathbb{L}|\times|\mathbb{P}|}$ is a matrix of partial regression coefficients, and $\boldsymbol{\varepsilon}_{z\lambda} \in \mathbb{R}^{|\mathbb{G}|\times|\mathbb{P}|}$ is a matrix containing the unexplained residuals.

The goal in fitting a linear model by the method of least-squares is usually to find estimates for the parameters, $\boldsymbol{\alpha}_{z\lambda}$ and $\boldsymbol{\beta}_{z\lambda}$, that minimise the sum of the squared residuals (error), and therefore maximise the explanatory (predictive) power of the model[g]. In our case, the goal is to find estimates of the parameters that uniquely minimise the sum of *population-weighted* squared residuals. In Box 3.2 we see that these estimates are given by

$$\hat{\boldsymbol{\alpha}}_{z\lambda} = \bar{\boldsymbol{z}} - \boldsymbol{\beta}_{z\lambda}^{\mathrm{T}}\bar{\boldsymbol{\lambda}} \quad \text{and} \tag{3.8}$$

$$\hat{\boldsymbol{\beta}}_{z\lambda} = (\mathbf{\Lambda}^{\mathrm{T}}\mathbf{\Sigma}\mathbf{\Lambda})^{-1}\mathbf{\Lambda}^{\mathrm{T}}\mathbf{\Sigma}\mathbf{Z}, \tag{3.9}$$

[f]Although our approach will typically work providing that there are more rows (genotypes, $|\mathbb{G}|$) than columns in the matrices defining the dependent (traits, $|\mathbb{P}|$) or explanatory variables (genetic factors, $|\mathbb{L}|$). Thus the theory holds just as well for simple linear regressions, multiple linear regressions or GLMs. If there are more explanatory or dependent variables than genotypes we expect there to be non-unique solutions to the system i.e. we expect to have an 'underdetermined' system.

[g]In terms of causality, the regression of traits on a multivariate set of genetic factors has the potential to provide greater explanatory (predictive) power than a standalone simple linear regression, since a GLM takes into account *correlations* between traits at the genetic level which would not otherwise be captured (Lande, 1979; Lande and Arnold, 1983).

respectively, where the carat symbol is used to denote that the choice of values for $\boldsymbol{\alpha}_{z\lambda}$ and $\boldsymbol{\beta}_{z\lambda}$ here are the ones that minimise the population-weighted sum of squared residuals, $\varsigma_{z\lambda}$.

Box 3.2 | Population-weighted least-squares parameters

We denote the sum of *population-weighted* squared residuals by $\varsigma_{z\lambda} := \varsigma_{z\lambda}(\boldsymbol{\varepsilon}_{z\lambda}) \in \mathbb{R}$. In vector-matrix notation, the sum is calculated as

$$\varsigma_{z\lambda} = \text{Tr}(\boldsymbol{\varepsilon}_{z\lambda}^{\text{T}}\mathbf{N}\boldsymbol{\varepsilon}_{z\lambda}) = N\text{Tr}(\boldsymbol{\varepsilon}_{z\lambda}^{\text{T}}\mathbf{X}\boldsymbol{\varepsilon}_{z\lambda}), \tag{3.10}$$

where $\mathbf{N} = \text{diag}(\boldsymbol{n})$ is the diagonalised composition vector, $\mathbf{X} = \text{diag}(\boldsymbol{x})$ is the diagonalised vector of relative frequencies, N is the population size, and the notation $\text{Tr}(\cdot)$ denotes the matrix trace operator, which is defined to be the sum of the diagonal elements of a matrix. We multiply the residuals by $\mathbf{N}$ so that the sum of squared residuals, $\varsigma_{z\lambda}$, is population-weighted. Substituting for $\boldsymbol{\varepsilon}_{z\lambda}$ from equation (3.21), using a standard transpose identity, and multiplying out the brackets, we obtain

$$\begin{aligned}\varsigma_{z\lambda} &= N\text{Tr}\left[(\mathbf{Z} - \mathbf{1}\boldsymbol{\alpha}_{z\lambda}^{\text{T}} - \boldsymbol{\Lambda}\boldsymbol{\beta}_{z\lambda})^{\text{T}}\mathbf{X}(\mathbf{Z} - \mathbf{1}\boldsymbol{\alpha}_{z\lambda}^{\text{T}} - \boldsymbol{\Lambda}\boldsymbol{\beta}_{z\lambda})\right] \\ &= N\text{Tr}\left[\mathbf{Z}^{\text{T}}\mathbf{X}\mathbf{Z} - \mathbf{Z}^{\text{T}}\mathbf{X}\mathbf{1}\boldsymbol{\alpha}_{z\lambda}^{\text{T}} - \mathbf{Z}^{\text{T}}\mathbf{X}\boldsymbol{\Lambda}\boldsymbol{\beta}_{z\lambda} - \boldsymbol{\alpha}_{z\lambda}\mathbf{1}^{\text{T}}\mathbf{X}\mathbf{Z} + \boldsymbol{\alpha}_{z\lambda}\mathbf{1}^{\text{T}}\mathbf{X}\mathbf{1}\boldsymbol{\alpha}_{z\lambda}^{\text{T}}\right. \\ &\qquad \left. + \boldsymbol{\alpha}_{z\lambda}\mathbf{1}^{\text{T}}\mathbf{X}\boldsymbol{\Lambda}\boldsymbol{\beta}_{z\lambda} - \boldsymbol{\beta}_{z\lambda}^{\text{T}}\boldsymbol{\Lambda}^{\text{T}}\mathbf{X}\mathbf{Z} + \boldsymbol{\beta}_{z\lambda}^{\text{T}}\boldsymbol{\Lambda}^{\text{T}}\mathbf{X}\mathbf{1}\boldsymbol{\alpha}_{z\lambda}^{\text{T}} + \boldsymbol{\beta}_{z\lambda}^{\text{T}}\boldsymbol{\Lambda}^{\text{T}}\mathbf{X}\boldsymbol{\Lambda}\boldsymbol{\beta}_{z\lambda}\right].\end{aligned} \tag{3.11}$$

Our goal now is to minimise $\varsigma_{z\lambda}$ with respect to the parameters. For a simple linear regression model, we would achieve this by taking the partial derivatives of the sum of squared residuals with respect to the pair of scalar parameters. Since we have a GLM, however, the parameters $\boldsymbol{\alpha}_{z\lambda}$ and $\boldsymbol{\beta}_{z\lambda}$ are not scalar quantities, but instead correspond to a $|\mathbb{P}| \times 1$ vector and a $|\mathbb{P}| \times |\mathbb{P}|$ matrix, respectively. We therefore use the notation we described in Box 2.5 of Chapter 2 to instead take the *gradient* of $\varsigma_{z\lambda}$ with respect to the parameters $\boldsymbol{\alpha}_{z\lambda}$ and $\boldsymbol{\beta}_{z\lambda}$. By standard identities from matrix calculus we obtain

$$\nabla_{\boldsymbol{\alpha}_{z\lambda}}[\varsigma_{z\lambda}] = -2N\mathbf{Z}^{\text{T}}\mathbf{X}\mathbf{1} + 2N\boldsymbol{\alpha}_{z\lambda}\mathbf{1}^{\text{T}}\mathbf{X}\mathbf{1} + 2N\boldsymbol{\beta}_{z\lambda}^{\text{T}}\boldsymbol{\Lambda}^{\text{T}}\mathbf{X}\mathbf{1} \qquad \text{and} \tag{3.12}$$

$$\nabla_{\boldsymbol{\beta}_{z\lambda}}[\varsigma_{z\lambda}] = -2N\mathbf{Z}^{\text{T}}\mathbf{X}\boldsymbol{\Lambda} + 2N\boldsymbol{\alpha}_{z\lambda}\mathbf{1}^{\text{T}}\mathbf{X}\boldsymbol{\Lambda} + 2N\boldsymbol{\beta}_{z\lambda}^{\text{T}}\boldsymbol{\Lambda}^{\text{T}}\mathbf{X}\boldsymbol{\Lambda}, \tag{3.13}$$

respectively. In minimising the sum of population-weighted squared residuals, $\varsigma_{z\lambda}$, we have made several important implicit assumptions about the values that the parameters can take. We describe these in Box 3.3. Let us proceed to identify the minimum points of the derivative functions $\nabla_{\boldsymbol{\alpha}_{z\lambda}}[\varsigma_{z\lambda}]$ and $\nabla_{\boldsymbol{\beta}_{z\lambda}}[\varsigma_{z\lambda}]$. To do this we set both equations equal to zero and simplify, which yields a system of 'normal' equations of the form

$$\mathbf{Z}^{\text{T}}\boldsymbol{x} = \boldsymbol{\alpha}_{z\lambda} + \boldsymbol{\beta}_{z\lambda}^{\text{T}}\boldsymbol{\Lambda}^{\text{T}}\boldsymbol{x}, \quad \text{and} \tag{3.14}$$

$$\mathbf{Z}^{\text{T}}\mathbf{X}\boldsymbol{\Lambda} = \boldsymbol{\alpha}_{z\lambda}\boldsymbol{x}^{\text{T}}\boldsymbol{\Lambda} + \boldsymbol{\beta}_{z\lambda}^{\text{T}}\boldsymbol{\Lambda}^{\text{T}}\mathbf{X}\boldsymbol{\Lambda}, \tag{3.15}$$

where we have used the property that the sum of all relative genotype frequencies is equal to one, $\mathbf{1}^{\mathrm{T}}\boldsymbol{x} = \boldsymbol{x}^{\mathrm{T}}\mathbf{1} = 1$, and the identities $\mathbf{X1} = \boldsymbol{x}$, and $\mathbf{1}^{\mathrm{T}}\mathbf{X} = \boldsymbol{x}^{\mathrm{T}}$. Hence, from equation (3.14), we obtain an expression for the population-weighted least-squares estimated intercept coefficients of the form

$$\hat{\boldsymbol{\alpha}}_{z\lambda} = \mathbf{Z}^{\mathrm{T}}\boldsymbol{x} - \boldsymbol{\beta}_{z\lambda}^{\mathrm{T}}\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{x} = \bar{\boldsymbol{z}} - \boldsymbol{\beta}_{z\lambda}^{\mathrm{T}}\bar{\boldsymbol{\lambda}}, \tag{3.16}$$

which corresponds to equation (3.8) in the main text. We use a carat symbol to denote that the choice of values for $\boldsymbol{\alpha}_{z\lambda}$ here are the ones that minimise the population-weighted sum of squared residuals, $\varsigma_{z\lambda}$. Note that $\bar{\boldsymbol{z}} = \mathbf{Z}^{\mathrm{T}}\boldsymbol{x}$ corresponds to the vector of average trait values in the population, and $\bar{\boldsymbol{\lambda}} = \boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{x}$ corresponds to a vector of the average frequencies of each genetic factor in the population.
To obtain an expression for $\boldsymbol{\beta}_{z\lambda}$, let us now substitute for $\hat{\boldsymbol{\alpha}}_{z\lambda}$ from equation (3.16) in place of $\boldsymbol{\alpha}_{z\lambda}$ in equation (3.15), to obtain

$$\mathbf{Z}^{\mathrm{T}}\mathbf{X}\boldsymbol{\Lambda} = (\mathbf{Z}^{\mathrm{T}} - \boldsymbol{\beta}_{z\lambda}^{\mathrm{T}}\boldsymbol{\Lambda}^{\mathrm{T}})\boldsymbol{x}\boldsymbol{x}^{\mathrm{T}}\boldsymbol{\Lambda} + \boldsymbol{\beta}_{z\lambda}^{\mathrm{T}}\boldsymbol{\Lambda}^{\mathrm{T}}\mathbf{X}\boldsymbol{\Lambda}. \tag{3.17}$$

After rearranging and simplifying, we then have

$$\mathbf{Z}^{\mathrm{T}}(\mathbf{X} - \boldsymbol{x}\boldsymbol{x}^{\mathrm{T}})\boldsymbol{\Lambda} = \boldsymbol{\beta}_{z\lambda}^{\mathrm{T}}\boldsymbol{\Lambda}^{\mathrm{T}}(\mathbf{X} - \boldsymbol{x}\boldsymbol{x}^{\mathrm{T}})\boldsymbol{\Lambda}. \tag{3.18}$$

This equation contains an expression that we have already encountered earlier in this thesis, namely, $\boldsymbol{\Sigma} = \mathbf{X} - \boldsymbol{x}\boldsymbol{x}^{\mathrm{T}}$ is the general symmetric covariance operator defined by equation (2.10) from Box 2.4 in Chapter 2. Making the substitution and transposing both sides, we have

$$\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{Z} = \boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{\Lambda}\boldsymbol{\beta}_{z\lambda}. \tag{3.19}$$

Under the assumption that the matrix $\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{\Lambda}$ is invertible (a point we address in Box 3.3), we obtain a unique expression for the population-weighted least-squares estimated partial regression coefficients of the form

$$\hat{\boldsymbol{\beta}}_{z\lambda} = (\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{\Lambda})^{-1}\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{Z} = \mathbf{L}^{-1}\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{Z}, \tag{3.20}$$

which corresponds to equation (3.9) in the main text. Again, we have used a carat symbol to denote that the choice of values for $\boldsymbol{\beta}_{z\lambda}$ here are the ones that minimise the population-weighted sum of squared residuals, $\varsigma_{z\lambda}$. Note that $\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{\Lambda}$ corresponds to the square symmetric variance-covariance matrix of genetic factors $\mathbf{L}$, and that $\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{Z}$ corresponds to a covariance matrix of genetic factors with trait values.

If we now re-write our original GLM equation (3.21) using our population-weighted least-

squares estimates we have

$$\mathbf{Z} = \mathbf{1}\hat{\boldsymbol{\alpha}}_{z\lambda}^{\mathrm{T}} + \boldsymbol{\Lambda}\hat{\boldsymbol{\beta}}_{z\lambda} + \hat{\boldsymbol{\varepsilon}}_{z\lambda}, \tag{3.21}$$

where $\hat{\boldsymbol{\varepsilon}}_{z\lambda}$ is the matrix containing the unexplained residuals corresponding to the population-weighted least-squares parameters $\hat{\boldsymbol{\alpha}}_{z\lambda}$ and $\hat{\boldsymbol{\beta}}_{z\lambda}$. Ordinary least-squares linear regression models are also often expressed in a standardised or mean-centred form. To do the same in our population-weighted least-squares world, we simply substitute for the definition of $\hat{\boldsymbol{\alpha}}_{z\lambda}$, given by equation (3.8), into equation (3.21), and rearrange, to obtain

$$\mathbf{Z} = \mathbf{1}\bar{\boldsymbol{z}}^{\mathrm{T}} + (\boldsymbol{\Lambda} - \mathbf{1}\bar{\boldsymbol{\lambda}}^{\mathrm{T}})\hat{\boldsymbol{\beta}}_{z\lambda} + \hat{\boldsymbol{\varepsilon}}_{z\lambda}, \tag{3.22}$$

where $\boldsymbol{\Lambda} - \mathbf{1}\bar{\boldsymbol{\lambda}}^{\mathrm{T}}$ expresses the matrix of genetic factors, $\boldsymbol{\Lambda}$, in terms of deviations from the relative frequency of genetic factors in the population at each locus, $\bar{\boldsymbol{\lambda}}$.

Box 3.3 | Assumptions of population-weighted least-squares theory

In deriving equation (3.22) we made several important assumptions. The main explicit assumption we made in our derivation was that the variance-covariance matrix $\mathbf{L} = \boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{\Lambda}$ is invertible. The potential problem with this assumption is that the explanatory variables could be highly correlated with one another, with the consequence that the matrix $\mathbf{L}$ might have dependent columns and therefore be singular. This might therefore seem like a stringent requirement, and could be seen to limit the generality of the population-weighted ordinary least-squares approach. Although theoretically true, in practical applications where this problem occurs there are several steps that can be taken to alleviate the problem. These are discussed by Lande and Arnold (1983) in their seminal paper describing the multivariate quantitative genetic approach. For instance, they suggest several approaches of matrix dimensionality reduction to ensure a non-singular matrix is obtained, including: *i*) averaging over highly correlated genetic factors; *ii*) retaining only one of the correlated genetic factors for the analysis; and *iii*) using principal components analysis to extract only the orthogonal components of variation among the genetic factors.

An implicit assumption[a] we made in our derivation was that the expected values of the residuals satisfying the population-weighted least-squares condition gives the zero vector, which we can express as $\hat{\boldsymbol{\varepsilon}}_{z\lambda}^{\mathrm{T}}\boldsymbol{x} = \mathbf{0}$. To prove that this is the case, let us rearrange equation (3.21), transpose, and post-multiply by $\boldsymbol{x}$, to get $\hat{\boldsymbol{\varepsilon}}_{z\lambda}^{\mathrm{T}}\boldsymbol{x} = \mathbf{Z}^{\mathrm{T}}\boldsymbol{x} - \hat{\boldsymbol{\beta}}_{z\lambda}^{\mathrm{T}}\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{x} - \hat{\boldsymbol{\alpha}}_{z\lambda}\mathbf{1}^{\mathrm{T}}\boldsymbol{x}$. We then simplify using $\mathbf{1}^{\mathrm{T}}\boldsymbol{x} = 1$, and substitute for $\hat{\boldsymbol{\alpha}}_{z\lambda} = \mathbf{Z}^{\mathrm{T}}\boldsymbol{x} - \hat{\boldsymbol{\beta}}_{z\lambda}^{\mathrm{T}}\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{x}$ from (3.8) to obtain

$$\hat{\boldsymbol{\varepsilon}}_{z\lambda}^{\mathrm{T}}\boldsymbol{x} = \hat{\boldsymbol{\alpha}}_{z\lambda} - \hat{\boldsymbol{\alpha}}_{z\lambda} = \mathbf{0}, \tag{3.23}$$

which proves that minimisation procedure requires us to assume that the expected values of the residuals are zero, $\hat{\boldsymbol{\varepsilon}}_{z\lambda}^{\mathrm{T}}\boldsymbol{x} = \mathbf{0}$.

A second implicit assumption we made in our derivation was that the explanatory variables and the residuals satisfying the population-weighted least-squares condition do not covary (are uncorrelated), which we can express as $\hat{\boldsymbol{\varepsilon}}_{z\lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{\Lambda} = \boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\hat{\boldsymbol{\varepsilon}}_{z\lambda} = \mathbf{0}$. To prove that this is the case, let us transpose equation (3.21), post-multiply by $\boldsymbol{\Sigma}\boldsymbol{\Lambda}$, and set the result equal to $\mathbf{0}$ to get $(\mathbf{Z}^{\mathrm{T}} - \hat{\boldsymbol{\alpha}}_{z\lambda}\mathbf{1}^{\mathrm{T}} - \hat{\boldsymbol{\beta}}_{z\lambda}^{\mathrm{T}}\boldsymbol{\Lambda}^{\mathrm{T}})\boldsymbol{\Sigma}\boldsymbol{\Lambda} = \mathbf{0}$.
We want to show that this equality holds. Multiplying out the brackets, transposing, and rearranging, we have $\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{Z} = \boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{1}\hat{\boldsymbol{\alpha}}_{z\lambda}^{\mathrm{T}} + \boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{\Lambda}\hat{\boldsymbol{\beta}}_{z\lambda}$. Since the term $\boldsymbol{\Lambda}\boldsymbol{\Sigma}\mathbf{1}\hat{\boldsymbol{\alpha}}_{z\lambda}^{\mathrm{T}}$ is a covariance matrix of explanatory variables with the intercept coefficients, it must be equal to the zero matrix (because the covariance of anything with a constant is always zero). Hence, we obtain

$$\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{Z} = \boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{\Lambda}\hat{\boldsymbol{\beta}}_{z\lambda}, \tag{3.24}$$

which is the same equality as that given by equation (3.19) in our derivation of $\hat{\boldsymbol{\beta}}_{z\lambda}$, and hence the equality we started with holds. Thus, we have proved that the process of population-weighted least-squares minimisation is equivalent to making the assumptions, in setting up the linear model, that the explanatory variables and the residuals do not covary (are uncorrelated), $\hat{\boldsymbol{\varepsilon}}_{z\lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{\Lambda} = \mathbf{0}$.

[a] The reason we made implicit assumptions is that we used a derivation from the 'geometrical' perspective of least-squares theory. An alternative derivation from the 'statistical' perspective of least-squares theory would have made the implicit assumptions more explicit, but the explicit assumptions implicit.

3.2.4 Average effects, genetic values, and environmental deviations

Having derived a method that we may use in the context of the population we studied in Chapter 2, let us now return to the causal analysis approach of Fisher (1918) to identify the key quantities of interest we mentioned previously. The first thing to note about equation (3.21) is that the $|\mathbb{L}| \times |\mathbb{P}|$ matrix of partial regression coefficients, $\hat{\boldsymbol{\beta}}_{z\lambda}$, serves to map the population-weighted least-squares estimated impact of each genetic factor onto each phenotypic trait at a particular point in time, t. It is therefore equivalent to a matrix of 'average effects' of the kind we mentioned previously (Fisher, 1918; Falconer and Mackay, 1995). Since the matrix of genetic factors, $\boldsymbol{\Lambda}$, contains only zeros or ones, the matrix multiplication $\boldsymbol{\Lambda}\hat{\boldsymbol{\beta}}_{z\lambda}$ corresponds to a sum of the average effects of genetic factors

for each individual in the population for each trait they hold (Fisher, 1918; Falconer and Mackay, 1995). We let the $|\mathbb{G}| \times |\mathbb{P}|$ matrix

$$\mathbf{V} = \boldsymbol{\Lambda}\hat{\boldsymbol{\beta}}_{z\lambda}, \tag{3.25}$$

hold these sums, where each element is given by a sum of the form $v_{ik} = \sum_{l=1}^{\mathbb{L}|} \lambda_{il}\hat{\beta}_{z\lambda lk}$. We refer to $\mathbf{V}$ as the 'matrix of sums of average effects'. Note that if we are interested in the average sum of average effects taken across all individuals in the population, this can be written as

$$\bar{\boldsymbol{v}} = \frac{1}{N}\mathbf{V}^{\mathrm{T}}\boldsymbol{n} = \mathbf{V}^{\mathrm{T}}\boldsymbol{x} = \hat{\boldsymbol{\beta}}_{z\lambda}^{\mathrm{T}}\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{x} = \hat{\boldsymbol{\beta}}_{z\lambda}^{\mathrm{T}}\bar{\boldsymbol{\lambda}}, \tag{3.26}$$

which is simply given by the product of the matrix of average effects, $\hat{\boldsymbol{\beta}}_{z\lambda}$, and the vector of the relative frequencies of each genetic factor in the population, $\bar{\boldsymbol{\lambda}}$. The average sums of average effects therefore corresponds to a relative-frequency-weighted sum of average effects.

The sum of the average effects of genetic factors for a trait held by an individual is key quantity of interest in evolutionary theory, and is often referred to as a 'breeding value' in quantitative genetics (Falconer and Mackay, 1995). As we discussed in Chapter 2, however, the true breeding value of a trait held by an individual is the expected value of the trait held by its descendants. In experimental settings, this is usually measured retrospectively, but in our continuous-time framework, we defined the *prospective* breeding values of traits at any time, t, by the matrix $\mathbf{Z}' = \mathbf{HZ}$, given by equation (2.22) in Chapter 2. How are these prospective breeding values related to the sums of average effects? To better understand the relationship, let us see what the implication would be if the two quantities were equal, so that $\mathbf{Z}' = \boldsymbol{\Lambda}\hat{\boldsymbol{\beta}}_{z\lambda}$. Pre-multiplying both sides of this equation by the quantity $(\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{\Lambda})^{-1}\boldsymbol{\Lambda}^{-1}\boldsymbol{\Sigma}$, we obtain the condition

$$\hat{\boldsymbol{\beta}}_{z'\lambda} = \hat{\boldsymbol{\beta}}_{z\lambda}, \tag{3.27}$$

where on the left-hand side $\hat{\boldsymbol{\beta}}_{z'\lambda} = (\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{\Lambda})^{-1}\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{Z}'$ can be interpreted as the matrix of average effects obtained from the regression of the matrix of prospective breeding values, $\mathbf{Z}'$, on the matrix of genetic factors, $\boldsymbol{\Lambda}$, and on the right-hand side we have simplified since $(\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{\Lambda})^{-1}\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{\Lambda} = \mathbf{I}$. Thus, we can interpret the condition expressed by equation

(3.27) as the following: if the average effects of genetic factors on traits are the same for descendants at the next instant in time, $t + \delta t$, as they are for individuals at time t, then the prospective breeding values are equal to the sums of the average effects of genetic factors.

Of course, the corollary of this is that if the average effects of genetic factors are different in descendants than they are in ancestors, so that $\hat{\boldsymbol{\beta}}_{z'\lambda} \neq \hat{\boldsymbol{\beta}}_{z\lambda}$, then it will also be the case that $\mathbf{Z}' \neq \mathbf{V}$. Nevertheless, when equation (3.27) does not hold exactly, we can see that the matrix of sums of the average effects, $\mathbf{V}$, may still be a good approximation to the matrix of prospective breeding values, $\mathbf{Z}'$, providing that there has not been dramatic changes in the population in the meantime[h]. As we will see in a later section, the sum of the average effects for a trait, v_{ik}, is an important quantity, since it corresponds to the part of a trait that is 'visible' to natural selection at any given instantaneous moment in time, t. The use of average effects in evolutionary theory is not, however, without controversy. There are two issues, in particular, which are thought to complicate evolutionary analyses.

The first relates to that which we have just discussed, which is that that the matrix of average effects, $\hat{\boldsymbol{\beta}}_{z\lambda}$, being a function of the composition of the population, $\boldsymbol{n}$, and the genotype-phenotype map, $\mathbf{Z}$, will generally not be constant, but will tend to vary as the composition of genotypes and phenotypes in the population changes through time. This is of course true, and if we wish we can take the derivative with respect to time of $\hat{\boldsymbol{\beta}}_{z\lambda}$ using a matrix calculus version of the quotient rule for inverse matrices to obtain a better understanding of why average effects are not constant. After doing this and rearranging, we obtain the somewhat complicated-looking expression

$$\begin{aligned}\dot{\hat{\boldsymbol{\beta}}}_{z\lambda} &= (\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{\Lambda})^{-1}\boldsymbol{\Lambda}^{\mathrm{T}}\dot{\boldsymbol{\Sigma}}\boldsymbol{\Lambda} - (\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{\Lambda})^{-1}(\boldsymbol{\Lambda}^{\mathrm{T}}\dot{\boldsymbol{\Sigma}}\boldsymbol{\Lambda})(\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{\Lambda})^{-1}\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{Z} + (\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{\Lambda})^{-1}\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\dot{\mathbf{Z}} \\ &= \mathbf{L}^{-1}\boldsymbol{\Lambda}^{\mathrm{T}}\dot{\boldsymbol{\Sigma}}\boldsymbol{\Lambda} - \mathbf{L}^{-1}(\boldsymbol{\Lambda}^{\mathrm{T}}\dot{\boldsymbol{\Sigma}}\boldsymbol{\Lambda})\hat{\boldsymbol{\beta}}_{z\lambda} + \hat{\boldsymbol{\beta}}_{\dot{z}\lambda} \\ &= \mathbf{L}^{-1}\boldsymbol{\Lambda}^{\mathrm{T}}\dot{\boldsymbol{\Sigma}}\boldsymbol{\Lambda}(\mathbf{I} - \hat{\boldsymbol{\beta}}_{z\lambda}) + \hat{\boldsymbol{\beta}}_{\dot{z}\lambda},\end{aligned} \tag{3.28}$$

where $\dot{\boldsymbol{\Sigma}}$ denotes the derivative of the covariance operator with respect to time, which accounts for changes in the relative population composition over time, $\dot{\mathbf{Z}}$ is the time derivative of the genotype-phenotype map given by equation (2.46) in Chapter 2, and we can interpret $\hat{\boldsymbol{\beta}}_{\dot{z}\lambda} = (\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{\Lambda})^{-1}\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\dot{\mathbf{Z}}$ as a matrix of partial regression coefficients

[h]Perhaps this is what Fisher (1930, pg. 32) was referring to when, in his typically opaque language, he said that 'the expected value [the sum of average effects?] will not necessarily represent the real stature, though it may be a good approximation to it [the true breeding value?], but its statistical properties will be more intimately involved in the inheritance of real stature than the properties of that variate itself.'

obtained from the regression of the derivative of the genotype-phenotype map, $\dot{\mathbf{Z}}$, on the matrix of genetic factors, $\mathbf{\Lambda}$. Thus equation (3.28) tells us that the matrix of average effects, $\hat{\boldsymbol{\beta}}_{z\lambda}$, changes over time because of changes in the summary statistics of genetic factors in the population, as determined by the term $\mathbf{L}^{-1}\mathbf{\Lambda}^{\mathrm{T}}\dot{\mathbf{\Sigma}}\mathbf{\Lambda}(\mathbf{I} - \hat{\boldsymbol{\beta}}_{z\lambda})$, and because of changes in the genotype-phenotype map, $\mathbf{Z}$, as determined by the term $\hat{\boldsymbol{\beta}}_{\dot{z}\lambda}$, which accounts for statistical associations between the genetic factors held by individuals and the changes taking place in their phenotypic trait values over time.

With multiple possible causes of changes in the average effects over time, there is debate among evolutionary theorists about the extent to which average effects can really provide any predictive (explanatory) power about the evolutionary response to natural selection, a process that may operate over timescales in which average effects are unlikely to be stable (Frank, 1998). The important point to make here, however, is that average effects can be calculated at every instantaneous moment in time, t, to provide insight into the dynamics of the evolutionary response to natural selection *at that time*. Natural selection has no foresight. Its effect on a population is temporally strictly local, so the fact that average effects may be different in the future has no bearing on how natural selection acts at the current instantaneous moment in time. If average effects *do* remain constant over a prolonged period of time, then the explanatory power of average effects calculated at any given moment will simply be extended over a longer period by comparison with a population in which they *do not* remain constant.

A second concern is that the relationship between genotype and phenotype is almost always a complicated one, and a linear model of the average effects of genetic factors on the value of phenotypic traits is hardly likely to be able to account for all the (non-linear) complexity of the true relationship (Frank, 1998). In particular, non-additive (but nonetheless genetic) effects like dominance and epistasis will tend to contribute toward the matrix of residuals in the model, $\hat{\boldsymbol{\varepsilon}}_{z\lambda}$, rather than the matrix of average effects, $\hat{\boldsymbol{\beta}}_{z\lambda}$. As Gardner et al. (2011) have said, however, 'gene interactions—such as dominance, epistasis and synergy... may mediate the overall additive effect of [a] gene, and hence impact upon the action of natural selection, but these effects are already taken into account within the regression analysis (they need not be assumed absent).' This is also true of the matrix of prospective breeding values, $\mathbf{Z}'$, which is calculated from linear combinations of the trait values in the genotype-phenotype map, $\mathbf{Z}$, which we know are arbitrarily complex functions. Ultimately, the key point is that, as Williams (1966) elegantly put it, 'no matter how functionally dependent a gene may be, and no matter how complicated its interactions with other genes and environmental factors, it must always be true that a given gene substitution will have an arithmetic mean effect.'

The sum of the average effects of genetic factors on traits plays a crucial in identifying the portion of the phenotype of individuals that can be explained by the genetic factors they carry. Recall that, according to Fisher (1918), the trait values defining an individual's phenotype can be causally decomposed into a genetic value and a statistically uncorrelated environmental deviation from this value. In the present context, Fisher's (1918) logic implies that we can decompose the genotype-phenotype map, $\mathbf{Z}$, into the addition of two matrices holding genetic values and environmental deviations, respectively. Given our work in the previous section, this is now simple to achieve. From equation (3.22) we simply let

$$\mathbf{A} = \mathbf{1}\bar{\boldsymbol{z}}^{\mathrm{T}} + (\boldsymbol{\Lambda} - \mathbf{1}\bar{\boldsymbol{\lambda}}^{\mathrm{T}})\hat{\boldsymbol{\beta}}_{z\lambda}, \quad \text{and} \tag{3.29}$$

$$\mathbf{U} = \hat{\boldsymbol{\varepsilon}}_{z\lambda}, \tag{3.30}$$

be the 'matrix of genetic values' and the 'matrix of environmental deviations', respectively. We can then re-write equation (3.22) as a causal decomposition of the form

$$\mathbf{Z} = \mathbf{A} + \mathbf{U}. \tag{3.31}$$

The causal decomposition of the genotype-phenotype map, $\mathbf{Z}$, into a matrix of genetic values, $\mathbf{A}$, and a matrix of environmental deviations, $\mathbf{U}$, is important because the genetic value of a trait, defined in terms of the average effects of genetic factors at a particular time, t, can be thought of as a best approximation to the heritable portion of the trait at that time[i]. The reason for this is that it is not genotypes or phenotypes *per se* that are transmitted between generations, but genetic factors with predictable average effects (Falconer and Mackay, 1995).

Genetic values and environmental deviations of traits are quantities measured on individuals, but it is ultimately phenotypic variation at the level of the *population* that defines whether or not natural selection can take place and drive adaptive evolutionary change (Lewontin, 1970; Godfrey-Smith, 2007). Let us therefore reinterpret the summary statistics of phenotypes from Chapter 2 in light of the causal decomposition equation (3.31).

[i]In the information-theoretic language we used in Chapter 2, we might say that $\mathbf{A}$ represents the component of the phenotype due to the particular assemblage of information held by an individual, and $\mathbf{E}$ a component due to the interaction of, and subsequent interpretation of, that information by the environment.

We start with the vector of average trait values in the population, $\bar{\boldsymbol{z}} = \mathbf{Z}^{\mathrm{T}}\boldsymbol{x}$. If we substitute into this equation for the genotype-phenotype map, $\mathbf{Z}$, given by the causal decomposition equation (3.31), we have

$$\bar{\boldsymbol{z}} = \mathbf{Z}^{\mathrm{T}}\boldsymbol{x} = (\mathbf{A}^{\mathrm{T}} + \mathbf{U}^{\mathrm{T}})\boldsymbol{x} = \mathbf{A}^{\mathrm{T}}\boldsymbol{x} + \mathbf{U}^{\mathrm{T}}\boldsymbol{x} = \bar{\boldsymbol{a}} + \bar{\boldsymbol{u}} = \bar{\boldsymbol{a}}, \tag{3.32}$$

where $\bar{\boldsymbol{u}} = \mathbf{U}^{\mathrm{T}}\boldsymbol{x} = \mathbf{0}$ follows from the assumption of population-weighted least-squares that the expected value of the residuals is always zero (see Box 3.3), and $\bar{\boldsymbol{a}} = \mathbf{A}^{\mathrm{T}}\boldsymbol{x}$ is a $|\mathbb{P}| \times 1$ vector containing the average genetic values in the population at any instant in time, t. Thus we see that the vector of average trait values in the population, $\bar{\boldsymbol{z}}$, is equal to the vector of average genetic values in the population, $\bar{\boldsymbol{a}}$, at any time t.

This finding is important because we expect the evolutionary response to natural selection to give rise to changes in the average phenotypic trait values over time, and equation (3.32) shows that we can study this change just as well using average genetic values, $\bar{\boldsymbol{a}}$, as we can using average phenotypic trait values, $\bar{\boldsymbol{z}}$. As Frank (1998, pg. 16) notes, under the assumption that the relationship between trait values and genetic values remains relatively constant through time, this property can help to greatly simplify evolutionary analyses as 'the difficulty for any method of describing character change between generations is that observed character values, z, will have many causes that are not easily understood... it would be much better if, instead of working with z as the character under study, we could focus on those predictors of the character that can be clearly identified.' For instance, whilst any given bull and cow will typically express very different phenotypic trait values for milk production, they both carry genes that are reliable predictors of milk production and therefore their genetic values for this trait will typically be very similar.

The genetic values of traits held by individuals in our population correspond to the portion of the phenotype that we can attribute to the average effect of genes. Since genetic values are measurable properties of individuals, we can write an alternative version of the Malthusian Price equation (2.48) to understand the total change in the average genetic values in the population, $\dot{\bar{a}}$. In vector-matrix notation the equation is given by

$$\dot{\bar{\boldsymbol{a}}} = \mathbf{A}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m} + (\Delta\mathbf{A})^{\mathrm{T}}\mathbf{X}\boldsymbol{b} + \dot{\mathbf{A}}^{\mathrm{T}}\boldsymbol{x}, \tag{3.33}$$

where all the references to the genotype-phenotype map, $\mathbf{Z}$, have once more been replaced by references to the matrix of genetic values, $\mathbf{A}$, so that $\mathbf{A}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m}$ is a vector of covariances

of genetic values with Malthusian fitness, $\Delta\mathbf{A}$ is the difference between the expected value of genetic values in descendants and their ancestors, and $\dot{\mathbf{A}}^{\mathrm{T}}\boldsymbol{x}$, gives the expected values of the derivative of the matrix of genetic values with respect to time, t. An important corollary of the equality $\bar{\boldsymbol{z}} = \bar{\boldsymbol{a}}$ given by equation (3.32), however, is that the total change of the average genetic values is equal to the total change in average trait values, so that $\dot{\bar{\boldsymbol{z}}} = \dot{\bar{\boldsymbol{a}}}$, and we can re-write equation (3.33) as

$$\dot{\bar{\boldsymbol{z}}} = \mathbf{A}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m} + (\Delta\mathbf{A})^{\mathrm{T}}\mathbf{X}\boldsymbol{b} + \dot{\mathbf{A}}^{\mathrm{T}}\boldsymbol{x}, \tag{3.34}$$

This equation provides us with a picture of the dynamics of natural selection that is somewhat intermediate between the phenotypic and genic perspectives we have described before. On the one hand, equation (3.34) suggests that we are studying the total change in average phenotypic values, $\bar{\boldsymbol{z}}$, but on the other it also suggests that we are studying change from the perspective of the genetic values associated with traits. Following the term used by Fisher (1930), we therefore refer to equation (3.34) as the 'genetical version' of the Malthusian Price equation[j].

The components of the genetical form of the Malthusian Price equation (3.34) can be interpreted, with care, in a similar way to those from the Malthusian Price equation (2.48) from Chapter 2. Whereas the Malthusian Price equation (2.49) focuses our attention on the phenotype of individuals, however, the genetical version of the Malthusian Price equation (3.34) focuses our attention on the portion of the phenotype of individuals that can be attributed to the average effects of genetic factors. Thus we have a component associated with natural selection, $\boldsymbol{A}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m}$, and transmission fidelity, $(\Delta\boldsymbol{A})^{\mathrm{T}}\mathbf{X}\boldsymbol{b}$, and change in the average effects of genes, $\dot{\mathbf{A}}^{\mathrm{T}}\boldsymbol{x}$. Since the genetic factors held by individuals are constant, one might expect that the matrix of genetic values, $\mathbf{A}$, would also be constant, but this is not case. Genetic values are calculated from the average effects of genes, and even in the absence of phenotypic plasticity and ecological inheritance mechanisms, average effects depend crucially on the composition of the population, $\boldsymbol{n}$, and so vary through time.

We are also interested in the variance in traits, since natural selection cannot act on a population in the absence of phenotypic variance (Lewontin, 1970; Godfrey-Smith, 2007). The phenotypic variances of each trait in the population are held by the diagonal elements

[j]The term 'genetical' was originally used by Fisher (1930), but has also been adopted by those studying kin (Hamilton, 1964; Gardner et al., 2011) and multi-level (Gardner, 2015) selection theory. In our population the term concerns genetic values associated with the set of traits, $\mathbb{P}$. It is not to be confused with the term 'genic', which concerns the set of genetic factors, $\mathbb{L}$.

of the variance-covariance matrix $\mathbf{P} = \mathbf{Z}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{Z}$, given by equation (2.12) in Chapter 2. If we substitute into this equation for the definition of the genotype-phenotype map, $\mathbf{Z}$, given by the causal decomposition equation (3.31), we obtain

$$\mathbf{P} = \mathbf{A}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{A} + \mathbf{A}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{U} + \mathbf{U}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{A} + \mathbf{U}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{U} = \mathbf{A}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{A} + \mathbf{U}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{U} = \mathbf{G} + \mathbf{E}, \tag{3.35}$$

where we have simplified using $\mathbf{A}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{U} = \mathbf{U}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{A} = \mathbf{0}$ which follows from the assumption of population-weighted least-squares that the explanatory variables and residuals are always uncorrelated (Box 3.3), $\mathbf{G} = \mathbf{A}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{A}$ is a square symmetric $|\mathbb{P}| \times |\mathbb{P}|$ variance-covariance matrix of genetic values, and $\mathbf{E} = \mathbf{U}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{U}$ is a square symmetric $|\mathbb{P}| \times |\mathbb{P}|$ variance-covariance matrix of environmental deviations. Thus we see that the total phenotypic variance of traits in the population, given by the diagonal elements of $\mathbf{P}$, can be decomposed at any instantaneous moment in time, t, into the variance explained by the average effects of the genetic factors held by individuals, given by the diagonal elements of $\mathbf{G}$, and the variance due to the environmental deviations about these average effects, given by the diagonal elements of $\mathbf{E}$.

When the causal decomposition expressed by equation (3.31) has been performed in experimental settings, data have suggested that the dominant proportion of phenotypic variance in most populations is attributable to genetic variance (Hill et al., 2008). Hence, the dominant proportion of phenotypic variance in natural populations appears to be best explained by variance in the effects of genetic factors, rather than variance attributable to environmental variables. The relationship between the phenotypic and genetic variance in populations is what gives rise to Fisher's (1918) notion of heritability. Before exploring this idea further, let us briefly explore the matrix $\mathbf{G} = \mathbf{A}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{A}$. By substituting into this equation for the matrix of genetic values, $\mathbf{A}$, from equation (3.29), we obtain, after expansion and simplification

$$\begin{aligned}
\mathbf{G} &= \left(\mathbf{1}\bar{\boldsymbol{z}}^{\mathrm{T}} + (\boldsymbol{\Lambda} - \mathbf{1}\bar{\boldsymbol{\lambda}}^{\mathrm{T}})\hat{\boldsymbol{\beta}}_{z\lambda}\right)^{\mathrm{T}} \boldsymbol{\Sigma} \left(\mathbf{1}\bar{\boldsymbol{z}}^{\mathrm{T}} + (\boldsymbol{\Lambda} - \mathbf{1}\bar{\boldsymbol{\lambda}}^{\mathrm{T}})\hat{\boldsymbol{\beta}}_{z\lambda}\right) \\
&= \bar{\boldsymbol{z}}\mathbf{1}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{1}\bar{\boldsymbol{z}}^{\mathrm{T}} + \bar{\boldsymbol{z}}\mathbf{1}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{\Lambda}\hat{\boldsymbol{\beta}}_{z\lambda} + \bar{\boldsymbol{z}}\mathbf{1}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{1}\bar{\boldsymbol{\lambda}}^{\mathrm{T}}\hat{\boldsymbol{\beta}}_{z\lambda} + \boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{1}\bar{\boldsymbol{z}}^{\mathrm{T}} + \hat{\boldsymbol{\beta}}_{z\lambda}^{\mathrm{T}}\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{\Lambda}\hat{\boldsymbol{\beta}}_{z\lambda} \\
&\quad + \boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{1}\bar{\boldsymbol{\lambda}}^{\mathrm{T}}\hat{\boldsymbol{\beta}}_{z\lambda} + \hat{\boldsymbol{\beta}}_{z\lambda}^{\mathrm{T}}\bar{\boldsymbol{\lambda}}\mathbf{1}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{1}\bar{\boldsymbol{z}}^{\mathrm{T}} + \hat{\boldsymbol{\beta}}_{z\lambda}^{\mathrm{T}}\bar{\boldsymbol{\lambda}}\mathbf{1}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{\Lambda}\hat{\boldsymbol{\beta}}_{z\lambda} + \hat{\boldsymbol{\beta}}_{z\lambda}^{\mathrm{T}}\bar{\boldsymbol{\lambda}}\mathbf{1}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{1}\bar{\boldsymbol{\lambda}}^{\mathrm{T}}\hat{\boldsymbol{\beta}}_{z\lambda} \\
&= \hat{\boldsymbol{\beta}}_{z\lambda}^{\mathrm{T}}\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{\Lambda}\hat{\boldsymbol{\beta}}_{z\lambda},
\end{aligned} \tag{3.36}$$

where any term involving a product of the covariance operator with a vector of ones, $\boldsymbol{\Sigma}\mathbf{1}$ or $\mathbf{1}^{\mathrm{T}}\boldsymbol{\Sigma}$, corresponds to the covariance of a quantity with a constant, and hence has

dropped out of the equation. Substituting for the definition of the matrix of the sums of average effects, $\mathbf{V} = \mathbf{\Lambda}\hat{\boldsymbol{\beta}}_{z\lambda}$ from equation (3.25), we see that the variance-covariance matrix $\mathbf{G}$ can be re-written as

$$\mathbf{G} = \mathbf{V}^{\mathrm{T}}\mathbf{\Sigma}\mathbf{V} = \hat{\boldsymbol{\beta}}_{z\lambda}^{\mathrm{T}}\mathbf{\Lambda}^{\mathrm{T}}\mathbf{\Sigma}\mathbf{\Lambda}\hat{\boldsymbol{\beta}}_{z\lambda} = \hat{\boldsymbol{\beta}}_{z\lambda}^{\mathrm{T}}\mathbf{L}\hat{\boldsymbol{\beta}}_{z\lambda}, \tag{3.37}$$

such that it equivalently represents a variance-covariance matrix for genetic values, $\mathbf{A}$, a variance-covariance matrix for the sums of average effects, $\mathbf{V}$, and an average-effect-weighted variance-covariance matrix for genetic factors, $\hat{\boldsymbol{\beta}}_{z\lambda}^{\mathrm{T}}\mathbf{L}\hat{\boldsymbol{\beta}}_{z\lambda}$. The importance of the matrix $\mathbf{G}$ in quantitative genetics stems from the fact that it holds the additive genetic variances from which we calculate the heritability of traits, and captures constraints on the evolutionary response to natural selection brought about correlations between different genetic factors due to phenomena such as pleiotropy, epistasis, and linkage disequilibrium (Arnold, 1992; Barton et al., 2000).

3.2.5 Heritability

Heritability (in the narrow-sense) is a statistical quantity defined as the proportion of the total phenotypic variance in a population that is attributable, in a causal sense, to the effect of a set of genetic factors (Fisher, 1918; Jacquard, 1983; Falconer and Mackay, 1995; Godfrey-Smith, 2007)[k]. It therefore allows a comparison of the relative importance of genetic factors or environmental effects in the determination of phenotypic variance in populations (Visscher et al., 2008).

To obtain the heritability of traits in the context of our population at any time, t, we first reverse the direction of the GLM equation (3.21) to regress the matrix of genetic values, $\mathbf{A}$, on the phenotypic trait values in the genotype-phenotype map, $\mathbf{Z}$, for which we obtain

$$\mathbf{A} = \mathbf{1}\hat{\boldsymbol{\alpha}}_{az}^{\mathrm{T}} + \mathbf{Z}\hat{\boldsymbol{\beta}}_{az} + \hat{\boldsymbol{\varepsilon}}_{az}. \tag{3.38}$$

[k]Sometimes heritability is described more abstractly as a direct measure of parent-offspring resemblance for a phenotypic trait (Godfrey-Smith, 2007), which is the sense in which (1970) used it in defining the principles that embody evolution by natural selection. A formal definition of this measure of resemblance between relatives is given by 'realised' or 'biometric' heritability (Jacquard, 1983; Falconer and Mackay, 1995).

where the vector $\hat{\boldsymbol{\alpha}}_{az} = \bar{\boldsymbol{a}} - \hat{\boldsymbol{\beta}}_{az}^{\mathrm{T}}\bar{\boldsymbol{z}}$ and the matrix $\hat{\boldsymbol{\beta}}_{az} = (\mathbf{Z}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{Z})^{-1}\mathbf{Z}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{A}$ hold the intercept coefficients and partial regression coefficients of the GLM, respectively, determined by the method of population-weighted least-squares, and the matrix $\hat{\boldsymbol{\varepsilon}}_{az} \in \mathbb{R}^{|\mathbb{G}|\times|\mathbb{P}|}$ contains the residuals from the regression.

Although regressing the genetic values on the trait values might seem like an unusual thing to do, it is useful because we can think of the partial regression coefficient matrix, $\hat{\boldsymbol{\beta}}_{az}$, as expressing a measure of the *reliability* of the phenotypic trait values as a guide to the *underlying* genetic value of traits (Falconer and Mackay, 1995)[1]. If we substitute into the equation for $\hat{\boldsymbol{\beta}}_{az}$ for the genotype-phenotype map, $\mathbf{Z}$, given by the causal decomposition equation (3.31), and simplify, we obtain

$$\begin{aligned}\hat{\boldsymbol{\beta}}_{az} &= (\mathbf{Z}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{Z})^{-1}(\mathbf{A}+\mathbf{U})^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{A} \\ &= (\mathbf{Z}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{Z})^{-1}(\mathbf{A}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{A}+\mathbf{U}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{A}) \\ &= (\mathbf{Z}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{Z})^{-1}\mathbf{A}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{A},\end{aligned} \tag{3.39}$$

where we have we have used the property that the covariance matrix of the explanatory variables and the residuals of a population-weighted least-squares linear model are always zero (Box 3.3), so that $\mathbf{U}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{A} = \mathbf{0}$. We can then substitute for the definition of the phenotypic variance-covariance matrix, $\mathbf{P} = \mathbf{Z}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{Z}$, and the variance-covariance matrix of genetic values, $\mathbf{G} = \mathbf{A}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{A}$ from equation (3.35), and transpose the equation so that the matrix of partial regression coefficients is given by

$$\hat{\boldsymbol{\beta}}_{az}^{\mathrm{T}} = \mathbf{G}\mathbf{P}^{-1}. \tag{3.40}$$

Hence we have shown that the matrix of partial regression coefficients, $\hat{\boldsymbol{\beta}}_{az}$, is equal to the product of the inverse of the phenotypic variance-covariance matrix, $\mathbf{P}^{-1}$, and the variance-covariance matrix of genetic values, $\mathbf{G}$.

In some sense we can view this matrix multiplication as $\mathbf{G}$ divided by $\mathbf{P}$, and can see that $\hat{\boldsymbol{\beta}}_{az}^{\mathrm{T}}$ therefore represents the *proportion* of the total phenotypic variance in a population, held in the matrix $\mathbf{P}$, that is attributable to the genetic values of traits, held in the matrix $\mathbf{G}$ (Fisher, 1918; Jacquard, 1983; Falconer and Mackay, 1995; Godfrey-Smith, 2007). The matrix $\hat{\boldsymbol{\beta}}_{az}$ therefore corresponds to a form of multivariate (narrow-sense)

[1]In fact, this idea can be formalised by considering the close relationship between $\hat{\boldsymbol{\beta}}_{az}$ and a multivariate form of what is called the 'coefficient of determination', R^2, in ordinary least squares theory.

heritability measure akin to that in the multivariate breeder's equation (3.2). Indeed, note that in the special case in which we are interested in a single trait only, say the kth phenotypic trait, equation (3.40) reduces to $\hat{\beta}_{a_{ik}z_{ik}} = \mathrm{Var}_{i\in\mathbb{G}}(a_{ik})/\mathrm{Var}_{i\in\mathbb{G}}(z_{ik}) = h^2_k$, which is Fisher's (1918) definition of (narrow-sense) heritability used in the univariate breeder's equation (3.1).

3.2.6 Selection coefficients

Let us now turn to exploring how the principles of evolutionary genetics can be used to summarise the phenotype-fitness relationship. There are two types of 'selection coefficients' in evolutionary genetics responsible for summarising this relationship. Firstly, the 'selection *differential*' is a dynamical measure defined by the change in the average value of traits brought about by the action of natural selection (Phillips and Arnold, 1989; Falconer and Mackay, 1995). For a single trait, this corresponds to the covariance terms in the Price equation (2.5) (Box 2.3, Chapter 2; Price, 1970; 1972a) and the univariate breeder's equation (3.1) (Box 3.1; Lush, 1937; Falconer, 1995). For multiple traits, it corresponds to the vector of covariances in the multivariate breeder's equation (3.2) (Box 3.1; Lande, 1979; Lande & Arnold, 1983). Secondly, the 'selection *gradient*' is a geometrical measure of the gradient of the adaptive landscape, which is a representation of population average fitness as a function of population average trait values (Lande, 1979; Lande and Arnold, 1983; Phillips and Arnold, 1989). Selection gradients are indicators of *directional* selection on each trait independently (ignoring the effects on fitness of other traits), whereas selection differentials reflect the impact of both *direct* selection on a focal trait as well as *indirect* selection on traits with which the focal trait is correlated. Here, we will explore both types of selection coefficient from three different perspectives: *phenotypic*—using the first term of the Malthusian Price equation (2.48) from Chapter 2, which describes changes in the average value of phenotypic traits due to natural selection; *ii*) *genic*—using the first term of the genic version of the Malthusian Price equation (3.6), which describes changes in the relative frequency of genetic factors in the population due to natural selection; and *iii*) *genetical*—using the first term of the genetical version of the Malthusian Price equation (3.6), which describes changes in the average value of the *heritable portion* of phenotypic traits due to natural selection. We will see that one of these perspectives formalises the requirement for an evolutionary response to natural selection (Lewontin, 1970; Godfrey-Smith, 2007).

3.2.6.1 Phenotypic

We start with phenotypic selection coefficients. Recall that the total change in the average trait values in the population, $\dot{\bar{\boldsymbol{z}}}$, over time is given by the Malthusian Price equation (2.48) we derived in Chapter 2. The selection differential is a dynamical measure defined by the change in the average value of traits brought about by the action of natural selection (Lush, 1937; Phillips and Arnold, 1989; Falconer and Mackay, 1995). The change in the average value of traits brought about by the action of natural selection in our population is given by the first term of the Malthusian Price equation (2.48) only, which we now denote by

$$\boldsymbol{s}_{zm} = \mathbf{Z}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m} = \begin{bmatrix} \mathrm{Cov}_{i\in\mathbb{G}}(z_{i1}, m_i) \\ \vdots \\ \mathrm{Cov}_{i\in\mathbb{G}}(z_{i|\mathbb{P}|}, m_i) \end{bmatrix}, \tag{3.41}$$

and refer to as the 'phenotypic version' of the vector of 'Malthusian selection differentials'. The vector is the Malthusian analogue in our framework to the vector $\boldsymbol{s}_{z\omega}$ in the multivariate breeder's equation (3.2) (Box 3.1; Lande, 1979; Lande & Arnold, 1983).

Selection differentials are equivalent to covariances between each trait and fitness. Thus, each element of the vector holds the statistical associations, $\mathrm{Cov}_{i\in\mathbb{G}}(z_{ik}, m_i)$, between the trait values held by individuals, z_{ik}, and their Malthusian fitness, m_i. Using this fact, Lande (1979) and Lande and Arnold (1983) showed that the selection differentials that present themselves in the dynamical equations for change in average traits can also be 'estimated' from phenotypic 'data' using ordinary least-squares linear regression.

At any point in time, t, we can similarly fit a multiple linear regression model in our population for the Malthusian fitness vector, $\boldsymbol{m}$, on the genotype-phenotype map, $\mathbf{Z}$, by the method of population-weighted least-squares to obtain

$$\boldsymbol{m} = \mathbf{1}\hat{\alpha}_{mz}^{\mathrm{T}} + \mathbf{Z}\hat{\boldsymbol{\beta}}_{mz} + \hat{\boldsymbol{\varepsilon}}_{mz}, \tag{3.42}$$

where the scalar $\hat{\alpha}_{mz} = \bar{m} - \hat{\boldsymbol{\beta}}_{mz}^{\mathrm{T}}\bar{\boldsymbol{z}}$ is the intercept coefficient from the linear model, the $|\mathbb{P}| \times 1$ vector $\hat{\boldsymbol{\beta}}_{mz} = (\mathbf{Z}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{Z})^{-1}\mathbf{Z}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m}$ contains the partial regression coefficients, and the $|\mathbb{G}| \times 1$ vector $\hat{bm}\varepsilon_{mz}$ contains the residuals from the regression. Equation (3.42)

represents a linear approximation to a selection surface that we will call the 'phenotypic version' of the 'Malthusian individual selection surface'[m].

The intercept coefficient, $\hat{\alpha}_{mz}$, can be thought of as the 'baseline' Malthusian fitness of individuals in our population before we have taken into account the trait values they express. The vector of partial regression coefficients, $\hat{\boldsymbol{\beta}}_{mz}$, summarises the statistical association between phenotypic traits and Malthusian fitness. It can be re-written in the form

$$\hat{\boldsymbol{\beta}}_{mz} = \mathbf{P}^{-1}\boldsymbol{s}_{zm}, \tag{3.43}$$

where $\mathbf{P} = \mathbf{Z}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{Z}$ is the $|\mathbb{P}| \times |\mathbb{P}|$ phenotypic variance-covariance matrix given by equation (2.12) in Chapter 2, and the $|\mathbb{P}| \times 1$ vector $\boldsymbol{s}_{zm} = \mathbf{Z}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m}$ is the phenotypic version of the vector of Malthusian selection differentials just described.

The kth element of $\hat{\boldsymbol{\beta}}_{mz}$ can be interpreted as the slope of the line that best describes a linear relationship between the Malthusian fitness of individuals in the population and the kth phenotypic trait value after holding the effects of all other traits constant (Phillips and Arnold, 1989). In this way, the vector of partial regression coefficients, $\hat{\boldsymbol{\beta}}_{mz}$, can be used as a measure of directional selection on traits, giving the direction of the steepest 'uphill' slope on a phenotypic version of the individual selection surface (Phillips and Arnold, 1989). We therefore refer to the vector of partial regression coefficients, $\hat{\boldsymbol{\beta}}_{mz}$, as the 'phenotypic version' of the 'Malthusian directional selection gradient'.

An important corollary of equation (3.43) is that we may re-write the phenotypic version of the vector of Malthusian directional selection differentials as

$$\boldsymbol{s}_{zm} = \mathbf{P}\hat{\boldsymbol{\beta}}_{mz}. \tag{3.44}$$

We can interpret this form as showing that change in the average value of the kth trait brought about by the action of natural selection can be partitioned into a sum of components due to *direct* selection on that trait, plus a set of components due to *indirect*

[m]The approach of formulating a least-squares linear regression-based approximation to the individual selection surface has been questioned in recent years (Allen et al., 2013). The least-squares approach used in quantitative genetics Lande (1979); Lande and Arnold (1983), is really very closely related the Taylor expansion approach used in the framework of *adaptive dynamics* (Hofbauer and Sigmund, 1990). Thus criticisms levelled at one framework would also largely hold true for the other, highlighting the need for plurality in evolutionary thinking.

selection on all other traits with which the kth trait is phenotypically correlated. In particular, the component of the sum given by $\text{Var}_{i\in\mathbb{G}}(z_{ik})\hat{\beta}_{mz,k}$ determines the impact of direct selection on the kth trait, whilst the set of components of the sum given by $\text{Cov}_{i\in\mathbb{G}}(z_{ik}, z_{il})\hat{\beta}_{mz,l}$ determine the impact of indirect selection due to a phenotypic correlation between the kth and lth traits.

Equation (3.44) is remarkable because it establishes a formal connection between population-weighted least-squares theory and the Malthusian Price equation (2.48) from Chapter 2. To some evolutionary theorists, the use of the least-squares theory in evolutionary biology is considered to be contrived and even counter-productive (van Veelen, 2005; Allen et al., 2013). Here, however, we see that it emerges perfectly naturally in the context of the phenotypic perspective of the dynamics of natural selection that we studied in Chapter 2. This is interesting because, as Crow (2008) has put it, it seems to suggest that 'nature discovered least squares long before Gauss.' That is, it seems to provide an indication that the process of least-squares *minimisation* is related in some way to the process of fitness *maximisation* brought about through the action of natural selection. In this way, it forms the foundations for a formal understanding of the process of evolution by natural selection as one of *optimisation* (Grafen, 2002). We will return to this point later when we consider the dynamics of the evolutionary response to selection as a process taking place on an adaptive landscape (Phillips and Arnold, 1989).

Another important point about equation (3.44), is that it formalises Fisher's (1930) claim that 'natural selection is not evolution', by showing that the component of the phenotypic version of the Malthusian Price equation (2.48) we associate with natural selection does not in fact correspond to that which we associate with the *evolutionary response* to natural selection (Lewontin, 1970; Godfrey-Smith, 2007). In particular, we now see that the natural selection component of the Malthusian Price equation (2.48), captures the requirement for phenotypic variation, via the variance-covariance matrix of phenotypic traits, $\mathbf{P}$, and the requirement for a statistical association between traits held by individuals and their Malthusian fitness, via the phenotypic version of the Malthusian directional selection gradient, $\hat{\boldsymbol{\beta}}_{mz}$, but crucially does not saying anything about a requirement for the *heritability* of traits (Lewontin, 1970; Godfrey-Smith, 2007).

3.2.6.2 Genic

Of course, since we didn't incorporate any of our knowledge about the genetic factors underlying the expression of phenotypic traits in the GLM equation (3.42), it is no surprise that we learnt nothing about heritability. It will also come as no surprise that to

understand heritability we need to study selection differentials involving genetic values, which constitute the heritable portion of phenotypic traits (Falconer and Mackay, 1995). Before doing this, however, let us focus on the underlying genetic factors of traits. The total change in the relative frequency of genetic factors in the population, $\dot{\bar{\boldsymbol{\lambda}}}$, is given by the genic version of the Malthusian Price equation (3.6). The change in the relative frequency of genetic factors brought about by the first term of this equation which we now denote by

$$\boldsymbol{s}_{\lambda m} = \boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m} = \begin{bmatrix} \mathrm{Cov}_{i\in\mathbb{G}}(\lambda_{i1}, m_i) \\ \vdots \\ \mathrm{Cov}_{i\in\mathbb{G}}(\lambda_{i|\mathbb{L}|}, m_i) \end{bmatrix}, \tag{3.45}$$

and refer to as the 'genic version' of the vector of 'Malthusian selection differentials'. Each element of the vector holds the statistical associations, $\mathrm{Cov}_{i\in\mathbb{G}}(\lambda_{il}, m_i)$, between the genetic factors held by individuals, λ_{il}, and their Malthusian fitness, m_i.

As we saw from a phenotypic perspective (Lande, 1979; Lande and Arnold, 1983), selection differentials can also be derived as a result of expressing fitness as a linear regression on trait values. Using the same approach for genetic factors, we can fit a multiple linear regression model in our population at any point in time, t, for the Malthusian fitness vector, $\boldsymbol{m}$, not on the genotype-phenotype map, $\mathbf{Z}$, but on the matrix of genetic values, $\boldsymbol{\Lambda}$, by the method of population-weighted least-squares to obtain

$$\boldsymbol{m} = \mathbf{1}\hat{\alpha}_{m\lambda}^{\mathrm{T}} + \boldsymbol{\Lambda}\hat{\boldsymbol{\beta}}_{m\lambda} + \hat{\boldsymbol{\varepsilon}}_{m\lambda}, \tag{3.46}$$

where the scalar $\hat{\alpha}_{m\lambda} = \bar{m} - \hat{\boldsymbol{\beta}}_{m\lambda}^{\mathrm{T}}\bar{\boldsymbol{\lambda}}$ is the intercept coefficient from the linear model, the $|\mathbb{L}| \times 1$ vector $\hat{\boldsymbol{\beta}}_{m\lambda} = (\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{\Lambda})^{-1}\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m}$ contains the partial regression coefficients, and the $|\mathbb{G}| \times 1$ vector $\hat{\boldsymbol{\varepsilon}}_{m\lambda}$ contains the residuals from the regression.

Once again, the intercept coefficient, $\hat{\alpha}_{m\lambda}$, can be thought of as the 'baseline' Malthusian fitness of individuals in our population before we have taken into account the effects of genetic factors held by individuals. The vector of partial regression coefficients, $\hat{\boldsymbol{\beta}}_{m\lambda}$, summarises the statistical association between the genetic factors held by individuals and their Malthusian fitness. It can be re-written in the form

$$\hat{\boldsymbol{\beta}}_{m\lambda} = \mathbf{L}^{-1}\boldsymbol{s}_{\lambda m}, \tag{3.47}$$

where $\mathbf{L} = \mathbf{\Lambda}^{\mathrm{T}}\mathbf{\Sigma}\mathbf{\Lambda}$ is the $|\mathbb{L}| \times |\mathbb{L}|$ variance-covariance matrix of genetic factors given by equation (3.5), and the $|\mathbb{L}| \times 1$ vector $\boldsymbol{s}_{z\lambda} = \mathbf{\Lambda}^{\mathrm{T}}\mathbf{\Sigma}\boldsymbol{m}$ is the genic version of the vector of Malthusian selection differentials just described.

Recall that in the regression of the genotype-phenotype map, $\mathbf{Z}$, on the matrix of genetic factors, $\mathbf{\Lambda}$, given by equation (3.21), we interpreted the matrix of partial regression coefficients $\hat{\boldsymbol{\beta}}_{z\lambda}$ as a matrix of 'average effects' of genes on trait values. Since the Malthusian fitness of individuals is really a special kind of phenotypic trait, we can similarly interpret the vector of partial regression coefficients, $\hat{\boldsymbol{\beta}}_{m\lambda}$, as a vector of average *fitness* effects. Alternatively, $\hat{\boldsymbol{\beta}}_{m\lambda}$ can be used as a measure of directional selection on each genetic factor, giving the direction of the steepest uphill slope on a population genetic version of the individual selection surface (Phillips and Arnold, 1989). We therefore refer to the vector of partial regression coefficients, $\hat{\boldsymbol{\beta}}_{m\lambda}$, as the 'genic version' of the 'Malthusian directional selection gradient'.

A corollary of equation (3.47) is that we may re-write the genic version of the vector of Malthusian selection differentials as

$$\boldsymbol{s}_{\lambda m} = \mathbf{L}\hat{\boldsymbol{\beta}}_{m\lambda}. \tag{3.48}$$

We can interpret these selection differentials as showing that change in the relative frequency of the lth genetic factor in the population brought about by the action of natural selection can be partitioned into a sum of components due to *direct* selection on that genetic factor, and a set of components due to *indirect* selection on all other genetic factors with which the lth genetic factor is *genetically* correlated. Indirect selection in this genetic context corresponds to a phenomenon known as 'genetic hitchhiking' (Maynard Smith and Haigh, 1974; Barton, 2000). The component of the sum given by $\mathrm{Var}_{i\in\mathbb{G}}(\lambda_{il})\hat{\beta}_{m\lambda,l}$ determines the impact of direct selection on the lth genetic factor, whilst the set of components of the sum given by $\mathrm{Cov}_{i\in\mathbb{G}}(\lambda_{ik}, \lambda_{il})\hat{\beta}_{m\lambda,k}$ determine the impact of indirect selection due to a genetic correlation between the lth and kth genetic factors. These genetic correlations correspond to a phenomenon known 'linkage disequilibrium', and may be brought about for numerous reasons, including because of the action of selection on the composition of the population, or because of features of genetic systems like mutation and recombination (Hill and Robertson, 1968; Falconer and Mackay, 1995).

Despite studying genetic change in our population, equation (3.48) still fails to capture the conditions required for a formal definition of the evolutionary response to natural selection. Once more we see that natural selection requires variation, in this case genetic

variation, via the variance-covariance matrix of genetic factors, $\mathbf{L}$, and the requirement for a statistical association between genetic factors held by individuals and their Malthusian fitness, via the genic version of the Malthusian directional selection gradient, $\hat{\boldsymbol{\beta}}_{m\lambda}$, but once more does not saying anything about a requirement for the *heritability* (Lewontin, 1970; Godfrey-Smith, 2007).

3.2.6.3 Genetical

So far we have seen that selection differentials calculated from a phenotypic and genic perspective fail to formalise the conditions required for an evolutionary response to natural selection (Lewontin, 1970; Godfrey-Smith, 2007). For this will now study selection differentials involving genetic values, which constitute the heritable portion of phenotypic traits (Falconer and Mackay, 1995). Once more we focus our attention on the component of change in the average value of traits brought about by the action of natural selection on the genetical values held by individuals. This is given by the first term of the genetical version of the Malthusian Price equation (3.34), which we denote by

$$\boldsymbol{s}_{am} = \mathbf{A}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m} = \begin{bmatrix} \mathrm{Cov}_{i\in\mathbb{G}}(a_{i1}, m_i) \\ \vdots \\ \mathrm{Cov}_{i\in\mathbb{G}}(a_{i|\mathbb{P}|}, m_i) \end{bmatrix}, \tag{3.49}$$

and refer to as the 'genetical version' of the vector of 'Malthusian selection differentials'. Each element of the vector holds the statistical associations, $\mathrm{Cov}_{i\in\mathbb{G}}(a_{ik}, m_i)$, between the genetic values held by individuals, z_{ik}, and their Malthusian fitness, m_i. We will see in the next section that this vector corresponds to a multivariate Malthusian form of the selection differential defining Robertson's (1966) equation, a central result in quantitative genetic theory (Falconer and Mackay, 1995).

As in the previous sections, our goal at this point is to use the approach of Lande (1979) and Lande and Arnold (1983) to explore the relationship between selection differentials and traits. Here, however, we will consider only the portion of trait values attributable to the action of genes held by individuals, that is, genetic values (Falconer and Mackay, 1995). In particular, at any point in time, t, we can fit a multiple linear regression model in our population for the Malthusian fitness vector, $\boldsymbol{m}$, not on the genotype-phenotype map, $\mathbf{Z}$, or the matrix of genetic factors, $\boldsymbol{\Lambda}$, but on the matrix of genetic values, $\mathbf{A}$, by the method of population-weighted least-squares to obtain

$$\boldsymbol{m} = \mathbf{1}\hat{\alpha}_{ma}^{\mathrm{T}} + \mathbf{A}\hat{\boldsymbol{\beta}}_{ma} + \hat{\boldsymbol{\varepsilon}}_{ma}, \tag{3.50}$$

where the scalar $\hat{\alpha}_{ma} = \bar{m} - \hat{\boldsymbol{\beta}}_{ma}^{\mathrm{T}}\bar{\boldsymbol{a}}$ is the intercept coefficient from the linear model, the $|\mathbb{P}| \times 1$ vector $\hat{\boldsymbol{\beta}}_{ma} = (\mathbf{A}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{A})^{-1}\mathbf{A}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m}$ contains the partial regression coefficients, and the $|\mathbb{G}| \times 1$ vector $\hat{\boldsymbol{\varepsilon}}_{ma}$ contains the residuals from the regression.

As always, the intercept coefficient, $\hat{\alpha}_{ma}$, can be thought of as the 'baseline' Malthusian fitness of individuals before we have taken into account the genetic values they hold, but the vector of partial regression coefficients, $\hat{\boldsymbol{\beta}}_{ma}$, now summarises the statistical association between genetic values and Malthusian fitness. In particular, it can be re-written as

$$\hat{\boldsymbol{\beta}}_{ma} = \mathbf{G}^{-1}\boldsymbol{s}_{am}, \tag{3.51}$$

where $\mathbf{G} = \mathbf{A}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{A}$ is the $|\mathbb{P}| \times |\mathbb{P}|$ variance-covariance matrix of genetic values defined by equation (3.35), and the $|\mathbb{P}| \times 1$ vector $\boldsymbol{s}_{am} = \mathbf{A}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m}$ is the genetical version of the vector of Malthusian selection differentials just described. The kth element of $\hat{\boldsymbol{\beta}}_{ma}$ can be interpreted as the slope of the line that best describes a linear relationship between the Malthusian fitness of individuals in the population and the kth genetic value after holding the genetic values of all other traits constant (Phillips and Arnold, 1989). In this way, the vector of partial regression coefficients, $\hat{\boldsymbol{\beta}}_{ma}$, can be used as a measure of directional selection on genetic values, giving the direction of the steepest uphill slope on a genetical version of the individual selection surface (Phillips and Arnold, 1989). We therefore refer to the vector of partial regression coefficients, $\hat{\boldsymbol{\beta}}_{ma}$, as the 'genetical version' of the 'Malthusian directional selection gradient'.

Equation (3.51) allows us to re-write the genetical version of the vector of Malthusian selection differentials as

$$\boldsymbol{s}_{am} = \mathbf{G}\hat{\boldsymbol{\beta}}_{ma}. \tag{3.52}$$

We can interpret this as showing that change in the average value of the kth trait brought about by the action of natural selection can be partitioned into a sum of components due to *direct* selection on the genetic value of the trait, plus a set of components due to *indirect* selection on the genetic values of all other traits with which the kth trait is *genetically*

correlated with. In particular, the component of the sum given by $\mathrm{Var}_{i\in\mathbb{G}}(a_{ik})\hat{\beta}_{ma,k}$ determines the impact of direct selection on the kth trait, whilst the set of components of the sum given by $\mathrm{Cov}_{i\in\mathbb{G}}(a_{ik}, a_{il})\hat{\beta}_{ma,l}$ determine the impact of indirect selection due to a *genetical* correlation between the kth and lth traits. Whereas it is fairly obvious what a phenotypic correlation and a genetic correlation are, it may be less obvious what a 'genetical' correlation is. From equation (3.37), however, we can see that it corresponds to an average-effect-weighted sum of genetic correlations in $\mathbf{L}$.

So far this all looks very similar to that which we obtained from the phenotypic and genic perspective of the Malthusian selection differentials, yet we can make a simple alteration here that we could not before. In particular, by post-multiplying the matrix $\mathbf{G}$ in equation (3.52) by $\mathbf{P}^{-1}\mathbf{P} = \mathbf{I}$, which clearly has no impact on the equality, we can re-write the genetical version of the vector of Malthusian selection differentials as

$$\boldsymbol{s}_{am} = \hat{\boldsymbol{\beta}}_{az}^{\mathrm{T}}\mathbf{P}\hat{\boldsymbol{\beta}}_{ma}. \tag{3.53}$$

where $\hat{\boldsymbol{\beta}}_{az}^{\mathrm{T}} = \mathbf{G}\mathbf{P}^{-1}$ is the multivariate analogue of Fisher's (1918) measure of heritability given by equation (3.40).

The important point about equation (3.53), is that it therefore now expresses the genetical version of the vector of Malthusian selection differentials as the product of three quantities that embody the conditions required for an *evolutionary response* to natural selection (Lewontin, 1970; Godfrey-Smith, 2007), namely: *i*) the variance-covariance matrix of phenotypic trait values, $\mathbf{P}$, captures the requirement for phenotypic variation; *ii*) the genetical form of the vector of Malthusian selection gradient, $\hat{\boldsymbol{\beta}}_{ma}$, captures the requirement for a statistical association between traits held by individuals and their fitness; and *iii*) the heritability matrix, $\hat{\boldsymbol{\beta}}_{az}$, summarises the relationship between genotypes and phenotypes in the population in terms of the heritability of traits.

Since the genetical version of the vector of Malthusian selection differentials, $\boldsymbol{s}_{am}$, formalises the definition of the evolutionary response to natural selection, it can also be used to formalise the claim we made earlier that natural selection only 'sees' the average effects of genetic factors in the population at any time, t. To understand why this is so, let us substitute into equation (3.49) for the definition of the matrix of genetic values, $\mathbf{A}$, given by equation (3.29). After rearrangement we obtain $\boldsymbol{s}_{am} = \bar{\boldsymbol{z}}\mathbf{1}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m} + (\boldsymbol{\Lambda}\hat{\boldsymbol{\beta}}_{z\lambda})^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m} - \hat{\boldsymbol{\beta}}_{z\lambda}^{\mathrm{T}}\bar{\boldsymbol{\lambda}}\mathbf{1}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m}$. By simplifying using the property that the covariance of anything with a constant is zero, so that $\bar{\boldsymbol{z}}\mathbf{1}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m} = \mathbf{0}$ and $\bar{\boldsymbol{\lambda}}\hat{\boldsymbol{\beta}}_{z\lambda}^{\mathrm{T}}\mathbf{1}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m} = \mathbf{0}$, and substituting for $\mathbf{V} = \boldsymbol{\Lambda}\hat{\boldsymbol{\beta}}_{z\lambda}$ from equation (3.25), we can re-write equation (3.49) as

$$\boldsymbol{s}_{am} = \mathbf{A}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m} = \mathbf{V}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m} = \boldsymbol{s}_{vm}, \tag{3.54}$$

where we see that the action of natural selection on the matrix of genetic values, $\mathbf{A}$, is equal to the action of natural selection on the matrix of sums of average effects, $\mathbf{V}$. Thus, at any instantaneous moment in time, t, any non-additive genetic effects on phenotypes due to pleiotropy, epistasis or linkage disequilibrium that are not already captured in $\mathbf{A}$ simply do not impact on the evolutionary response to natural selection *at that time* (Frank, 1997, 1998).

3.3 The dynamics of the evolutionary response to natural selection

The evolutionary response to natural selection is defined as the portion of phenotypic change in a population over time due to the action of natural selection on the underlying heritable basis of phenotypes (Lush, 1937; Falconer and Mackay, 1995). Evolutionary theorists are particularly interested in this component of change, because it provides an explanation for the adaptations exhibited by biological organisms in the natural world (Gardner, 2009). In this section, we bring together all the principles of evolutionary genetics we have studied so far to formalise the evolutionary response to natural selection in our population at any instantaneous moment in time, t. We discuss the relationship between the dynamics of the evolutionary response to natural selection in our population and Robertson's (1966) secondary theorem of natural selection as well as Fisher's (1930) fundamental theorem of natural selection. We then show that the formulation of these equations leads us to consider the dynamics of the evolutionary response to natural selection in our population from three complementary perspectives: *i*) *phenotypic*—in terms of heritability, phenotypic variance, and a phenotypic selection gradient; *ii*) *genic*—in terms of the average effects of genes, genetic variance, and a genic selection gradient; and; *iii*) *genetical*—in terms of heritability, phenotypic variance, and a genetical selection gradient. We discuss how each of these perspectives can be visualised using the concept of an *adaptive landscape*.

3.3.1 Robertson's secondary theorem of natural selection

The approach used in evolutionary genetics to formalise the dynamics of the evolutionary response to natural selection is to decompose the change in the average trait values in a

population into two *partial* changes (Frank, 1998): *i*) the partial change brought about *natural selection*; and *ii*) the partial change due to *environmental effects* or other causes not associated with natural selection. In the context of our population, the approach suggests that at any time, t, we can formulate a causal decomposition of the time derivative for the change in the average trait values of the form

$$\dot{\bar{\boldsymbol{z}}} = \frac{\partial_{NS}\bar{\boldsymbol{z}}}{\partial t} + \frac{\partial_{EC}\bar{\boldsymbol{z}}}{\partial t}, \tag{3.55}$$

where $\partial_{NS}\bar{\boldsymbol{z}}/\partial t$ represents the change brought about by natural selection and $\partial_{EC}\bar{\boldsymbol{z}}/\partial t$ represents change due to the environment. The notation used here is similar to that used to describe the 'total derivative' of a function. It is an atypical use of notation, but one which has historical precedent, being used by Price (1972b) to provide clarity on Fisher's (1930) 'fundamental theorem of natural selection'[n]. In the last section we saw that the genetical version of the vector of Malthusian selection differentials, $\boldsymbol{s}_{am}$, suitably summarises the action of natural selection on our population in terms of the conditions required to bring about evolutionary change (Lewontin, 1970; Godfrey-Smith, 2007). It is therefore straightforward to define the dynamics of the evolutionary response to natural selection in our population as $\partial_{NS}\bar{\boldsymbol{z}}/\partial t = \boldsymbol{s}_{am}$, which is equivalent to

$$\frac{\partial_{NS}\bar{\boldsymbol{z}}}{\partial t} = \mathbf{A}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m}. \tag{3.56}$$

This is a multivariate Malthusian analogue of a result due to Robertson (1966) and expanded upon by Price (1970). The vector-matrix notation we have used, however, somewhat obscures its similarity to those classical results. Switching to 'moment' notation (Box 2.4, Chapter 2) we may re-write equation (3.56) as

$$\begin{bmatrix} \partial_{NS}\mathrm{E}_{i\in\mathbb{G}}(z_{i1})/\partial t \\ \vdots \\ \partial_{NS}\mathrm{E}_{i\in\mathbb{G}}(z_{i|\mathbb{P}|})/\partial t \end{bmatrix} = \begin{bmatrix} \mathrm{Cov}_{i\in\mathbb{G}}(a_{i1}, m_i) \\ \vdots \\ \mathrm{Cov}_{i\in\mathbb{G}}(a_{i|\mathbb{P}|}, m_i) \end{bmatrix}. \tag{3.57}$$

To emphasise that equation (3.56) is based on a continuous-time definition of Malthusian fitness, rather than the discrete-time measure of absolute or relative fitness used

[n]Price (1972b) argued that Fisher's (1930) unwillingness to employ a 'slight sacrifice of strict mathematical propriety' led to 'forty years of bewilderment about what he meant'.

throughout quantitative genetics, we refer to equation (3.57) as the 'Malthusian Robertson equation'.

Roberton's (1966) original equation is somewhat less general than the Price equation (2.5) (Frank, 1997), and the same is true of the Malthusian Robertson equation (3.57) by comparison with the phenotypic version of the Malthusian Price equation (2.49) from Chapter 2. Firstly, the Malthusian Robertson equation (3.57) clearly only deals with the partial change in the average phenotypic trait values, $\partial_{NS}\mathrm{E}_{i\in\mathbb{G}}(z_{ik})/\partial t$, whereas the phenotypic version of the Malthusian Price equation (2.49) deals with the total change in the average trait values, $\dot{\mathrm{E}}_{i\in\mathbb{G}}(z_{ik})$. Secondly, the Malthusian Robertson equation (3.57) requires us to have a well-formed model of particulate inheritance for which the assumptions required of the theory of population-weighted least-squares hold, whereas the phenotypic version of the Malthusian Price equation (2.49) can be formulated for a dynamical system describing any population, regardless of the model of inheritance used. Despite the loss of generality associated with Roberton's (1966) equation, it is often referred to as the 'secondary theorem of natural selection', because it holds true for the vast majority of systems and neatly links all of the central principles and dynamical equations of change in evolutionary genetics together in one (relatively) simple expression (Frank, 2012a).

3.3.2 Fisher's fundamental theorem of natural selection

The Malthusian Robertson equation (3.56) describes the action of natural selection on any of the traits in the genotype-phenotype map, $\mathbf{Z}$. As we discussed in Chapter 2, the Malthusian fitness of individuals is, strictly speaking, a phenotypic trait like any other. This suggests that at any time, t, we can formulate a causal decomposition of the time derivative for the change in the average Malthusian fitness of the form

$$\dot{\bar{m}} = \frac{\partial_{NS}\bar{m}}{\partial t} + \frac{\partial_{EC}\bar{m}}{\partial t}, \tag{3.58}$$

where $\partial_{NS}\bar{m}/\partial t$ represents the change brought about by natural selection and $\partial_{EC}\bar{m}/\partial t$ represents change due to the environment.

If we let $\boldsymbol{m} = \boldsymbol{a}_{\bullet m} + \boldsymbol{e}_{\bullet m}$ be the causal decomposition of the Malthusian fitness vector, $\boldsymbol{m}$, into its genetical, $\boldsymbol{a}_{\bullet m}$, and environmental, $\boldsymbol{e}_{\bullet m}$, components then by the Malthusian Robertson equation (3.56), the evolutionary response to natural selection of Malthusian

fitness itself can be written $\partial_{NS}\bar{m}/\partial t = \boldsymbol{a}_{\bullet m}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m}$. If we substitute into this equation for the causal decomposition of the Malthusian fitness vector, $\boldsymbol{m}$, then we obtain

$$\frac{\partial_{NS}\bar{m}}{\partial t} = \boldsymbol{a}_{\bullet m}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{a}_{\bullet m}. \tag{3.59}$$

This is an analogue in our framework to an important result reached by Fisher (1930). The result is clearer if we again switch notation to moment notation (Box 2.4, Chapter 2). In particular, we have

$$\frac{\partial_{NS}\mathrm{E}_{i\in\mathbb{G}}(m_i)}{\partial t} = \mathrm{Cov}_{i\in\mathbb{G}}(a_{im}, a_{im}) = \mathrm{Var}_{i\in\mathbb{G}}(a_{im}), \tag{3.60}$$

which shows that the change in average Malthusian fitness that can be attributed to the action of natural selection at any time, t, is simply given by the variance in the genetical component of Malthusian fitness, $\mathrm{Var}_{i\in\mathbb{G}}(a_{im})$. Since the variance of a quantity is always non-negative, this indicated to Fisher (1930) that the evolutionary response to natural selection is a process of *optimisation* that will lead organisms to appear designed as if to maximise their fitness. Fisher (1930, pg. 35) called his result the 'fundamental theorem of natural selection', stating that, 'the rate of increase in fitness of any organism at any time is equal to its genetic variance in fitness at that time.' The '*at that time*' aspect of Fisher's (1930, pg. 35) definition is important because it stresses that even though the result has only been proved for one moment in time, it will also be true for every other instant in time.

It is also important to realise that Fisher's (1930) interpretation stems from the fact that the fundamental theorem concerns the partial change in average Malthusian fitness due to natural selection, $\partial_{NS}\bar{m}/\partial t$, and not the total change, $\dot{\bar{m}}$ (Price, 1972b; Ewens, 1989; Frank and Slatkin, 1992). Clearly the average Malthusian fitness of most populations, $\bar{m}$, does not generally increase continually over time, but instead is likely to remain at zero because population growth is constrained by space or the availability of resources. In order that this be the case, it follows that the partial change in the average Malthusian fitness due to the environment, $\partial_{EC}\bar{m}/\partial t$, is often negative (so that it cancels out the non-negative component of the total change, $\partial_{NS}\bar{m}/\partial t$). This 'deterioration of the environment' as Fisher (1930) referred to it was explained eloquently by Price (1972b) who wrote, 'what Fisher's theorem tells us is that natural selection... at all times acts to increase the fitness of a species to live under the conditions that existed an instant earlier. But since the standard of "fitness" changes from instant to instant, this constant

improving tendency of natural selection does not necessarily get anywhere in terms of increasing "fitness" as measured by any fixed standard, and in fact M [average Malthusian fitness] is about as likely to decrease under natural selection as to increase.' Or, to put it another way Fisher's (1930) result suggests (Grafen, 2002): 'that the natural selection part of evolution tends to improve design, while the environmental change part is essentially non-constructive.'

The optimising aspect of Fisher's (1930) result does seem to formalise that which we observe in nature: the fact that organisms often appear designed as if to maximise their individual survival and reproduction (Darwin, 1859). There are claims that a general optimisation principle of evolutionary theory cannot exist, because most of the time natural selection is frequency-dependent (Allen et al., 2013). It is important to stress that the version of the fundamental theorem of natural selection we have obtained, however, holds for any type of mating system, population growth model, or model of phenotypic plasticity. Thus there is always a way to identify the *partial* optimising component of evolutionary change, no matter how small. Nevertheless, Fisher's (1930) optimisation component of natural selection does require us to make specific assumptions about the underlying heritable basis of traits and more generally about the relationship between the genotype and phenotype map, and consequently the theorem will continue to provoke controversy until a more abstract generalisation of Fisher's (1930) optimisation principle is obtained (see Ewens (1992); Grafen (2002, 2003); Metz et al. (2008); Grafen (2008); Ewens (2014) for developments and discussion).

3.3.3 Adaptive landscapes and multivariate breeder's equations

An alternative, somewhat competing (see Frank (2012b)), view of the action of natural selection as an optimising principle is given by viewing a population as residing on a form of *adaptive landscape* (Wright, 1932; Simpson, 1944; Phillips and Arnold, 1989). In the opening to this chapter, we saw that the evolutionary response to natural selection can be characterised as a hill-climbing process on an adaptive landscape formalised by the directional selection gradient, $\boldsymbol{\beta}_{wz}$, of the multivariate breeder's equation (3.2) derived by Lande (1979); Lande and Arnold (1983). In the present context, Simpson's (1944) adaptive landscape concept suggests that we can visualise our population at any time, t, as residing at a point, $(\bar{\boldsymbol{z}}, \bar{m})$, on a form of landscape where the average Malthusian fitness, $\bar{m}$, gives us the elevation of the population on the vertical axis of the landscape, and the vector of average trait values, $\bar{\boldsymbol{z}}$, tells us the location of the population on the horizontal axes of the landscape. We can then use the three different directional selection gradients we encountered in an earlier section to characterise the dynamics of the evolutionary

response to natural selection in our population as taking place on: *i*) a landscape formalised by the *phenotypic* version of the Malthusian directional selection gradient, $\hat{\boldsymbol{\beta}}_{mz}$; *ii*) a landscape formalised by the *genic* version of the Malthusian directional selection gradient, $\hat{\boldsymbol{\beta}}_{m\lambda}$; and *iii*) a landscape formalised by the *genetical* version of the Malthusian directional selection gradient, $\hat{\boldsymbol{\beta}}_{ma}$.

3.3.3.1 Phenotypic perspective

The relationship between the dynamics of the evolutionary response to natural selection and an adaptive landscape is not particularly apparent from the Malthusian Robertson equation (3.56) as it is currently written. We can re-write the partial change in the average trait values over time, $\partial_{NS}\bar{\boldsymbol{z}}/\partial t$, however, by first substituting into the Malthusian Robertson equation (3.56) for the matrix of genetic values, $\mathbf{A}$, given by the GLM equation (3.38). After rearrangement we obtain $\partial_{NS}\bar{\boldsymbol{z}}/\partial t = \hat{\boldsymbol{\alpha}}_{az}^{\mathrm{T}}\mathbf{1}^{\mathrm{T}}\boldsymbol{\Sigma m} + \hat{\boldsymbol{\beta}}_{az}^{\mathrm{T}}\mathbf{Z}^{\mathrm{T}}\boldsymbol{\Sigma m} + \hat{\boldsymbol{\varepsilon}}_{az}^{\mathrm{T}}\boldsymbol{\Sigma m}$. By simplifying using the property that the covariance of anything with a constant is zero (Box 3.3), so that $\hat{\boldsymbol{\alpha}}_{az}^{\mathrm{T}}\mathbf{1}^{\mathrm{T}}\boldsymbol{\Sigma m} = \mathbf{0}$, we can re-write the Malthusian Robertson equation (3.56) as

$$\frac{\partial_{NS}\bar{\boldsymbol{z}}}{\partial t} = \hat{\boldsymbol{\beta}}_{az}^{\mathrm{T}}\boldsymbol{s}_{zm} + \hat{\boldsymbol{\varepsilon}}_{az}^{\mathrm{T}}\boldsymbol{\Sigma m}, \tag{3.61}$$

where $\hat{\boldsymbol{\beta}}_{az}^{\mathrm{T}} = \mathbf{G}\mathbf{P}^{-1}$ is the heritability matrix given by equation (3.40), $\boldsymbol{s}_{zm} = \mathbf{Z}^{\mathrm{T}}\boldsymbol{\Sigma m}$ is the phenotypic version of the vector of Malthusian selection differentials given by equation (3.44), and $\hat{\boldsymbol{\varepsilon}}_{az}^{\mathrm{T}}\boldsymbol{\Sigma m}$ represents the covariance of the Malthusian fitness vector, $\boldsymbol{m}$, with the residuals from the GLM given by equation (3.38). At this point it is tempting to think that the term $\hat{\boldsymbol{\varepsilon}}_{az}^{\mathrm{T}}\boldsymbol{\Sigma m}$ may also drop out by the assumption of the population-weighted least-squares theory that the residuals and the explanatory variables are uncorrelated (Box 3.3). This is not the case here, however, since the Malthusian fitness vector, $\boldsymbol{m}$, is not one of the explanatory variables in the GLM equation (3.38) from which the matrix of residuals, $\hat{\boldsymbol{\varepsilon}}_{az}$, is derived.

Despite there being no mathematical justification for $\hat{\boldsymbol{\varepsilon}}_{az}^{\mathrm{T}}\boldsymbol{\Sigma m} = \mathbf{0}$, Frank (1997) points out that evolutionary theorists often implicitly ignore these forms of 'error covariance' on the basis that they seem to have little relevance for the evolutionary response to natural selection[o]. Thus, following this tradition and ignoring the term $\hat{\boldsymbol{\varepsilon}}_{az}^{\mathrm{T}}\boldsymbol{\Sigma m}$, we can re-write equation (3.61) in the form

[o]See Frank (1997) and Okasha (2006) for a discussion of the consequences of ignoring such terms.

$$\frac{\partial_{NS}\bar{\boldsymbol{z}}}{\partial t} = \mathbf{G}\mathbf{P}^{-1}\boldsymbol{s}_{zm} = \mathbf{G}\hat{\boldsymbol{\beta}}_{mz} = \hat{\boldsymbol{\beta}}_{az}^{\mathrm{T}}\mathbf{P}\hat{\boldsymbol{\beta}}_{mz}, \tag{3.62}$$

where we have substituted for the definition of the heritability matrix, $\hat{\boldsymbol{\beta}}_{az}^{\mathrm{T}} = \mathbf{G}\mathbf{P}^{-1}$, given by equation (3.40), then substituted for the phenotypic version of the Malthusian directional selection gradient, $\hat{\boldsymbol{\beta}}_{mz} = \mathbf{P}^{-1}\boldsymbol{s}_{zm}$, given by equation (3.41), and post-multiplied the matrix $\mathbf{G}$ by $\mathbf{P}\mathbf{P}^{-1} = \mathbf{I}$ (which clearly has no impact on the equality). This equation is a Malthusian analogue in our framework of of the multivariate breeder's equation (3.2) (Box 3.1). We refer to it as the 'phenotypic version' of the 'Malthusian multivariate breeder's equation'.

Like the multivariate breeder's equation (3.2), we see that the phenotypic version of the Malthusian multivariate breeder's equation (3.62) can be written in three equivalent ways, each of which illuminates a different aspect of the dynamics of the evolutionary response to natural selection: *i*) as the product of a heritability measure, $\mathbf{G}\mathbf{P}^{-1}$, and a selection differential, $\boldsymbol{s}_{zm}$; *ii*) as the product of a measure of genetic variance, $\mathbf{G}$, and a directional selection gradient of traits on fitness, $\hat{\boldsymbol{\beta}}_{mz}$; and *iii*) as the product of a heritability measure, $\hat{\boldsymbol{\beta}}_{az}^{\mathrm{T}}$, a measure of phenotypic variance, $\mathbf{P}$, and a directional selection gradient of traits on fitness, $\hat{\boldsymbol{\beta}}_{mz}$.

The form that interests us most here is $\partial_{NS}\bar{\boldsymbol{z}}/\partial t = \mathbf{G}\hat{\boldsymbol{\beta}}_{mz}$, which shows that, like the multivariate breeder's equation (3.2), the phenotypic version of the Malthusian multivariate breeder's equation (3.62) formalises the visualisation of the dynamics of the evolutionary response to natural selection in terms of a form of Simpson's (1944) adaptive landscape. The direction of steepest uphill ascent on the adaptive landscape at any time t will be indicated by the phenotypic version of the Malthusian directional selection gradient, $\hat{\boldsymbol{\beta}}_{mz}$ (Phillips and Arnold, 1989), whilst the nature of genetic constraints on the population will be indicated by the 'genetic line of least resistance' for the population as obtained from the eigendecomposition of the matrix $\mathbf{G}$ (Schluter, 1996; Arnold et al., 2008).

The advantage of the phenotypic perspective on the dynamics of the evolutionary response to natural selection is that it is based on a selection differential, $\boldsymbol{s}_{zm}$, relating phenotypic trait values to Malthusian fitness. In practical settings this will be much easier quantity to measure than selection coefficients relating to underlying genetic factors or genetic values. Nevertheless, the phenotypic perspective does come with the disadvantage that it requires us to make the additional assumption $\hat{\boldsymbol{\varepsilon}}_{az}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m} = \mathbf{0}$, an assumption that made be perfectly reasonable or totally unacceptable depending on the biological circumstances.

3.3.3.2 Genic perspective

Let us now consider an alternative genic perspective on the dynamics of the evolutionary response to natural selection. This perspective will not require us to make an assumption of the form $\hat{\boldsymbol{\varepsilon}}_{az}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m} = \mathbf{0}$, and will also help formalise our claim that natural selection only 'sees' average effects.

We begin by first substituting into the Malthusian Robertson equation (3.56) for the matrix of genetic values, $\mathbf{A}$, given not by the GLM equation (3.38), but by equation (3.29) which we used to perform the causal decomposition of the genotype-phenotype map, $\mathbf{Z}$. After rearrangement we now obtain $\partial_{NS}\bar{\boldsymbol{z}}/\partial t = \bar{\boldsymbol{z}}\mathbf{1}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m} + \hat{\boldsymbol{\beta}}_{z\lambda}^{\mathrm{T}}\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m} - \hat{\boldsymbol{\beta}}_{z\lambda}^{\mathrm{T}}\bar{\boldsymbol{\lambda}}\mathbf{1}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m}$. By simplifying using the property that the covariance of anything with a constant is zero, so that $\bar{\boldsymbol{z}}\mathbf{1}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m} = \mathbf{0}$ *and* $\hat{\boldsymbol{\beta}}_{z\lambda}^{\mathrm{T}}\bar{\boldsymbol{\lambda}}\mathbf{1}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m} = \mathbf{0}$, we can re-write the Malthusian Robertson equation (3.56) as

$$\frac{\partial_{NS}\bar{\boldsymbol{z}}}{\partial t} = \hat{\boldsymbol{\beta}}_{z\lambda}^{\mathrm{T}}\boldsymbol{s}_{\lambda m}, \tag{3.63}$$

where $\hat{\boldsymbol{\beta}}_{z\lambda}^{\mathrm{T}} = \mathbf{Z}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{\Lambda}(\boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{\Lambda})^{-1}$ is the matrix of of average effects given by equation (3.9), and $\boldsymbol{s}_{\lambda m} = \boldsymbol{\Lambda}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m}$ is the vector of Malthusian selection differentials given by equation (3.48). Importantly, note that we have now obtained an alternative form of the Malthusian Robertson equation (3.56) which did not require us to make the additional assumption $\hat{\boldsymbol{\varepsilon}}_{az}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m} = \mathbf{0}$. We can now re-write equation (3.63) in the form

$$\frac{\partial_{NS}\bar{\boldsymbol{z}}}{\partial t} = \hat{\boldsymbol{\beta}}_{z\lambda}^{\mathrm{T}}\mathbf{L}\hat{\boldsymbol{\beta}}_{m\lambda}, \tag{3.64}$$

where we have substituted for the genic version of the Malthusian directional selection gradient, $\hat{\boldsymbol{\beta}}_{m\lambda} = \mathbf{L}^{-1}\boldsymbol{s}_{\lambda m}$, given by equation (3.45). This equation provides an alternative genic perspective on the multivariate breeder's equation (3.2) (Box 3.1). We refer to it as the 'genic version' of the 'Malthusian multivariate breeder's equation'.

This form is important, because it formalises the idea that, providing our assumption about the causal effects of genetic factors on trait values is correct, the evolutionary response to natural selection is brought about by the average effects of genes on traits. That is, it formalises the notion that at any instantaneous moment in time, t, natural selection only 'sees' average effects. It does not, however, provide us with an alternative way to visualise the dynamics of the evolutionary response to natural selection. The direction

of steepest uphill ascent at any time t indicated by the genic version of the Malthusian directional selection gradient, $\hat{\boldsymbol{\beta}}_{m\lambda}$, is a measure of the slope on Wright's (1932) landscape of gene frequencies, $\bar{\boldsymbol{\lambda}}$, not Simpson's (1944) landscape of average phenotypic trait values, $\bar{\boldsymbol{z}}$. If we observed this genic adaptive landscape, the eigendecomposition of $\mathbf{L}$ would, however, possibly provide us with an analogous visualisation of the genetic line of least resistance (Schluter, 1996; Arnold et al., 2008). The component $\hat{\boldsymbol{\beta}}_{z\lambda}^{\mathrm{T}}$ would essentially map our genic adaptive landscape into phenotypic space, but it is not clear how we would visualise this effect geometrically.

3.3.3.3 Genetical perspective

Finally, we can also re-write the partial change in the average trait values over time, $\partial_{NS}\bar{\boldsymbol{z}}/\partial t$, from a genetical perspective which also does not require the assumption $\hat{\boldsymbol{\varepsilon}}_{az}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m} = \mathbf{0}$ that we were required to make when considering a phenotypic perspective. The genetical perspective is reached considerably faster than the genic or phenotypic perspective. We simply multiply the Malthusian Robertson equation (3.56) by $\mathbf{G}\mathbf{G}^{-1} = \mathbf{I}$ (which has no effect on the equality) and then re-write as

$$\frac{\partial_{NS}\bar{\boldsymbol{z}}}{\partial t} = \mathbf{G}\hat{\boldsymbol{\beta}}_{ma} = \hat{\boldsymbol{\beta}}_{za}^{\mathrm{T}}\mathbf{P}\hat{\boldsymbol{\beta}}_{ma}, \tag{3.65}$$

where we have substituted for the definition of the genetical version of the Malthusian directional selection gradient, $\hat{\boldsymbol{\beta}}_{ma} = \mathbf{G}^{-1}\boldsymbol{s}_{\lambda m}$, given by equation (3.49), post-multiplied the matrix $\mathbf{G}$ by $\mathbf{P}\mathbf{P}^{-1} = \mathbf{I}$ (which as always does not impact the equality), and then substituted for the definition of the heritability matrix, $\hat{\boldsymbol{\beta}}_{az}^{\mathrm{T}} = \mathbf{G}\mathbf{P}^{-1}$. This equation provides an alternative genetical perspective on the multivariate breeder's equation (3.2) (Box 3.1). We refer to it as the 'genetical version' of the 'Malthusian multivariate breeder's equation'.

This form provides us with an alternative way to visualise the dynamics of the evolutionary response to natural selection on a form of Simpson's (1944) adaptive landscape. This follows from the fact that $\bar{\boldsymbol{z}} = \bar{\boldsymbol{a}}$ from equation (3.32). The direction of steepest uphill ascent on the adaptive landscape at any time t is now indicated by the genetical version of the Malthusian directional selection gradient, $\hat{\boldsymbol{\beta}}_{ma}$, whilst the nature of genetic constraints on the population will be indicated by the 'genetic line of least resistance' for the population as obtained from the eigendecomposition of the matrix $\mathbf{G}$ (Schluter, 1996; Arnold et al., 2008).

The advantage of the genetical perspective on the dynamics of the evolutionary response to natural selection is that it is based on a selection differential, $\boldsymbol{s}_{am}$, that 'absorbs' the component $\hat{\boldsymbol{\varepsilon}}_{az}^{\mathrm{T}}\boldsymbol{\Sigma m}$ from the phenotypic perspective. In this way, it provides a complete description of the evolutionary response to natural selection where the phenotypic perspective would require of us an assumption that may not be justified (Frank, 1997). The disadvantage of the genetical perspective, however, is that the genetical version of the Malthusian directional selection gradient, $\hat{\boldsymbol{\beta}}_{ma}$ is likely to be a harder quantity to obtain in practical applications than the phenotypic analogue, $\hat{\boldsymbol{\beta}}_{ma}$.

3.4 Concluding remarks

To summarise, natural selection can drive evolutionary change only insofar as traits are heritable. Evolutionary genetics provides tools for predicting this change given information about heritability and the direction of selection acting on traits. Only through an understanding of the relative magnitudes of the strength of selection, and the degree to which genetic constraints impact on the dynamics of the evolutionary response to natural selection can we hope to truly understand how natural selection brings about adaptations in the natural world and the timescales over which this is expected to happen. In this chapter we have extended the dynamical systems framework we developed in Chapter 2 to integrate it with some of the core principles of evolutionary genetics. Under the assumption of an underlying genetic model for traits in the genotype-phenotype map, $\mathbf{Z}$, we have derived expressions for genetic values, measures of heritability, selection differentials and directional selection gradients. Since these expressions can be calculated at any instantaneous moment in time, t, by solving the Malthusian selection equation (2.28) from Chapter 2, these quantities can all be studied over arbitrary lengths of time to better understand the long-term dynamics of the evolutionary response to natural selection.

Chapter 4

The dynamics of social evolution

4.1 Introduction

Social evolution theory seeks to explain the evolution of social adaptations in the natural world. In evolutionary terms, social traits are defined as those that have evolved because of the impact they have on the fitness of the individual expressing them (the 'actor'), and the fitness of individuals with whom the actor interacts (the 'recipients') (West et al., 2007c). Evolutionary theorists distinguish between four classes of social trait, typically described as 'mutualistic', 'selfish', 'altruistic', and 'spiteful' (Table 4.1). Why natural selection should favour the evolution of mutualistic or selfish traits is relatively easy to explain using Darwin's (1859) logic. These types of traits ultimately lead to a direct fitness benefit for the actor and should therefore be positively selected. Why natural selection should favour the evolution of altruistic or spiteful traits is much harder to explain using Darwin's (1859) logic. These types of traits are common in the natural world (West et al., 2007b), yet they lead to a direct fitness cost for the actor and it seems they should therefore be selected against.

As far back as Fisher (1930), evolutionary theorists realised that the heritable component of traits can, however, be favoured by both direct and indirect routes. Hamilton (1963; 1964) proposed that to understand how natural selection can favour the evolution of certain classes of social traits one should think in terms of population genetics. More specifically, Hamilton (1963) identified that a gene promoting the expression of an altruistic trait by a focal actor might also be shared by the neighbours with whom the actor interacts. An altruistic trait could therefore spread in a population, despite its direct fitness cost, by providing sufficient indirect fitness benefits to neighbours that share the heritable basis for the trait. The formal treatment of this idea led Hamilton (1964, 1970) to derive a simple elegant inequality, now known as 'Hamilton's rule' (Charnov, 1977),

Table 4.1: **Social traits** | A categorisation of social traits according to fitness effects they confer on a focal actor and interacting recipients. There are four types of traits: *i*) *mutualistic*, where the focal actor and recipients both benefit from the effects of the trait; *ii*) *selfish*, where the trait provides gains for the focal actor at the expense of recipients; *iii*) *altruistic*, where the trait is costly to the focal actor, but benefits recipients; and *iv*) *spiteful*, where the trait is costly to the focal actor and detrimental to recipients. Table reproduced from West et al. (2007c).

	Recipient effect	
	+	−
Actor effect		
−	Altruistic	Spiteful
+	Mutualistic	Selfish

which states that natural selection favours the evolution of a trait when $rb - c > 0$, where r is the 'relatedness' between the actor and recipients (interpreted as a measure of the likelihood that the actor and recipients share a heritable basis for the cooperative trait (Orlove, 1975; Michod and Hamilton, 1980; Grafen, 1985)), b is the indirect fitness effect of the actor's social trait on recipients, and c is the direct fitness effect of the actor's trait on its own fitness. The product rb constitutes the overall indirect fitness effect of a trait (Brown, 1980; West et al., 2007b). The concept of relatedness is a crucial one in social evolution theory, for in its absence ($r = 0$), Hamilton's rule predicts that no amount of indirect fitness benefits, b, can bring about the social evolution of altruistic or spiteful traits (Gardner and West, 2006; Foster et al., 2006; West and Gardner, 2010).

The sum of the direct fitness and overall indirect fitness effects constitutes the 'inclusive fitness' of the actor (Fig. 4.1A; Hamilton, 1964). A mathematically equivalent accounting method for fitness effects known as 'neighbour-modulated fitness' sees the benefit, b, become the fitness effect on the actor rather than the recipients (Fig. 4.1B; Hamilton, 1970). These two accounting methods add up to the same aggregate effect, but lead to different measures of fitness from an individual perspective (Taylor et al., 2007). Despite their mathematical equivalence, there are advantages and disadvantages to both accounting methods. In particular, neighbour-modulated fitness is, practically speaking, usually found to be somewhat easier to calculate (West and Gardner, 2013), whilst inclusive fitness is more closely aligned with the Darwinian notion of fitness as something that organisms should appear designed to maximise (Gardner, 2009; West and Gardner, 2013).

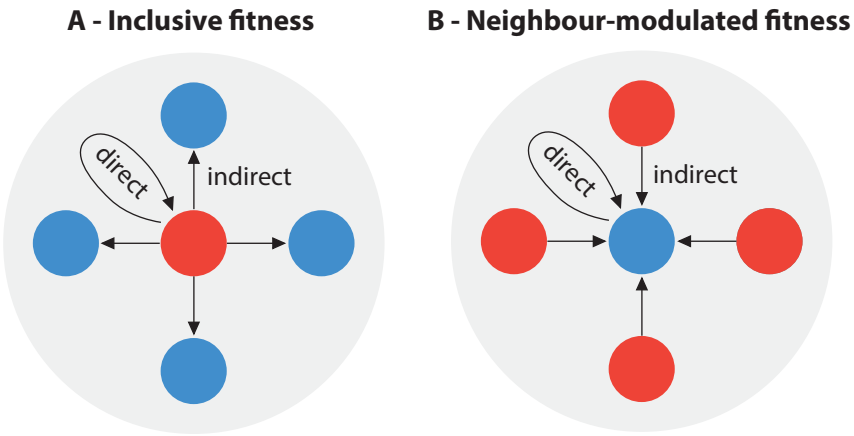


Figure 4.1: Direct and indirect fitness effects | There are two accounting methods for describing the direct and indirect fitness effects of a social trait (Taylor et al., 2007): *i*) through *inclusive-fitness* effects conferred upon recipients by a focal actor (Hamilton, 1964); and *ii*) through *neighbour-modulated* effects conferred upon the actor by neighbouring social partners (Hamilton, 1970). A crucial distinction between these two accounting approaches is that inclusive fitness is calculated in terms of the focal actor's own traits, whereas neighbour-modulated fitness is calculated in terms of the traits of many socially interacting individuals. Inclusive fitness is therefore a property of an individual, a social trait in its own right, whereas neighbour-modulated fitness might more properly be described as a property of the population. Inclusive fitness, unlike neighbour-modulated fitness, therefore shares the property of Darwinian fitness in that it is something individuals might become appear designed to maximise through social evolution (West and Gardner, 2013). Figure adapted from Wenseleers et al. (2010).

The selection process that favours traits like altruism because of their overall indirect fitness consequences (taking into account relatedness-weighted fitness effects) was named by Maynard Smith (1964) as 'kin selection'[a]. An intuitive way to think about the process of kin selection is that when a focal actor helps relatives (kin) survive and reproduce, this results in an increase in the spread of the actor's own genes (Dawkins, 1976). J. B. S. Haldane famously summed up this idea when he, allegedly, said that he would only be prepared to 'lay down my life for two brothers or eight cousins.' Although the name kin selection suggests a process limited to selection on relatives, the only real requirement for kin selection to operate is that there is mechanism by which the focal actor can preferentially interact with individuals that share a heritable basis for a social trait (Hamilton, 1970). Kin selection might therefore also occur if social partners display a recognisable and reliable tag, such as a 'green beard' through which suitable social

[a]As a brief semantic point, it is important to distinguish between kin selection the *process*, which can (and does) operate in natural populations, and the body of kin selection *theory*, which is the study of how natural selection impacts on the heritable components of social traits through direct and indirect routes (Gardner et al., 2011).

partners can be recognised (Dawkins, 1976; Gardner and West, 2010).

Although Hamilton's (1963; 1964) original work was grounded in population genetics theory, it was eventually superseded by derivations of Hamilton's rule that are grounded in *quantitative* genetics theory (Queller, 1992a,b; Frank, 1997; Gardner et al., 2011) and proceed via the covariance mathematics of Robertson (1966) and Price (1970). The advantage of derivations taking this route is that they endow kin selection theory with a similar degree of generality as the Price equation (2.5) (Box 2.3, Chapter 2; Price, 1970; 1972a) itself (Queller, 1992a). Several authors even go as far to say that they endow kin selection theory with the same generality as the theory of natural selection itself (Gardner et al., 2011). Certainly, the logic underlying kin selection theory is sound, and its explanatory power in terms of understanding adaptations to social environments has been demonstrated across a vast range of taxa over a period of 50 years or more (see Abbot et al. (2011), Bourke (2011), and West and Gardner (2013) for discussion).

One of the most common ways kin selection theory is employed is in conjunction with an optimisation methodology (Maynard Smith, 1978c). A typical approach is to construct a model, obtain a definition for fitness by re-writing the model in terms of the covariance mathematics of Robertson (1966) and Price (1970), and try to find a solution that maximises fitness (Taylor and Frank, 1996). This approach does not rest on any explicit description of dynamics; the solution to the optimisation problem acts as a prediction for the types of adaptations we would expect to see in the natural world *given* the assumptions we put in (Maynard Smith, 1978c). The approach follows from a direct extension of the logic Darwin (1859) used to formulate his theory. If we do not see the adaptations the model predicts in nature, this implies that the model is missing a key component of natural selection. In the case of social evolution, models that ignore the impact of fitness effects on social partners often lead to false conclusions about whether or not traits like altruism or spite can evolve (West et al., 2007b; West and Gardner, 2010; Queller, 2011). When indirect fitness effects are accounted for, the predictions are much better. Thus, when combined with the phenotypic gambit (Grafen, 1984), the optimisation approach in kin selection theory is a very simple but powerful explanatory tool (Maynard Smith, 1978c; West et al., 2007b; Gardner et al., 2011).

Despite many empirical successes in social evolution theory, however, the theoretical underpinnings of kin selection analyses continue to generate controversy (Traulsen and Nowak, 2006; Lehmann et al., 2007; Nowak et al., 2010; Traulsen, 2010; Gardner et al., 2011; Marshall, 2011; Allen et al., 2013; Simon, 2014; Liao et al., 2015; Nowak and Allen, 2015; Queller et al., 2015; Birch and Okasha, 2015). Following from the confusions of specific kin selection methods with the general theory of kin selection (Gardner et al.,

2011), there has now been a tendency among critics of kin selection theory to confuse the derivation of the general foundations of kin selection theory, which rests on using genetic values in conjunction with the Price equation (Box 2.3, Chapter 2; Price, 1970; 1972a), with the process of kin selection itself.

The Price equation is not a dynamical model of anything, and any modifications that arise in the process of deriving the foundations of kin selection theory also do not give rise to a dynamical model (Frank, 1995; Gardner, 2008). The utility of the Price equation is its generality. Through it we can convert between seemingly very different processes and frameworks. Thus, using the Price equation to derive the foundations of kin selection theory has the advantage that it shows that kin selection theory has the same (or at least a similar) level of generality as the Price equation itself (Gardner et al., 2011). One of the disadvantages of this more general derivation is, however, that it means that it is often not easy to see how one can incorporate explicit dynamics into kin selection theory (Queller, 2011). The absence of dynamics is not a problem for using kin selection theory in optimisation models. Yet there is nothing preordained about kin selection theory that should restrict its use to optimisation approaches. The challenges with incorporating dynamics means that questions about the timescales over which kin selection favours the evolution of a social adaptation, as well as questions about how quantities of interest like r, b, and c from Hamilton's rule change over time, have received relatively little attention. These kind of questions naturally arise in the study of social evolution in microbes, for instance, where populations are often in constant flux (Damore and Gore, 2012).

Our aim in this chapter is therefore to develop a framework in which to study the dynamics of social evolution resulting from kin selection. More specifically, our goal is to use the foundations of the dynamical systems framework we developed in Chapter 2, in conjunction with our study of the dynamics of selection on correlated traits in Chapter 3, to derive a Hamilton's rule that predicts the direction of evolutionary change in social traits at every instantaneous moment in continuous time. First, we study a focal trait of interest and partition the Malthusian fitness of individuals into its neighbour-modulated form using a simplified form of the least-squares approach we developed in Chapter 3. We then generalise this procedure to multivariate phenotypes using an extension of the quantitative genetic approach pioneered by Lande (1979); Lande and Arnold (1983). We then derive a univariate form of Hamilton's rule in continuous-time using the genetical form of the Malthusian Price equation (3.34) derived in Chapter 3, and a novel multivariate form of Hamilton's rule in which relatedness is no longer scalar valued function, r, but instead becomes a matrix of partial regression coefficients, $\mathbf{R} \equiv \hat{\boldsymbol{\beta}}_{aa^*}$. Finally, we end with a discussion of the scenarios in which we might benefit from studying dynamics

of social evolution, focussing on applications of kin selection theory to understand the evolution of social traits in microbes.

4.2 The principles of kin selection

How do social interactions impact on the fitness of individuals? In some sense, social partners can be viewed as merely another part of an individual's environment. Yet social partners are different from other aspects of the environment in that they are themselves under the action of natural selection. This introduces a strategic aspect into evolutionary theory (Maynard Smith and Price, 1973). In particular, it suggests that adaptations can evolve via social evolution because of the impact they have on the fitness of other individuals (West et al., 2007c). A key question, however, is how evolutionary theorists should account for the fitness effects of social interactions in their analyses. In this section, our goal is to revisit the population we studied in Chapters 2 and 3 to investigate the principles of kin selection theory, which is the study of how selection impacts on the fitness of individuals through direct and indirect routes (Gardner et al., 2011). We begin by deriving a partition of the Malthusian fitness of individuals into its *neighbour-modulated* form (Hamilton, 1970) using the quantitative genetic approach of Queller (1992a,b). In Section 4.3, we then use this neighbour-modulated form of Malthusian fitness in conjunction with the covariance mathematics of Robertson (1966) and Price (1970) to explore the dynamics of social evolution, unifying the work in this thesis with the key results of Hamilton (1964, 1970).

4.2.1 Univariate neighbour-modulated Malthusian fitness

Disentangling the direct effects on fitness of a particular phenotypic trait from the effects of the environment and other phenotypic traits is a difficult task. In Chapter 3, however, we saw that one way of achieving this in a non-social context is given by the quantitative genetic approach of Lande (1979) and Lande and Arnold (1983). In particular, we found that the vector of partial regression coefficients, $\hat{\boldsymbol{\beta}}_{ma}$, from the multiple linear regression equation (3.50) of Malthusian fitness, $\boldsymbol{m}$, on the matrix of genetic values, $\mathbf{A}$, gave us a measure of *directional selection* on the genetic value of each trait, assuming the genetic values of all other traits were held constant. In social evolution theory, the decomposition of fitness into its 'neighbour-modulated' form represents a simple extension of this approach to take into account social partners (Queller, 1992a,b; Frank, 1995; Gardner et al., 2011).

To understand the decomposition approach in the context of our population, let us denote by $\mathbf{A}^* := \mathbf{A}^*(t, \boldsymbol{n}, \mathbf{Z}) \in \mathbb{R}^{|\mathbb{G}|\times|\mathbb{P}|}$ a matrix holding the average genetic values of all traits in the social partners of each genotype[b]. For any time t, the ith row vector $\boldsymbol{a}^*_{i\bullet} \in \mathbb{R}^{|\mathbb{P}|}$ denotes a vector of average genetic values an i-genotype individual is expected to encounter in social partners, and the kth column vector $\boldsymbol{a}^*_{\bullet k} \in \mathbb{R}^{|\mathbb{G}|}$ gives the distribution of the average genetic values of the kth trait in social partners for all genotypes. Let us focus on an arbitrary trait, say the kth trait. We can decompose the Malthusian fitness of individuals into its neighbour-modulated form at any point in time, t, by fitting a multiple-linear regression for the Malthusian fitness vector, $\boldsymbol{m}$, on the kth vector of genetic values, $\boldsymbol{a}_{\bullet k}$, *and* the kth vector of average genetic values of social partners, $\boldsymbol{a}^*_{\bullet k}$, by the method of population-weighted least-squares. In doing so, we obtain

$$\begin{aligned}\boldsymbol{m} &= \mathbf{1}\hat{\alpha}^{\mathrm{T}}_{ma_k a^*_k} + \boldsymbol{a}_{\bullet k}\hat{\beta}_{ma_k|a^*_k} + \boldsymbol{a}^*_{\bullet k}\hat{\beta}_{ma^*_k|a_k} + \hat{\boldsymbol{\varepsilon}}_{ma_k a^*_k} \\ &= \mathbf{1}\hat{\alpha}^{\mathrm{T}}_{ma_k a^*_k} + (\boldsymbol{a}_{\bullet k}, \boldsymbol{a}^*_{\bullet k})(\hat{\beta}_{ma_k|a^*_k}, \hat{\beta}_{ma^*_k|a_k})^{\mathrm{T}} + \hat{\boldsymbol{\varepsilon}}_{ma_k a^*_k}.\end{aligned} \tag{4.1}$$

where, the scalar $\hat{\alpha}_{ma_k a^*_k} = \bar{m} - \hat{\beta}^{\mathrm{T}}_{ma_k|a^*_k}\bar{a}_k - \hat{\beta}^{\mathrm{T}}_{ma^*_k|a_k}\bar{a}^*_k$ contains the intercept coefficients from the linear model, $\hat{\beta}_{ma_k|a^*_k}$ and $\hat{\beta}_{ma^*_k|a_k}$ represent scalar partial regression coefficients, and the vector $\hat{\boldsymbol{\varepsilon}}_{ma_k a^*_k}$ contains the residuals from the regression.

Equation (4.1) is really just an alternative formulation of the genetical version of the Malthusian individual selection surface given by equation (3.50) in Chapter 3, but it now constitutes a decomposition of the Malthusian fitness vector, $\boldsymbol{m}$, into its neighbour-modulated fitness form (Queller, 1992a,b; Frank, 1995; Gardner et al., 2011). The key difference between the two equations is that here, rather than decomposing Malthusian fitness into components resulting from the effects of multiple traits in each genotype's own phenotype, we are accounting for the effects of a single trait in each genotype's own phenotype *and* the effects of the same trait held by each genotype's average social partner.

4.2.1.1 Direct and indirect fitness effects

The intercept coefficient, $\hat{\alpha}_{ma_k a^*_k}$, of the multiple linear regression equation (4.1) can be thought of as the 'baseline' Malthusian fitness of individuals before we have taken into account the effect of the kth trait expressed by themselves or their social partners. We can

[b]Practically speaking, a model of social interactions might be given by a right-stochastic symmetric matrix, $\boldsymbol{\Xi} := \boldsymbol{\Xi}(t, \boldsymbol{n}, \mathbf{Z}) \in [0,1]^{|\mathbb{G}|\times|\mathbb{G}|}$ indicating the probability, $\xi_{ij} \in [0,1]$, that at any time, t, an i-genotype individual and a j-genotype individual socially interact. We would then have $\mathbf{A}^* = \boldsymbol{\Xi}\mathbf{A}$.

use 'block matrix' notation to re-write the partial regression coefficients from equation (4.1) in the form

$$\begin{bmatrix} \hat{\beta}_{ma_k|a_k^*} \\ \hat{\beta}_{ma_k^*|a_k} \end{bmatrix} = \begin{bmatrix} \boldsymbol{a}_{\bullet k}^{\mathrm{T}} \boldsymbol{\Sigma} \boldsymbol{a}_{\bullet k} & \boldsymbol{a}_{\bullet k}^{*\mathrm{T}} \boldsymbol{\Sigma} \boldsymbol{a}_{\bullet k}) \\ \boldsymbol{a}_{\bullet k}^{\mathrm{T}} \boldsymbol{\Sigma} \boldsymbol{a}_{\bullet k} & \boldsymbol{a}_{\bullet k}^{*\mathrm{T}} \boldsymbol{\Sigma} \boldsymbol{a}_{\bullet k}^{*}) \end{bmatrix}^{-1} \begin{bmatrix} \boldsymbol{a}_{\bullet k}^{\mathrm{T}} \boldsymbol{\Sigma} \boldsymbol{m} \\ \boldsymbol{a}_{\bullet k}^{*\mathrm{T}} \boldsymbol{\Sigma} \boldsymbol{m} \end{bmatrix}, \tag{4.2}$$

or perhaps more clearly using the equivalent moment notation favoured by Price (1970) as

$$\begin{bmatrix} \hat{\beta}_{ma_k|a_k^*} \\ \hat{\beta}_{ma_k^*|a_k} \end{bmatrix} = \begin{bmatrix} \mathrm{Var}_{i \in \mathbb{G}}(a_{ik}) & \mathrm{Cov}_{i \in \mathbb{G}}(a_{ik}, a_{ik}^*) \\ \mathrm{Cov}_{i \in \mathbb{G}}(a_{ik}, a_{ik}^*) & \mathrm{Var}_{i \in \mathbb{G}}(a_{ik}^*) \end{bmatrix}^{-1} \begin{bmatrix} \mathrm{Cov}_{i \in \mathbb{G}}(a_{ik}, m_i) \\ \mathrm{Cov}_{i \in \mathbb{G}}(a_{ik}^*, m_i) \end{bmatrix}, \tag{4.3}$$

where $\hat{\beta}_{ma_k|a_k^*}$ can be thought of as the *direct* fitness effect of the kth trait on individuals, holding the average genetic value of the kth trait in social partners constant, and $\hat{\beta}_{ma_k^*|a_k}$ can be thought of as the *indirect* fitness effect of the average genetic value of the kth trait held by social partners, holding constant the genetic value of the kth trait of individuals (Queller, 1992a,b; Frank, 1995; Gardner et al., 2011).

It is important to note that the direct and indirect fitness effects of a trait are statistical associations dependent on time, t, the composition of the population, $\boldsymbol{n}$, and the genotype-phenotype map, $\mathbf{Z}$. As time proceeds, and the genotypic and phenotypic composition of our population changes, so too will the statistical associations determining the direct and indirect fitness effects of traits. Nevertheless, at any time, t, the partial regression coefficients $\hat{\beta}_{ma_k|a_k^*}$ and $\hat{\beta}_{ma_k^*|a_k}$ will always provide an indication of the direct and indirect fitness effects of the kth trait *at that time*. The explanatory power of the regression approach will clearly depend strongly on whether or not there is a true causal relationship between traits and fitness or simply a correlation (Queller, 2011), but practically speaking the approach will work in any case for which the matrix in equation (4.3) is invertible.

Allen and Nowak (2015) have recently claimed that this is not the case, since the neighbour-modulated fitness approach, they claim, cannot be performed for a 2-player matrix model. In particular, they have stated that there is a problem with the regression coefficients in such a scenario which, 'arises because we are trying to fit a model with four undetermined parameters to a "dataset" with only two distinct points (one for cooperators and one for defectors). Geometrically, an infinite number of hyperplanes pass through these two points.' This claim initially seems plausible, but the mistake in the

reasoning is that there are not just two data points. There may just be two *genotypes* in the model of Allen and Nowak (2015), 'cooperator, and 'defector', but these two genotypes should be *weighted* by the their abundance in the population, as per the theory of population-weighted least-squares regression we developed in Chapter 3. Thus, whereas Allen and Nowak (2015) find that 'the quantity of inclusive fitness does not exist for general games', our analysis suggests that it will tend to exist for any game (system of differential equations) for which equality (4.3) is well defined. This will be any scenario in which the determinant of the matrix in equation (4.3) is non-zero, an analysis of which may warrant further exploration, but which we can see may hold quite generally for 2-player games.

4.2.1.2 Selection coefficients and relatedness

An important property of equation (4.3) is that it provides us with an alternative definition for the genetical version of the Malthusian selection differential, $s_{am,k} = \mathrm{Cov}_{i\in\mathbb{G}}(a_{ik}, m_i)$, for the kth trait of interest. This, in turn, leads us naturally to a definition of relatedness (Michod and Hamilton, 1980; Grafen, 1985; Queller, 1992a; Gardner et al., 2011). In particular, using the standard rules of matrix multiplication, we can pre-multiply both sides of equation (4.3) by the inverse of the inverse matrix on the RHS of equation (4.3). Then focussing on the first element of the result, we have

$$\begin{aligned} s_{am,k} &= \mathrm{Var}_{i\in\mathbb{G}}(a_{ik})\hat{\beta}_{ma_k|a_k^*} + \mathrm{Cov}_{i\in\mathbb{G}}(a_{ik}, a_{ik}^*)\hat{\beta}_{ma_k^*|a_k} \\ &= \mathrm{Var}_{i\in\mathbb{G}}(a_{ik})\left(\hat{\beta}_{ma_k|a_k^*} + r_k\hat{\beta}_{ma_k^*|a_k}\right), \end{aligned} \tag{4.4}$$

where $r_k \equiv \hat{\beta}_{a_k a_k^*} = \mathrm{Cov}_{i\in\mathbb{G}}(a_{ik}, a_{ik}^*)/\mathrm{Var}_{i\in\mathbb{G}}(a_{ik})$ is equivalent to a definition of relatedness for our focal kth trait (Michod and Hamilton, 1980; Grafen, 1985; Queller, 1992a; Gardner et al., 2011).

We can see that relatedness is defined by the slope coefficient, $\beta_{a_k a_k^*}$, from a regression of each individual's own genetic value for the focal trait, $\boldsymbol{a}_{\bullet k}$, on the average genetic value of their social partners, $\boldsymbol{a}_{\bullet k}^*$. Note that if we perform $|\mathbb{P}|$ separate multiple linear regressions, we obtain

$$\boldsymbol{s}_{am} = \begin{bmatrix} \mathrm{Var}_{i\in\mathbb{G}}(a_{i1})\left(\hat{\beta}_{ma_1|a_1^*} + r_1\hat{\beta}_{ma_1^*|a_1}\right) \\ \vdots \\ \mathrm{Var}_{i\in\mathbb{G}}(a_{i|\mathbb{P}|})\left(\hat{\beta}_{ma_{|\mathbb{P}|}|a_{|\mathbb{P}|}^*} + r_{|\mathbb{P}|}\hat{\beta}_{ma_{|\mathbb{P}|}^*|a_{|\mathbb{P}|}}\right) \end{bmatrix}, \tag{4.5}$$

which provides us with an alternative definition of the genetical version of the vector of Malthusian selection differentials given by equation (3.49) in Chapter 3. As we will see shortly, this formulation is important, because we can substitute it back into the genetical version of the Malthusian Price equation (3.34) or Malthusian Robertson equation (3.56) from Chapter 3 to understand the evolutionary response to social selection (i.e. social evolution).

Like the direct and indirect fitness effects of our focal trait, $\hat{\beta}_{ma_k|a_k^*}$ and $\hat{\beta}_{ma_k^*|a_k}$, it is important to stress that the relatedness coefficient $r_k \equiv \hat{\beta}_{a_k a_k^*}$ is a property of the population, rather than a value relating to any pair of socially interacting individuals, and is therefore not constant, but a variable quantity that may change as the composition of the population, $\boldsymbol{n}$, and the trait values expressed by individuals, $\mathbf{Z}$, also change through time. Given the state of the population at some time t, relatedness provides a measure of the statistical association across the population between the genetic value of individuals, $\boldsymbol{a}_{\bullet k}$, and the genetic values of individuals with which social interactions are likely to occur, $\boldsymbol{a}_{\bullet k}^*$, at that particular time.

4.2.2 Multivariate neighbour-modulated Malthusian fitness

There has been a large emphasis on the action of natural selection on a single phenotypic trait in social evolution theory (particularly an 'altruistic' trait), but we know from Chapter 3 that greater explanatory power can sometimes be obtained from quantitative genetics models by considering multivariate phenotypes. In particular, by going from the univariate breeder's equation (3.1) to the multivariate breeder's equation (3.2), evolutionary theorists have been able to better understand how statistical associations between traits—brought about by pleiotropy, epistasis, linkage disequilibrium, and so on—can lead to constraints on the direction of the evolutionary response to natural selection (Lande, 1979; Lande and Arnold, 1983). To date, there has been relatively little theoretical research on the importance of genetic details like pleiotropy, epistasis and linkage disequilibrium in social evolution (Foster, 2011). Although some progress has been made (Gardner et al., 2007), much more work is needed to understand the processes by which genetic details shape social evolution and how social evolution, in turn, shapes genetic details (Foster, 2011). For this reason, let us now explore an extension of the univariate analysis we have just undertaken to a multivariate analysis that accounts for the possibility of statistical associations between multiple traits. The connection between this approach and the approach of Lande (1979) and Lande and Arnold (1983) we described in Chapter 3 will be even more apparent in this context.

Indeed, the approach requires that we now generalise the multiple linear regression equation (4.1) to consider multiple traits. Rather than simply focus on the kth trait, at any point in time, t, we now fit a multiple linear regression model in our population for the Malthusian fitness vector, $\boldsymbol{m}$, on the entire *matrix* of genetic values, $\mathbf{A}$, and the entire matrix of genetic values, $\mathbf{A}^*$, corresponding to the genetic values held by each genotype's average social parter. Using the method of population-weighted least-squares, we now have

$$\begin{aligned}\boldsymbol{m} &= \mathbf{1}\hat{\alpha}^{\mathrm{T}}_{maa^*} + \mathbf{A}\hat{\boldsymbol{\beta}}_{ma|a^*} + \mathbf{A}^*\hat{\boldsymbol{\beta}}_{ma^*|a} + \hat{\boldsymbol{\varepsilon}}_{maa^*} \\ &= \mathbf{1}\hat{\alpha}^{\mathrm{T}}_{maa^*} + (\mathbf{A}, \mathbf{A}^*)(\hat{\boldsymbol{\beta}}_{ma|a^*}, \hat{\boldsymbol{\beta}}_{ma^*|a})^{\mathrm{T}} + \hat{\boldsymbol{\varepsilon}}_{maa^*},\end{aligned} \tag{4.6}$$

where the scalar $\hat{\alpha}_{maa^*} = \bar{m} - \hat{\boldsymbol{\beta}}^{\mathrm{T}}_{ma|a^*}\bar{\boldsymbol{a}} - \hat{\boldsymbol{\beta}}^{\mathrm{T}}_{ma^*|a}\bar{\boldsymbol{a}}^*$ again contains the intercept coefficients from the linear model, the $|\mathbb{P}| \times 1$ vectors $\hat{\boldsymbol{\beta}}_{mz|z^*}$ and $\hat{\boldsymbol{\beta}}_{mz^*|z}$ contain the partial regression coefficients, and the vector $\hat{\boldsymbol{\varepsilon}}_{ma_k a_k^*}$ contains the residuals.

Equation (4.6) is now clearly an extension of the Malthusian individual selection surface given by (3.50) in Chapter 3 to incorporate the effects on fitness of social partners. It constitutes a multivariate decomposition of the Malthusian fitness vector, $\boldsymbol{m}$, into its neighbour-modulated fitness form (Queller, 1992a,b; Frank, 1995; Gardner et al., 2011).

4.2.2.1 Direct and indirect fitness effects

Once more, the intercept coefficient, $\hat{\alpha}_{maa^*}$, can be thought of as the 'baseline' Malthusian fitness of individuals before we have taken into account the effect of traits expressed by themselves or their social partners. We can again use 'block matrix' notation to re-write the partial regression coefficients from equation (4.6) in the form

$$\begin{bmatrix}\hat{\boldsymbol{\beta}}_{ma|a^*} \\ \hat{\boldsymbol{\beta}}_{ma^*|a}\end{bmatrix} = \begin{bmatrix}\mathbf{A}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{A} & \mathbf{A}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{A}^* \\ \mathbf{A}^{*\mathrm{T}}\boldsymbol{\Sigma}\mathbf{A} & \mathbf{A}^{*\mathrm{T}}\boldsymbol{\Sigma}\mathbf{A}^*\end{bmatrix}^{-1}\begin{bmatrix}\mathbf{A}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m} \\ \mathbf{A}^{*\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m}\end{bmatrix}, \tag{4.7}$$

or, using the notation defined in Chapter 3, as

$$\begin{bmatrix}\hat{\boldsymbol{\beta}}_{ma|a^*} \\ \hat{\boldsymbol{\beta}}_{ma^*|a}\end{bmatrix} = \begin{bmatrix}\mathbf{G} & \mathbf{A}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{A}^* \\ \mathbf{A}^{*\mathrm{T}}\boldsymbol{\Sigma}\mathbf{A} & \mathbf{G}^*\end{bmatrix}^{-1}\begin{bmatrix}\boldsymbol{s}_{am} \\ \boldsymbol{s}_{a^*m}\end{bmatrix}, \tag{4.8}$$

where $\mathbf{G} = \mathbf{A}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{A}$ is the $|\mathbb{P}| \times |\mathbb{P}|$ variance-covariance matrix of genetic values defined by equation (3.35), $\mathbf{G}^* = \mathbf{A}^{*\mathrm{T}}\boldsymbol{\Sigma}\mathbf{A}^*$ is an equivalent variance-covariance matrix of genetic values for average social partners, the $|\mathbb{P}| \times 1$ vector $\boldsymbol{s}_{am} = \mathbf{A}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m}$ is the genetical version of the vector of Malthusian selection differentials defined by equation (3.49), and $\boldsymbol{s}_{am} = \mathbf{A}^{*\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m}$ is an equivalent vector for the genetic values of traits held by average social partners.

The vector of partial regression coefficients $\hat{\boldsymbol{\beta}}_{ma|a^*}$ can be thought of as representing the *direct* fitness effects of each trait on individuals, holding constant the genetic value of all other traits and the average genetic value of all other traits held by social partners. The vector of partial regression coefficients $\hat{\boldsymbol{\beta}}_{ma^*|a}$ can be thought of as the *indirect* fitness effect of each trait on individuals brought about by social partners, holding constant the average genetic value of all other traits held by social partners, and the genetic value of all traits held by individuals (Hamilton, 1970; Queller, 1992b,a; Frank, 1995; Taylor and Frank, 1996; Gardner et al., 2011).

4.2.2.2 Selection coefficients and relatedness

Similarly to the univariate scenario, equation (4.8) provides us with an alternative definition for the genetic version of the vector of Malthusian selection differentials, $\boldsymbol{s}_{am} = \mathbf{A}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m}$ defined by equation (3.49) in Chapter 3. Again, using standard rules of matrix multiplication, we can pre-multiply both sides of equation (4.8), by the inverse of the inverse matrix on the RHS of equation (4.8). Then, focussing on the first element of the result once more, we have

$$\begin{aligned} \boldsymbol{s}_{am} &= \mathbf{G}\hat{\boldsymbol{\beta}}_{ma|a^*} + \mathbf{A}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{A}^*\hat{\boldsymbol{\beta}}_{ma^*|a} \\ &= \mathbf{G}\left(\hat{\boldsymbol{\beta}}_{ma|a^*} + \mathbf{R}\hat{\boldsymbol{\beta}}_{ma^*|a}\right), \end{aligned} \tag{4.9}$$

where $\mathbf{R} \equiv \hat{\boldsymbol{\beta}}_{aa^*} = \mathbf{G}^{-1}\mathbf{A}^{\mathrm{T}}\boldsymbol{\Sigma}\mathbf{A}^*$ is now a multivariate equivalent of the definition of relatedness for all traits held by individuals in our population (Michod and Hamilton, 1980; Grafen, 1985; Queller, 1992a; Gardner et al., 2011). We call it the 'relatedness matrix'.

Equation (4.9) represents yet another alternative formulation of the genetical version of the vector of Malthusian selection differentials given by equation (3.49) in Chapter 3. Shortly we will see that this formulation is important because we can substitute it back into the genetical version of the Malthusian Price equation (3.34) or Malthusian

Robertson equation (3.56) from Chapter 3 to understand the evolutionary response to social selection in the presence of within-genotype and between-social-partner statistical associations.

The relatedness matrix plays the same role as the scalar version of relatedness, $r_k \equiv \hat{\beta}_{a_k a_k^*}$, we derived in the univariate case, but now also accounts for correlations among individuals expressing different traits. In mathematical terms, it is a $|\mathbb{P}| \times |\mathbb{P}|$ square symmetric covariance matrix of the form

$$\mathbf{R} = \begin{array}{c} \\ \mathbb{P}_1 \\ \mathbb{P}_2 \\ \vdots \\ \mathbb{P}_{|\mathbb{P}|} \end{array} \begin{array}{c} \begin{array}{cccc} \mathbb{P}_1 & \mathbb{P}_2 & \cdots & \mathbb{P}_{|\mathbb{P}|} \end{array} \\ \begin{bmatrix} r_{11} & r_{12} & \cdots & r_{1|\mathbb{P}|} \\ r_{21} & r_{22} & \cdots & r_{2|\mathbb{P}|} \\ \vdots & \vdots & \ddots & \vdots \\ r_{|\mathbb{P}|1} & r_{|\mathbb{G}|2} & \cdots & r_{|\mathbb{P}||\mathbb{P}|} \end{bmatrix} \end{array}, \tag{4.10}$$

equivalent to a matrix of partial regression coefficients, $\hat{\boldsymbol{\beta}}_{aa^*}$, obtained from the regression of the matrix of genetic values, $\mathbf{A}$, on the matrix of genetic values held by average social partners, $\mathbf{A}^*$. The diagonal elements, r_{kk}, represent the relatedness coefficients for the kth trait of the usual kind (Michod and Hamilton, 1980; Grafen, 1985; Queller, 1992a; Gardner et al., 2011). The off-diagonal elements, r_{kl}, however, measure statistical associations in interactions between individuals with respect to the kth and lth traits (i.e. different types of traits). We therefore refer to them as *partial* relatedness coefficients.

Relatedness coefficients of a similar ilk have been derived before (Queller, 1985; Frank, 1994; Doebeli and Knowlton, 1998; Foster and Wenseleers, 2006; Fletcher and Doebeli, 2009; Queller, 2011). In particular, Frank (1994), Doebeli and Knowlton (1998) and Foster and Wenseleers (2006) have all identified similar partial-relatedness coefficients in their models on the evolution of between-species mutualisms. To understand why non-zero values of partial regression coefficients might come about, consider a population consisting of flowering plants and pollinating insects. Non-zero partial-relatedness coefficients might come about in this context owing to a correlation between the heritable basis of a foraging trait held by insects and the heritable basis for a nectar production trait (i.e. an entirely different trait) held by flowering plants. Indeed, Frank (1994) called his version of the partial-relatedness coefficients 'between-species relatedness coefficients'.

In some sense, partial-relatedness coefficients represent a measure of 'reciprocity', but it is an odd kind of genetical reciprocity, distinct from the process that we usually associate with phenotypes (Frank, 1994). That is, it is not the same kind of reciprocity as that

which is involved in 'partner choice' or 'partner-fidelity feedbacks', discussed elsewhere (Trivers, 1971; Sachs et al., 2004; Foster and Wenseleers, 2006), which can lead to a type of social selection process Queller (2011) has called 'kith selection'.

4.3 The dynamics of social evolution

Social evolution occurs via an evolutionary response to *social* selection. Like the evolutionary response to natural selection (Lush, 1937; Falconer and Mackay, 1995) we studied in Chapter 3, social evolution is defined as the portion of phenotypic change in a population over time due to the action of social selection on the underlying heritable basis of social phenotypes (Hamilton, 1970; Queller, 1992b,a; Frank, 1995; Taylor and Frank, 1996; Gardner et al., 2011). Evolutionary theorists are particularly interested in this component of change, because it provides an explanation for the *social* adaptations exhibited by biological organisms in the natural world (Gardner, 2009; West and Gardner, 2013). Thus, Hamilton (1964) wrote in his seminal paper, 'species following the model should tend to evolve behaviour such that each organism appears to be attempting to maximize its inclusive fitness.' In this section, we bring together the two neighbour-modulated forms of fitness we have derived to explore two alternative perspectives on how kin selection shapes the dynamics of social evolution. We discuss the relationship between the dynamics of the social evolution in our population and Robertson's (1966) secondary theorem of natural selection, and show his this relationship leads us naturally to the unification of our dynamical systems theory with Hamilton's (1964; 1970) rule. We end with a comparison of the univariate and multivariate perspective on how kin selection shapes the dynamics of social evolution and possible applications of theory.

4.3.1 Robertson's secondary theorem of natural selection revisited

Recall from Chapter 3, that the approach used in evolutionary genetics to formalise the dynamics of the evolutionary response to natural selection is to decompose the change in the average trait values in a population into two *partial* changes (Frank, 1998): *i*) the partial change brought about *natural selection*; and *ii*) the partial change due to *environmental effects* or other causes not associated with natural selection. We identified the genetical version of the vector of Malthusian selection differentials, $\boldsymbol{s}_{am}$, as a working definition of the partial change due to natural selection, and used it to derive an analogue in our dynamical systems framework of a result due to Robertson (1966), and expanded

upon by Price (1970), which we called the Malthusian Robertson equation (3.56). The equation is given by

$$\frac{\partial_{NS}\bar{\boldsymbol{z}}}{\partial t} = \mathbf{A}^{\mathrm{T}}\boldsymbol{\Sigma}\boldsymbol{m}, \tag{4.11}$$

where the unusual notation, $\partial_{NS}\bar{\boldsymbol{z}}/\partial t$, due to Price (1972b), identifies the partial change in the average value of phenotypic traits in the population due to natural selection. In the present context, our goal is to reformulate this equation in a way that allows us to study the dynamics of social evolution. Since we have already obtained alternative formulations of the genetical version of the vector of Malthusian selection differentials, given by equations (4.5) and (4.9), this goal is now easily met.

4.3.2 Univariate Malthusian Hamilton's rule

Firstly, with regards to our univariate analysis of Malthusian fitness, we can simply substitute for the genetical version of the vector of Malthusian selection differentials, $\boldsymbol{s}_{am}$, given by equation (4.5), into the Malthusian Robertson equation (3.56) to obtain

$$\frac{\partial_{NS}\bar{\boldsymbol{z}}}{\partial t} = \begin{bmatrix} \mathrm{Var}_{i\in\mathbb{G}}(a_{i1})\left(\hat{\beta}_{ma_1|a_1^*} + r_1\hat{\beta}_{ma_1^*|a_1}\right) \\ \vdots \\ \mathrm{Var}_{i\in\mathbb{G}}(a_{i|\mathbb{P}|})\left(\hat{\beta}_{ma_{|\mathbb{P}|}|a_{|\mathbb{P}|}^*} + r_{|\mathbb{P}|}\hat{\beta}_{ma_{|\mathbb{P}|}^*|a_{|\mathbb{P}|}}\right) \end{bmatrix}, \tag{4.12}$$

where we see that the evolutionary response to social selection, can be partitioned into change resulting from direct and indirect fitness consequences. On the one hand, the evolutionary change brought about by social selection depends upon the direct fitness effect of each trait k on individuals expressing the trait themselves, $\beta_{ma_k|a_k^*}$. On the other hand, it also depends upon the indirect fitness effect of each trait k resulting from the interactions of individuals with social partners expressing the trait, $r_k\beta_{ma_k^*|a_k}$.

To obtain an analogue of Hamilton's rule, we are interested in when natural selection favours an increase in the average trait value, $\bar{z}_k$, of an arbitrary trait, k, in the population. We can see from equation (4.12) that this happens when $\partial_{NS}\bar{z}_k/\partial t > 0$, or equivalently, when

$$\beta_{ma_k|a_k^*} + r_k\beta_{ma_k^*|a_k} > 0. \tag{4.13}$$

This inequality is equivalent to a neighbour-modulated fitness form of Hamilton's rule for our population. We refer to it as a 'univariate version' of 'Malthusian Hamilton's rule'. It predicts whether the heritable basis of our focal trait is favoured by social selection at any instantaneous moment in time, t.

Goodnight (2013a) has recently outlined some of the similarities between the neighbour-modulated fitness approach to studying social evolution and several other approaches in evolutionary theory including the 'contextual analysis' approach often used in multilevel selection theory. Goodnight (2013a) points out that the formulation of Hamilton's rule is based on an optimality assumption in the tradition of evolutionary game theory (Maynard Smith, 1978c), since the goal is to identify when $\partial_{NS}\bar{z}_k/\partial t > 0$. Whilst this is certainly true, it is important to point out that the decision to study optimality versus rates of evolutionary change in social evolution theory is one of common preference, not one necessity. In the present context one simply chooses whether or not to study the dynamics of social evolution over an extended period of time using equation (4.12), or to identify whether or not natural selection favours a particular phenotype or not at a specific moment in time using the univariate version of Malthusian Hamilton's rule (4.13).

In many contexts, formulating a dynamical model of social evolution might not contribute much to our understanding of a system. For instance, consider the problem of why a worker honeybee should sacrifice her own reproductive success and lay down her life to protect the hive and queen. Clearly she doesn't gain a direct benefit from doing this, which means that such behaviours could not have evolved through the usual route identified by Darwin (1859). To find an answer we could specify a model for the population dynamics of honeybees, solve the necessary equations, and come to some conclusion, but whether this would yield much insight is doubtful. It might make a prediction for a particular model, but we would gain no insight into the phenomenon of eusocial insect societies more generally. In this case an optimisation approach might be more appropriate and yield more general predictions. From this perspective we might hypothesise that sterile workers have been favoured by kin selection because the gains from indirect fitness benefits of performing altruistic behaviours outweigh any direct fitness costs. This would lead to the prediction that altruism is directed towards individuals that share a heritable basis for the behaviour, a prediction that we could go straight to the field and test empirically. Indeed, this approach has been the basis for much of our understanding about the evolution of eusociality in insect societies for the past 50 years (Ratnieks and Visscher, 1989; Queller, 1994; Queller and Strassmann, 1998; Ratnieks and Wenseleers, 2008; Hughes et al., 2008; Abbot et al., 2011; Liao et al., 2015).

The circumstances in which it is likely to be most desirable to study social evolution using a dynamical model are those in which non-linear population dynamics interact strongly with the selection process. One area of research in which this is typically the case is in the study of social evolution in microbes (Damore and Gore, 2012). Microbial populations exhibit many peculiarities that require special attention as compared to the more traditional domains of study in social evolution theory (West et al., 2006, 2007a). For instance, the spatial and temporal scales over which selection occurs can have important consequences for the evolution and stability of social adaptations (Michod and Roze, 2001; West and Buckling, 2003). The challenge with the rapid generation times of microbes and the resulting short temporal scales over which natural selection acts is illustrated in work by Smith et al. (2010), who studied social evolution in an experimental population of sporulating *Myxococcus* bacteria. They measured the fitness of different bacterial genotypes based on their relative abundance in spores before and after a period of growth and sporulation, and then formulated a version of Hamilton's rule. From their analysis, they concluded that Hamilton's rule 'confounds fitness effects with population structure, obscures the biological causes of selection, and limits the usefulness of Hamiltons rule as an interpretive tool.' They then attempted to overcome this perceived limitation by 'generalising' Hamilton's rule using a Taylor series expansion (up to the 30th order) for fitness. One of the key limitations of the analysis of Smith et al. (2010), however, is that it rests on an attempt to try to force a discrete-generation model on what is an inherently continuous-time process. Rather than modify the discrete-time version of Hamilton's rule to accommodate their particular experimental system, a perhaps more obvious solution would have been to calculate Hamilton's rule at a much shorter timescale to predict the direction of evolutionary change at the next *instant* in time (just like we would do for any other differential equation model) (Wu et al., 2013). Equation (4.12) and the univariate version of Malthusian Hamilton's rule (4.13) would be suitable for such a purpose.

4.3.3 Multivariate Malthusian Hamilton's rule

Let us now turn to our multivariate analysis of Malthusian fitness. Again, we can simply substitute the genetical version of the vector of Malthusian selection differentials, $\boldsymbol{s}_{am}$, this time given by equation (4.9), into the Malthusian Robertson equation (3.56) to obtain

$$\frac{\partial_{NS}\bar{\boldsymbol{z}}}{\partial t} = \mathbf{G}\left(\boldsymbol{\beta}_{ma|a^*} + \mathbf{R}\boldsymbol{\beta}_{ma^*|a,}\right), \tag{4.14}$$

where we see that the evolutionary response to social selection, now taking into account the multivariate nature of phenotypes, can again be partitioned into change resulting from the direct fitness effects of traits, $\hat{\boldsymbol{\beta}}_{ma|a^*}$, and the relatedness-weighted indirect fitness effects of traits, $\mathbf{R}\hat{\boldsymbol{\beta}}_{ma^*|a}$.

The genetic variance-covariance matrix, $\mathbf{G}$, in equation (4.14) replaces the variance components, $\mathrm{Var}_{i\in\mathbb{G}}(a_{ik})$, from equation (4.12). Unlike our univariate analysis, the multivariate analysis thus emphasises that genetic correlations can occur between traits within genotypes to ultimately constrain the 'genetic line of least resistance' in our population (Schluter, 1996). We have already discussed these types of genetic correlations in Chapter 3, but it is worth mentioning why these may be especially important in the context of social evolution. The key point is that a social and non-social trait might become correlated with one another in a population because of linkage-disequilibrium or pleiotropy (Foster et al., 2004; Mitri and Foster, 2016). This within-genotype association could then play an important role in contributing to a type of within-genotype indirect fitness effect. That is, any fitness effects conferred by the non-social trait could become entwined with the fitness effects conferred by the social trait.

Consider, for instance, an altruistic trait k that confers a fitness benefit on social partners and a direct fitness cost upon its bearers. In the absence of genetic correlations, mutant individuals not expressing this altruistic trait might be expected to 'cheat' and outcompete their altruistic neighbours (West et al., 2007c; Ghoul et al., 2014). In the presence of genetic correlations, however, mutant individuals not expressing the altruistic trait might also experience adverse fitness effects through the impact of the mutation on linked non-social traits. Thus, the genetic line of least resistance for this population might be orientated in the direction of increased altruism, even if the selection gradient were not. Indeed, there is now good empirical evidence that such linkage of social and non-social traits can play an important role in the stability of cooperative traits in both microbes (Foster et al., 2004; Dandekar et al., 2012; Mitri and Foster, 2016) and somatic selection in multicellular organisms (Evan and Littlewood, 1998; Lowe et al., 2004).

Equation (4.14) is equivalent to the genetical version of the Malthusian multivariate breeder's equation (3.65) from Chapter 3, where the genetical version of the Malthusian selection gradient, $\hat{\boldsymbol{\beta}}_{ma}$, has been decomposed to give

$$\hat{\boldsymbol{\beta}}_{ma} = \hat{\boldsymbol{\beta}}_{ma|a^*} + \mathbf{R}\hat{\boldsymbol{\beta}}_{ma^*|a}. \tag{4.15}$$

To understand why this is important, recall from Chapter 3 that the genetical version of the Malthusian selection gradient, $\hat{\boldsymbol{\beta}}_{ma}$, gives the direction of the steepest uphill slope on genetical versions of the individual selection surfaces for direct and indirect fitness effects (Phillips and Arnold, 1989), and therefore provides the basis for viewing the dynamics of the evolutionary response to natural selection using Simpson's (1944) adaptive landscape (Steppan et al., 2002; Arnold et al., 2008). Equation (4.15) therefore shows that we can partition the adaptive landscape into two separate *social* landscapes, corresponding to the *i*) direct fitness effects of traits, $\hat{\boldsymbol{\beta}}_{ma|a^*}$, and; *ii*) relatedness-weighted indirect fitness effects of traits, $\mathbf{R}\hat{\boldsymbol{\beta}}_{ma^*|a}$.

By analogy with the approach used in multivariate quantitative genetics (Steppan et al., 2002; Arnold et al., 2008), the eigendecomposition of the relatedness matrix, $\mathbf{R}$, could perhaps be used to represent a 'social line of least resistance' on the landscape of indirect fitness effects, in a similar way to how the eigendecomposition of the matrix $\mathbf{G}$ can used to represent the genetic line of least resistance (Schluter, 1996). In terms of visualising the dynamics, a social trait would be then be seen to be favoured by social selection at any time t, when any movement of the population down a slope on one of the landscapes was offset by a corresponding movement of the population up the slope of the other landscape. To formalise this idea, we observe that a trait is under positive selection when $\partial_{NS}\bar{\boldsymbol{z}}/\partial t > 0$, or equivalently,

$$\boldsymbol{\beta}_{ma|a^*} + \mathbf{R}\boldsymbol{\beta}_{ma^*|a} > \mathbf{0}, \tag{4.16}$$

which represents a neighbour-modulated fitness, multivariate form of Hamilton's rule in continuous-time. It tells us the conditions required for all $|\mathbb{P}|$ traits in the genotype-phenotype map, $\mathbf{Z}$, to be favoured by social selection at every instantaneous moment in time, t. For a focal trait, say the kth trait, inequality (4.16) can be re-written in scalar notation as

$$\beta_{ma|a^*,k} + r_{kk}\,\beta_{ma^*|a,k} + \sum_{l\neq k}^{|\mathbb{P}|} r_{lk}\,\beta_{ma^*|a,k} > 0, \tag{4.17}$$

where $\beta_{ma|a^*,k}$ is the direct fitness effect of the focal trait on each individual, $r_{kk}\,\beta_{ma^*|a,k}$, is the relatedness-weighted indirect fitness effect of the focal trait on individuals resulting from their interaction with social partners, and $\sum_{l\neq k}^{|\mathbb{P}|} r_{kl}\,\beta_{ma^*|a,l}$ accounts for the indirect

fitness effects attributable to traits other than the focal trait held by social partners. We call this inequality the 'multivariate version' of 'Malthusian Hamilton's rule'.

It is important to stress that the univariate version of Malthusian Hamilton's rule (4.13) and the multivariate version of Malthusian Hamilton's rule (4.17) predict the same conditions under which the kth trait is favoured by social selection, they just decompose the impact of selection in different ways. In particular, the multivariate version of Malthusian Hamilton's rule (4.17) makes more explicit the role that partial-relatedness-weighted indirect fitness effects contribute to determining whether or not natural selection favours a trait at time t. These partial-relatedness-weighted indirect fitness effects are also accounted for in the univariate version of Malthusian Hamilton's rule (4.13), but they are absorbed by individual components of that rule in a way that does not make their impact particularly obvious.

We might ask where it is that these types of partial-relatedness-weighted indirect fitness effects arise in natural systems such that we should be interested in them? One of the common theme among the models of Frank (1994), Doebeli and Knowlton (1998), and Foster and Wenseleers (2006) is that unrelated individuals can sometimes be co-located across generations, leading to statistical associations between different types of traits held by different species. The idea is that social selection can then act on these 'functionally coherent' units (Frank, 1994), and bring the reproductive interests of unrelated parties into alignment with one another. This type of scenario has surely played out in a number of the major transitions in evolution (Szathmáry and Maynard Smith, 1995; Szathmáry, 2015). For instance, it certainly seems to have been the case in the formation of the very first eukaryotic organisms (Margulis, 1970). Thus, the multivariate version of Malthusian Hamilton's rule (4.17) may help provide new perspectives on the dynamics of social evolution in the context of the major transitions in evolution or in other circumstances in which between-species social interactions occur.

4.3.4 Concluding remarks

To sum up, when phenotypic traits are social, natural selection operates both directly, through the impact of a trait upon a focal individual's own survival and reproduction, and indirectly, via the impact of the trait upon the fitness of the individual's related social partners. This idea is formalised by Hamilton's rule: $rb - c > 0$, where rb is the indirect fitness effect of the trait on social partners, and $-c$ is the direct fitness effect of the trait on the focal individual. Here, we have extended the dynamical systems framework we introduced in Chapter 2, and our work on the dynamics of selection on correlated traits in

Chapter 3, to derive an expanded continuous-time multivariate version of Hamilton's rule that takes into account the dynamics of natural selection and incorporates phenotypes comprised of multiple traits. We thus provide a general framework for studying how Hamilton's rule changes through time as a system evolves. It is important to note that we do not strictly *need* to formulate the Malthusian form of Hamilton's rule (4.13) to describe the dynamics of natural selection in our population. To do that, we need only solve the Malthusian selection equation (2.28) that we described in Chapter 2. Like the adaptive landscape we discussed in Chapter 3, however, the power of reformulating Hamilton's rule lies in its partitioning of selection into meaningful components that can be compared and contrasted across seemingly very different models and moreover to experiments.

Chapter 5

The dynamics of interdemic group selection

5.1 Introduction

The natural world seems to form a nested hierarchy of organisation (Szathmáry and Maynard Smith, 1995; Okasha, 2006; Bourke, 2011). For instance, starting with multicellular organisms we can move down the hierarchy to find cells, organelles, chromosomes, and genes. Moving up the hierarchy we find populations, species, and whole ecosystems. In principle, any entities from within this nested hierarchy can form populations which exhibit variation, differential reproductive success, and heritability, and therefore be subject to evolution by natural selection (Lewontin, 1970; Godfrey-Smith, 2007). When selection acts across multiple hierarchical levels simultaneously, it is known as 'multi-level' selection (MLS) (Okasha, 2006). When MLS is characterised by a *two*-level selection process, it is often referred to instead as 'group' selection, consisting of selection between entities within groups and selection between groups themselves (Maynard Smith, 1964).

Although historically group selection referred to the process by which selection acts on groups of individual organisms, today it is widely recognised that the terms 'individual' and 'group' are relative definitions that could apply to any two levels of the hierarchy (Okasha, 2006). Thus, a group could represent an entire clade (Nunney, 1999), species (Stanley, 1975; Arnold and Fristrup, 1982), ecosystem (Dunbar, 1960), population (Lewontin, 1970), multicellular organism (Michod, 1997), superorganism (Queller and Strassmann, 2009), microbial colony (Shapiro, 1998), chromosome (Maynard Smith and Száthmary, 1993), and so on. The key requirement is that whatever definition of group we use, the entities in question must embody the principles of evolution by natural selection (Lewontin, 1970; Godfrey-Smith, 2007). Thus, Maynard Smith (1976) argued,

'the extinction of some groups and the "reproduction" of others are essential features of evolution by group selection. If groups are the units of selection, then they must have the properties of variation, multiplication, and heredity required if natural selection is to operate on them.'

The selection process Maynard Smith (1976) was referring to is one of two types of group selection that evolutionary theorists now distinguish between. In particular, it is a process known more specifically as 'interdemic selection' (Reeve and Keller, 1999; West et al., 2007c). Interdemic selection corresponds to the 'MLS2' variety of group selection (Mayo and Gilinsky, 1987; Damuth and Heisler, 1988; Okasha, 2006). It is characterised by two focal levels of selection: groups and individuals within groups. The other type of group selection is known as 'intrademic selection' (Reeve and Keller, 1999; West et al., 2007c). Intrademic selection corresponds to the 'MLS1' variety of group selection (Mayo and Gilinsky, 1987; Damuth and Heisler, 1988; Okasha, 2006). It is characterised by a single focal level of selection: individuals within a population that happens to be group-structured.

There is ongoing debate about the extent to which these two distinctions represent two extremes of a continuum or whether they are distinct processes (Okasha, 2006; Bourrat, 2015a,b; Gardner, 2015). Part of this debate is centred around what definition of fitness is appropriate for groups—should the number of descendants propagated by a group be described in terms of descendant individuals or descendant groups? Intrademic selection is ultimately about selection on individuals, and the fitness of a group is therefore defined in terms of descendant individuals and specifically measured in terms of the aggregate fitness of the individuals comprising it. Interdemic selection concerns selection on both individuals and groups, where group fitness is defined in terms of descendant groups and measured as an independent 'emergent' property (that perhaps bears no clear relationship to the fitness of individuals within a group). In this chapter we will focus on the dynamics of MLS2 and interdemic selection. In the Discussion chapter, however, we will give a short analysis of an equivalent intrademic selection process. Whereas Gardner (2015) has recently shown that intrademic and interdemic definitions of fitness can be reconciled using the notion of genetic value, and Goodnight (2015) has argued for a reconciliation based on a method of contextual analysis, we will briefly explore in the Discussion how the Malthusian fitness of individuals naturally accommodates group-level effects when viewing them from an intrademic selection *perspective*. Thus we will argue that interdemic and intrademic selection processes are not really distinct, but represent different views on the same underlying evolutionary process (contra Okasha (2006)).

One of the common characteristics of interdemic selection is that it typically operates on different timescales at different levels of the biological hierarchy (Fig. 5.1; Williams, 1966; Lewontin, 1970). These different timescales can play an important role in shaping the strength of selection at each level. Indeed, this idea played an important role in the discrediting of Wynn-Edwards' (1962) group selection paradigm by Williams (1966) and others (Maynard Smith, 1964; Dawkins, 1976; Grafen, 1984). Wynne-Edwards (1962) assumed that within-group selection is negligible, and therefore posited that a form of interdemic selection, now sometimes referred to as 'naive' or 'old' group selection (Reeve, 2000; West et al., 2007c), could provide an *explanatory principle* for the evolution of individual-level adaptations that are 'for the good of the group'. The major problem with this, as Williams (1966) pointed out, is that within-group is not negligible, or even weak, but actually likely to outweigh between-group selection, since individuals reproduce on a much shorter timescale than the equivalent processes that take place in groups (Fig. 5.1).

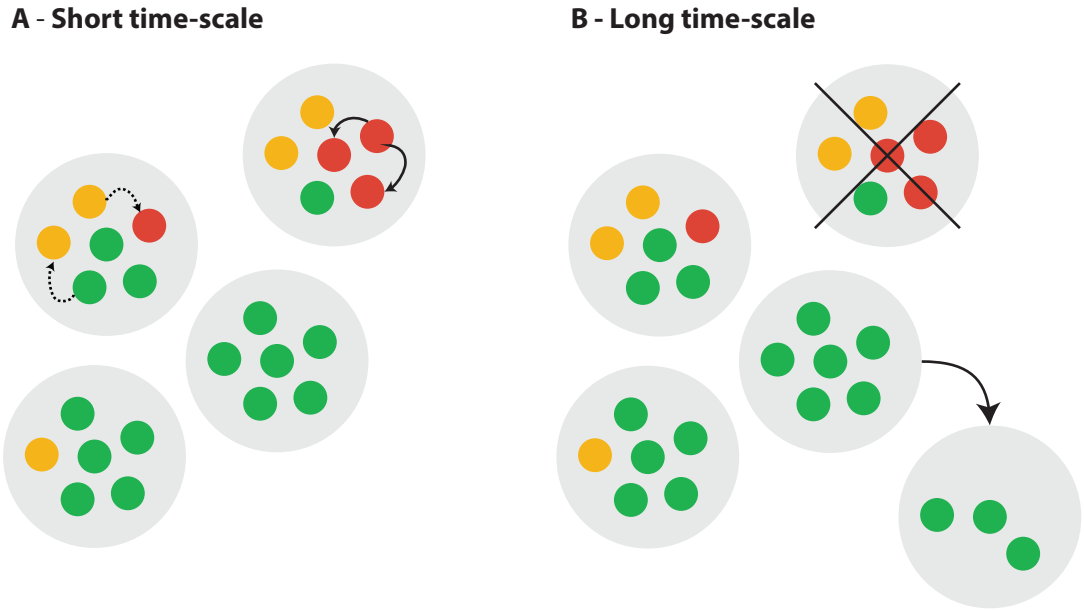


Figure 5.1: The timescales of interdemic selection | Interdemic selection takes place at two focal levels: between groups (large grey circles) and between individuals within groups (small coloured circles). Panel A depicts selection on a short timescale in which there is differential survival and reproduction of individuals within groups. Non-cooperative individuals (orange and red) emerge (dotted arrow), and then survive and reproduce faster than cooperative individuals (green) so tend to spread (black arrow) within groups. Panel B depicts selection on a longer timescale, in which there is differential survival and reproduction of groups. Groups comprised largely of non-cooperative individuals have a higher propensity to become extinct (black cross), whilst those that are comprised of more cooperative individuals have a higher propensity to survive and 'seed' new groups (black arrow). In this schematic, the timescales of selection are favourable for the evolution of cooperation. If individual-level selection were to take place on a much faster timescale than group-level selection, however, as will be the case in many biological systems (Williams, 1966), then groups will tend to become dominated by non-cooperators and the timescales will be unfavourable for the evolution of individual-level cooperation.

Thanks to Hamilton (1964; 1975), we now know that the evolution of traits that give the impression of being 'for the good of the group' are far more parsimoniously explained by the process of kin selection that we discussed in Chapter 4. Following the success of kin selection theory and, in particular, the demonstration that the process of kin selection is mathematically equivalent to that of intrademic selection (Wade, 1985; Queller, 1992b), interdmic selection became a topic rarely discussed in contemporary evolutionary theory. One of the reasons for this is that interdemic selection has been perceived to be too easily conflated with the group selection of old (see West et al. (2007c, 2008) and Wilson (2008) for a discussion)[a].

In recent years, however, there has been a resurgence of interest in interdemic group selection and MLS2 more generally, partly driven by an increasing appreciation of the importance of MLS in the context of the major transitions in evolution (Michod, 1996, 1997; Michod and Roze, 1999; Michod, 2000; Okasha, 2005, 2006; Grosberg and Strathmann, 2007; Bourke, 2011; Goodnight, 2013b; Szathmáry, 2015; West et al., 2015). In particular, it has been claimed that the major evolutionary transition of a population containing one unit of selection to one comprising a hierarchy of two units of selection requires a shift from intrademic to interdemic group selection (MLS1 to MLS2) (Michod, 2000; Okasha, 2005, 2006). That is, cooperative groups of entities form, and are transformed in the course of evolution into an integrated individual that can be considered a new unit of selection in its own right (Maynard Smith and Száthmary, 1997; Bourke, 2011; West et al., 2015). This has been characterised as a transition in which 'group fitness becomes decoupled from the fitness of its lower-level components' (Michod and Nedelcu, 2003).

A key challenge in exploring this hypothesis further, however, again comes back to the different timescales on which selection acts at different levels of the hierarchy (Fig. 5.1). In particular, (Okasha, 2006, pg. 75) argues that the different timescales over which both the higher-level and lower-level units reproduce are 'incommensurate'. A consequence of this is that from a theoretical perspective it is generally not possible to use the discrete-time covariance mathematics of Price (1970, 1972a) to study these two levels of selection

[a]To be clear, interdemic selection is a process that can and does happen across the biological hierarchy in many natural systems (Maynard Smith, 1976). By contrast, old group selection is a limiting case of interdemic selection that occurs when within-group selection is falsely assumed to be weak or non-existent. Thus, whereas old group selection leads to the conclusion that group-level selection can act as an *explanatory principle* for the evolution of individual-level cooperative traits (Wade, 1978), interdemic group selection leads to no such conclusion. Most importantly, there is no empirical evidence supporting the role of old group selection as an important force in shaping evolutionary change, whereas a response to interdemic selection has been demonstrated in a large number of experiments (Wade, 1976; Avilés, 1993; Goodnight and Stevens, 1997; Aspi et al., 2003; Donohue, 2004; Eldakar et al., 2010; Muir et al., 2013; Pruitt and Goodnight, 2014).

simultaneously as an interdemic group selection and interdemic group selection process. Indeed, Arnold and Fristrup (1982) noted many years ago that the choice of a particular timescale suitable for one level of selection immediately limits our ability to understand selection at the other if the timescales are out of sync.

In recent years, however, a number of theorists have departed from the study of MLS using the abstract covariance mathematics of Price (1970, 1972a) to develop a new class of continuous-time group selection models (Simon, 2010; Simon et al., 2013). These new models rest on the derivation of partial differential equations (PDE) that describe the deterministic dynamics of selection in terms of the rates at which groups and individuals within groups survive and reproduce. This enables them explore the impact of the relative timescales over which selection at the within-group and between-group level occurs. The timescales of selection at the two levels are commensurate in these models because they are both instantaneous. Moreover, the authors have shown that it is also possible to use the PDE to explore the impact of modes of group reproduction like fission and fusion that are seldom studied in models grounded in the more traditional frameworks in evolutionary theory (Simon et al., 2013). The extent to which these models a represent a *general* theory of group selection, as Simon et al. (2013) claim, however, is not yet clear. Moreover, it is difficult to relate these models to the existing literature, since Simon et al. (2013) seem to be claiming that their work bears little conceptual relation to the descriptions of group selection and MLS we have given above. In particular, they have made the claim that: 'it is doubtful that the Price equation can be modified in a reasonable way to apply to the models of two-level population dynamics we have described here'.

In this chapter, our aim is to extend dynamical systems theory of natural selection to study the dynamics of interdemic selection. First, we reiterate the general principles of interdemic selection and MLS2 in the context of the work undertaken in previous chapters, developing a general conceptual framework in which to describe a population of groups that operate as units of selection in their own right (Lewontin, 1970; Maynard Smith, 1976). Second, we then extend the Malthusian selection equation (2.28) from Chapter 2 to account for selection between and within groups. This recovers a generalised form of the group-selection PDE derived by (Simon, 2010), in which all modes of group reproduction are represented in abstract terms akin to the approach we described in Chapter 2. Third, we derive interdemic forms of the Malthusian growth-selection equation (2.39), the Malthusian replicator equation (2.45) and the Malthusian Price equation (2.49) from Chapter 2. Hence, we show that the dynamics of interdemic selection can be described from ecological, genotypic, and phenotypic perspectives, just like the dynamics of natural

selection we discussed in Chapter 2. Moreover, we identify a quantity we call 'Malthusian group fitness' using Kimura's (1958) definition, that holds for all modes of group reproduction. Fourth, we discuss how the phenotypic perspective of interdemic selection, centred on the derivation of an interdemic form of the Malthusian Price equation (2.49), provides a formal demonstration of the links between the work of Simon et al. (2013) and the covariance mathematics of Price (1970, 1972a) (contrary to their expectation). Finally, we end with a short discussion of the scenarios in which we might benefit from studying dynamics of interdemic selection, focussing on applications of the theory developed herein to understand the dynamics involved in major evolutionary transitions and to the evolution of conflict resolution mechanisms in the context of cancer.

5.2 The abstract principles of interdemic selection

In this section, we develop a general model for an arbitrary population of groups undergoing evolution by interdemic group selection. Following the approach taken in Chapter 2, we start by considering the characteristics the group population must embody to enable it to be acted on by natural selection, namely, phenotypic variation, differential survival and reproduction, and heritability (Lewontin, 1970; Maynard Smith, 1976). In subsequent sections, we then explore how best to describe the dynamics of interdemic group selection in the model, concluding that just as there were for the individuals we studied in Chapter 2, there are three complementary perspectives that illuminate the impact of ecological and evolutionary forces on the group population.

5.2.1 Units of selection

Entities on which natural selection can act are known formally as 'units of selection' (Lewontin, 1970). Units of selection are members of a population that exhibits phenotypic variation, differential survival and reproduction, and heritability (Lewontin, 1970; Godfrey-Smith, 2007). It doesn't really matter what the units of selection are, providing they exhibit the properties just described. In Chapter 2 we considered arbitrary individuals within a population as our focal units of selection. In this chapter, our aim is to extend beyond a single focal unit, and explore a dynamical system with two levels of selection. In particular, we now consider a system with multiple sub-populations of individuals. For simplicity, we refer to a particular sub-population in the composition space as a 'group'. As we mentioned above, the groups we consider could, in principle, represent anything, including an entire clade (Nunney, 1999), species (Stanley, 1975; Arnold

and Fristrup, 1982), ecosystem (Dunbar, 1960), population (Lewontin, 1970), multicellular organism (Michod, 1997), superorganism (Queller and Strassmann, 2009), microbial colony (Shapiro, 1998), chromosome (Maynard Smith and Száthmary, 1993), and so on. The important thing is that the groups are units of selection in their own right. That is, they must occupy a population, express some form of group phenotype, exhibit differential rates of survival and reproduction, and produce new groups with inherited properties (Lewontin, 1970; Maynard Smith, 1976).

As we did in Chapter 2, we assume that phenotypic variation, differential survival and reproduction, and heritability, both of groups and individuals within group, all result from variation in the biological *information* held by different entities (Maynard Smith, 2000). Whereas an individual within a group is defined by its genotype, a group the genotypic composition of individuals, $\boldsymbol{n}$, that is it comprised of, which can be thought of as its location within the composition space Ω. Hence, we refer to a group at a particular point in space as an '$\boldsymbol{n}$-composition group'. Note that the composition space contains all possible group compositions.

5.2.2 Population

To study the dynamics of group selection, we need a group-population. Let $\theta := \theta(t, \boldsymbol{n}) \in \mathbb{R}_+$ denote a group density scalar field that associates every point $\boldsymbol{n}$ in the composition space with the density of groups at that point at some time t. That is, the density of $\boldsymbol{n}$-composition groups in the group-population at some time t is given by θ. We denote the finite size of the group-population by $\Theta := \Theta(t) \in \mathbb{R}_+$. We can calculate the group-population size at any time t by simply integrating over the group density scalar field to give: $\Theta = \int_\Omega \theta \, d\Omega$. We may also calculate the *relative* density of $\boldsymbol{n}$-composition groups, rather than their absolute density. The relative density of $\boldsymbol{n}$-composition groups in the group-population is simply given by the scalar field $\mathcal{X} = \theta/\Theta$. Note that the total relative group density is simply unity, that is $\int_\Omega \mathcal{X} \, d\Omega = \int_\Omega \theta \, d\Omega/\Theta = \Theta/\Theta = 1$.

If we focus on a particular $\boldsymbol{n}$-composition group, we see it is just like the population of entities we described in Chapter 2. The genotypic composition of the group is given by $\boldsymbol{n}$, its finite size is given by N, and its relative composition given by $\boldsymbol{x}$. The main difference is that in Chapter 2 each of these quantities was defined for a particular point in time, but in the present context each of the quantities must be defined at every point in the composition space. Since we now have many groups, we distinguish between any two of them using hat notation. For instance, the composition vectors $\boldsymbol{n}$ and $\hat{\boldsymbol{n}}$ represent the composition of groups at two separate positions in the composition space, Ω.

5.2.3 Phenotypes

For natural selection to act on our groups, there must be variation among the group-level phenotypes they express (Lewontin, 1970; Godfrey-Smith, 2007). The approach we take here to define these phenotypes is almost identical to that taken in Chapter 2. The phenotype of a group is simply a set of observable characteristics or 'quantitative traits' associated with it (Falconer and Mackay, 1995). We index each trait of interest by $k \in \mathbb{Q}$, where $\mathbb{Q}$ is the index set of all group traits. The total number of group traits is given by the size of the set, $|\mathbb{Q}|$.

For the kth trait, let $\mathcal{Z}_k := \mathcal{Z}_k(t, \boldsymbol{n}) \in \mathbb{R}$ denote the 'value' of the group trait expressed by $\boldsymbol{n}$-composition groups at time t. The values of all $|\mathbb{Q}|$ traits expressed by $\boldsymbol{n}$-composition groups at time t define their group-level phenotype at that time. The phenotypes expressed by all groups are given by a $|\mathbb{K}| \times |\mathbb{P}|$ vector of scalar fields

$$\boldsymbol{\mathcal{Z}} = \begin{array}{c} \begin{matrix} \mathbb{Q}_1 & \mathbb{Q}_2 & \cdots & \mathbb{Q}_{|\mathbb{Q}|} \end{matrix} \\ \begin{bmatrix} \mathcal{Z}_{\boldsymbol{n}1} & \mathcal{Z}_{\boldsymbol{n}2} & \cdots & \mathcal{Z}_{\boldsymbol{n}|\mathbb{Q}|} \end{bmatrix} \end{array}. \tag{5.1}$$

We refer to this vector as the 'composition-phenotype map', by analogy with the genotype-phenotype map, $\mathbf{Z}$, that we defined in Chapter 2. Although we have represented this as a finite vector, the set of all possible group traits is infinitely large, since it is always possible to take a linear combination of two or more group traits to arrive at another 'new' group trait.

Just as in Chapter 2, it is important to note that the information held by a group does not determine its phenotype directly, but rather influences the functional form of some kind of mapping function, $\mathcal{Z}_k$, that *does* determine its phenotype. Many evolutionary theorists make the distinction between so-called 'aggregate' and 'emergent' group traits (Okasha, 2006, pg. 48-49). An aggregate group trait typically refers to a trait that is measured as a summary statistic of the trait values measured on individuals within the group. An emergent group trait typically refers to one that is measurable only at the level of the group itself. For instance, suppose our groups represent 'clumps' of the budding-yeast *Saccharomyces cerevisiae*, which are known to secrete hydrolytic enzymes in order to obtain nutrients from the breakdown of more complex organic molecules in their environment. The *rate* of enzyme secretion by a clump represents an aggregate trait since it scales linearly with the rate of secretion by individual cells within the clump. That is, we can measure the rate of enzyme secretion separately at the level of the cell and group. Clumping of cells provides several advantages over a free-living

state, since it leads to a local concentration build up of secreted enzyme within the group (Koschwanez et al., 2011). The *concentration* of secreted enzyme within a clump represents an emergent trait that cannot be measured without including all features of the group. We could say that cells have the measurable property of living within a group that has a particular concentration of secreted enzyme, but this would correspond to what evolutionary theorists refer to as a 'contextual trait' (Goodnight et al., 1992; Okasha, 2006), which we will discuss briefly in Chapter 5 in the context of intrademic group selection.

It is important to note that overall, the phenotype of a group emerges from the interpretation of the information it holds, *given* the 'environment' it experiences. The environment here refers to the state of the system the group occupies at time t. That is, *anything* in the system can be viewed as an environmental or ecological variable. The key point is that phenotypic traits can be specified as arbitrary functions that may or may not vary through time. We will discuss the causes and implications of time-dependent group phenotypes in a later section when we consider group phenotypic *dynamics*.

As we discussed in Chapter 2, if we are interested in evolutionary change in group phenotypes, we will typically be interested not in any particular group, but in the overall summary statistics for groups in the group population (Okasha, 2006). Integrating over the composition space and weighting by the group density θ at each point, we can obtain the *average* value of the kth group trait in the population at time t, which we denote by

$$\bar{\mathcal{Z}}_k = \frac{1}{\Theta}\int_\Omega \theta \mathcal{Z}_k \, d\Omega = \int_\Omega \mathcal{X}\mathcal{Z}_k \, d\Omega. \tag{5.2}$$

We denote the average values of all group traits in the group-population by a $|\mathbb{Q}|\times 1$ vector $\bar{\boldsymbol{\mathcal{Z}}} = \frac{1}{\Theta}\int_\Omega \theta \boldsymbol{\mathcal{Z}} \, d\Omega = \int_\Omega \mathcal{X}\boldsymbol{\mathcal{Z}} \, d\Omega$. An alternative notation and several other summary statistics of potential interest are given in Box 5.1.

Box 5.1 | A note on statistical notation for group phenotypes

The expected value of a group trait is a measure of the centre of its distribution in the group-population at time t. In this context, the expected value of the kth group trait is simply equal to the average from equation (5.2), which we re-write as

$$\mathrm{E}_{\boldsymbol{n}\in\Omega}(\mathcal{Z}_{ik}) = \bar{\mathcal{Z}}_k, \tag{5.3}$$

where the notation $\boldsymbol{n} \in \Omega$ indicates that the expectation is taken over all groups in the composition space Ω. As in Chapter 2, writing the average in this 'moment' no-

tation is useful, because we can easily see the relations to other summary statistics that may be of interest (Robertson, 1966; Price, 1970, 1972a; Falconer and Mackay, 1995). For instance, the covariance between two group traits, say the kth and lth group traits, gives a measure of their statistical association in the population. We calculate the covariance as

$$\mathrm{Cov}_{\boldsymbol{n}\in\Omega}(\mathcal{Z}_k, \mathcal{Z}_l) \equiv \mathrm{E}_{\boldsymbol{n}\in\Omega}(\mathcal{Z}_k\mathcal{Z}_l) - \mathrm{E}_{\boldsymbol{n}\in\Omega}(\mathcal{Z}_k)\mathrm{E}_{\boldsymbol{n}\in\Omega}(\mathcal{Z}_l) \tag{5.4}$$

The covariance between a group trait k and itself gives the variance of the trait in the group-population, which is a measure of its dispersal around the group-population average, $\bar{\mathcal{Z}}_k$. We calculate the variance as

$$\begin{aligned}\mathrm{Var}_{\boldsymbol{n}\in\Omega}(\mathcal{Z}_k) &\equiv \mathrm{Cov}_{\boldsymbol{n}\in\Omega}(\mathcal{Z}_k, \mathcal{Z}_k) \\ &= \mathrm{E}_{\boldsymbol{n}\in\Omega}(\mathcal{Z}_k^2) - \mathrm{E}_{\boldsymbol{n}\in\Omega}(\mathcal{Z}_k)^2.\end{aligned} \tag{5.5}$$

5.2.4 Survival and reproduction

Now that we have a description of the phenotypes groups express, the second principle of evolution by natural selection that our group-population must meet is that there is some form of differential survival and reproduction among groups (Lewontin, 1970; Godfrey-Smith, 2007). Note that since we are describing interdemic group selection we must define group survival and reproduction in terms of changes in the abundance of *groups* (rather than changes in the abundance of *entities*, which is the approach usually taken in descriptions of intrademic group selection). Just as the logic of natural selection does not depend on what the units of selection in question are, or how how we measure their phenotypes, it also does not depend on what the specific processes are that influence the gain or loss of copies particular units of selection in a population. We demonstrated this with an abstract notion of survival and reproduction in Chapter 2, and will take the same approach here. Indeed, an exact definition of exactly what constitutes group survival and reproduction is not widely agreed upon (Okasha, 2006). This isn't really surprising since, as we noted above, a group could represent an entire clade (Nunney, 1999), species (Stanley, 1975; Arnold and Fristrup, 1982), ecosystem (Dunbar, 1960), population (Lewontin, 1970), multicellular organism (Michod, 1997), superorganism (Queller and Strassmann, 2009), microbial colony (Shapiro, 1998), chromosome (Maynard Smith and Száthmary, 1993), and so on.

To understand the abstract formulation of group survival and reproduction we take, it may help the reader to return to Chapter 2 and see the more detailed description we give

there. The most obvious processes that lead to gain or loss of particular groups are births and deaths, but only if our groups represent organisms in their own right. Some of the other modes of group reproduction we must also consider include splitting, sending out propagules, mating-pool reproduction, fusion, and fission (Maynard Smith, 1976; Wade, 1978; Okasha, 2006; Simon et al., 2013). Yet, as we argued in Chapter 2, these diverse processes too can be thought of in terms of the gain and loss of a group. For instance, if a group fissions (splits into two or more pieces), the density on the composition space at one point decreases, but group density is gained at two other points corresponding to whatever composition defines the resulting smaller groups. Similarly, if two groups fuse, the group-population loses two groups, but gains a new one corresponding to whatever composition the newly fused group is defined by.

Again, following Chapter 2, we use the term 'ancestor' to describe any group alive at time t that contributes information (vicariously through the transfer of individuals) to the creation of a new 'descendant' group some instant later at $t + \delta t$. Since Simon et al. (2013) claim that group fusion and fission cannot be represented in terms of a Price equation, which we dispute, we will focus on these processes here. Thus, our abstract characterisation of group survival and reproduction is depicted for group fusion and fission in Figure 5.2. We will see in a later section that the abstract approach leads us to be able to define a measure for the Malthusian fitness of a group using Kimura's (1958) definition, and then to relate the group selection PDE models of Simon (2010) and Simon et al. (2013) to the covariance mathematics of Price (1970, 1972a).

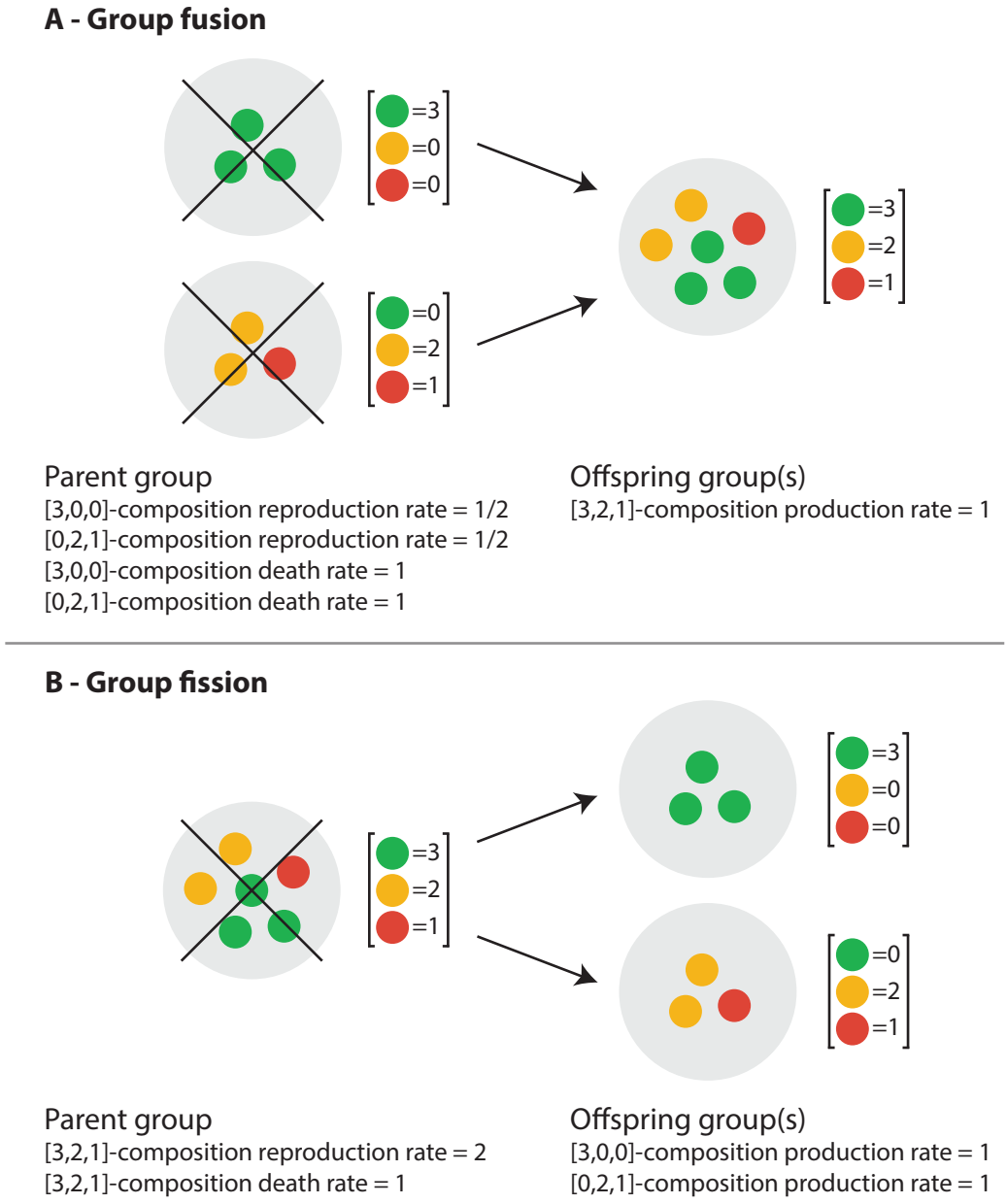


Figure 5.2: Group fusion and fission | We use an abstract notion of group survival and reproduction by thinking about all processes that lead to changes in the composition of the group population through the gain and loss of groups. We say that ancestral groups *reproduce*, and descendants groups are *produced*. That is, we emphasise that these are two different processes that are intimately related and happen to occur at the same time. We give two examples that Simon et al. (2013) claim are not given sufficient attention in the literature on group selection. In panel **A** we depict the fusion of an $(3, 0, 0)$-composition ancestral group with a $(0, 2, 1)$-composition ancestral group giving rise to the production of an $(3, 2, 1)$-composition descendant group. In panel **B** we depict the fission of an $(3, 2, 1)$-composition ancestral group to produce a $(3, 0, 0)$-composition descendant group and a $(0, 2, 1)$-composition descendant group. Note that in both panels the reproduction rate of each ancestral group is scaled so that the total rate of reproduction always equals the total rate of production.

Whatever process of group survival and reproduction we consider, the ancestors and descendants involved must always be defined somewhere in the composition space Ω. It is therefore possible to assign rates – measurable in units of time^{-1} – to existing groups that account for the gain and loss of new groups. Beginning with processes that cause the loss of groups, let $\mathcal{D} := \mathcal{D}(t, \boldsymbol{n}) \in \mathbb{R}$ denote the 'death' rate of $\boldsymbol{n}$-composition groups at time t. We use the term death loosely; As we have discussed, death of a group might happen because groups fuse or fission, but it might also happen because groups die in the usual sense. The average death rate in the group-population at time t, is given by

$$\bar{\mathcal{D}} = \frac{1}{\Theta} \int_{\Omega} \theta \mathcal{D} \, d\Omega = \int_{\Omega} \mathcal{X} \mathcal{D} \, d\Omega. \tag{5.6}$$

We can always think of the death rate as being a trait in the composition-phenotype map, $\boldsymbol{\mathcal{Z}}$, since it is a measurable property of groups. Just like other traits in the composition-phenotype map, the group death rate is not necessarily a static trait, but may change through time. For example, if resources are scarce there might be an upper limit on how many tribes can occupy a given territory.

Moving on to processes that cause the gain of a copy of a particular group, things get a little more complicated, just as they did at the same point in Chapter 2. As we stated then, it might seem natural to simply define another function, say $\mathcal{B}$, denoting the 'birth' rate of $\boldsymbol{n}$-composition group ancestors at time t and continue from there. As we have previously discussed, however, the rate of reproduction *by* a ancestor is not usually the same as the rate of increase of that type of ancestor in the population at that time. If our groups 'reproduce' by any process like fusion, fission or propagule emission, they will certainly give rise to descendants with a different composition to themselves. Also of interest to us, therefore, is the rate of 'production' of descendants of a specified composition.

The solution to obtaining both the rates of reproduction and production in the population rests on defining pairwise rates, just as they did in Chapter 2. Here, though, we do not have discrete genotypic types, but a continuum of different group compositions. Therefore, let the integral transform $\mathcal{F}(\boldsymbol{n}, \hat{\boldsymbol{n}}) := \mathcal{F}(\boldsymbol{n}, \hat{\boldsymbol{n}}, t) \in \mathbb{R}_+$ denote a *compound* group fidelity rate, giving the rate at which $\boldsymbol{n}$-composition group ancestors reproduce *and* give rise to the production of $\hat{\boldsymbol{n}}$-composition group descendants. This kernel plays a similar role in this chapter to the reproduction fidelity matrix, $\mathbf{F}$, that we introduced in Chapter 2. In particular, it gives the *conditional* rate at which $\hat{\boldsymbol{n}}$-composition group offspring are produced by a particular $\boldsymbol{n}$-composition parent group, *given* that the specified

parent group is alive at time t. We can think of the first argument of the fertility kernel, $\boldsymbol{n}$, as pertaining to an ancestral group, and the second argument, $\hat{\boldsymbol{n}}$, as pertaining to an descendant group. It is important to note that to specify the fidelity rate transform we need to know specific details about the mode of reproduction of reproduction of groups, and the mechanisms of group inheritance. We will return to this point shortly.

For now we can return to the goal we started with and let $\mathcal{B} := \mathcal{B}(\boldsymbol{n}, t) \in \mathbb{R}_+$ denote the rate of reproduction of $\boldsymbol{n}$-composition ancestral groups. From the fidelity rate kernel $\mathbf{F}$ we can now see that the reproduction rate is simply given by the integral over the rates at which $\boldsymbol{n}$-composition ancestral groups reproduce and give rise to descendants of *any* other composition:

$$\mathcal{B} = \int_{\hat{\Omega}} \mathcal{F}_{\boldsymbol{n}\hat{\boldsymbol{n}}} \, d\hat{\Omega}. \tag{5.7}$$

Just like the death rate, we can always think of the birth rate as being a trait in the composition-phenotype map, $\boldsymbol{\mathcal{Z}}$, since it is also a measurable property of a group. Like other traits in the composition-phenotype map, the reproduction rate is also dependent on time t. It is also therefore not necessarily a static trait, but may change through time. For example, if our groups reproduce by fissioning, then the rate of reproduction might depend on the size of a group at time t, with larger groups more likely to fission than smaller groups. For instance, this was the assumption in the MLS model of Traulsen and Nowak (2006).

Now let us turn to the rate at which new group variants are created in the group-population. Let $\mathcal{P} := \mathcal{P}(\boldsymbol{n}, t) \in \mathbb{R}_+$ denote the rate of production of $\boldsymbol{n}$-composition descendant groups. This is simply given by integrating over the rate at which $\hat{\boldsymbol{n}}$-composition ancestral groups (weighted by their group density) reproduce and give rise to $\boldsymbol{n}$-composition descendant groups:

$$\mathcal{P} = \int_{\hat{\Omega}} \hat{\theta} \mathcal{F}_{\hat{\boldsymbol{n}}\boldsymbol{n}} \, d\hat{\Omega}. \tag{5.8}$$

Unlike the reproduction rate and death rate, we cannot think of the production rate as a trait in the composition-phenotype map, $\boldsymbol{\mathcal{Z}}$, since it is *not* a measurable property of any particular group, but instead a measurable property of the group-population. As we highlighted in Chapter 2, the rate of production of an entity is more like a demographic rate from population ecology (Maynard Smith, 1978a).

Although the rate of reproduction and production of any given group are not equivalent, we pointed out in Chapter 2 that it *is* logically the case that the total, and hence the average, reproduction and production rates of all groups are the same at any time t. That is because the production of a group implies that another individual reproduced and vice versa. To prove that this is indeed the case, let us start by denoting the average rate of reproduction in the population by

$$\bar{\mathcal{B}} = \frac{1}{\Theta}\int_{\Omega} \theta\mathcal{B}\, d\Omega = \int_{\Omega} \mathcal{X}\mathcal{B}\, d\Omega. \tag{5.9}$$

Similarly, the average rate of production of all groups is given by

$$\bar{\mathcal{P}} = \frac{1}{\Theta}\int_{\Omega} \mathcal{P}\, d\Omega = \frac{1}{\Theta}\int_{\Omega}\int_{\hat{\Omega}} \hat{\theta}\mathcal{F}_{\hat{\boldsymbol{n}}\boldsymbol{n}}\, d\hat{\Omega}\, d\Omega = \int_{\Omega}\int_{\hat{\Omega}} \hat{\mathcal{X}}\mathcal{F}_{\hat{\boldsymbol{n}}\boldsymbol{n}}\, d\hat{\Omega}\, d\Omega. \tag{5.10}$$

where we have substituted for $\mathcal{P}$ from equation (5.8). If we now take the integral over Ω inside the integral over $\hat{\Omega}$ in equation (5.10), and then switch the order of integration (which has no effect on the equality), we obtain

$$\bar{\mathcal{P}} = \int_{\hat{\Omega}} \hat{\mathcal{X}} \int_{\Omega} \mathcal{F}_{\hat{\boldsymbol{n}}\boldsymbol{n}}\, d\Omega\, d\hat{\Omega} = \int_{\Omega} \mathcal{X} \int_{\hat{\Omega}} \mathcal{F}_{\boldsymbol{n}\hat{\boldsymbol{n}}}\, d\hat{\Omega}\, d\Omega = \int_{\Omega} \mathcal{X}\mathcal{B}\, d\Omega = \bar{\mathcal{B}}, \tag{5.11}$$

where we have substituted for $\mathcal{B} = \int_{\hat{\Omega}} \mathcal{F}_{\boldsymbol{n}\hat{\boldsymbol{n}}}\, d\hat{\Omega}$ from equation (5.7) and $\bar{\mathcal{B}} = \int_{\Omega} \mathcal{X}\mathcal{B}\, d\Omega$ from equation (5.9). Hence, we have proved that average rate of reproduction given by equation (5.9) is equivalent to the average rate of production given by equation (5.10).

An important consequence of this equality is that the fidelity rate of an $\boldsymbol{n}$-composition ancestral group, $\mathcal{F}(\boldsymbol{n}, \hat{\boldsymbol{n}})$, should be weighted by the ratio of the average number of descendants produced to the average number of reproducing ancestors involved in reproduction, #avg. descendants/#avg. ancestors. For instance, if an ancestral group fissions into 10 pieces, the rate of reproduction of the ancestor must be weighted by #descendants/#ancestors = 10/1, whereas if it fuses with 4 other groups, the rate of reproduction of all 4 ancestral groups must be weighted by #descendants/#ancestors = 1/4. Thus, we have the prediction that, like the famous 'two-fold cost of sex' described by Maynard Smith (1978b), reproduction by group fusion represents a poor form of group selection mechanism from a dynamical perspective (although possibly not for other reasons). Indeed, it is even worse than sexual reproduction, because the group-population size is *reduced* by the process of fusion, rather than increased. Yet we can

see that group fissions could represent a powerful group selection mechanism, because they increase the group-population size and group-population variance, which is the raw currency of natural selection.

The cost of describing group survival and reproduction, and other related group-level processes, in the abstract way we have defined in this section is that it clearly obscures the biology behind the process we are interested in. In the papers by Simon (2010) and Simon et al. (2013), they illuminate many interesting group-level processes that can be independently captured by the specification of process-related functions. They have a fusion function, a fission function, and so on. Their approach and the approach we have described here will ultimately give rise to the same group-population dynamics, but the specification of rates for group-level processes in the way we have done represents a more abstract, general approach. We will see in a later section that it a key requirement for being able to translate the dynamics of this model into the covariance mathematics of Price (1970, 1972a).

5.2.5 Inheritance

Now that we have a description of the ways in which groups 'reproduce', the third principle of evolution by natural selection that our population must meet is that there is heritability (Lewontin, 1970; Godfrey-Smith, 2007). Again, it will come as no surprise to learn that we can use exactly the same logic as that we applied in Chapter 2 to think about group-level inheritance. The main distinction is that in Chapter 2, we assumed individuals transmit *information* to their descendants when they reproduce. Here, however, whilst information is still transmitted between group ancestors and their descendants, it is vicariously through individuals themselves.

The phenotype expressed by descendant groups depends on their composition, which they inherited from the ancestors that gave rise to them, and how the information they hold gets interpreted by the environment. As we discussed in Chapter 2, all our knowledge about modes of group reproduction has already gone into the specification of the fidelity rate transform $\mathcal{F}(\boldsymbol{n}, \hat{\boldsymbol{n}})$. Clearly, to know the rate at which $\hat{\boldsymbol{n}}$-composition descendant groups are produced when an $\boldsymbol{n}$-composition ancestral group 'reproduces', we need to know how it reproduced, did it fission, fuse, etc.

To give an illustration of why this is the case, consider the model organism *Dictyostelium discoidium* as an example. *D. discoidium* is a type of slime mould with both a single-celled amoebic state and multi-celled mobile slug state (Crespi, 2001; West et al., 2007a; Foster, 2010). To represent the process by which the slug forms using the fertility kernel, we must

take into account the rates at which single-celled amoebae – which can be thought of as groups of size 1 – meet and aggregate (fuse), which will in turn depend on the composition of the entire population of cells, the composition of cells within a particular developing slug, the phenotypes expressed, and so on. Similarly, when the slug forms a stalk and disperses spores (fission), the fertility kernel must take into account the rates at which different types of cells are dispersed, which in turn will depend on the composition of the slug/stalk, the phenotypes cells' express, and so on. Despite the inherent complexity of the fertility kernel, we can use it in a quite general way to obtain several other quantities of interest.

5.2.5.1 Expected composition distribution of descendant groups

By analogy with the approach in population genetics of studying relative genotype frequencies rather than absolute numbers (Crow and Kimura, 1970), we can gain a clearer perspective on the mechanisms of group inheritance in our framework by exploring the question: what composition do we expect group offspring to inherit from their $\boldsymbol{n}$-composition group parents? For instance, suppose our groups represent ant colonies of the species *Formica truncorum*. These ants are characterised by a high degree of inter-colony variation in intra-colony sex-ratio (Sundström, 1994). In this context, we might therefore be interested in what the expected composition of males and females is in offspring colonies resulting from the 'reproduction' of a given parent colony.

To answer this question, let us introduce a group 'inheritance kernel', $\mathcal{H}_{\boldsymbol{n}\hat{\boldsymbol{n}}} := \mathcal{H}_{\boldsymbol{n}\hat{\boldsymbol{n}}}(\mathbf{Z}, \hat{\mathbf{Z}}, \boldsymbol{n}, \hat{\boldsymbol{n}}, \boldsymbol{\mathcal{Z}}, \theta, t) \in \mathbb{R}$. The inheritance kernel gives the *conditional* probability[b] that an $\boldsymbol{n}$-composition group produces $\hat{\boldsymbol{n}}$-composition group descendants, *given* that is has reproduced. The kernel is defined by dividing the group fertility kernel, $\mathcal{F}_{\boldsymbol{n}\hat{\boldsymbol{n}}}$, by the group reproduction rate, $\mathcal{B}$, to give

$$\mathcal{H}_{\boldsymbol{n}\hat{\boldsymbol{n}}} = \frac{\mathcal{F}_{\boldsymbol{n}\hat{\boldsymbol{n}}}}{\mathcal{B}}. \tag{5.12}$$

The inheritance kernel is a dimensionless quantity that we may interpret as a probability *density* function over the composition space Ω. It gives a measure of the likelihood that an $\boldsymbol{n}$-composition group produces $\hat{\boldsymbol{n}}$-composition group descendants, *given* that is has reproduced. It plays a similar role to the inheritance matrix, $\mathbf{H}$, that we introduced in

[b]Recall from basic probability theory that the conditional probability of an event A given an event B is given by $\mathbb{P}(A|B) = \mathbb{P}(A \cap B)/\mathbb{P}(A)$, where $\cap$ denotes the intersection of two events (i.e. a compound event).

Chapter 2. Indeed, it shares a similar property to the inheritance matrix, in that the integral over its second argument is always equal to 1. That is, we have $\int_{\hat{\Omega}} \mathcal{H}_{\boldsymbol{n}\hat{\boldsymbol{n}}}\, d\hat{\Omega} = 1/\mathcal{B} \int_{\hat{\Omega}} \mathcal{F}_{\boldsymbol{n}\hat{\boldsymbol{n}}}\, d\hat{\Omega} = \mathcal{B}/\mathcal{B} = 1$.

The inheritance kernel provides the answer to the question we posed at the start of this section by giving us the *expected* distribution of an $\boldsymbol{n}$-composition groups descendants over the composition space Ω at any time t. That is, it tells us how likely an $\boldsymbol{n}$-composition ancestral group is to undergo fission, fusion, and so on and to produce a given type of descendant group. Another useful property of the inheritance kernel is that it gives us an indication of how likely group reproduction is to generate diversity in the group-population. If the probability density function represented by $\mathcal{H}_{\boldsymbol{n}\hat{\boldsymbol{n}}}$ has a large variance, we can infer that group reproduction involves a lot of random fusion or fission events that 'redistribute' group density across the composition space. If the density function has a small variance we can infer that group reproduction involves more events like the occasional emission of a propagule that have a less dramatic impact on the distribution of group density. In the special case where all groups reproduce and produce groups with the same composition as themselves (which corresponds to clonal group reproduction and the perfect transmission of information), the variance of the probability density function tends toward zero, and the inheritance kernel becomes the identity kernel, also known as the 'Dirac delta function', $\mathcal{H}_{\boldsymbol{n}\hat{\boldsymbol{n}}} = \delta(\boldsymbol{n})$.

5.2.5.2 Expected phenotypic distribution of descendant groups

Now let us turn to answering the question: what group phenotype do we expect descendants to inherit from the $\boldsymbol{n}$-composition group ancestors that give rise to them? Since the inheritance kernel represents a type of probability density function, we note that taking the integral of a product of the inheritance kernel with an arbitrary quantitative trait from the group composition-phenotype map, say trait k, represents an expected value of the group in an $\boldsymbol{n}$-composition ancestral group's potential descendants. We denote this by

$$\mathrm{E}'_{\boldsymbol{n}\in\Omega}(\mathcal{Z}_{\boldsymbol{n}k}) = \int_{\hat{\Omega}} \mathcal{H}_{\hat{\boldsymbol{n}}\boldsymbol{n}} \hat{\mathcal{Z}}_{\boldsymbol{n}k}\, d\hat{\Omega} = \mathcal{Z}'_{\boldsymbol{n}k}, \tag{5.13}$$

where the notation $\mathrm{E}'(\cdot)$ indicates that we have taken the expectation using the group inheritance kernel $\mathcal{H}_{\boldsymbol{n}\hat{\boldsymbol{n}}}$. The symbol $\mathcal{Z}'_{\boldsymbol{n}k} := \mathcal{Z}'_{\boldsymbol{n}k}(\boldsymbol{n}, \hat{\boldsymbol{n}}, \mathbf{Z}, \hat{\mathbf{Z}}, \theta, \boldsymbol{\mathcal{Z}}) \in \mathbb{R}$ is an alternative short-hand notation we use for the expected trait values in group offspring. Now let the

vector of scalar fields $\boldsymbol{\mathcal{Z}}' = [\mathcal{Z}'_{\boldsymbol{n}k}] \in \mathbb{R}^{|\mathbb{Q}|}$ denote the group composition-phenotype map for expected group descendants. We have:

$$\boldsymbol{\mathcal{Z}}' = \int_{\hat{\Omega}} \mathcal{H}_{\hat{\boldsymbol{n}}\boldsymbol{n}} \hat{\boldsymbol{\mathcal{Z}}} \, d\hat{\Omega}, \tag{5.14}$$

It is important to note that these quantities are *prospective* or *conditional* values that group descendants will express, if we assume that they have been produced. That is, these values exist independently of whether or not a particular parent group actually reproduces or not (we can always predict what the phenotypic trait values its group descendants would express if they *were* produced). Note that in the special limiting case where groups reproduce and produce groups with the same composition as themselves, the inheritance kernel becomes the identity kernel, $\mathcal{H}_{\boldsymbol{n}\hat{\boldsymbol{n}}} = \delta(\boldsymbol{n})$, so that $\boldsymbol{\mathcal{Z}}' = \int_{\hat{\Omega}} \delta(\boldsymbol{n}) \hat{\boldsymbol{\mathcal{Z}}} \, d\hat{\Omega} = \boldsymbol{\mathcal{Z}}$, and we find that the expected trait values of group descendants are identical to the values of their group parents, as we would expect. In the more general case where group reproduction is not a case of like begets like, there will be differences between the trait values of ancestral groups and the expected trait values of group descendants. Let us therefore define another vector of scalar fields $\Delta\boldsymbol{\mathcal{Z}} = [\Delta\mathcal{Z}_{\boldsymbol{n}k}] \in \mathbb{R}^{|\mathbb{Q}|}$ to hold these differences. The vector is simply given by

$$\Delta\boldsymbol{\mathcal{Z}} = \boldsymbol{\mathcal{Z}}' - \boldsymbol{\mathcal{Z}}. \tag{5.15}$$

It is important to note that that $\boldsymbol{\mathcal{Z}}'$ and $\Delta\boldsymbol{\mathcal{Z}}$ may vary continuously through time as the the inheritance kernel changes due to changes in the composition of the group-population.

5.3 The dynamics of interdemic selection

We now have a population of groups that has the potential exhibit phenotypic variation, differentially reproduce and survive as a result of the phenotypes they express, and pass on their phenotypes to their group descendants (Lewontin, 1970; Godfrey-Smith, 2007). In this section, we therefore now turn to exploring the dynamics of interdemic selection. Like we did in Chapter 2, we view these dynamics from three perspectives: *i*) ecological—in terms of the changing frequencies of different types of groups and changes in the overall group-population size; *ii*) genotypic—in terms of changes in the relative frequencies of groups of different compositions in the group population; and *iii*) phenotypic—in terms of the changes in the average group trait values in the group-population.

5.3.1 Ecological perspective

As we have said, a change in the group-population composition over time can be pictured as the flow of group density across the composition space, Ω. To describe this flow, we need a *dynamical law*, analogous to the Malthusian selection equation (2.28) we derived in Chapter 2. That is, we need a rule for predicting the future group density, θ, at every point, $\boldsymbol{n}$, in the composition space, Ω, given the current state of the system at time t.

5.3.1.1 Within-group dynamics

We start by considering how the dynamics of selection within groups drives changes in the composition of the group-population. In Chapter 2 we showed that the dynamics of natural selection within an arbitrary population (corresponding to a group in this chapter) of individuals are described by the Malthusian selection equation (2.28). We described this selection equation as giving the velocity, $\boldsymbol{n} = d\boldsymbol{n}/dt \equiv \dot{\boldsymbol{n}}$, of the population as it traces out a trajectory on the composition space, Ω. In the present context, we now have multiple groups (sub-populations) each tracing out its own trajectory. Thus, we now have a velocity vector *field*, $\boldsymbol{v} \equiv \dot{\boldsymbol{n}}$, defined by the equivalent of a Malthusian selection equation (2.28) at every point in the composition space Ω. A change in the structure of the composition of the group-population can now be pictured as the 'flow' of group density, θ, across the composition space. Our aim in this section is to derive a selection equation for all groups that describes how group density flows over the composition space due to the velocity of within-group selection dynamics defined by the within-group Malthusian selection equation (2.28).

Let us denote the flux of group density by a vector field $\mathbf{J} := \mathbf{J}(\boldsymbol{v}, \theta) \in \mathbb{R}^{|\mathbb{G}|}$. This is simply given by multiplying the group density scalar field, θ, by the velocity vector field, $\boldsymbol{v}$, to obtain $\mathbf{J} = \theta\boldsymbol{v}$. We want to find a relation between the how the group density scalar field, θ, changes over time and the flux, $\mathbf{J}$. To do this, let us now consider a fixed arbitrary control space, C whose boundary is denoted by ∂C. We want to understand how the total group density within this control space, C, changes over time. Let us assume for a moment that groups are not undergoing reproduction or death. In the absence of processes that increase or decrease the density of groups, we expect that the total group density in the arbitrary control space should only increase or decrease over time due to net gain or loss of groups moving across its boundary, ∂C. We describe this formally by applying a conservation of mass constraint to the arbitrary control space C, giving

$$\frac{d}{dt}\int_C \theta \; dC = -\int_{\partial C} \mathbf{J}\boldsymbol{\eta}^{\mathrm{T}} \; d\partial C, \tag{5.16}$$

where $\boldsymbol{\eta}^{\mathrm{T}}$ is a surface vector that is normal to the boundary of the control space, ∂C. The term on the LHS describes the rate of change with respect to time of the mass within the control space C, and the term on the RHS side is the total flux across the control space boundary ∂C. The negative sign indicates that the surface normal vector $\boldsymbol{\eta}$ is outward-facing. The notation $\nabla_{\boldsymbol{n}}$ denotes the gradient operator that we defined by equation (2.26) in Box 2.5 of Chapter 2. It can be thought of a partial derivative taken with respect to the composition vector, $\boldsymbol{n}$. Assuming the scalar group density function, θ, and flux function, $\mathbf{J}$, are sufficiently smooth we apply the divergence theorem to derive the relationship between the flux and the partial time derivative of the group density within the control space. This gives

$$\frac{d}{dt}\int_C \theta \; dC = -\int_C \nabla_{\boldsymbol{n}}[\mathbf{J}] \; dC, \tag{5.17}$$

Providing that θ and its partial derivative with respect to time, $\partial_t\theta$ are both continuous functions over the control space, C, we can use Leibniz' integral rule and take the derivative operator inside the integral on the LHS, and rearrange, to obtain

$$\int_C \left(\partial_t\theta + \nabla_{\boldsymbol{n}}[\mathbf{J}]\right) \; dC = 0. \tag{5.18}$$

Since C is an *arbitrary* control space, equation (5.18) holds for *any* point in the composition space, Ω, which implies a continuity equation for the group density scalar field. That is, we obtain a PDE that describes change in the group density, θ, with respect to time, t, over the composition space, Ω, owing to the dynamics of selection within groups:

$$\partial_t\theta = -\nabla_{\boldsymbol{n}} \cdot [\theta \boldsymbol{v}], \tag{5.19}$$

where we have back-substituted for the definition of the flux, $\mathbf{J} = \theta\boldsymbol{n}$. This equation is a generalisation of the Malthusian selection equation (2.28) from Chapter 2 to a scenario in which we have multiple sub-divided populations with no migration. It is important to note that this equation does not describe the dynamics of group selection, since we have

only considered selection dynamics within groups at this stage. The boundary conditions for this PDE are naturally defined as zero-flux boundary conditions. These arise from the within-group selection dynamics given by the Malthusian selection equation (2.28) from Chapter 2. That is, since a negative number or an infinite number of i-genotype individuals within a particular group is not possible, we have Neumann zero-flux boundary conditions of the form

$$\theta \boldsymbol{v} \boldsymbol{\eta}^{\mathrm{T}} = 0, \tag{5.20}$$

where $\boldsymbol{\eta}$ again denotes the outward facing normal vector to the boundary of the composition space. Note that these conditions simply specify that there is zero flux of the group density scalar field, θ, across the boundary of the composition space, $\partial\Omega$.

5.3.1.2 Between-group dynamics

Now let us consider how the group density scalar field, θ, changes with respect to time, t, when groups themselves undergo reproduction and death, as we defined these processes previously. In this case we no longer expect that group density to be conserved as it is in the solution to the PDE equation (5.19).

Clearly, the rate of change of the density of groups now depends upon the rates at which they are being produced, and the rate at which they are dying. Our goal in this section is therefore to derive an extended selection equation to account for these group-level events. We do so by including source and sink terms in the RHS of equation (5.19) to get

$$\partial_t \theta = \int_{\hat{\Omega}} \hat{\theta} \hat{\mathcal{B}} \mathcal{H}_{\hat{\boldsymbol{n}}\boldsymbol{n}} \, d\hat{\Omega} - \theta \mathcal{D} - \nabla_{\boldsymbol{n}} \cdot [\theta \boldsymbol{v}], \tag{5.21}$$

where $\mathcal{P} = \int_{\hat{\Omega}} \hat{\theta} \mathcal{F}_{\hat{\boldsymbol{n}}\boldsymbol{n}} \, d\hat{\Omega} = \int_{\hat{\Omega}} \hat{\theta} \hat{\mathcal{B}} \mathcal{H}_{\hat{\boldsymbol{n}}\boldsymbol{n}} \, d\hat{\Omega}$ is the rate at which $\hat{\boldsymbol{n}}$-composition parent groups reproduce *and* produce descendant of a composition $\boldsymbol{n}$, $\theta\mathcal{D}$is the rate at which $\boldsymbol{n}$-composition groups die, and $\nabla_{\boldsymbol{n}} \cdot [\theta \boldsymbol{v}]$ represents the rate at which $\boldsymbol{n}$-composition groups are being created and lost due to flow across the composition space driven by within-group selection dynamics. We call this the 'Malthusian interdemic group selection equation'. It is a non-linear PDE that describes the rate of change of the density of $\boldsymbol{n}$-composition groups in the population with respect to time due to selection within and between groups. By solving the this equation, we obtain the complete picture of interdemic group selection dynamics over the composition space Ω.

The Malthusian interdemic group selection equation (5.21) is the same form of PDE derived by Simon (2010). Here, however, we have derived our PDE as an extension of the Malthusian selection equation (2.28) that we derived in Chapter 2 using dynamical systems theory, whereas Simon (2010) derived his PDE using a probabilistic interpretation (Simon, 2008). The two types of PDE are essentially the same. The main difference between them is that we have proposed a framework in which almost any type of group selection process can be studied, whereas Simon (2010) and Simon et al. (2013) chose to focus on the development of specific examples of group selection processes. Our approach therefore goes some way towards validating the claim of Simon et al. (2013) that their PDE models represents a general theory of group selection.

We do not, however, endorse the view of Simon et al. (2013) that their PDE represents a different type of selection process from those studied in the more traditional frameworks in evolutionary theory. Their argument stems from a focus on group-level events like fissioning and fusion, which they claim cannot be represented in the more traditional approaches. Here, we have used a more abstract formulation of group survival and reproduction which has allowed us to incorporate all kinds of group-level events, including fission and fusion, into the source terms on the RHS of the Malthusian interdemic group selection equation (5.21). In a later section we will see that this abstract formulation allows us to formulate a form of Price equation for interdemic group selection dynamics, which provides a formal demonstration that the group selection PDE models of Simon et al. (2013) can be represented using covariance mathematics of Price (1970, 1972a), contrary to their claims.

5.3.1.3 Absence of within-group dynamics

In the special case in which there are no within-group Malthusian selection dynamics, so that $\boldsymbol{v} = \mathbf{0}$, we obtain the single-level group selection equation

$$\partial_t \theta = \int_{\hat{\Omega}} \hat{\theta} \hat{\mathcal{B}} \mathcal{H}_{\hat{\boldsymbol{n}}\boldsymbol{n}} \, d\hat{\Omega} - \theta \mathcal{D}. \tag{5.22}$$

This equation represents a generalisation of the original Malthusian selection equation (2.28) from Chapter 2 to a scenario in which individuals are defined not by particular distinct configurations of the units of information they hold, but by particular mixed or continuous configurations of the units of information they hold. This is similar to the concept of a mixed strategy in evolutionary game theory. Similar equations have been derived in this context in both economic (Oechssler and Riedel, 2001) and evolutionary

(Hofbauer and Sigmund, 2003) game theory. Again, we include this here merely to illustrate the numerous connections between the dynamical systems theory of natural selection we are developing and other branches of evolutionary theory.

5.3.1.4 Group-population growth

The Malthusian interdemic selection equation (5.21) we have derived provides an ecological perspective on how the dynamics of natural selection shape the composition of the group-population over time. To complete this ecological perspective, however, we should also like to know how the group-population size, Θ, changes over time. Let $\dot{\Theta} \equiv d\Theta/dt$ denote the derivative of the group-population size, Θ, with respect to time t. We have

$$\dot{\Theta} = \frac{d}{dt}\int_{\Omega} \theta \; d\Omega = \int_{\Omega} \partial_t \theta \; d\Omega, \tag{5.23}$$

where we have we have assumed θ and $\partial_t \theta$ are sufficiently smooth functions and hence used Leibniz' integral rule to take the derivative operator inside the integral on the RHS. This operation is allowable since the composition space, Ω, is not itself a function of time. Now substituting for $\partial_t \theta$ from the Malthusian multi-level selection equation (5.21), and simplifying, we obtain

$$\begin{aligned} \dot{\Theta} &= \int_{\Omega} \left(\int_{\hat{\Omega}} \hat{\theta}\hat{\mathcal{B}}\mathcal{H}(\hat{\boldsymbol{n}}, \boldsymbol{n}) \; d\hat{\Omega} - \theta\mathcal{D} - \nabla_{\boldsymbol{n}} \cdot [\theta \boldsymbol{v}] \right) \; d\Omega \\ &= \int_{\Omega}\int_{\hat{\Omega}} \hat{\theta}\hat{\mathcal{B}}\mathcal{H}(\hat{\boldsymbol{n}}, \boldsymbol{n}) \; d\hat{\Omega} \; d\Omega - \int_{\Omega} \theta\mathcal{D} \; d\Omega - \int_{\Omega} \nabla_{\boldsymbol{n}} \cdot [\theta \boldsymbol{v}] \; d\Omega. \end{aligned} \tag{5.24}$$

By the divergence theorem, we may re-write the third term on the RHS as $\int_{\Omega} \nabla_{\boldsymbol{n}} \cdot [\theta \boldsymbol{v}] \; d\Omega = \int_{\partial\Omega} \theta \boldsymbol{v} \boldsymbol{\eta}^{\mathrm{T}} \; d\partial\Omega$, where $\boldsymbol{\eta}^{\mathrm{T}}$ is the outward-facing surface normal vector to the composition space boundary $\partial\Omega$. Thus, from the boundary conditions specified by equation (5.20) we can see that this term drops out. We are left with

$$\dot{\Theta} = \int_{\Omega}\int_{\hat{\Omega}} \hat{\theta}\hat{\mathcal{B}}\mathcal{H}(\hat{\boldsymbol{n}}, \boldsymbol{n}) \; d\hat{\Omega} \; d\Omega - \int_{\Omega} \theta\mathcal{D} \; d\Omega. \tag{5.25}$$

In the first term on the RHS we now take the integral over Ω inside the integral over $\hat{\Omega}$ and then switch the order of integration (which has no effect on the equality), to get

$$\begin{aligned}\dot{\Theta} &= \int_{\hat{\Omega}} \hat{\theta}\hat{\mathcal{B}} \int_{\Omega} \mathcal{H}(\hat{\boldsymbol{n}}, \boldsymbol{n})\, d\Omega\, d\hat{\Omega} - \int_{\Omega} \theta\mathcal{D}\, d\Omega \\ &= \int_{\Omega} \theta\mathcal{B} \int_{\hat{\Omega}} \mathcal{H}(\boldsymbol{n}, \hat{\boldsymbol{n}})\, d\hat{\Omega}\, d\Omega - \int_{\Omega} \theta\mathcal{D}\, d\Omega.\end{aligned} \tag{5.26}$$

We now simplify using the property of the group inheritance kernel, $\mathcal{H}(\boldsymbol{n}, \hat{\boldsymbol{n}})$, that the integral over its second argument is equal to 1 (see description of equation (5.12)). We are left with

$$\begin{aligned}\dot{\Theta} &= \int_{\Omega} \theta\mathcal{B}\, d\Omega - \int_{\Omega} \theta\mathcal{D}\, d\Omega \\ &= \int_{\Omega} \theta(\mathcal{B} - \mathcal{D})\, d\Omega \\ &= \Theta \int_{\Omega} \mathcal{X}(\mathcal{B} - \mathcal{D})\, d\Omega \\ &= \Theta(\bar{\mathcal{B}} - \bar{\mathcal{D}}).\end{aligned} \tag{5.27}$$

This equation is now in a form similar to the Malthusian growth equation (2.1) from population ecology (Turchin, 2001), and the Malthusian growth-selection equation (2.39) we derived in Chapter 2. This equation tells us that the rate of growth of the group-population is simply proportional to the quantity $\int_{\Omega} \mathcal{X}(\mathcal{B} - \mathcal{D})\, d\Omega = \bar{\mathcal{B}} - \bar{\mathcal{D}}$. As we discussed in Chapter 2, this quantity has a special interpretation in population genetics.

5.3.1.5 Malthusian group fitness

In particular, Kimura (1958) defined the Malthusian fitness of a genotype to be the net relative contribution it makes to the growth-rate of a population[c]. If we denote the Malthusian fitness of $\boldsymbol{n}$-composition groups by $\mathcal{M} := \mathcal{M}(t, \boldsymbol{n}) \in \mathbb{R}$, we can see by inspection from equation (5.27) that this quantity is simply given by

$$\mathcal{M} = \mathcal{B} - \mathcal{D}, \tag{5.28}$$

which is just the difference between the rate at which a $\boldsymbol{n}$-composition groups produce descendants, $\mathcal{B}$, and the rate at which they die, $\mathcal{D}$. Identifying this as measure of Malthusian

[c]See Charlesworth (1970) for a description of the difference between Kimura's (1958) definition and the definition of Malthusian fitness given by Fisher (1930).

group fitness might seem somewhat trivial, but we do it here to emphasise the general approach outlined by Kimura (1958). We will see in the Discussion chapter that the Malthusian fitness of an entity is not always such an 'obvious' quantity. Moreover, in taking this approach we emphasise that fitness is generally a quantity that emerges from the dynamics of selection, rather than one that we define up-front in order to dictate the dynamics of populations (Ariew and Lewontin, 2004).

Since Malthusian group fitness is a quantitative trait, measurable in units of $(\text{time})^{-1}$, it is part of a group's phenotype, in the same way that the within-group Malthusian fitness of an i-genotype individual, m_i, is part of *its* phenotype. As we emphasised in Chapter 2, in some sense fitness is the most important group trait of all, since it is through Malthusian group fitness that all other group traits become 'visible' to selection (Mayr, 1997). We denote the average Malthusian group fitness in the group-population by $\bar{\mathcal{M}} = \bar{\mathcal{M}}(t, \boldsymbol{n}) \in \mathbb{R}$. We calculate this as

$$\bar{\mathcal{M}} = \frac{1}{\Theta} \int_{\Omega} \theta \mathcal{M} \, d\Omega = \int_{\Omega} \mathcal{X} \mathcal{M} \, d\Omega. \tag{5.29}$$

By substituting for the definition of Malthusian group fitness given by equation (5.28) it is easy to see that the average Malthusian group fitness is equal to the difference between the average rate of group reproduction and the average rate of group death, $\bar{\mathcal{M}} = \bar{\mathcal{B}} - \bar{\mathcal{D}}$. Hence, returning to the dynamics of group-population growth, we may re-write equation (5.27) as

$$\dot{\Theta} = \Theta \bar{\mathcal{M}}. \tag{5.30}$$

With this equation we have shown that the Malthusian interdemic group selection equation (5.21) gives rise to group-population dynamics that are a generalised form of those described by the Malthusian growth equation from population ecology (Turchin, 2001). Thus, we call equation (5.30) the 'Malthusian group growth-selection equation'. The virtue of equation (5.30) is that it tells us that the instantaneous growth-rate of the group-population is proportional to the average Malthusian group fitness, $\bar{\mathcal{M}} = \bar{\mathcal{B}} - \bar{\mathcal{D}}$, which is simply equal to the difference between the average group reproduction and group death rates in the group-population.

5.3.2 Genotypic perspective

The dynamics of natural selection in the group-population can only ultimately be understood in full by solving the Malthusian interdemic group selection equation (5.21). In many cases, however, these dynamics may not provide us with the most intuitive picture of evolutionary change. To give an example of why this is the case, consider a scenario in which the Malthusian interdemic group selection equation (5.21) tells us that the abundance of $\boldsymbol{n}$-composition groups is increasing in the group-population, $\partial_t \theta > 0$, at some time t. Unfortunately, this information does not really tell us very much about how successful those groups are in an evolutionary sense. If the abundance of all other $\hat{\boldsymbol{n}}$-composition groups is increasing at a much greater rate then we wouldn't consider $\boldsymbol{n}$-composition groups to be particularly 'fit' in the classic sense, since they would be becoming less and less frequent in the group-population over time. One way to avoid this problem is to consider the dynamics of the *relative* abundance of different types of groups in the group-population.

Recall that the relative abundance of $\boldsymbol{n}$-composition groups in the group-population is given by the scalar field $\mathcal{X} = \theta/\Theta$. We are interested in how this relative abundance changes with respect to time. Taking the (partial) derivative with respect to time using the quotient rule, we have

$$\partial_t \mathcal{X} = \frac{\partial_t[\theta]\theta - \theta\dot{\Theta}}{\Theta^2} = \frac{\partial_t[\theta]}{\Theta} - \frac{\theta}{\Theta}\frac{\dot{\Theta}}{\Theta}. \tag{5.31}$$

Substituting for $\partial_t \theta$ from the Malthusian multi-level selection equation (5.21), and for $\dot{\Theta}$ from the Malthusian group growth-selection equation (5.30), and rearranging, we have

$$\partial_t \mathcal{X} = \frac{\int_{\hat{\Omega}} \hat{\theta}\hat{\mathcal{B}}\mathcal{H}(\hat{\boldsymbol{n}}, \boldsymbol{n})\, d\hat{\Omega} - \theta\mathcal{D} - \nabla_{\boldsymbol{n}} \cdot [\theta \boldsymbol{v}]}{\Theta} - \frac{\theta}{\Theta}\frac{\theta\bar{\mathcal{M}}}{\Theta}. \tag{5.32}$$

Now substituting for the definition of the relative composition scalar field, $\mathcal{X} = \theta/\Theta$, and rearranging, we obtain

$$\partial_t \mathcal{X} = \int_{\hat{\Omega}} \hat{\mathcal{X}}\hat{\mathcal{B}}\mathcal{H}(\hat{\boldsymbol{n}}, \boldsymbol{n})\, d\hat{\Omega} - \mathcal{X}\mathcal{D} - \mathcal{X}\bar{\mathcal{M}} - \nabla_{\boldsymbol{n}} \cdot (\mathcal{X}\boldsymbol{v}), \tag{5.33}$$

which is now in a form similar to the replicator equation (2.3) from the replicator dynamics framework (Page and Nowak, 2002; Nowak and Sigmund, 2004) and the Malthusian

replicator equation (2.45) we derived in Chapter 2. We call equation (5.33) the 'Malthusian interdemic replicator equation'.

5.3.2.1 Absence of within-group dynamics

In the special case where there are no between-group dynamics, so that $\int_{\hat{\Omega}} \hat{\mathcal{X}}\hat{\mathcal{B}}\hat{\mathcal{H}}(\hat{\boldsymbol{n}}, \boldsymbol{n})\, d\hat{\Omega} - \mathcal{X}\mathcal{D} - \mathcal{X}\bar{\mathcal{M}} = 0$, equation (5.33) reduces to the single-level replicator equation

$$\partial_t \mathcal{X} = -\nabla_{\boldsymbol{n}} \cdot (\mathcal{X}\boldsymbol{v}). \tag{5.34}$$

This equation can be viewed as describing the dynamics of natural selection among isolated groups of individuals. Alternatively, $\mathcal{X}$ can viewed as a probability density function that gives the likelihood that a single group is in a particular state $\boldsymbol{n}$ at a particular time t, and the equation then describes the *probabilistic* time evolution of the system. This interpretation derives from the fact that this equation is equivalent to an equation known as the 'Louiville equation', which appears in the context of statistical mechanics and is used to describe the evolution of the phase space distribution of Hamiltonian dynamical systems (see, for example Magpantay and Perez (2013)). More recently the Liouville equation has been derived during attempts at generalising the celebrated Kimura (1962) equation from population genetics (Chalub and Souza, 2014).

5.3.3 Phenotypic perspective

We have now seen that interdemic group selection dynamics can lead to changes in composition of the group-population, θ, its size, Θ, and its relative composition, $\mathcal{X}$. Now let us turn to exploring how the dynamics of interdemic group selection translate into the evolutionary dynamics of group traits. On the face of it, however, the Malthusian interdemic equation (5.21) seems to say little about the dynamics of group *phenotypic* change. In our framework, we distinguish between non-genetic change in individual trait values, $\mathcal{Z}_k$, and genetic change in the summary statistics of phenotypes, $\bar{\mathcal{Z}}_k$, which corresponds to an evolutionary response to selection (Falconer and Mackay, 1995).

5.3.3.1 Group-level

Before turning to evolutionary change in the summary statistics of phenotypes, let us first return to the composition-phenotype map, $\boldsymbol{\mathcal{Z}}$, and gain a better understanding of why

it is not constant, but may vary through time. The reasons are, unsurprisingly, similar to those we described in the corresponding section of Chapter 2. The dynamical laws for traits in the composition-phenotype map is found, by the chain rule, to be given by

$$\dot{\boldsymbol{\mathcal{Z}}} = \nabla_{\boldsymbol{n}}[\boldsymbol{\mathcal{Z}}]\boldsymbol{v} + \partial_t[\boldsymbol{\mathcal{Z}}]. \tag{5.35}$$

This equation indicates that the dynamical law describing phenotypic change must specify two reasons why the trait values change. The first corresponds to *phenotypic plasticity* in group trait expression (Via and Lande, 1985; Stearns, 1989; Miner et al., 2005). Secondly, if a group trait is dependent on time, t, the trait values may be functions of the values held by the ancestors that gave rise to them in the past. This corresponds to a non-genetic mechanism of inheritance, that is sometimes called 'ecological inheritance' (Danchin and Wagner, 2010; Danchin et al., 2011). Both these points were discussed in more detail in Chapter 2, but let us briefly give a couple of examples.

Phenotypic plasticity

Plasticity might arise, for instance, because group phenotypes respond to their environment (Via and Lande, 1985; Stearns, 1989; Miner et al., 2005). This response could be driven by abiotic or biotic changes in the environment. It might even result from a social frequency-dependent type of plasticity, such that the trait values groups express depend on the detection of the presence or absence of another group. For instance, if our groups represent microbial colonies, a detection of the presence of another colony (competition sensing) in the environment might lead to stress responses, toxin production, or biofilm formation (Cornforth and Foster, 2013).

Ecological inheritance

Group phenotypes might also depend on the past state of the system, such that the trait values they express now depend on some feature of the environment at an earlier moment in time. This emerges from the functional dependence of the composition-phenotype map on time t. For instance, if our groups represent hunter-gatherer tribes, they might construct a niche for themselves as part of an 'extended' group phenotype (Dawkins, 1982; Odling-Smee et al., 2003). The associated trait values might be subject to change as the niche is 'ecologically inherited' across generations (Laland et al., 2001), or subject to biotic and abiotic forces that slowly degrade the niche over time. These would be examples of a group-level 'Lamarckian' inheritance mechanism, in which descendant groups inherit the acquired characteristics of the ancestral groups that gave rise to them (Jablonka and Lamb, 1999; Danchin et al., 2011).

5.3.3.2 Group-population-level

If the traits in the composition-phenotype map, $\boldsymbol{\mathcal{Z}}$, are selectively significant, we might expect their population averages, given by the $|\mathbb{Q}| \times 1$ vector $\bar{\boldsymbol{\mathcal{Z}}}$ from equation (5.2), to change over time due to the impact of *selection* on the composition of the group-population, θ. The population average trait values depend on the trait values in the composition-phenotype map, $\boldsymbol{\mathcal{Z}}$, and the relative composition, $\mathcal{X}$. Taking the derivative with respect to time t, using the product rule, we obtain

$$\dot{\bar{\boldsymbol{\mathcal{Z}}}} = \frac{d}{dt}\int_{\Omega} \mathcal{X}\boldsymbol{\mathcal{Z}}\, d\Omega = \int_{\Omega} \partial_t[\mathcal{X}]\boldsymbol{\mathcal{Z}}\, d\Omega \tag{5.36}$$

This doesn't yield much insight into the the action of natural selection in our group population, other than to identify that it is the net result of changes in the composition-phenotype map due to the aforementioned processes of phenotypic plasticity and ecological inheritance. After a considerable amount of algebra and multivariate calculus, however, we show in Box 5.2, that equation (5.36) can be re-written as

$$\dot{\bar{\boldsymbol{\mathcal{Z}}}} = \int_{\Omega} \mathcal{X}\mathcal{M}\boldsymbol{\mathcal{Z}}\, d\Omega - \bar{\mathcal{M}}\int_{\Omega} \mathcal{X}\boldsymbol{\mathcal{Z}}\, d\Omega + \int_{\Omega} \mathcal{X}\mathcal{B}\Delta\boldsymbol{\mathcal{Z}}\, d\Omega + \int_{\Omega} \mathcal{X}\dot{\boldsymbol{\mathcal{Z}}}\, d\Omega. \tag{5.37}$$

where $\mathcal{M}$ is the Malthusian group fitness defined by equation (5.28), $\Delta\boldsymbol{\mathcal{Z}}$ is the difference between the expected trait values in group descendants and the ancestors that gave rise to them, defined by equation (5.15), and finally $\dot{\boldsymbol{\mathcal{Z}}}$ is the derivative of the composition-phenotype map with respect to time from equation (5.35), which we discussed in the last section. In fact, this equation is now written in a similar form to the Price equation (2.5) (Box 2.3; Chapter 2), but the integral notation we have used obscures its similarity to Price's (1970; 1972a) original work. Switching to the more traditional 'moment' notation Price (1970, 1972a) used, which corresponds to the notation that we introduced in Box 5.1, equation (5.37) can be re-written as

$$\begin{bmatrix} \dot{\mathrm{E}}_{\boldsymbol{n}\in\Omega}(\mathcal{Z}_{\boldsymbol{n}1}) \\ \vdots \\ \dot{\mathrm{E}}_{\boldsymbol{n}\in\Omega}(\mathcal{Z}_{\boldsymbol{n}|\mathbb{Q}|}) \end{bmatrix} = \begin{bmatrix} \mathrm{Cov}_{\boldsymbol{n}\in\Omega}(\mathcal{M}, \mathcal{Z}_{\boldsymbol{n}1}) \\ \vdots \\ \mathrm{Cov}_{\boldsymbol{n}\in\Omega}(\mathcal{M}, \mathcal{Z}_{\boldsymbol{n}|\mathbb{Q}|}) \end{bmatrix} + \begin{bmatrix} \mathrm{E}_{\boldsymbol{n}\in\Omega}(\mathcal{B}\Delta\mathcal{Z}_{\boldsymbol{n}1}) \\ \vdots \\ \mathrm{E}_{\boldsymbol{n}\in\Omega}(\mathcal{B}\Delta\mathcal{Z}_{\boldsymbol{n}|\mathbb{Q}|}) \end{bmatrix} + \begin{bmatrix} \mathrm{E}_{\boldsymbol{n}\in\Omega}(\dot{\mathcal{Z}}_{\boldsymbol{n}1}) \\ \vdots \\ \mathrm{E}_{\boldsymbol{n}\in\Omega}(\dot{\mathcal{Z}}_{\boldsymbol{n}|\mathbb{Q}|}) \end{bmatrix}, \tag{5.38}$$

where $\dot{\mathrm{E}}_{\boldsymbol{n}\in\Omega}(\mathcal{Z}_{\boldsymbol{n}k}) \equiv d\mathrm{E}(\mathcal{Z}_{\boldsymbol{n}k})/dt$ gives the instantaneous rate of total change of the expected value of all traits in the group composition-phenotype map, $\boldsymbol{\mathcal{Z}}$, with respect to time. Note that this equation is almost identical to the Malthusian Price equation (2.49) we introduced in Chapter 2, except that all the relevant quantities are now associated with groups rather than individuals. Of course, this shouldn't be too surprising, because the $\boldsymbol{n}$-composition groups in this chapter are units of selection for exactly the same reasons that i-genotype individuals were in Chapter 2 (Lewontin, 1970; Godfrey-Smith, 2007). We refer to equation (5.38) as the 'Malthusian interdemic Price equation'. A similar discrete-time version has also described by Okasha (2006, p. 74-75) in his discussion of MLS2.

Using the convention made popular by Frank (1995), let us take each of the terms on the RHS of this equation to see what they pertain to. The first term, $\mathrm{Cov}_{\boldsymbol{n}\in\Omega}(\mathcal{M}, \mathcal{Z}_k)$, represents the covariance between Malthusian group fitness, $\mathcal{M}$, and a group trait value, $\mathcal{Z}_k$. Using Frank's (1995) convention, we may interpret this as the partial change in the average group trait values due to group-level *selection* on group traits. Importantly, unlike the equivalent component of the discrete-time version of this equation described by Okasha (2006, p. 74-75), this covariance term not only tells about selection, but also about the timescale over which selection takes place.

The second term, $\mathrm{E}_{\boldsymbol{n}\in\Omega}(\mathcal{B}\Delta\mathcal{Z}_k)$, in the equation represents the expected value of the quantity $\mathcal{B}_{\boldsymbol{n}\in\Omega}\Delta\mathcal{Z}_k$ over all groups. Again, using Frank's (1995) approach, we can interpret this as the partial change in the average trait values due to imperfect *fidelity of transmission* of group traits from parent groups to their descendant, $\Delta\mathcal{Z}_k$, when group reproduction occurs. That is, if parent groups produce descendant groups with very different characteristics to themselves, then this term will be large.

The third term, $\mathrm{E}_{\boldsymbol{n}\in\Omega}(\dot{\mathcal{Z}}_k)$, represents the expected value of the derivative of the kth group trait value with respect to time. That is, it corresponds to the average rate at which group phenotypes are changing for reasons that are unrelated to group survival and reproduction. The phenotype held by a group can change within its lifetime for numerous reasons that we will come to shortly. Before we consider these reasons, however, it is important to note that there is no anologous term in the covariance mathematics of Price (1970, 1972a), and hence we cannot borrow our interpretation of this term from Frank (1995) as we did for the first two terms. It might seem strange that we have gained an extra term when the discrete-time Price equation is an 'exact and complete description for evolutionary change' (Frank, 1995). The reason is that the Price equation maps between a an ancestral generation and descendant generation separated by a *discrete period of time* of arbitrary length. If there is phenotypic plasticity in the expression of traits

that takes effect between the period in which parent phenotypes are measured, then any parent-descendant differences resulting from this plasticity will be allocated in the term of the Price equation that we associate with transmission fidelity. In our continuous-time model, however, we know the relationship between group phenotype and environment at every instantaneous moment in time, and can therefore identify phenotypic plasticity as a distinct causal effect.

Box 5.2 | Derivation of a Malthusian interdemic group selection form of the Price equation

We start by taking the derivative with respect to time of the average trait values (given by equation (5.2)) using the product rule, to obtain

$$\dot{\bar{\boldsymbol{\mathcal{Z}}}} = \frac{d}{dt}\int_{\Omega} \mathcal{X}\boldsymbol{\mathcal{Z}}\, d\Omega = \int_{\Omega} \partial_t[\mathcal{X}]\boldsymbol{\mathcal{Z}}\, d\Omega + \int_{\Omega} \mathcal{X}\partial_t[\boldsymbol{\mathcal{Z}}]\, d\Omega, \tag{5.39}$$

where we have again used Leibniz' integral rule to take the derivative operator inside the integral on the RHS. Next, substituting for $\partial_t\mathcal{X}$ from the Malthusian interdemic replicator equation (5.33) and simplifying, we obtain

$$\begin{aligned}\dot{\bar{\boldsymbol{\mathcal{Z}}}} &= \int_{\Omega}\left(\int_{\hat{\Omega}} \hat{\mathcal{X}}\hat{\mathcal{B}}\mathcal{H}(\hat{\boldsymbol{n}},\boldsymbol{n})\, d\hat{\Omega} - \mathcal{X}\mathcal{D} - \mathcal{X}\bar{\mathcal{M}} - \nabla_{\boldsymbol{n}}\cdot[\mathcal{X}\boldsymbol{v}]\right)\boldsymbol{\mathcal{Z}}\, d\Omega + \int_{\Omega}\mathcal{X}\partial_t[\boldsymbol{\mathcal{Z}}]\, d\Omega \qquad (5.40)\\ &= \int_{\Omega}\int_{\hat{\Omega}} \hat{\mathcal{X}}\hat{\mathcal{B}}\mathcal{H}(\hat{\boldsymbol{n}},\boldsymbol{n})\, d\hat{\Omega}\boldsymbol{\mathcal{Z}}\, d\Omega - \int_{\Omega}\mathcal{X}\mathcal{D}\boldsymbol{\mathcal{Z}}\, d\Omega - \bar{\mathcal{M}}\int_{\Omega}\mathcal{X}\boldsymbol{\mathcal{Z}}\, d\Omega\\ &\quad - \int_{\Omega}\left(\nabla_{\boldsymbol{n}}\cdot[\mathcal{X}\boldsymbol{v}]\right)\boldsymbol{\mathcal{Z}}\, d\Omega + \int_{\Omega}\mathcal{X}\partial_t[\boldsymbol{\mathcal{Z}}]\, d\Omega,\end{aligned}$$

Using the high-dimensional analogue of integration by parts, we may re-write the fourth term on the RHS as

$$\int_{\Omega}\left(\nabla_{\boldsymbol{n}}\cdot[\mathcal{X}\boldsymbol{v}]\right)\boldsymbol{\mathcal{Z}}\, d\Omega = \int_{\partial\Omega}\mathcal{X}\nabla_{\boldsymbol{n}}[\boldsymbol{\mathcal{Z}}]\boldsymbol{v}\boldsymbol{\eta}^{\mathrm{T}}\, d\partial\Omega - \int_{\Omega}\mathcal{X}\nabla_{\boldsymbol{n}}[\boldsymbol{\mathcal{Z}}]\boldsymbol{v}\, d\Omega, \tag{5.41}$$

where $\boldsymbol{\eta}^{\mathrm{T}}$ is the outward facing surface normal vector to the composition space boundary $\partial\Omega$. We see from the boundary conditions specified by equation (5.20), that the first term on the RHS term drops out. Substituting the expression back in, and rearranging, we have

$$\begin{aligned}\dot{\bar{\boldsymbol{\mathcal{Z}}}} &= \int_{\Omega}\int_{\hat{\Omega}} \hat{\mathcal{X}}\hat{\mathcal{B}}\mathcal{H}(\hat{\boldsymbol{n}},\boldsymbol{n})\, d\hat{\Omega}\boldsymbol{\mathcal{Z}}\, d\Omega - \int_{\Omega}\mathcal{X}\mathcal{D}\boldsymbol{\mathcal{Z}}\, d\Omega - \bar{\mathcal{M}}\int_{\Omega}\mathcal{X}\boldsymbol{\mathcal{Z}}\, d\Omega \qquad (5.42)\\ &\quad + \int_{\Omega}\mathcal{X}\left(\nabla_{\boldsymbol{n}}[\boldsymbol{\mathcal{Z}}]\boldsymbol{v} + \partial_t[\boldsymbol{\mathcal{Z}}]\right)\, d\Omega\end{aligned}$$

Now looking at the fourth term on the RHS, we can see it is simply the total derivative of the group composition-phenotype map with respect to time given by equation (5.35).

$$\dot{\bar{\boldsymbol{\mathcal{Z}}}} = \int_{\Omega}\int_{\hat{\Omega}} \hat{\mathcal{X}}\hat{\mathcal{B}}\mathcal{H}(\hat{\boldsymbol{n}},\boldsymbol{n})\, d\hat{\Omega}\boldsymbol{\mathcal{Z}}\, d\Omega - \int_{\Omega}\mathcal{X}\mathcal{D}\boldsymbol{\mathcal{Z}}\, d\Omega - \bar{\mathcal{M}}\int_{\Omega}\mathcal{X}\boldsymbol{\mathcal{Z}}\, d\Omega + \int_{\Omega}\mathcal{X}\dot{\boldsymbol{\mathcal{Z}}}\, d\Omega. \tag{5.43}$$

In the first term on the RHS we now take the integral over Ω inside the integral over $\hat{\Omega}$ and then switch the order of integration (which has no effect on the equality), to get

$$\begin{aligned}\dot{\bar{\boldsymbol{\mathcal{Z}}}} &= \int_{\hat{\Omega}} \hat{\mathcal{X}}\hat{\mathcal{B}}\int_{\Omega}\mathcal{H}(\hat{\boldsymbol{n}},\boldsymbol{n})\boldsymbol{\mathcal{Z}}\, d\Omega\, d\hat{\Omega} - \int_{\Omega}\mathcal{X}\mathcal{D}\boldsymbol{\mathcal{Z}}\, d\Omega - \bar{\mathcal{M}}\int_{\Omega}\mathcal{X}\boldsymbol{\mathcal{Z}}\, d\Omega + \int_{\Omega}\mathcal{X}\dot{\boldsymbol{\mathcal{Z}}}\, d\Omega \\ &= \int_{\Omega}\mathcal{X}\mathcal{B}\int_{\hat{\Omega}}\mathcal{H}(\boldsymbol{n},\hat{\boldsymbol{n}})\boldsymbol{\mathcal{Z}}\, d\hat{\Omega}\, d\Omega - \int_{\Omega}\mathcal{X}\mathcal{D}\boldsymbol{\mathcal{Z}}\, d\Omega - \bar{\mathcal{M}}\int_{\Omega}\mathcal{X}\boldsymbol{\mathcal{Z}}\, d\Omega + \int_{\Omega}\mathcal{X}\dot{\boldsymbol{\mathcal{Z}}}\, d\Omega.\end{aligned} \tag{5.44}$$

We can now simplify by substituting for the definition of the expected trait values in group offspring, $\boldsymbol{\mathcal{Z}}' = \int_{\hat{\Omega}}\mathcal{H}(\boldsymbol{n},\hat{\boldsymbol{n}})\boldsymbol{\mathcal{Z}}\, d\hat{\Omega}$, given by equation (5.13). We are left with

$$\dot{\bar{\boldsymbol{\mathcal{Z}}}} = \int_{\Omega}\mathcal{X}\mathcal{B}\boldsymbol{\mathcal{Z}}'\, d\Omega - \int_{\Omega}\mathcal{X}\mathcal{D}\boldsymbol{\mathcal{Z}}\, d\Omega - \bar{\mathcal{M}}\int_{\Omega}\mathcal{X}\boldsymbol{\mathcal{Z}}\, d\Omega + \int_{\Omega}\mathcal{X}\dot{\boldsymbol{\mathcal{Z}}}\, d\Omega. \tag{5.45}$$

At this point we simultaneously subtract and add (thereby not altering the equality) the expression $\int_{\Omega}\mathcal{X}\mathcal{B}\boldsymbol{\mathcal{Z}}\, d\Omega$ after the first term on the RHS, and rearrange, to get

$$\begin{aligned}\dot{\bar{\boldsymbol{\mathcal{Z}}}} &= \int_{\Omega}\mathcal{X}\mathcal{B}\boldsymbol{\mathcal{Z}}'\, d\Omega - \int_{\Omega}\mathcal{X}\mathcal{B}\boldsymbol{\mathcal{Z}}\, d\Omega + \int_{\Omega}\mathcal{X}\mathcal{B}\boldsymbol{\mathcal{Z}}\, d\Omega - \int_{\Omega}\mathcal{X}\mathcal{D}\boldsymbol{\mathcal{Z}}\, d\Omega \\ &\quad - \bar{\mathcal{M}}\int_{\Omega}\mathcal{X}\boldsymbol{\mathcal{Z}}\, d\Omega + \int_{\Omega}\mathcal{X}\dot{\boldsymbol{\mathcal{Z}}}\, d\Omega \\ &= \int_{\Omega}\mathcal{X}\mathcal{B}(\boldsymbol{\mathcal{Z}}' - \boldsymbol{\mathcal{Z}})\, d\Omega + \int_{\Omega}\mathcal{X}(\mathcal{B}-\mathcal{D})\boldsymbol{\mathcal{Z}}\, d\Omega - \bar{\mathcal{M}}\int_{\Omega}\mathcal{X}\boldsymbol{\mathcal{Z}}\, d\Omega + \int_{\Omega}\mathcal{X}\dot{\boldsymbol{\mathcal{Z}}}\, d\Omega.\end{aligned} \tag{5.46}$$

Now substituting for the definition of the difference between the expected trait values in group offspring and their group parents, $\Delta\boldsymbol{\mathcal{Z}} = \boldsymbol{\mathcal{Z}}' - \boldsymbol{\mathcal{Z}}$, from equation (5.15), and the definition of Malthusian group fitness, $\mathcal{M} = \mathcal{B} - \mathcal{D}$, from equation (5.28), and reordering the terms for convenience, we have

$$\dot{\bar{\boldsymbol{\mathcal{Z}}}} = \int_{\Omega}\mathcal{X}\mathcal{M}\boldsymbol{\mathcal{Z}}\, d\Omega - \bar{\mathcal{M}}\int_{\Omega}\mathcal{X}\boldsymbol{\mathcal{Z}}\, d\Omega + \int_{\Omega}\mathcal{X}\mathcal{B}\Delta\boldsymbol{\mathcal{Z}}\, d\Omega + \int_{\Omega}\mathcal{X}\dot{\boldsymbol{\mathcal{Z}}}\, d\Omega. \tag{5.47}$$

This gives equation (5.37) in the main text.

This result is important, for as we mentioned in the introduction, attempts to study the dynamics of interdemic group selection and MLS2 more generally have not met with great success (Arnold and Fristrup, 1982; Okasha, 2006). One of the advantages of the Malthusian interdemic Price equation (5.37) is that it holds true for every instantaneous moment in time, whereas the discrete-time MLS2 Price equation discussed by (Okasha, 2006, pg. 75) cannot be iterated through time. This challenge arises from the fact that discrete time is not commensurate between the two levels of selection. As Arnold and Fristrup (1982) said, 'the choice of a single measure of evolutionary change restricts the context in which "other level" processes will be perceived.' This point has also been made much more recently by Bourrat (2015a,b), saying, 'if different proxies of fitness reflecting different time scales are used at the organism and species levels, this will have the consequence of measuring selection pressures over two different sets of environmental conditions. This can lead one to confound the existence of one unique process of selection over two different periods of time with two ontologically distinct processes of selection, one for each level.' Indeed, problems with the timescales of selection in MLS2 have led Okasha (2006, pg. 59) to assert that 'MLS1 and MLS2 are distinct processes that can occur in nature; whether either occurs in a particular case is a matter of objective fact.' We will see in the Discussion chapter that this claim is untrue in the context of the dynamical systems theory of natural selection, and that the two types of MLS are merely different perspectives on the same underlying dynamical processes.

Although the Malthusian interdemic Price equation (5.37) was derived from the same class of interdemic selection equation studied by Simon et al. (2013), the natural conclusions one arrives at from our analysis of the same problem are very different. There are three arguments put forward by Simon et al. (2013) that we consider to be inconsistent with the work undertaken here: *i*) argument #1—on the generality of the Price equation, Simon et al. (2013) claimed that, 'it is doubtful that the Price equation can be modified in a reasonable way to apply to the models of two-level population dynamics we have described here.'; *ii*) argument #2—on the utility of the Price equation in predicting evolutionary change, Simon et al. (2013) stated that: 'but even if it could be [that is, the PDE could be written in terms of a Price equation], it would still not provide the information needed to predict long-term evolutionary dynamics; and as we have argued, long-term dynamics is crucial to understanding the phenomenon of group selection'; and *iii*) argument #3—on the utility of the Price equation in providing a definition of group selection Simon et al. (2013) claimed that, 'no definitive opinion about the merits of group selection can be drawn from ... the Price equation, or Hamiltons equation, because they inadequately address the most important features of two-level population dynamics.'

By deriving the Malthusian interdemic Price equation (5.37) from the same class of PDE as Simon et al. (2013), we have clearly demonstrated that argument #1 to be false. Indeed, we need not have derived the Malthusian interdemic Price equation (5.37) to make the point, since the argument put forth by Simon et al. (2013) stems from the misconception that the Price equation is some sort of model that is limited to certain types of populations with well-defined birth and death regimens. Frank (2012a) makes clear that the Price equation, being a mathematical identity, is not restrictive in any way: 'it is important to realize that everything truly means every possible force that might arise and that is not accounted for by the particular expression for selection. Lightning may strike. New food sources may appear. The Price equation in its general and abstract form is a mathematical identity.'

Argument #2 is fundamentally true, but Simon et al. (2013) use it as a 'straw man' against which to argue. Again, this is made clear by a quote from Frank (1995) who wrote over 20 years ago, 'I have sometimes heard the question: "What problems can the Price equation solve that cannot be solved by other methods?" The answer is, of course, none, because the Price equation is derived from, and is no more than, a set of notational conventions. It is a mathematical tautology... the Price equation works well because it provides nothing more than a way to relate a problem to the fundamental properties of evolutionary change.' The Price equation is used as a way to partition evolutionary change into components that can be ascribed to different biological processes, such as natural selection and fidelity of transmission. The reality is that the Price equation itself is therefore not strictly 'modified' to apply to anything—the reality is that there is no such thing as *the* Price equation, but instead a Price equation *corresponding* to every single model of selection.

Lastly, argument #3 is used as a means to justify the development of their own definition of group selection. Based on their analogue of the Malthusian interdemic selection equation (5.21) (corresponding to equation (8) in Simon et al. (2013)) Simon et al. (2013), formulated their own definition as: *'If a trait establishes itself in a model of two-level population dynamics when group-level events are present, and does not establish itself in the same model when they are absent, then the trait evolves by group selection.'*. On the face of it this definition might seem quite logical, but it actually emphasises exactly why the covariance mathematics of Price (1970, 1972a) is useful in defining what interdemic group selection is! In particular, whereas the Malthusian interdemic Price equation (5.37) partitions the total change in the group population into distinct causal components, leading naturally to a definition of the action of natural selection on the group population irrespective of what types of group-level reproductive processes are occurring to impact

on Malthusian group fitness, $\mathcal{M}$, the definition of Simon et al. (2013) sidesteps defining what the fitness of groups even is. Moreover, in failing to identify what might be meant by a group-level inheritance, or the fidelity of transmission of group phenotypes between group ancestors and group descendants, the definition of Simon et al. (2013) also confounds the process of change with the process of change *due to* selection, and the change due to selection with the change due to an evolutionary response to selection (Falconer and Mackay, 1995).

5.4 Implications

As we mentioned in the introduction to this chapter, one of the main reasons for a resurgence of interest in group selection and MLS more generally is that there is an a increasing appreciation of the importance of MLS in the context of the major transitions in evolution (Michod, 1996, 1997; Michod and Roze, 1999; Michod, 2000; Okasha, 2005, 2006; Grosberg and Strathmann, 2007; Bourke, 2011; Goodnight, 2013b; Szathmáry, 2015; West et al., 2015). These transitions have been characterised as processes that lead to the creation of new units of selection in the hierarchy of life. For example, cooperating archaea and bacteria came together to form eukaryotic cells (Margulis, 1970), which, in turn, came together to form multicellular organisms (Grosberg and Strathmann, 2007).

Key questions yet to be answered, however, are what types of conditions favoured the formation of cooperative groups in the first place, and once a major transition has occurred, what processes maintain cooperation among within-group individuals and prevent conflict (West et al., 2015)? Since we cannot wind back the clock or study major evolutionary transitions in the laboratory, the solutions to these problems will no doubt require a large theoretical component. Moreover, the characteristics of major evolutionary transitions are not clearly adaptations like, say, a birds wing, that we can study using the traditional optimisation approaches from evolutionary theory. More than ever it is clear that we will need to incorporate both dynamics and optimisation in models to better understand how these transitions are brought about. The framework we have developed in this chapter may help bridge the theoretical divide between these two traditions.

Cancer is increasingly viewed as an evolutionary process whereby the inevitable mutations that occur during growth and development generate somatic cell lineages that differ in their propensity to survive and reproduce in a manner that is both irregular and harmful to organismal function (Leroi et al., 2003; Crespi and Summers, 2005; Merlo et al., 2006; Greaves and Maley, 2012). The evolutionary dynamics of cancer can be captured in

interdemic group selection terms as two different levels at which natural selection can operate (Trivers, 2006; Foster, 2011).

On a relatively short timescale, selection acts within organisms on heritable variation in the propensity of somatic cells to survive and reproduce, promoting cancer progression (Fig. 5.1A; Nunney, 1999). Intuitively, long-lived, larger organisms with many cell divisions per lifetime should therefore be subject to higher rates of cancer than organisms with fewer cell divisions and shorter generation times, but this is only half the story. On a relatively long timescale selection acts between organisms on heritable variation in their propensity to develop cancer, promoting cancer suppression (Fig. 5.1B; Nunney, 2013). On the one hand, the fact that we do not generally observe higher-rates of cancer in long-lived, larger organisms—so-called 'Peto's paradox' (Peto et al., 1975; Caulin and Maley, 2011)—suggests that organism-level selection promotes the evolution of anti-cancer adaptations (Leroi et al., 2003; Trivers, 2006; Nunney, 2013; Korolev et al., 2014). On the other hand, the fact that cancer has been discovered in almost all multicellular organisms in which we have searched for it—from *Hydra* Domazet-Lošo et al. (2014) to elephants (Abegglen et al., 2015)—suggests that interdemic group selection generates a type of balancing selection between the two levels, a sort of evolutionary 'arms race' which can never be won (Ridley, 1994). To date there has been relatively little theoretical work on this type of process. Yet the framework we have developed here could be readily applied to these kinds of problems.

5.5 Concluding remarks

As Maynard Smith (1976) once said, 'group selection will have evolutionary consequences; the only question is how important these consequences have been.' In this chapter, we have developed a general framework in which to study the dynamics of interdemic group selection in order to be able to answer Maynard Smith's question. In particular, we have generalised Malthusian selection equation (2.28) presented in Chapter 2, to obtain the Malthusian interdemic group selection equation (5.21). We have shown the the Malthusian interdemic group selection equation (5.21) is a generalised form of the group selection PDE derived by Simon (2010). We showed that the dynamics of interdemic group selection can be described from ecological, genotypic, and phenotypic perspectives. Hence, we have added support to the claim of Simon (2010) and Simon et al. (2013) that they do indeed represent a general theory of group selection, but we have also formally proved that they are incorrect to dismiss the similarities of the processes they study with those that have been well-described for many years (Williams, 1966; Lewontin,

1970; Price, 1970, 1972a; Maynard Smith, 1976). Overall, we have further extended our dynamical systems theory of natural selection and further highlighted its unifying properties with respect to other major frameworks in evolutionary theory.

Chapter 6

The dynamics of natural selection in microbial systems

6.1 Introduction

Biological systems are complex. There are many possible genotypes, and many different environments in which genotypes may find themselves. Each genotype may map to infinitely many phenotypes in ways that may or may not depend crucially on the environment at the time the phenotype is observed. To make sense of this complexity, evolutionary biologists have, broadly speaking, taken two alternative approaches to developing theory.

On the one hand, there has been the development of theory that aims to uncover the abstract principles of evolution by natural selection—those that hold true in a general sense across all conceivable biological systems. Darwin's (1859) verbal description of evolution by natural selection is the most obvious example of a body of theory of the general, abstract kind. Other notable examples include the replicator equation (Schuster and Sigmund, 1983), Price's (1970; 1972a) covariance mathematics, the univariate and multivariate breeder's equations (Lush, 1937; Lande, 1979; Lande and Arnold, 1983; Falconer and Mackay, 1995), and Hamilton's (1963; 1964) kin selection theory. The goal of this kind of work has been to deal with complexity by formulating abstract principles and concepts, such as fitness, heritability, selection, and so on, that apply to any arbitrary biological system of interest. Indeed, this has been the focus of the majority of the theory developed in this thesis.

On the other hand, there has been the development of theory that is designed to address problems regarding a specific biological system or answer questions about a particular biological phenomenon. Much of this 'streamlined' theory has tended to employ an

approach known as the 'phenotypic gambit' (often in conjunction with an optimisation procedure) to explore the kinds of adaptations one might expect to find in nature under a set of greatly simplifying assumptions (Grafen, 1984). One reason this type of approach has been favoured by evolutionary theorists is that it has enabled them to distil much of the inherent complexity of biological systems down into a set of key characteristics. For instance, this approach has revealed evolutionary principles underlying generalised categories of life strategies, such as predators and their prey, cooperators and defectors, signallers and receivers, single-celled and multi-celled organisms, and so on. Another reason for the commonality of the phenotypic gambit and other streamlined approaches, however, has been the absence of sufficient data with which more detailed models could have been constructed.

In recent years, this absence of data has become much less of an issue. Advances in molecular biology have been married to a research programme focused heavily on the evolution of microbial systems (Elena and Lenski, 2003; West et al., 2006, 2007a; Kawecki et al., 2012), providing evolutionary theorists with a vast amount of data with which to develop and test new hypotheses and formulate different types of models. There are numerous advantages to working with microbes, not least because their short generations times allow evolutionary timescales to be observed, and their genetics are considerably less complex than those of multi-cellular organisms and can therefore be manipulated experimentally relatively easily.

Whereas models developed using the phenotypic gambit and other streamlined approaches have typically rested heavily on the identification of key qualitative features of biological systems, the new class of models tend to incorporate more of a physical sciences or 'systems biology' type methodology. This approach tends to involve perturbing systems, taking quantitative measurements in a carefully controlled experimental set-up, and modelling the dynamics of a system explicitly using deterministic or stochastic models. For instance, Xavier and Foster (2007) studied the evolution of cooperation and conflict in microbial biofilms using a stochastic individual-based model of microbial growth coupled to a differential equation for the diffusion-reaction effects of secreted polymers. As another example, Sanchez and Gore (2013) combined game-theoretic deterministic differential equations with experimental data to explore feedback loops between population dynamics and evolutionary dynamics using a model laboratory yeast population. Whereas the goal in the more traditional evolutionary models has been typically to make a general prediction applicable to a diverse range of taxa, the goal of the new types of models is more often to make predictions about the future of a particular system—such

as the dynamical changes taking place, or the probability and/or time to fixation of a mutant.

In the thesis so far, I have focussed almost entirely on the development of theory of the general, abstract kind. In this chapter, we now turn to exploring how this general theory can be applied to specific questions of interest under a set of simplifying assumptions. In particular, our goal is to demonstrate how simple models can be constructed and solved (numerically) to obtain different perspectives on the dynamics of natural selection. Inspired by research on evolution in microbial populations, we focus on two examples of an idealised population of asexually reproducing microbes. Firstly, we develop a series of models of increasing complexity to study the processes of horizontal gene transfer and phenotypic plasticity, focussing on the ecological, genotypic, and phenotypic perspectives on the dynamics of natural selection we introduced in Chapter 2. Secondly, we develop another series of models of increasing complexity that incorporates genetic details about epistatic mutations and phenotypic plasticity, focussing on the adaptive landscape perspective of evolutionary change we introduced in Chapter 3. The examples we study are primarily chosen to highlight some of the important characteristics of the dynamical systems theory when it is applied in a streamlined methodology, but they are also selected on the basis of being open problems that are thought to be somewhat difficult to tackle using existing theory[a].

6.2 The dynamics of natural selection in populations with horizontal gene transfer and phenotypic plasticity

In our first example, we develop a series of relatively simple models designed to highlight some of the important characteristics of the dynamical systems theory from Chapter 2 when it is applied in the form of a streamlined methodology. In particular, we develop models of an asexually reproducing population of microbes that incorporates the processes of horizontal gene transfer and phenotypic plasticity.

Horizontal transfer of genetic material is widespread in the natural world, particularly among microbes (Thomas and Nielsen, 2005). Many mobile plasmids transferred among bacteria, for instance, encode genes whose expression can be modulated according to the nutrient, toxin or competition levels of the environment a bacterium finds itself in

[a]It is important to stress, however, that we do not aim to study quantitatively, or necessarily even qualitatively, 'realistic' models for now, which are beyond the scope of this thesis.

(a type of phenotypic plasticity), helping migrant bacterial genotypes to rapidly adapt to new environments (Raz and Tannenbaum, 2010). Niehus et al. (2015) have recently shown that the rapidity with which horizontal gene transfer can provide fitness benefits to bacteria can lead to the formation of ecological niches that are defined not by the abundance of particular species, but rather by the abundance of particular sets of mobile genes. This is one of the reasons why horizontal gene transfer is thought to be one of the dominant causes of the spread of antibiotic resistance in bacteria, since it is antiobiotic resistance *genes*, rather than antibiotic resistant *species*, that come to rapidly colonise antibiotic-containing niches (Ochman et al., 2000).

Horizontal gene transfer poses problems for evolutionary theorists, however, for it complicates the notion of a phylogenetic lineage by providing evolutionary 'short-cuts' to potentially radically different genotypes and phenotypes (Gogarten and Townsend, 2005). Moreover, evolutionary theorists do not yet agree on how one should conceptualise the process of horizontal gene transfer in terms of selection and transmission, and it is therefore a matter of debate how exactly horizontal gene transfer influences adaptive evolution. For instance, Birch (2014) characterises the process as a kind of frequency-dependent developmental process when he says, 'we cannot talk of an organism's genotype *simpliciter*; we can talk only of an organism's genotype at a particular stage in its life cycle.' Whereas many evolutionary theorists think of the process as akin to a form of microbial sexual reproduction (Redfield et al., 1997; Shapiro et al., 2012; Papke and Gogarten, 2012; Cohan and Aracena, 2012). We discussed this conceptualisation in Chapter 2, where we characterised the process as two microbes of different genotypes coming together to produce a 'descendant' genotype containing genetic information from two genetically different 'ancestors'[b].

To explore some of these ideas in the context of the dynamical systems theory of natural selection, our focus will be on the dynamics of population composition, $\boldsymbol{n}$, the relative composition of the population, $\boldsymbol{x}$, and the phenotypic trait values in the genotype-phenotype map, $\mathbf{Z}$, and their population averages, $\bar{\boldsymbol{z}}$. This will allow us to explore the utility of the ecological, genotypic, and phenotypic perspectives on the dynamics of natural selection that we emphasised in Chapter 2. By using the the general framework we outlined in that chapter, we demonstrate how one can construct simplified models of horizontal gene transfer and phenotypic plasticity. Solving the resulting equations numer-

[b]On the face of it these different conceptualisations might seem to be based on mere semantic differences, but this is not quite true. The reason is that evolutionary theorists are primarily concerned with adaptive evolutionary change, and this can only be studied if we can identify the part of a process that impacts on natural selection.

ically in a restricted parameter regime, we identify conditions in which these processes bring about or disrupt stable mixed equillibria in populations.

6.2.1 Model with no phenotypic plasticity and no horizontal gene transfer

To keep our models relatively simple, the context we consider here is a population of asexually reproducing microbes undergoing logistic growth. That is, we assume that the population size, N, grows until it reaches some limiting carrying capacity, K. As a suitable timescale, we specify the units of time, t, as hours, and consider a period of growth over four days, so that the population growth is from $t = 0$ to $t = 96$. We suppose that there is some focal trait of interest (so that we have $|\mathbb{P}| = 1$) whose trait value indicates how well the average microbe of each genotype acquires or degrades some resource in the environment. We further assume, for simplicity, that there are just two genotypes of any significance in our system, a 'resident' and a 'migrant' (so that we have $|\mathbb{G}| = 2$), that differ with respect to the focal trait of interest. To represent this system, we initialise a genotype-phenotype map at time $t = 0$ of the form

$$\mathbf{Z} = \begin{bmatrix} 1 \\ 1/2 \end{bmatrix}. \tag{6.1}$$

The assumption being made here is that the resident (the first genotype) is somewhat (two-fold) better at obtaining or degrading the resource in the environment than the migrant (the second genotype). For now, we also assume that the trait values of both types of microbes do not change through time i.e. that they are constant. This implies that $\dot{\mathbf{Z}} = \mathbf{0}$. At time $t = 0$, we initialise the population with $n_1 = 1000$ resident and $n_2 = 500$ migrant microbes.

Now let us turn to the question of how the trait influences the ability of the microbes to survive and reproduce. We assume that the resource degrading ability of the trait (linearly) increases the *relative* ability of a genotype to reproduce[c]. With a baseline reproduction rate of 1, and a selection strength of trait of ς, we initialise the fidelity rate matrix for this population at time $t = 0$ as

[c]The alternative would be a trait whose expression increased the absolute ability of a genotype to reproduce, but these kind of traits are likely to be rare in nature, since it is almost always the benefit relative to others in the environment that dictates an individual's success.

$$\mathbf{F} = \begin{bmatrix} \rho\left(\frac{(1-\varsigma)+\varsigma z_1}{(1-\varsigma)+\varsigma\bar{z}}\right) & 0 \\ 0 & \rho\left(\frac{(1-\varsigma)+\varsigma z_2}{(1-\varsigma)+\varsigma\bar{z}}\right) \end{bmatrix}, \tag{6.2}$$

where the fidelity rates f_{ij} are normalised by the average reproduction fidelity rate, $(1-\varsigma)+\varsigma\bar{z}_1$, to ensure that any reproductive benefit acquired from trait expression is strictly relative, and we recall that $\bar{z} = \mathbf{Z}^{\mathrm{T}}\boldsymbol{x}$ is the definition of the average value of the trait in the population. The rate parameter ρ scales how fast the population as a whole is growing. From this fidelity rate matrix, it follows that the vector of reproduction rates and vector of production rates are given by

$$\boldsymbol{b} = \begin{bmatrix} \rho\left(\frac{(1-\varsigma)+\varsigma z_{11}}{(1-\varsigma)+\varsigma\bar{z}_1}\right) \\ \rho\left(\frac{(1-\varsigma)+\varsigma z_{21}}{(1-\varsigma)+\varsigma\bar{z}_1}\right) \end{bmatrix}, \quad \text{and} \quad \boldsymbol{p} = \begin{bmatrix} \rho n_1\left(\frac{(1-\varsigma)+\varsigma z_{11}}{(1-\varsigma)+\varsigma\bar{z}_1}\right) \\ \rho n_2\left(\frac{(1-\varsigma)+\varsigma z_{21}}{(1-\varsigma)+\varsigma\bar{z}_1}\right) \end{bmatrix}, \tag{6.3}$$

respectively. Remember, the vector of reproduction rates, $\boldsymbol{b}$, specifies the rates at which an individual of each genotype produces descendants, whereas the vector of production rates, $\boldsymbol{p}$, specifies the rate at which individuals of a given genotype are being produced in the population. That is, whereas $\boldsymbol{p}$ is a population rate, $\boldsymbol{b}$ is a *per capita* rate.

We also further assume that the quantitative trait we study has a negligible effect on the differential survival rate of either genotype. We initialise the death rate vector at time $t = 0$ as

$$\boldsymbol{d} = \begin{bmatrix} \rho\frac{N}{K} \\ \rho\frac{N}{K} \end{bmatrix}. \tag{6.4}$$

The assumption here is that the rate of death of individuals of each genotype is proportional to the ratio of the population size, N, to its carrying capacity, K. In natural systems this is usually the case whenever there is some limiting resource being used up by the population that is necessary for survival.

One of the implicit assumptions of the way we have specified the fidelity rate matrix $\mathbf{F}$ is that reproduction always leads to the production of the same genotype (i.e. we assume

that there is no mutation or horizontal gene transfer). We can tell this is the case by noting that all the off-diagonal entries of the matrix are zero. Since like begets like during reproduction, the inheritance matrix for this population for all t is therefore simply equal to the identity matrix, $\mathbf{H} = \mathbf{I}$.

To understand the dynamics of our system, we need to formulate the key dynamical equations we identified in Chapter 2. Firstly, suppose that we are interested in how the population composition, $\boldsymbol{n}$, changes over time. To find this change, we formulate the Malthusian selection equation (2.28) for this population, which is given by

$$\dot{\boldsymbol{n}} = \mathbf{F}^{\mathrm{T}}\boldsymbol{n} - \mathbf{N}\boldsymbol{d} = \begin{bmatrix} \rho n_1 \left(\frac{(1-\varsigma)+\varsigma z_{11}}{(1-\varsigma)+\varsigma \bar{z}_1} - \frac{N}{K} \right) \\ \rho n_2 \left(\frac{(1-\varsigma)+\varsigma z_{21}}{(1-\varsigma)+\varsigma \bar{z}_1} - \frac{N}{K} \right) \end{bmatrix}, \tag{6.5}$$

where $\mathbf{N} = \mathrm{diag}(\boldsymbol{n})$ is the diagonalised composition vector. This equation provides us with one part of the ecological perspective on the dynamics of natural selection, and the timescales over which each genotype is growing in the population. To find how the population size as a whole, N, changes over time, we use the Malthusian growth-selection equation (2.39). Before doing so, however, recall that we need to calculate the Malthusian fitness vector, $\boldsymbol{m}$, for the genotypes. Using the details from the reproduction and death rates of the two genotypes, the Malthusian fitness vector takes the form

$$\boldsymbol{m} = \begin{bmatrix} \rho \left(\frac{(1-\varsigma)+\varsigma z_{11}}{(1-\varsigma)+\varsigma \bar{z}_1} - \frac{N}{K} \right) \\ \rho \left(\frac{(1-\varsigma)+\varsigma z_{21}}{(1-\varsigma)+\varsigma \bar{z}_1} - \frac{N}{K} \right) \end{bmatrix}. \tag{6.6}$$

Note that from the definitions of $\boldsymbol{b}$ and $\boldsymbol{d}$ the average rate of reproduction is simply given by $\bar{b} = \rho$, and the average rate of death is simply given by $\bar{d} = \rho N/K$. The average Malthusian fitness in the population is then simply given by $\bar{m} = \bar{b} - \bar{d} = \rho\,(1 - N/K)$. Using this in conjunction with the Malthusian growth-selection equation (2.39), we find that the rate of change of the overall population size is given by

$$\dot{N} = \rho N \left(1 - \frac{N}{K} \right). \tag{6.7}$$

This equation is important because it completes our ecological perspective on the dynamics of natural selection. In particular, the form of this equation confirms that at each instant in time, t, the population growth is logistic in nature (Box 2.1; Chapter 2).

Now suppose that we are interested in changes in the relative composition of the population, $\boldsymbol{x}$. To find this change, we must use the Malthusian replicator equation (2.45) for this population, which is given by

$$\dot{\boldsymbol{x}} = \begin{bmatrix} \rho x_1 \left(\frac{(1-\varsigma)+\varsigma z_{11}}{(1-\varsigma)+\varsigma \bar{z}_1} - \frac{N}{K} - \bar{m} \right) \\ \rho x_2 \left(\frac{(1-\varsigma)+\varsigma z_{21}}{(1-\varsigma)+\varsigma \bar{z}_1} - \frac{N}{K} - \bar{m} \right) \end{bmatrix}. \tag{6.8}$$

This equation is important because it defines the genotypic perspective on the dynamics of natural selection. Recall that the rates of change of the relative frequencies of genotypes will often be more intuitive to us from an evolutionary perspective, because it is a genotype's relative ability to compete that determines its evolutionary success, rather than just its ability to grow *per se*. Thus, in the early stages of logistic growth we may see that both genotypes are increasing in absolute abundance, but that one of the genotypes is actually decreasing in terms of its overall relative frequency in the population.

Finally, suppose that we are interested not in the microbes themselves, but in some aspect of their phenotypes. In terms of phenotypic change over time, we have already said that the genotype-phenotype map, $\mathbf{Z}$, does not change, so that $\dot{\mathbf{Z}} = \mathbf{0}$. Nevertheless, we expect there to be changes in the average phenotypic trait value in the population, $\bar{z}$, over time if the relative composition of the population, $\boldsymbol{x}$, is also changing. This change is given by the Malthusian Price equation (2.49), which here takes the form

$$\dot{\bar{\boldsymbol{z}}} = \mathrm{Cov}_{i \in \mathbb{G}}(z_{i1}, m_i). \tag{6.9}$$

This equation is important because it defines the phenotypic perspective on the dynamics of natural selection. Note that we only have the first term of the Malthusian Price equation (2.49) from Chapter 2. This term is the *natural selection* component corresponding to the statistical association between the trait values held by individuals, z_{ik}, and their Malthusian fitness, m_i. The other two components have dropped out in the present context because of the assumptions we have made. In particular, since there is no mutation or horizontal gene transfer there can be no transmission biases, and since there

is no change in the phenotypic values over time there can be no phenotypic plasticity or ecological inheritance.

We have now formulated a simple model of an asexually reproducing population of microbes, demonstrating how the general theory from Chapter 2 can be used in conjunction with greatly simplifying assumptions to generate streamlined theory suitable for a particular example. Let us now observe how the dynamics of natural selection play out in our simple model over a period of four days, from time $t = 0$ to $t = 96$. To illustrate the workings of the theory we use arbitrary values of $\varsigma = 1/4$, for the strength of selection parameter, $\rho = 1/2$ for the population growth parameter, and $K = 1 \times 10^8$ for the carrying capacity. Although the model we have constructed is relatively simple, the presence of several non-linear terms among $\dot{\boldsymbol{n}}$ means that a closed-form analytical solution to our system is unlikely to be tractable to solve for. Nevertheless, we can solve the system numerically[d].

Observing the population from an ecological perspective, we see that the absolute abundances of both the resident and the migrant increase until the population reaches its carrying capacity, K, at which point the absolute abundance of the migrant rapidly decreases as it is out-competed by the resident (Fig. 6.1A). The population size itself follows logistic growth as we expected from the model set-up. Despite the increase in absolute abundance of both genotypes early on, the genotypic perspective tells a slightly different story as we suggested it might. In particular, we see that the relative frequency of the resident genotype increases monotonically, whilst the relative frequency of the migrant genotype *decreases* monotonically (Fig. 6.1B). Note that the genotypic perspective therefore tells us that the migrant genotype suffers a growth disadvantage from the outset, despite the ecological perspective suggesting that it enjoys an initially positive growth rate.

[d]We do so here using custom built MATLAB scripts centred around the ode45 function.

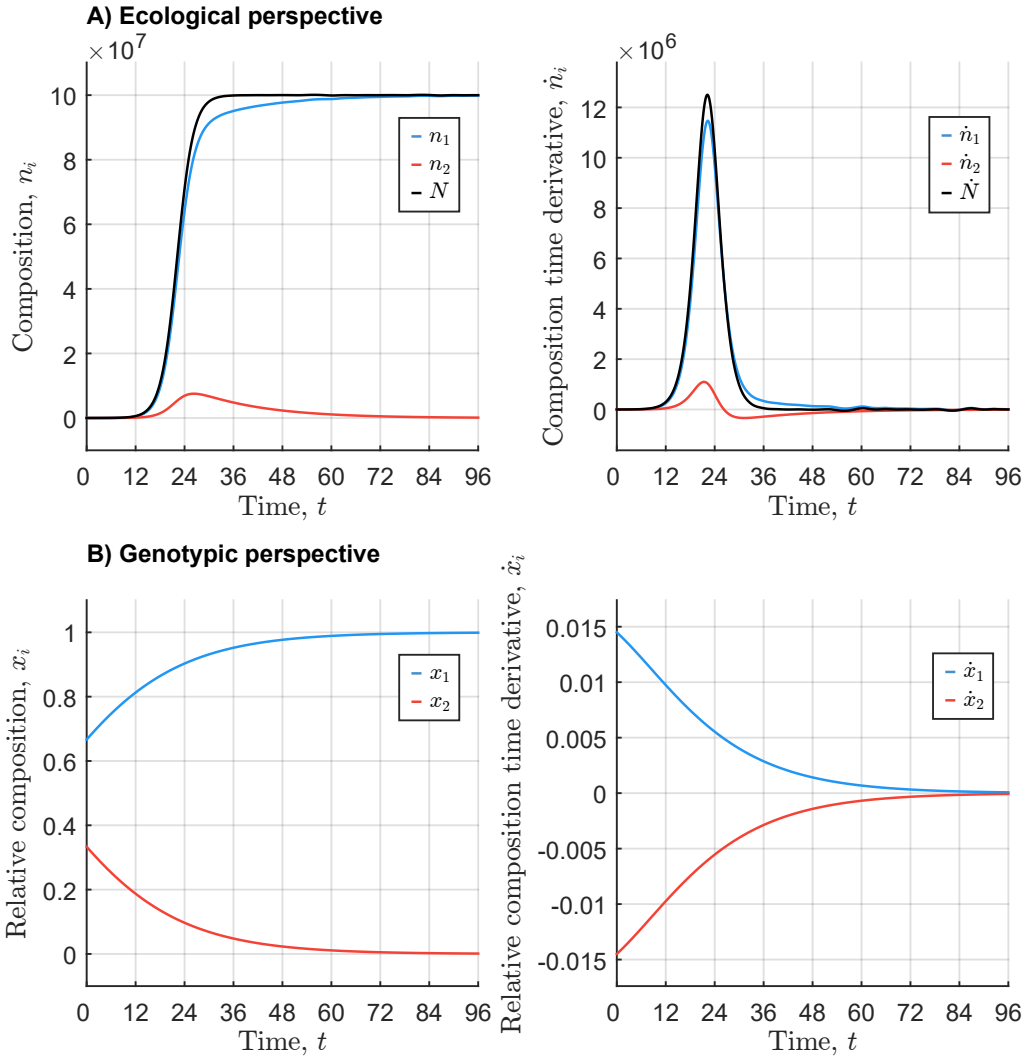


Figure 6.1: Ecological and genotypic perspective of model dynamics. A) Ecological perspective on the dynamics. On the left, the abundance of each genotype and the population size over time are plotted. On the right, the derivatives of the abundance of each genotype and the population size over time are shown. These correspond to the elements of the Malthusian selection equation (2.28), and Malthusian growth-selection equation (2.39), respectively. B) Genotypic perspective on the dynamics. On the left, the relative frequency of each genotype over time is plotted. On the right, the derivatives of the relative frequencies of each genotype over time are shown. These correspond to the elements of the Malthusian replicator equation (2.45). All graphs are plotted over a period of 96 hours. Parameters used in the model were: $\rho = 1/2$, $\varsigma = 1/4$, and $K = 1 \times 10^8$.

Now let us look at the phenotypic dynamics. Clearly there is no change in the trait values of the genotypes themselves since we specified that they were constants in the model set-up (Fig. 6.2A). Yet, despite the absence of change in the individual trait values, the average trait value, $\bar{z}$, does change over time as the population composition changes, monotonically increasing in-line with the increase in frequency of the resident genotype (Fig. 6.2B). When we look at the derivative of this quantity, we can see from the components of the Malthusian Price equation (2.49) that the change is entirely due to natural selection i.e change over time of the selection coefficient $\mathrm{Cov}_{i\in\mathbb{G}}(z_{i1}, m_i)$ (Fig. 6.2B).

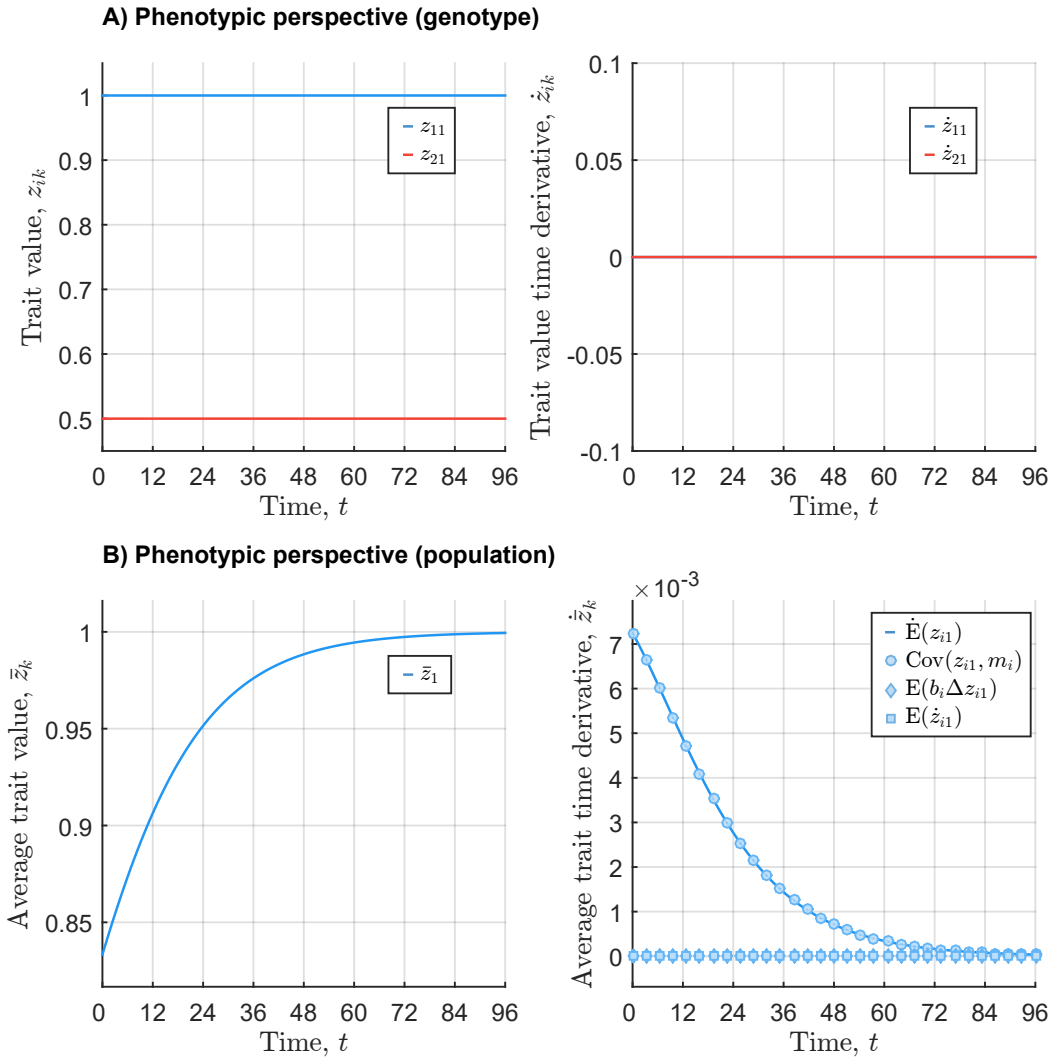


Figure 6.2: Phenotypic perspective of model dynamics. A) Phenotypic perspective on the dynamics at the level of the individual genotype. On the left, the trait values of each genotype are plotted over time. On the right, the derivatives of the trait values of each genotype over time are shown. These correspond to the elements of equation (2.46) for the time derivative of the genotype-phenotype map. B) Phenotypic perspective on the dynamics at the population level. On the left, the average trait value in the population over time are plotted. On the right, the derivative of the average trait value in the population over time is shown, decomposed into three separate components corresponding to those from the Malthusian Price equation (2.49) from Chapter 2. Each component has a different interpretation: the covariance term $\mathrm{Cov}_{i\in\mathbb{G}}(z_{ik}, m_i)$ is the component of change in average trait value, $\bar{z}_k$, in the population we attribute to the action of *natural selection*; *ii*) the term reproduction-rate-weighted expectation $\mathrm{E}_{i\in\mathbb{G}}(b_i \Delta z_{ik})$ is the component of change in average trait values due to *transmission fidelity*; and *iii*) the expectation term $\mathrm{E}_{i\in\mathbb{G}}(\dot{z}_{ik})$ is the component of change due to *phenotypic plasticity* and *ecological inheritance*. All graphs are plotted over a period of 96 hours. Parameters used in the model were: $\rho = 1/2$, $\varsigma = 1/4$, and $K = 1 \times 10^8$.

Despite the simplicity of the model, there is an important take-home message from these results. Namely, that each of the ecological, genotypic, and phenotypic perspectives provide their own unique insight into the dynamics of natural selection. Without the ecological perspective, we would not know that the population of microbes we are studying grows logistically. In particular, we see that it is the availability of resources that determines the overall rate of growth of microbes initially, rather than differences in their ability to compete with one another. Without the genotypic perspective, it would be far less obvious to us that the the resident genotype benefits from a Malthusian fitness advantage immediately (from time $t = 0$), out-competing the migrant genotype even while both are increasing in absolute abundance. Finally, without the phenotypic perspective, we would have little indication as to why the absolute and relative frequencies of the genotypes change over time. As it is, without even knowing about the underlying equations, we can see from the dynamics alone that the resident genotype has a different trait value to that of the migrant and that this trait value is statistically associated with the ability of the resident to survive and reproduce, providing the variation in the population on which natural selection can act.

6.2.2 Model incorporating phenotpyic plasticity

Now let us introduce another dimension to the population dynamics. Let us suppose that there is a second phenotypic trait that enables the degradation of some other resource in the environment (so that we now have $|\mathbb{G}| = 2$ and $|\mathbb{P}| = 1$). Unlike the first trait, however, we now assume that this trait is only expressed by the migrant genotype (in other words, resident microbes have a value for this trait of $z_{12} = 0$). We initialise the new genotype-phenotype map at time $t = 0$ as

$$\mathbf{Z} = \begin{bmatrix} 1 & 0 \\ 1/2 & 1/20 \end{bmatrix}. \tag{6.10}$$

If we assume that this second trait value contributes to the reproductive success of each genotype in the same way that the first trait does then, as we have described the system so far, we should expect only a small change in the dynamics (since the migrant is now able to acquire a small amount of additional resources for reproduction). To illustrate the potential importance of phenotypic plasticity in trait values, however, let us assume

that the phenotypic trait value of the migrant is a variable quantity that is sensitive to changes in the environment.

We know that, in the natural world, microbes exhibit a number of specialised adaptations for detecting the presence of other microbes, and that they regulate the expression of certain classes of genes as a result (Cornforth and Foster, 2013). This type of plasticity in microbe phenotypes is potentially very useful. It allows microbes to 'spend' additional metabolic resources on the attack or defence of other genotypes when necessary. Let us therefore suppose that the migrant genotype responds to the abundance of the other genotype in the population by regulating its trait value z_{22}. To incorporate this process in our model, let us specify that the genotype-phenotype map, $\mathbf{Z}$, now changes over time. In particular, let us suppose that the derivative of the genotype-phenotype map is given by

$$\dot{\mathbf{Z}} = \begin{bmatrix} 0 & 0 \\ 0 & \varphi n_1 z_{22}(1 - z_{22}) \end{bmatrix}. \tag{6.11}$$

The assumption being made here is that the trait value z_{22} is a form of logistic function related to the *abundance* of the resident genotype. The parameter φ simply scales the rate of change (again, for practical reasons we will simply choose a value for this parameter to be $\varphi = 5/K$). If $n_1 > 0$ and $z_{11} < 1$, we can see that there will be a positive increase (up-regulation) of the trait value z_{22} by migrant microbes. This is not a complete model of what we might expect to see in the natural world, since it does not allow for the trait levels to decrease. Nevertheless, it serves to illustrate how one can incorporate such assumptions in the framework we have developed in a fairly intuitive way. In a moment we will introduce an alternative function which does allow for the trait levels to decrease. For now though, note that under these new assumptions the change in the average phenotypic trait values in the population, which are given by the Malthusian Price equation (2.49), take the form

$$\dot{\bar{\boldsymbol{z}}} = \begin{bmatrix} \mathrm{Cov}_{i\in\mathbb{G}}(z_{i1}, m_i) \\ \mathrm{Cov}_{i\in\mathbb{G}}(z_{i2}, m_i) \end{bmatrix} + \begin{bmatrix} \mathrm{E}_{i\in\mathbb{G}}(\dot{z}_{i1}) \\ \mathrm{E}_{i\in\mathbb{G}}(\dot{z}_{i2}) \end{bmatrix}. \tag{6.12}$$

Note that we now have two rows in our Malthusian Price equation (2.49), one for each trait, and that we have both the first and third terms, the *natural selection* component

corresponding to the statistical association between the trait values held by individuals, z_{ik}, and their Malthusian fitness, m_i, as well as the *plasticity* component corresponding to the expected value of the change in phenotypic trait values, $\dot{z}_{ik}$. With these changes in place, let us now see what effect they have on the dynamics of natural selection.

In the previous model, we found that the resident genotype out-competes the migrant genotype and eventually dominates the population. In this model, however, this is no longer the case. Again, starting with the ecological perspective, we see that at the early stages of the numerical solution, the growth of both genotype is fairly similar to that which we observed before (compare Fig. 6.1A and 6.3A). However, as the population grows, we see that the migrant is now able to reproduce at a faster rate than the resident and hence it is this genotype that now comes to dominate the population (Fig. 6.3A). As before, the story of evolutionary, rather than ecological, change is told more clearly from the genotypic perspective by looking at how the relative frequency of the two genotypes changes over time (Fig. 6.3B). In the previous model, the relative abundances of both genotypes were monotonically increasing or decreasing functions of time, but we now see that the direction of change of these curves change as time proceeds corresponding to a change of direction in which genotype natural selection favours.

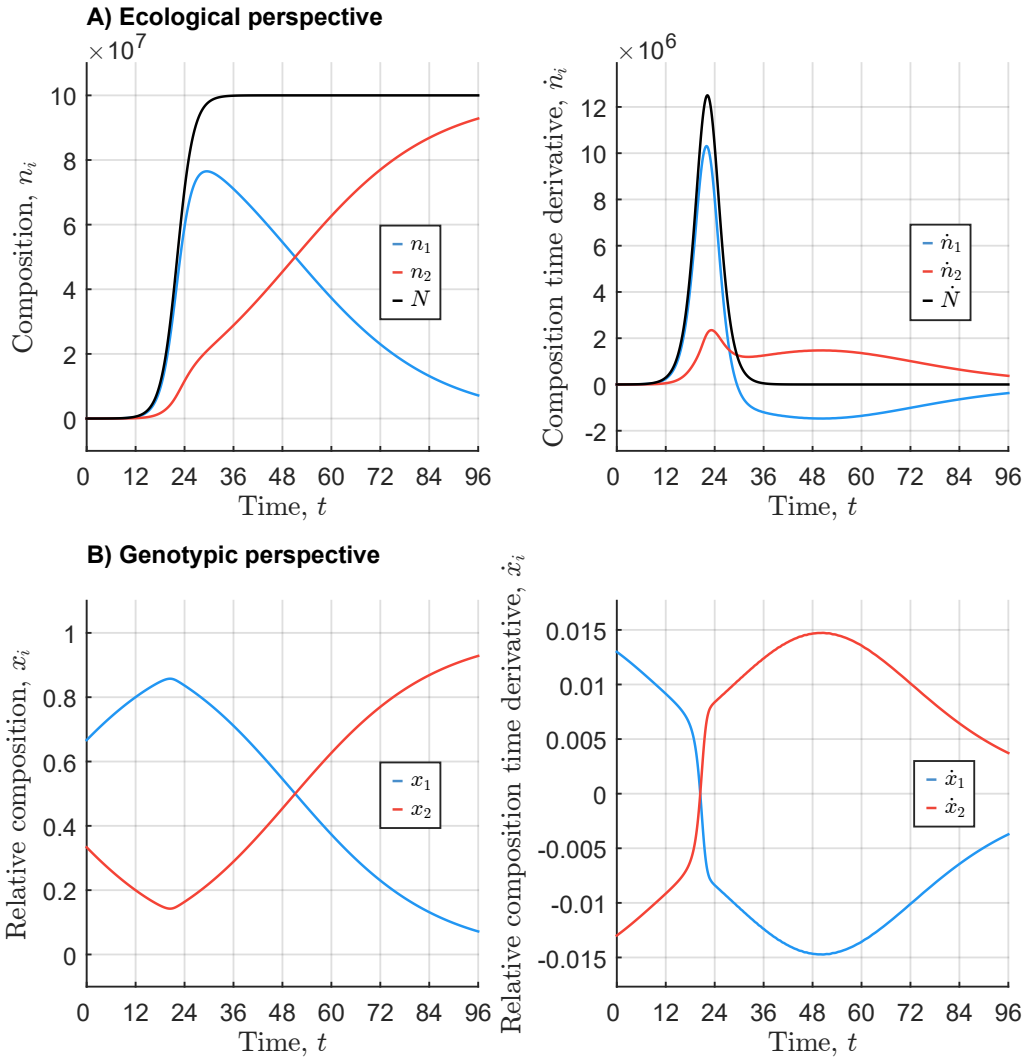


Figure 6.3: Ecological and genotypic perspective of phenotypic plasticity model dynamics. A) Ecological perspective on the dynamics. Note how the increasing growth rate of the migrant genotype allows it to begin to grow faster (at around $t = 24$) than the resident and eventually come to dominate the population. B) Genotypic perspective on the dynamics. Note the sudden change in direction of the trajectory of the relative genotypic frequencies around time $t = 24$, indicating that natural selection changes from favouring the resident to favouring the migrant genotype. All graphs are plotted over a period of 96 hours. Parameters used in the model were: $\rho = 1/2$, $\varsigma = 1/4$, $K = 1 \times 10^8$, and $\varphi = 5/K$.

As before, from the phenotypic perspective at the level of individuals there is no change in the first trait value. There is, however, now a change in the second trait value over time as we expect from our new model assumptions. Since the abundance of the resident genotype is positive from the start, we have $\dot{z}_{22} > 0$, and we see a corresponding increase in the second trait value by the migrant (Fig. 6.4A). We can think of this as the migrant increasing its competitiveness by up-regulating the value of this trait. The expression of this trait increases to a maximum value of $z_{22} = 1$ by time $t = 24$, at which point it ceases to change any more (Fig. 6.4A). Crucially, by this time the resident expresses a total phenotypic trait value of $z_{11} + z_{12} = 1$, whereas the migrant expresses a total phenotypic trait value of $z_{21} + z_{22} = 3/2$. Since the total phenotypic trait expression is related to the relative reproductive rate of the microbes, the migrant gains the upper-hand at this point.

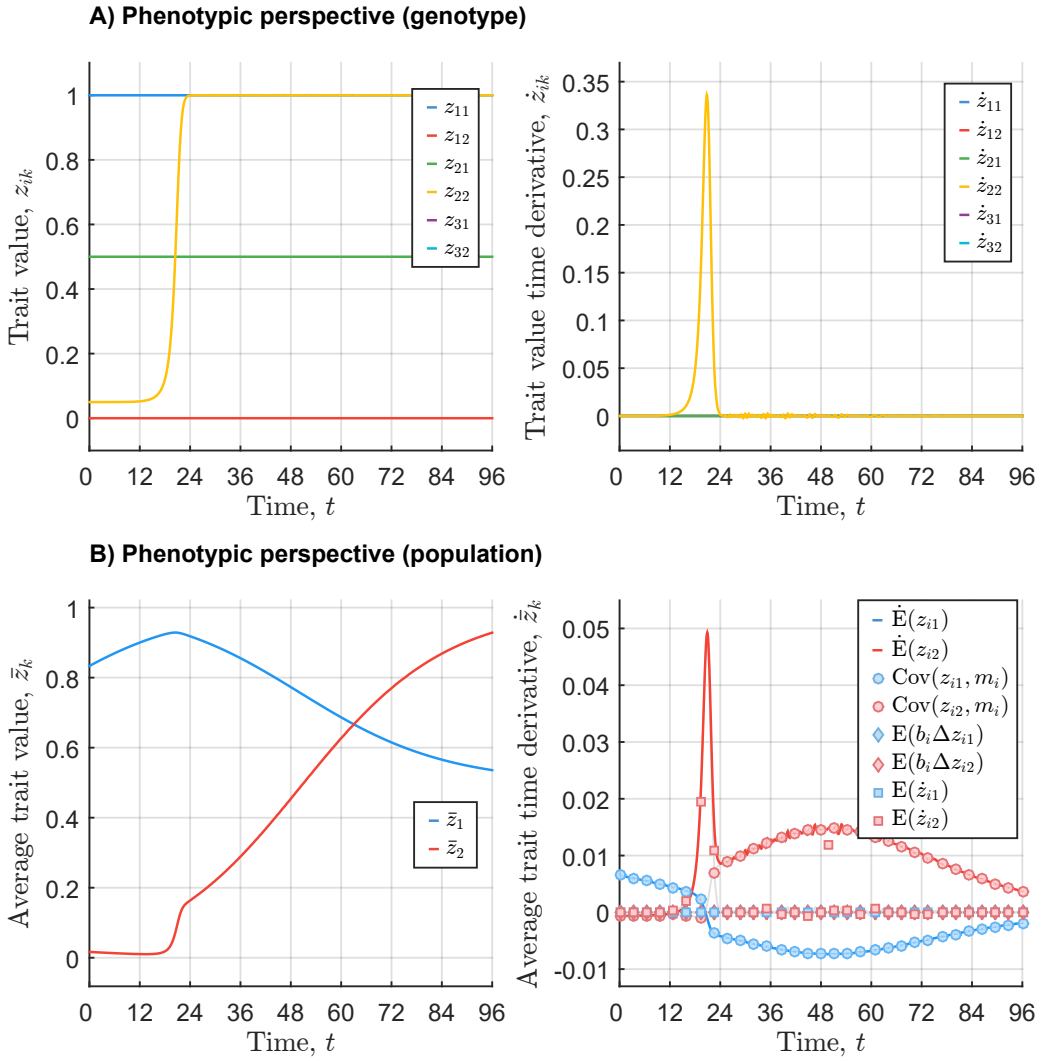


Figure 6.4: Phenotypic perspective of plasticity model dynamics. A) Phenotypic perspective on the dynamics at the level of the individual genotype. Note how the trait value z_{22} rapidly increases from its initial value $z_{22} = 1/20$ to a value of $z_{22} = 1$ by time $t = 24$. B) Phenotypic perspective on the dynamics at the population level. On the left, the average trait value in the population over time are plotted. On the right, the derivative of the average trait value in the population over time is shown, decomposed into three separate components corresponding to those from the Malthusian Price equation (2.49) from Chapter 2. Each component has a different interpretation: the covariance term $\mathrm{Cov}_{i\in\mathbb{G}}(z_{ik}, m_i)$ is the component of change in average trait value, $\bar{z}_k$, in the population we attribute to the action of *natural selection*; *ii*) the term reproduction-rate-weighted expectation $\mathrm{E}_{i\in\mathbb{G}}(b_i \Delta z_{ik})$ is the component of change in average trait values due to *transmission fidelity*; and *iii*) the expectation term $\mathrm{E}_{i\in\mathbb{G}}(\dot{z}_{ik})$ is the component of change due to *phenotypic plasticity* and *ecological inheritance*. The red lines demonstrate that change in the average trait value $\bar{z}_2$ is driven initially by the $\mathrm{E}_{i\in\mathbb{G}}(\dot{z}_{i2})$ component of the derivative corresponding to plasticity, but eventually by the $\mathrm{Cov}_{i\in\mathbb{G}}(z_{i2}, m_i)$ component of the derivative corresponding to natural selection. All graphs are plotted over a period of 96 hours. Parameters used in the model were: $\rho = 1/2$, $\varsigma = 1/4$, $K = 1 \times 10^8$, and $\varphi = 5/K$.

In addition to the individual trait values, the evolution of the average trait value across the population are now very interesting too. Initially, we see that it is the first trait value, $\bar{z}_1$, that is increasing on average in the population, before the second trait, $\bar{z}_2$, rapidly increases (Fig. 6.4B). In itself, this change only tells part of the story. As we discussed in Chapter 2, however, when we look at the derivatives of the average trait values, we can see that the increase in the second trait value is initially driven by the component of change corresponding to plasticity, $\mathrm{E}_{i\in\mathbb{G}}(\dot{z}_{i1})$, but eventually driven by the component of change corresponding to selection, $\mathrm{Cov}_{i\in\mathbb{G}}(m_i, z_{21})$ (Fig. 6.4B). Identifying these two different components of change is important, because evolutionary adaptations can only be brought about through selection. Thus, the initial change in trait value by the migrant does not correspond to selection, even though it eventually gives rise to a selective advantage. To identify whether or not selection favours phenotypic plasticity itself, one would need to look at the derivatives of the trait values to see if *they* covary with Malthusian fitness (strictly speaking the derivatives of trait values are traits in their own right, since they are a measurable property of an individual).

Before moving on to look at horizontal gene transfer, recall that we said above that the specification of the migrant trait value z_{22} as a type of logistic function of n_1 is not a particularly realistic model of phenotypic plasticity, since it does not account for times when microbes might benefit from decreasing their expression of the trait. A simple way to incorporate up- and down-regulation of the trait is to suppose that its expression depends not on the abundance of the resident genotype, n_1, but on the *rate of change* of the abundance of that genotype, $\dot{n}_1$. One way in which microbes might respond to the rate of change in abundance of other genotypes is through monitoring resource gradients. Many species of bacteria, for instance, are known to respond to variability in nutrient gradients through a process known as 'chemotaxis' in order to adapt the speed and direction of their motility (Sourjik and Wingreen, 2012). To incorporate this change, let us suppose that the derivative of the genotype-phenotype map is now given by

$$\dot{\mathbf{Z}} = \begin{bmatrix} 0 & 0 \\ 0 & \varphi\dot{n}_1 z_{22}(1-z_{22}) \end{bmatrix}. \tag{6.13}$$

Note the subtle change here from equation (6.11), that the second trait held by the migrant is now a function of $\dot{n}_1$ rather than n_1 as before. The assumption we are making here is therefore that the trait value z_{22} is a form of logistic function related to the rate of change in abundance of the resident genotype. As before, the parameter φ simply scales

the rate of change. With this seemingly minor tweak to our assumptions let us explore the dynamics once more.

In the last model, we found that the migrant genotype out-competes the resident genotype and eventually dominates the population. In this model, however, the result is different once more. In our previous models, the steady-states of the populations appeared to be represented by populations in which one or the other genotype dominates. In this model, however, something more interesting happens: the ecological perspective shows us that the population appears to tend towards a mixed equillibrium, supporting sub-populations of both genotypes (Fig. 6.5A). As in previous examples, the story of evolutionary change is told more clearly by looking at how the relative frequency of the two genotypes changes over time. Here, the genotypic perspective clearly shows us that the resident genotype initially out-competes the migrant, but that this benefit does not last for long before the two genotypes approach a steady-state relative frequency of roughly 60% and 40%, respectively (Fig. 6.5B).

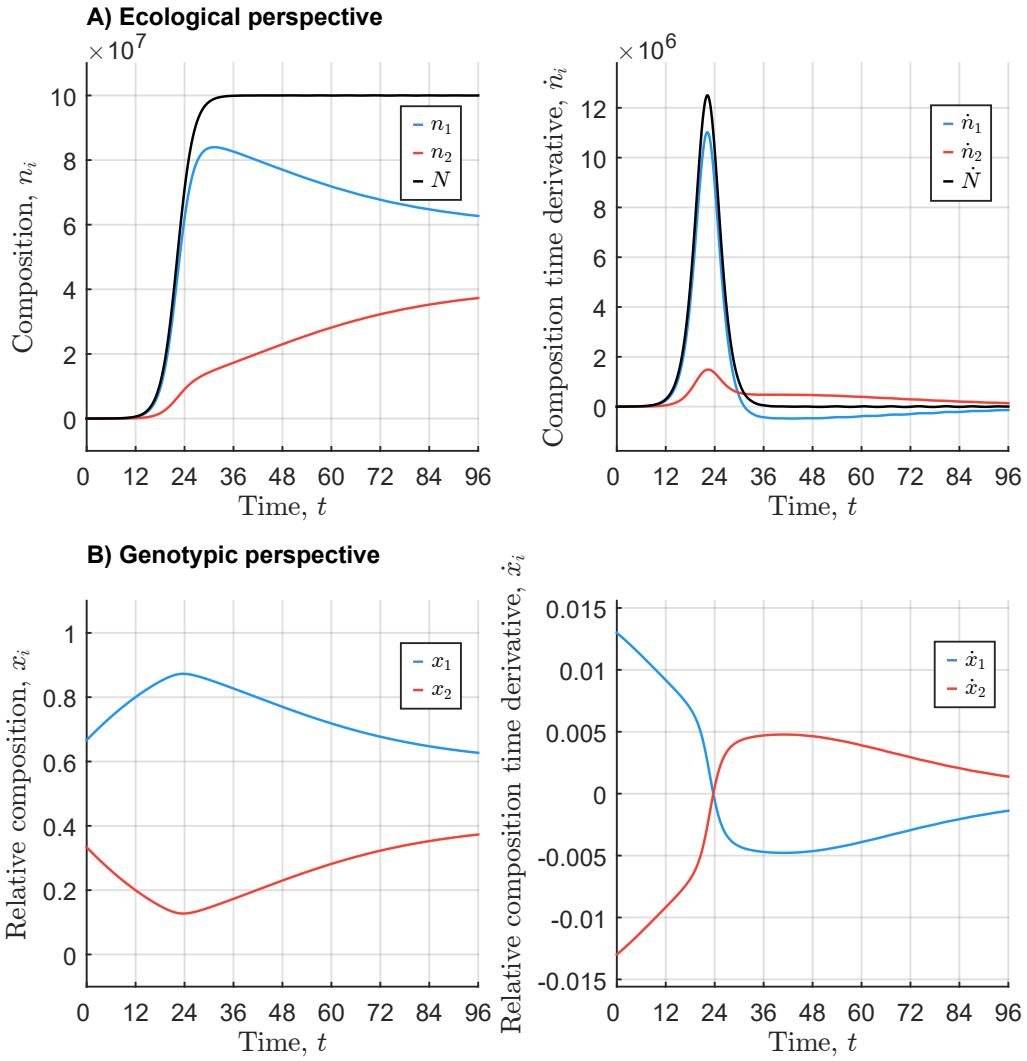


Figure 6.5: Ecological and genotypic perspective of second plasticity model dynamics. A) Ecological perspective on the dynamics. Note how the absolute abundances of both genotypes tends towards a positive value representing a proportion of the total population size—a mixed equillibrium—rather than one genotype or the other coming to dominate the population and the other going extinct. B) Genotypic perspective on the dynamics. Note how between time $t = 0$ and time $t = 24$ natural selection favours the resident genotype, and then how it shifts to favour the migrant genotype between time $t = 24$ and $t = 96$, but to a lesser and lesser extent. Parameters used in the model were: $\rho = 1/2$, $\varsigma = 1/4$, $K = 1 \times 10^8$, and $\varphi = 5/K$.

We can see more clearly why the population approaches a mixed equilibrium between the two genotypes by exploring the phenotypic perspective. The migrant genotype up-regulates the expression of its second trait as the resident genotype undergoes growth (i.e. with $\dot{n}_1 > 0$). When, however, the increased expression of the trait gives the migrant genotype a selective advantage, the resident decreases its expression of the trait, which decreases its selective advantage. This feedback loop continues until there is no change in the system, which appears to occur, as one might predict, when the expression of the second trait by the migrant approaches a level that gives the two genotypes equivalent *total* phenotypic trait values (albeit of different traits) (Fig. 6.6A).

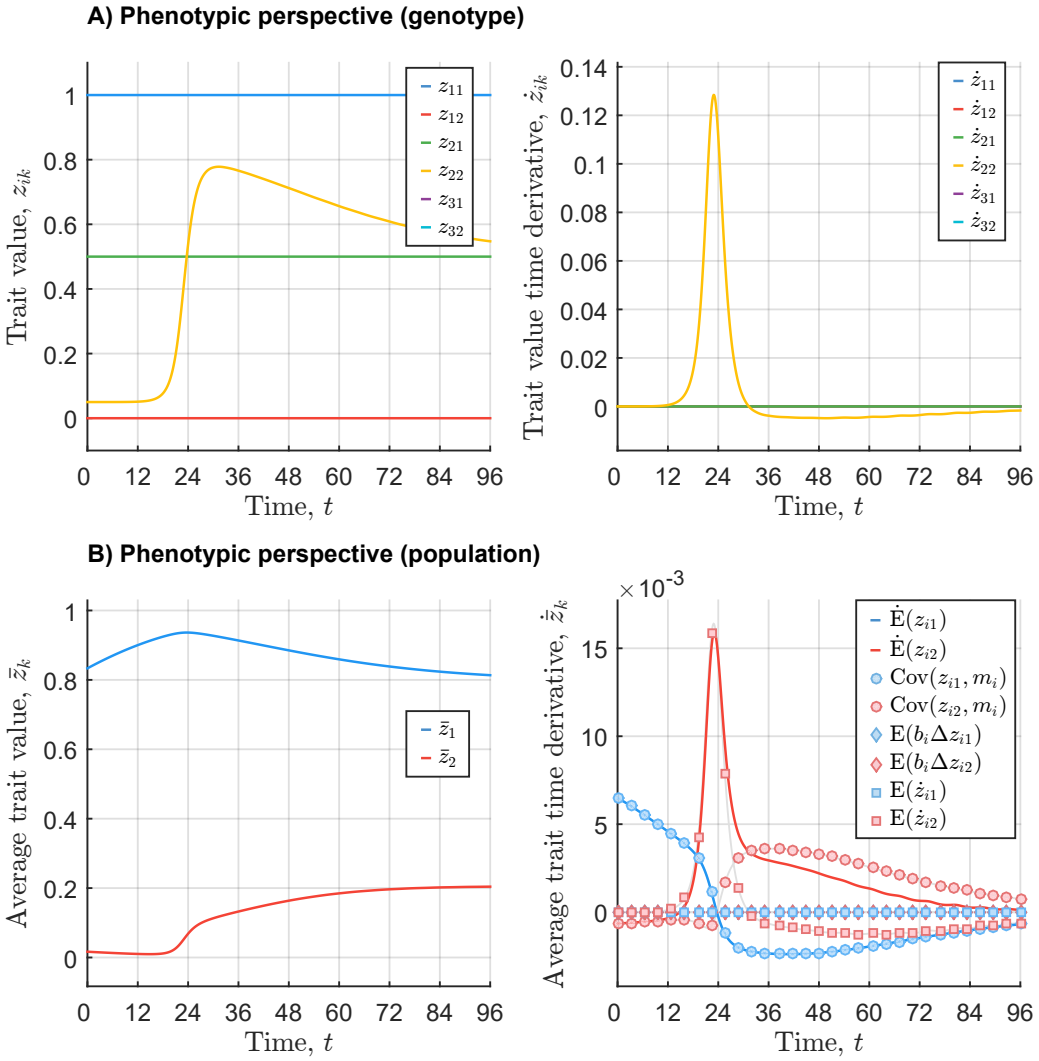


Figure 6.6: Phenotypic perspective of second plasticity model dynamics. A) Phenotypic perspective on the dynamics at the level of the individual genotype. Note how the trait value z_{22} held by the migrant initially increases up to time $t = 24$ before tending towards a value of $z_{22} = 1/2$ by time $t = 96$. B) Phenotypic perspective on the dynamics at the population level. On the left, the average trait value in the population over time are plotted. On the right, the derivative of the average trait value in the population over time is shown, decomposed into three separate components corresponding to those from the Malthusian Price equation (2.49) from Chapter 2. Each component has a different interpretation: the covariance term $\mathrm{Cov}_{i\in\mathbb{G}}(z_{ik}, m_i)$ is the component of change in average trait value, $\bar{z}_k$, in the population we attribute to the action of *natural selection*; *ii*) the term reproduction-rate-weighted expectation $\mathrm{E}_{i\in\mathbb{G}}(b_i \Delta z_{ik})$ is the component of change in average trait values due to *transmission fidelity*; and *iii*) the expectation term $\mathrm{E}_{i\in\mathbb{G}}(\dot{z}_{ik})$ is the component of change due to *phenotypic plasticity* and *ecological inheritance*. Note that the average trait value $\bar{z}_2$ is pulled in different directions by the different components of selection after time $t = 24$. At this time the $\mathrm{E}_{i\in\mathbb{G}}(\dot{z}_{i2})$ component of the derivative corresponding to plasticity is negative indicating the trait is on average being down-regulated, but the $\mathrm{Cov}_{i\in\mathbb{G}}(z_{i2}, m_i)$ component of the derivative is positive indicating that selection favours an increase in the trait. All graphs are plotted over a period of 96 hours. Parameters used in the model were: $\rho = 1/2$, $\varsigma = 1/4$, $K = 1 \times 10^8$, and $\varphi = 5/K$.

Of course, with a mixed equilibrium being approached, the average trait value changes are now much less pronounced (Fig. 6.6B), but once more we can gain a clearer understanding of the evolutionary dynamics by observing the different components of change from the Malthusian Price equation (2.49) (Fig. 6.6B).

6.2.3 Model incorporating phenotpyic plasticity and horizontal gene transfer

In the previous models, we assumed that the population consisted of two genotypes, namely a resident and a migrant (so that we had $|\mathbb{G}| = 2$). Now let us assume that the migrant genotype carries with it a transmissible plasmid on which the gene(s) encoding the second trait are carried. Upon transferring its plasmid to one of the resident microbes, a new genotype is created (so that we now have $|\mathbb{G}| = 3$), that we will call the 'transformed' genotype. Since the possession of the the plasmid is also something measurable about a genotype, it is also a trait in the overall phenotype of each microbe (as is any other genetic feature), so that we now also have $|\mathbb{P}| = 3$. At time $t = 0$, we initialise the population as before, but we now specify that there are $n_3 = 0$ microbes of the transformed genotype. The genotype-phenotype map at time $t = 0$ is now given by

$$\mathbf{Z} = \begin{bmatrix} 1 & 0 & 0 \\ 1/2 & 1/20 & 1 \\ 1 & 1/20 & 1 \end{bmatrix}, \tag{6.14}$$

such that the transformed genotype expresses the same level of the first trait as the resident, $z_{31} = z_{11}$, and the same level of expression of the second trait as the migrant, $z_{32} = z_{22}$. For a transformed genotype to be created in the first place, we need to model a rate of horizontal gene transfer, which we can assume is relatively rapid (Dionisio et al., 2002). As we discussed in Chapter 2, a transfer event can be thought of as the reproduction of both a resident and migrant, followed by the immediate death of the resident and the immediate production of a transformed genotype. What matters in terms of the dynamics of the population is that we capture the change in the composition of the population, $\boldsymbol{n}$, induced by transfer events correctly.

In order that the transfer can happen, we must assume that residents and migrants interact at some rate. For simplicity, we shall we assume that the rate at which a given resident meets any migrant is x_2 (that is, proportional to the relative frequency of the

migrant genotype in the population). Equivalently, the rate at which a given migrant meets a resident is x_1. When an interaction has occurred, the rate at which the plasmid is transferred is given by a parameter ζ. As we discussed in Chapter 2, we normalise the rate at which transfer happens by multiplying by the ratio of 'descendants' produced over the number of 'ancestors' involved in the transfer. In this case, we multiply by 1/2 since a horizontal transfer event involves a single descendant and two ancestors. Putting this all together with the models we introduced previously, we initialise the fidelity rate matrix for this population with

$$\mathbf{F} = \begin{bmatrix} \rho\left(\frac{(1-\varsigma)+\varsigma(z_{11}+z_{12})}{(1-\varsigma)+\varsigma(\bar{z}_1+\bar{z}_2)}\right) & \frac{1}{2}\zeta x_2 & 0 \\ 0 & \rho\left(\frac{(1-\varsigma)+\varsigma(z_{21}+z_{22})}{(1-\varsigma)+\varsigma(\bar{z}_1+\bar{z}_2)}\right) & \frac{1}{2}\zeta x_1 \\ 0 & 0 & \rho\left(\frac{(1-\varsigma)+\varsigma(z_{31}+z_{32})}{(1-\varsigma)+\varsigma(\bar{z}_1+\bar{z}_2)}\right) \end{bmatrix}. \tag{6.15}$$

Note that we now have non-zero off-diagonal entries in the fidelity rate matrix indicating that the inheritance matrix, $\mathbf{H}$, will not be equivalent to the identity matrix. We will come back to this in a moment. First, let us note that vector of reproduction rates and vector of production rates are given by

$$\boldsymbol{b} = \begin{bmatrix} \rho\left(\frac{(1-\varsigma)+\varsigma(z_{11}+z_{12})}{(1-\varsigma)+\varsigma(\bar{z}_1+\bar{z}_2)}\right) + \frac{1}{2}\zeta x_2 \\ \rho\left(\frac{(1-\varsigma)+\varsigma(z_{21}+z_{22})}{(1-\varsigma)+\varsigma(\bar{z}_1+\bar{z}_2)}\right) + \frac{1}{2}\zeta x_1 \\ \rho\left(\frac{(1-\varsigma)+\varsigma(z_{31}+z_{32})}{(1-\varsigma)+\varsigma(\bar{z}_1+\bar{z}_2)}\right) \end{bmatrix}, \quad \text{and} \quad \boldsymbol{p} = \begin{bmatrix} \rho n_1\left(\frac{(1-\varsigma)+\varsigma(z_{11}+z_{12})}{(1-\varsigma)+\varsigma(\bar{z}_1+\bar{z}_2)}\right) \\ \rho n_2\left(\frac{(1-\varsigma)+\varsigma(z_{21}+z_{22})}{(1-\varsigma)+\varsigma(\bar{z}_1+\bar{z}_2)}\right) \\ \zeta N x_1 x_2 + \rho n_3\left(\frac{(1-\varsigma)+\varsigma(z_{31}+z_{32})}{(1-\varsigma)+\varsigma(\bar{z}_1+\bar{z}_2)}\right) \end{bmatrix}, \tag{6.16}$$

respectively. As in previous models, we take the rate of death of each genotype to be proportional to the ratio of the population size to its carrying capacity. Additionally, however, in this model we have a source of 'death' for the resident genotype, since its abundance is decreased when horizontal gene transfer events take place. Thus, the death rate vector $\boldsymbol{d}$ is given by

$$\boldsymbol{d} = \begin{bmatrix} \rho\frac{N}{K} + \zeta x_2 \\ \rho\frac{N}{K} \\ \rho\frac{N}{K} \end{bmatrix}. \tag{6.17}$$

Although the abundance of the resident genotype is decreased by a type of 'death', this is clearly exactly offset by the increase in abundance of the transformed genotype due to a type of 'birth'. Hence, despite the difference in the death rate vector, $\boldsymbol{d}$, there is no net increase or decrease of microbes resulting from horizontal gene transfer, and the average rate of reproduction in the population is still $\bar{b} = \rho$, and the average rate of death is still given by $\bar{d} = \rho N/K$.

Unlike in previous models, however, the inheritance matrix for this population is not simply the identity matrix, $\mathbf{H} \neq \mathbf{I}$, since horizontal gene transfer acts like a type of reproduction in which descendants are produced that are defined by different units of information to their ancestors. Here we have

$$\mathbf{H} = \begin{bmatrix} \frac{1}{1+\frac{\zeta x_2((1-\varsigma)+\varsigma(\bar{z}_1+\bar{z}_2))}{2\rho((1-\varsigma)+\varsigma(z_{11}+z_{12}))}} & \frac{1}{1+\frac{2\rho((1-\varsigma)+\varsigma(z_{11}+z_{12}))}{\zeta x_2((1-\varsigma)+\varsigma(\bar{z}_1+\bar{z}_2))}} & 0 \\ 0 & \frac{1}{1+\frac{\zeta x_1((1-\varsigma)+\varsigma(\bar{z}_1+\bar{z}_2))}{2\rho((1-\varsigma)+\varsigma(z_{21}+z_{22}))}} & \frac{1}{1+\frac{2\rho((1-\varsigma)+\varsigma(z_{21}+z_{22}))}{\zeta x_1((1-\varsigma)+\varsigma(\bar{z}_1+\bar{z}_2))}} \\ 0 & 0 & 1 \end{bmatrix}. \tag{6.18}$$

Again, it is worth noting that since the the average Malthusian fitness in the population is given by $\bar{m} = \bar{b} - \bar{d}$, and the average rates of reproduction and death have not changed, the rate of change of the overall population size is still given by

$$\dot{N} = \rho N \left(1 - \frac{N}{K}\right). \tag{6.19}$$

Finally, as we specified in the model description, the second phenotypic trait has a degree of plasticity such that its value changes through time. The derivative of the genotype-phenotype map in this model is therefore given by

$$\dot{\mathbf{Z}} = \begin{bmatrix} 0 & 0 & 0 \\ 0 & \varphi\dot{n}_1 z_{22}(1-z_{22}) & 0 \\ 0 & \varphi\dot{n}_1 z_{22}(1-z_{22}) & 0 \end{bmatrix}. \tag{6.20}$$

Again, this assumption means that as the abundance of the resident genotype changes, so too does the trait values of any genotype holding the plasmid. In other words, the plasmid trait has a density- and frequency-dependence associated with its expression.

Since the inheritance matrix, $\mathbf{H}$, is no longer simply given by the identity matrix, $\mathbf{I}$, the change in the average phenotypic trait values in the population, which are given by the Malthusian Price equation (2.49), now take the form

$$\dot{\bar{\boldsymbol{z}}} = \begin{bmatrix} \mathrm{Cov}_{i\in\mathbb{G}}(z_{i1}, m_i) \\ \mathrm{Cov}_{i\in\mathbb{G}}(z_{i2}, m_i) \\ \mathrm{Cov}_{i\in\mathbb{G}}(z_{i3}, m_i) \end{bmatrix} + \begin{bmatrix} \mathrm{E}_{i\in\mathbb{G}}(b_i \Delta z_{i1}) \\ \mathrm{E}_{i\in\mathbb{G}}(b_i \Delta z_{i2}) \\ \mathrm{E}_{i\in\mathbb{G}}(b_i \Delta z_{i3}) \end{bmatrix} + \begin{bmatrix} \mathrm{E}_{i\in\mathbb{G}}(\dot{z}_{i1}) \\ \mathrm{E}_{i\in\mathbb{G}}(\dot{z}_{i2}) \\ \mathrm{E}_{i\in\mathbb{G}}(\dot{z}_{i3}) \end{bmatrix}. \tag{6.21}$$

We now have three rows in our Malthusian Price equation (2.49), one for each trait, and we have all three terms: the *natural selection* component corresponding to the statistical association between the trait values held by individuals, z_{ik}, and their Malthusian fitness, m_i, the *transmission fidelity* component corresponding to the average difference in trait values expressed by ancestors and their descendants, $b_i \Delta z_{i1}$, and the *phenotypic plasticity* component corresponding to the expected value of the change in phenotypic trait values, $\dot{z}_{ik}$. With these changes in place, let us now see what effect they have on the dynamics of natural selection.

In the previous model, we found that the migrant genotype and the resident genotype formed a stable mixed equilibrium when the migrant expresses a plastic trait that is responsive to the rate of growth of the resident. In this model, once more, we now find that things are very different when we introduce horizontal gene transfer into the system. In particular, although the rate of horizontal gene transfer is low relative to the reproduction rate (we specify one horizontal gene transfer event per 100 interactions among microbes, $\zeta = 0.01$), we see from the ecological perspective that the transformed genotype (comprising information from both the resident and the migrant) now establishes itself as the dominant genotype (Fig. 6.7A). By looking at the genotypic perspective (Fig. 6.7B), we

can see that there are points when natural selection favours each of the different genotypes, but that it *consistently* favours the transformed genotype (that is, the function describing the change in relative frequency of the transformed genotype monotonically increases).

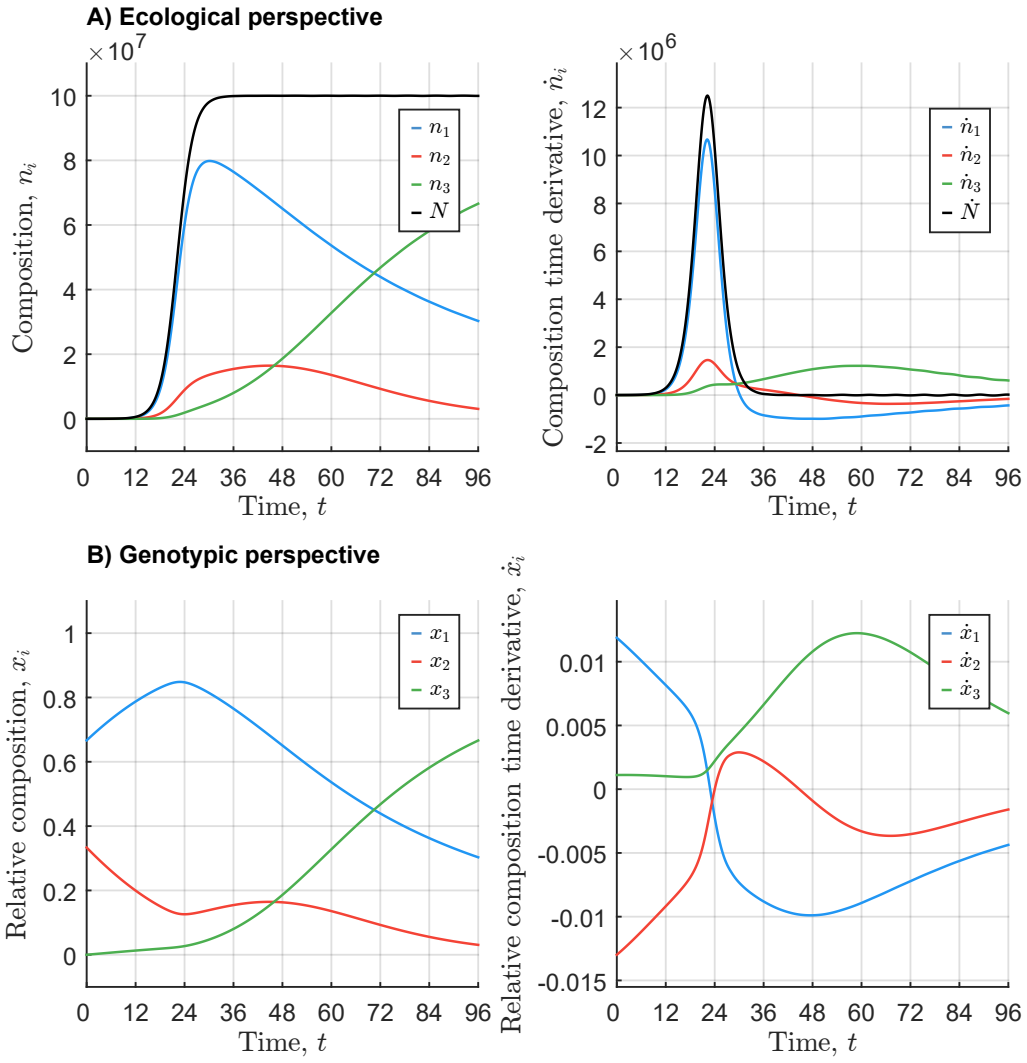


Figure 6.7: Ecological and genotypic perspective of plasticity and horizontal gene transfer model dynamics. A) Ecological perspective on the dynamics. Note that despite starting with an initial abundance of $n_3 = 0$ the transformed genotype outcompetes the other two genotypes to dominate the population. B) Genotypic perspective on the dynamics. Note how natural selection favours all three genotypes at particular points in time, so that $x_1, x_2, x_3 > 0$ at certain times, but *consistently* favours the transformed genotype (i.e. $x_3 > 0 \ \forall t$). All graphs are plotted over a period of 96 hours. Parameters used in the model were: $\rho = 1/2$, $\varsigma = 1/4$, $K = 1 \times 10^8$, $\varphi = 5/K$, and $\zeta = 0.01$.

When looking to the phenotypic dynamics for individual genotypes, we see little difference from the previous model, as we would expect (Fig. 6.8A).

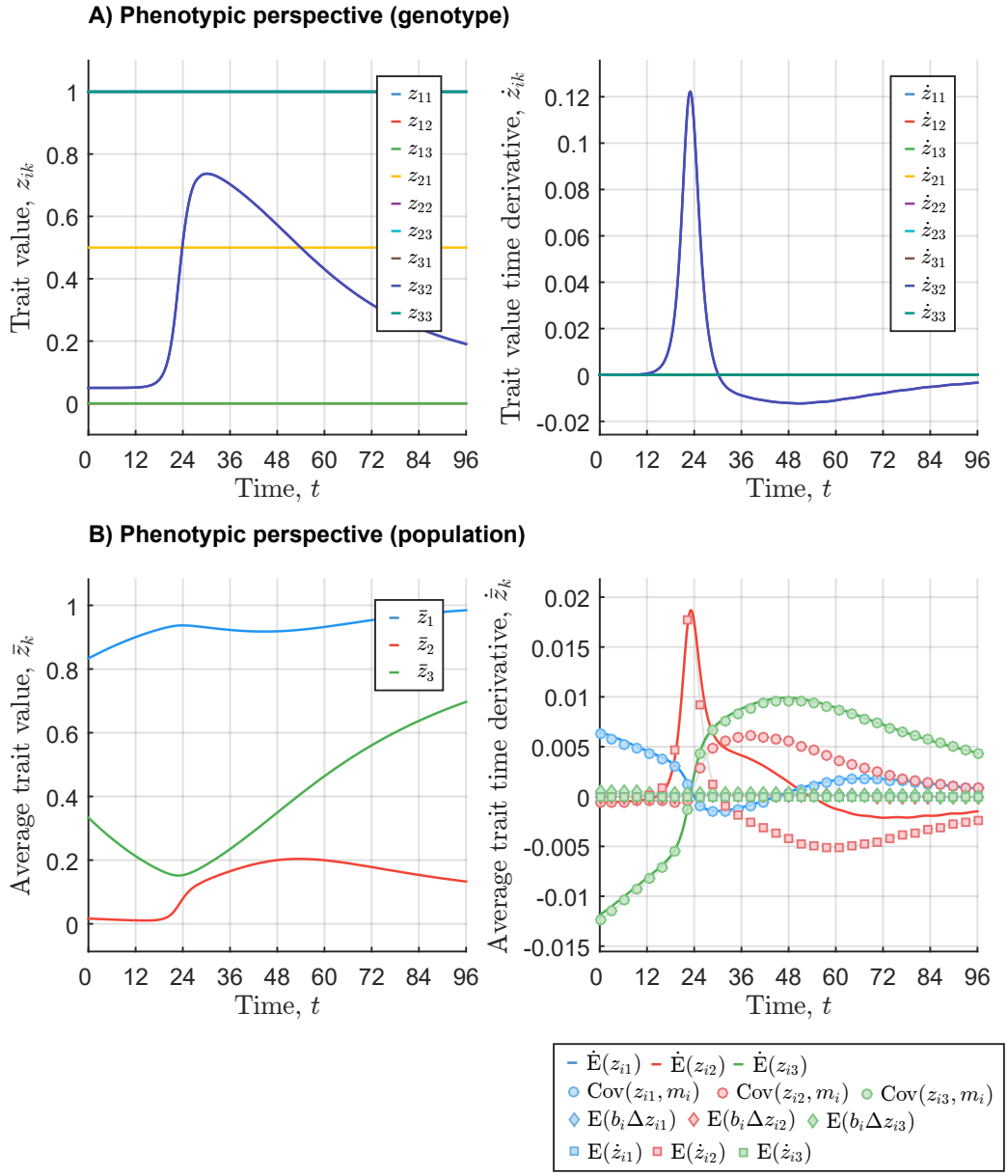


Figure 6.8: Phenotypic perspective of plasticity and horizontal gene transfer model dynamics. A) Phenotypic perspective on the dynamics at the level of the individual genotype. B) Phenotypic perspective on the dynamics at the population level. On the left, the average trait value in the population over time are plotted. On the right, the derivative of the average trait value in the population over time is shown, decomposed into three separate components corresponding to those from the Malthusian Price equation (2.49) from Chapter 2. Each component has a different interpretation: the covariance term $\mathrm{Cov}_{i\in\mathbb{G}}(z_{ik}, m_i)$ is the component of change in average trait value, $\bar{z}_k$, in the population we attribute to the action of *natural selection*; *ii*) the term reproduction-rate-weighted expectation $\mathrm{E}_{i\in\mathbb{G}}(b_i \Delta z_{ik})$ is the component of change in average trait values due to *transmission fidelity*; and *iii*) the expectation term $\mathrm{E}_{i\in\mathbb{G}}(\dot{z}_{ik})$ is the component of change due to *phenotypic plasticity* and *ecological inheritance*. Note that some lines are not visible because the trajectories are hidden by lines of a different colour following the same trajectory. Parameters used in the model were: $\rho = 1/2$, $\varsigma = 1/4$, $K = 1 \times 10^8$, $\varphi = 5/K$, and $\zeta = 0.01$.

When looking to the phenotypic dynamics at the population level, however, one might expect that the changes in abundance of transformed genotype might drive a significant portion of change in phenotypes due to a transmission bias (i.e change in time of the component $\mathrm{E}_{i\in\mathbb{G}}(b_i\Delta z_{ik})$ in the Malthusian Price equation (2.49)) owing to horizontal gene transfer. Yet we see that this is clearly not the case when looking at the components of the change over time. Instead, selection (i.e change in time of the selection differential, $\mathrm{Cov}_{i\in\mathbb{G}}(z_{ik}, m_i)$) is the overriding driver of changes in the average phenotypic values in the population over time (Fig. 6.8B).

6.3 The dynamics of the evolutionary response to natural selection in populations with mutation and phenotypic plasticity

In our second example, we develop a series of relatively simple models designed to highlight some of the important characteristics of the dynamical systems theory from Chapter 3 when it is applied in the form of a streamlined methodology. In particular, we develop models of an asexually reproducing population of microbes that incorporates phenotypic plasticity, and details about genetic systems including epistasis and mutation.

Epistatic gene interactions are thought to be commonplace in the natural world (Mackay, 2014). They arise as a natural consequence of the evolution of the complex genetic architectures that comprise the molecular networks of most living things (Phillips, 2008). In theory, epistatic interactions between genetic loci should lead to a substantial amount of non-additive genetic variance in populations. Since natural selection acts on additive genetic variance in populations, it is therefore a matter of considerable debate among evolutionary theorists how gene interactions shape the course of adaptive evolution (Paixão and Barton, 2016).

One issue is that in the absence of epistatic interactions, natural selection should quickly exhaust genetic variation for traits, leading a population rapidly to a locally 'optimum' phenotype. It is therefore thought that epistatic interactions might influence adaptive evolution by prolonging the evolutionary response to natural selection in populations, providing new sources of genetic variance on which natural selection can continually act (Carlborg et al., 2006). The idea is that mutation or recombination brings together new sets of genes with an effect on the fitness of individuals that it is somewhat unpredictable (for it depends crucially on their genetic background). Thus, instead of reducing the additive genetic variation in natural populations, there is a growing appreciation that

epistatically interacting loci might actually *contribute* to the creation of the apparent, that is, statistical, additive genetic variance that we observe in natural populations (Mackay, 2014).

Whilst the role of mutation in shaping genetic variance in populations has been considered for some time, there is comparatively little research on the impact of phenotypic plasticity on genetic variance in populations. Two possibilities are that phenotypic plasticity might: *i*) enable different genotypes to each create a niche for themselves leading to an environment that supports increased genetic variance; or *ii*) enable certain genotypes to rapidly adapt and out-compete other variants leading to a collapse of genetic variance. Yet difficulties understanding how the **G**-matrix (which determines genetic variance in populations) evolves over time under different types of model have limited the extent to which the possibilities have been explored.

To explore some of these ideas in the context of the dynamical systems theory of natural selection, our focus will be on the dynamics of the **G**-matrix and its movement on the adaptive landscape. This will allow us to explore the utility of viewing the dynamics of natural selection using some of the key principles of evolutionary genetics. By studying the dynamics of **G**-matrix evolution, we demonstrate how mutation and phenotypic plasticity can act in concert with epistasis to alter the timescales of selection and lead a population to different peaks on the adaptive landscape.

6.3.1 Model with genetic details, but no phenotypic plasticity and no mutation

We build on the models developed in the last section, keeping the assumption that the traits held by microbes in our population influence their relative reproductive rate. For now, we return to the simple case where there is no phenotypic plasticity (so that $\dot{\mathbf{Z}} = \mathbf{0}$) and no mutation or horizontal gene transfer (so that $\mathbf{H} = \mathbf{I}$). We modify the previous models, however, by supposing that we now have a limited amount of information about the genetic features held by different genotypes. In particular, we suppose that we have two loci of interest ($|\mathbb{L}| = 2$), and take it to be the case that the genetic features may be in an 'active' or 'inactive' form so that we have four genotypes ($|\mathbb{G}| = 4$). The matrix of genetic features corresponding to this system is given by

$$\mathbf{\Lambda} = \begin{bmatrix} 1 & 1 \\ 1 & 0 \\ 0 & 1 \\ 0 & 0 \end{bmatrix}, \tag{6.22}$$

where the first row identifies a genotype that we can think of as the being the 'wild-type' (since it carries active forms of the genetic features of interest at both loci), and the remaining rows identify genotypes that can be thought of as single and double 'mutants', respectively. The composition of the population at time $t = 0$ is given by $\boldsymbol{n} = (1000, 500, 0, 100)^{\mathrm{T}}$. For the sake of incorporating assumptions about epistasis into the model, we assume there are two traits of interest to us ($|\mathbb{P}| = 2$) with a genotype-phenotype map at time $t = 0$ of the form

$$\mathbf{Z} = \begin{bmatrix} 3 & 0 \\ 1 & 0 \\ 1 & 2 \\ 0 & 1 \end{bmatrix}. \tag{6.23}$$

Note that in specifying the matrices $\mathbf{\Lambda}$ and $\mathbf{Z}$ in this way, the causal relationship between the genetic features and phenotypic trait values is represented *implicitly*. Had we wanted to, we could have defined the trait values as *explicit* functions of the genetic features (as well as the composition of the population, $\boldsymbol{n}$, and time, t). This would require us to incorporate detailed knowledge detailed knowledge about genetic details and molecular pathways into our example. The case we have represented therefore resembles the kind of situation evolutionary biologists often find themselves in when studying natural populations, whereby they have access to a degree of detail about the characteristics of genotypes and phenotypes, but limited knowledge about the true underlying causal relationship(s) that connects them.

Although we have not defined the relationship between genotypes and phenotypes explicitly, we can try to infer something about the possible relationships between them. In particular, let us try to infer something about the potential for *epistatic interactions* between the genetic features at the two loci. Inference about epistatic interactions between

loci is usually made on the basis of whether or not the effect of a genetic feature at one locus depends upon the presence or absence of genetic features at other loci. If there is a dependence, then epistatic mutations will tend to have different effects in combination than individually. In other words, epistatic mutations will mean that the effect of double mutants cannot be predicted from a simple additive model of the effects measured on single mutants.

Using this definition here we find that with respect to the first trait, the mapping between each genotype and the trait represents an example of 'positive' mutational epistasis, since all single mutant genotypes express a lower trait value than the wild-type, $z_{11} > z_{21} = z_{31} > z_{41}$, but the double mutant has a higher than expected level of trait value than that we would predict from an additive model alone, $(z_{41} - z_{11}) > (z_{21} - z_{11}) + (z_{31} - z_{11})$. The mapping between each genotype and the second trait, on the other hand, represents an example of 'negative' mutational epistasis, since the mutant genotypes tend to express a higher trait value than the wild-type, $z_{32} > z_{42} > z_{22} > z_{12}$, and the double mutant has a lower than expected level of trait value than that we would predict from an additive model alone, since $(z_{42} - z_{12}) < (z_{32} - z_{12}) + (z_{22} - z_{12})$.

Now that we have a specified a simple model inclusive of information about the genetic features held by different genotypes, let us explore how the dynamics of natural selection play out. In the absence of processes that help generate diversity, quantitative genetic theory predicts that a population will quickly exhaust its genetic variation and come to rest at a steady-state (Falconer and Mackay, 1995). In Figure 6.9 we show the dynamics of the average trait values in the population from the perspective of an adaptive landscape (the space of average trait values, $\bar{\boldsymbol{z}}$).

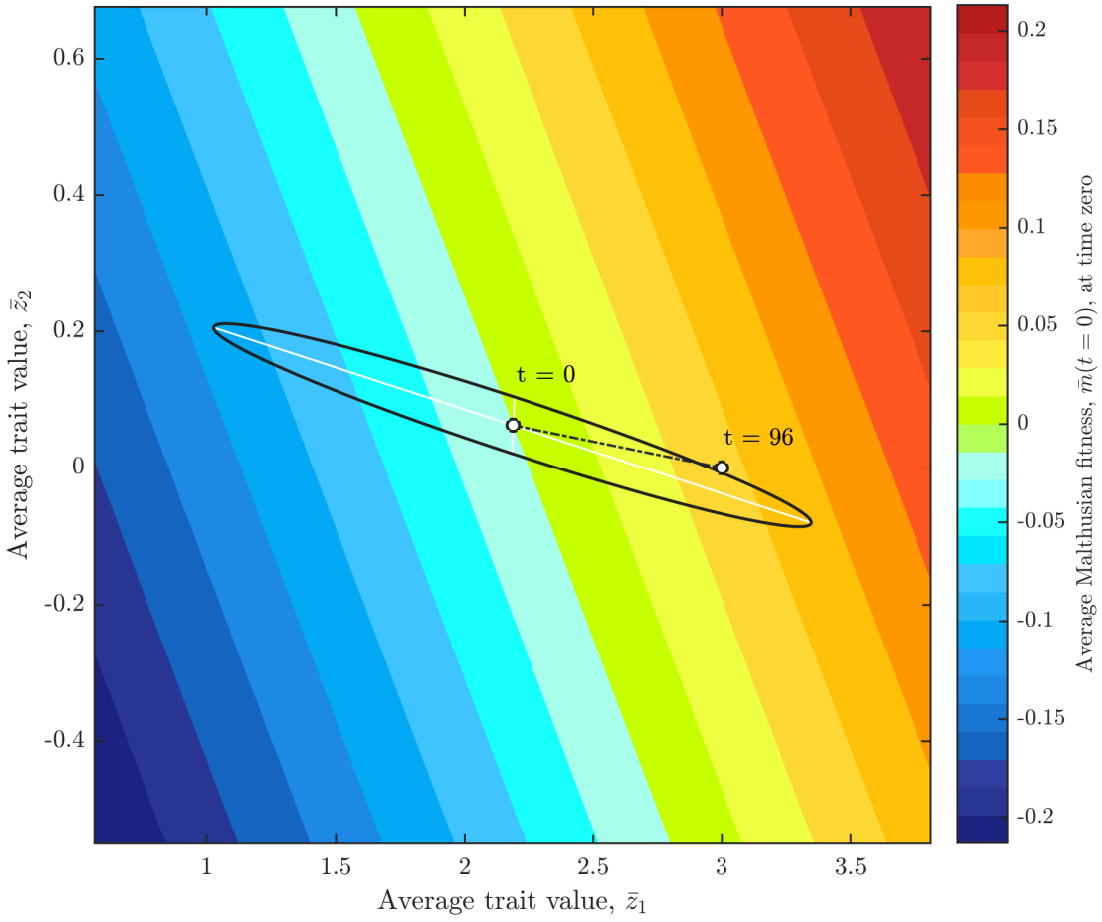


Figure 6.9: G-matrix evolution. The first order term of the linear approximation to the adaptive landscape at time $t = 0$ is illustrated by the contour map (which is represented as a plane in 2-dimensional trait space). The population average trait values, $\bar{\boldsymbol{z}}$ at time $t = 0$ (light grey) and time $t = 96$ (dark grey) are plotted as circles on the landscape, and the **G**-matrix of additive genetic variance is represented at time $t = 0$ and $t = 96$ as an ellipse centred at the average trait values. The change in population average trait values over time is indicated by a trajectory represented by a dashed black line. Parameters used in the model were: $\rho = 1/2$, $\varsigma = 1/4$, and $K = 1 \times 10^8$.

The contour map indicates that at time $t = 0$ microbes expressing higher trait values tend to have a higher fitness. Over the short-term, we should therefore expect that selection drives changes in the population composition which lead to an increase in the average trait values. The trajectory of the population over time confirms that there is indeed such an increase, but that the observed change is not in the direction of steepest ascent on the landscape.

That is because the direction is naturally guided by a trade-off between the direction of steepest ascent and the genetic line of least resistance, which corresponds to the leading *eigenvector* of the **G**-matrix (the major axis of the ellipse) (Schluter, 1996). These factors influencing the trajectory are both themselves continually changing through time. We cannot see the change in the approximation to the adaptive landscape given by the contour map because Figure 6.9 is static. We can, however, plot the ellipse representing the **G**-matrix at multiple points along the trajectory of the population (large ellpise centred at the light grey circle). In doing so, we see that its shape changes considerably over time, shrinking from a large elongated ellipse at time $t = 0$, to a circle too small to see at time $t = 96$. This indicates that genetic variance in both phenotypic traits has decreased dramatically between the two time points.

The final resting point of the population at time $t = 96$ is thus best explained by the fact that our assumptions have constrained the 'optimal' phenotype available for natural selection to discover. In particular, adaptive evolution is constrained in our model by the set of all possible genotypes, by the absence of mutation and phenotypic plasticity, and by the initial composition of the population. Both the wild-type and the second single loss-of-function mutant express the same overall level of traits ($z_{11} + z_{12} = z_{31} + z_{32}$) and so should be equally fit, but since there are no microbes of this mutant genotype in the population at time $t = 0$, and no means by which this genotype can come into existence through mutation, the movement of the population is toward the trait values held by the wild-type. There isn't a genotype that expresses an infinite level of both traits, and so the best natural selection can achieve is to carry the population as far up the slope of average Malthusian fitness, $\bar{m}$, as the genetic variation available, **G**, allows for. It is only if there were no genetic constraints on phenotypic evolution (a key assumption of the phenotypic gambit approach (Grafen, 1984)) that adaptive evolution would carry the population up the slope in the direction of steepest ascent.

The importance of using this approach in conjunction with a dynamical systems model derives from the fact that it allows one to test assumptions about the dynamics of natural selection under a given model of constraint. One of the limitations of the adaptive landscape view of evolutionary change, however, is that it hides the *pace* of change. The

pace of evolutionary change is determined by a trade-off between the magnitude of the slope of the adaptive landscape and the degree of genetic variance along each phenotypic dimension. For monitoring the pace of evolutionary change we may simply revert to using one of the other complementary perspectives of evolutionary change outlined in the previous section. When we view the same results from different perspectives new insights on the dynamics and process of natural selection reveal themselves.

6.3.2 Model with genetic details and mutation, but no phenotypic plasticity

In the previous model, we found that in the absence of processes that act as a source of genetic variation a population quickly comes to exhaust its genetic variance. It is, however, thought that epistatic mutations might influence adaptive evolution by prolonging the evolutionary response to natural selection in populations, providing new sources of genetic variance on which natural selection can continually act (Carlborg et al., 2006). Let us therefore make a single change to our earlier model by assuming that there is now a low rate of loss-of-function mutation, μ, affecting the transmission of genetic features between parent microbes and their offspring. For now we will continue to assume there is no phenotypic plasticity in traits ($\dot{\mathbf{Z}} = \mathbf{0}$). In this circumstance, the inheritance matrix is now equal to a $|\mathbb{G}| \times |\mathbb{G}|$ *mutation* matrix of the form

$$\mathbf{H} = \begin{bmatrix} 1-2\mu-\mu^2 & \mu & \mu & \mu^2 \\ 0 & 1-\mu & 0 & \mu \\ 0 & 0 & 1-\mu & \mu \\ 0 & 0 & 0 & 1 \end{bmatrix}. \tag{6.24}$$

The assumptions governing the form of this matrix are: *i*) loss-of-function mutation changes an active allele to an inactive allele; *ii*) gain-of-function mutations occur with a negligible frequency and can be ignored.

In Figure 6.10 we again show the dynamics of the average trait values in the population, $\bar{\boldsymbol{z}}$, from the adaptive landscape perspective. Since the initial population composition is the same as that from the previous model, the contour map and the ellipse centred at the population average trait values at time $t = 0$ is the same as that in Figure 6.9. Yet the trajectory of the population over time shows a very different trend to that displayed

for the previous model. In particular, the effect of epistatic mutations now plays a key role in shaping the dynamics.

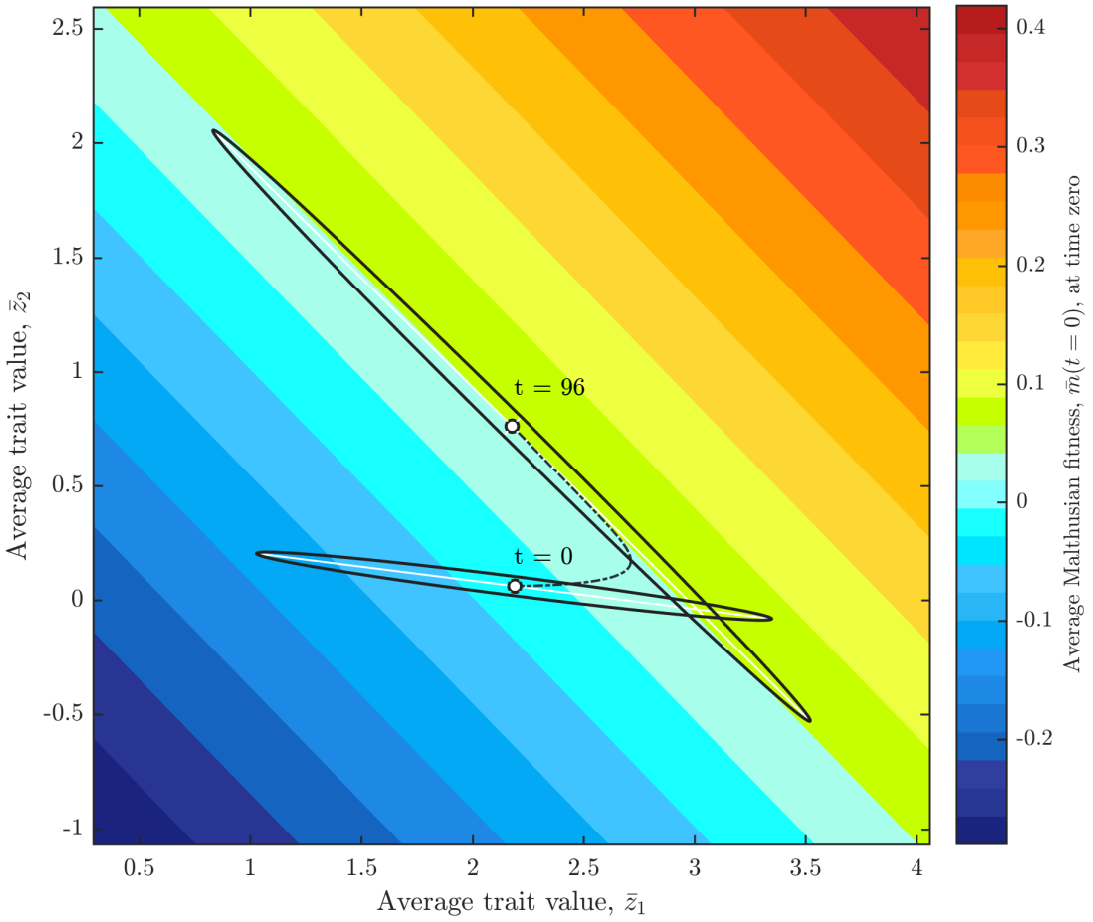


Figure 6.10: G-matrix evolution with mutation. The first order term of the linear approximation to the adaptive landscape at time $t = 0$ is illustrated by the contour map (which is represented as a plane in 2-dimensional trait space). The population average trait values, $\bar{\boldsymbol{z}}$ at time $t = 0$ (light grey) and time $t = 96$ (dark grey) are plotted as circles on the landscape, and the **G**-matrix of additive genetic variance is represented at time $t = 0$ and $t = 96$ as an ellipse centred at the average trait values. The change in population average trait values over time is indicated by a trajectory represented by a dashed black line. Parameters used in the model were: $\rho = 1/2$, $\varsigma = 1/4$, $K = 1 \times 10^8$, and $\mu = 0.001$.

Owing to what we identified as positive mutational epistasis in the second trait of the second loss-of-function mutant genotype, these microbes express the same overall level of

trait as the wild-type ($z_{11} + z_{12} = z_{31} + z_{32} = 3$) and therefore have the same Malthusian fitness at any instant in time. Thus in Figure 6.10 we see that although the trajectory of the population is initially in the same direction as that from our earlier model, the creation of genetic variance by mutation, and the subsequent action of natural selection on that genetic variance, leads to a change in direction of the population away from the direction of steepest ascent on the adaptive landscape.

The **G**-matrix for our new population undergoes significant changes over time, leading to an ellipse that increases in size and becomes oriented along its major axis in a different direction. The increase in genetic variance is not driven by mutation alone, but by a complex interplay between mutation, epistatic gene interactions and selection. In particular, mutation leads to the creation of a genotype with equal fitness to that of the wild-type (which is true only because we assumed gene interactions were epistatic), which can then be acted on by selection leading to a mutation-selection equillibrium. Our finding is that, as quantitative genetic theory predicts, *non-additive* gene interactions can act in concert with mutation to increase *additive* genetic variance in the population (Carlborg et al., 2006).

6.3.3 Model with genetic details, mutation, and phenotypic plasticity

In the previous model, we found that a population subject to mutation acting on genes interacting epistatically can exhibit a sustained period of genetic variance. To study the impact of phenotypic plasticity on our population, let us suppose that in addition to a low rate of loss-of-function mutation, μ, one of the trait values, z_{32}, exhibits phenotypic plasticity. The time derivative of the genotype-phenotype map takes the form

$$\dot{\mathbf{Z}} = \begin{bmatrix} 0 & 0 \\ 0 & 0 \\ 0 & \varphi \dot{n}_1 z_{32}(\varrho - z_{32}) \\ 0 & 0 \end{bmatrix}. \tag{6.25}$$

The assumptions governing the functional form of z_{32} here are that the expression of the trait is sensitive to changes in the abundance of the wild-type genotype in the population. The value of the trait remains constant only when the trait value reaches its maximum, ϱ, or when there is no change in the abundance of the wild-type genotype, so that $\dot{n}_1 = 0$.

Figure 6.11 shows the dynamics of the average trait values, $\bar{\boldsymbol{z}}$, under these new assumptions from the perspective of an adaptive landscape. The trajectory of the population over time initially shows similar trends to that displayed for the previous models, but eventually diverges significantly from that seen in either of them. This highlights how phenotypic plasticity can play a key role in shaping adaptive evolution, both in terms of genetic variance and movement up an adaptive landscape.

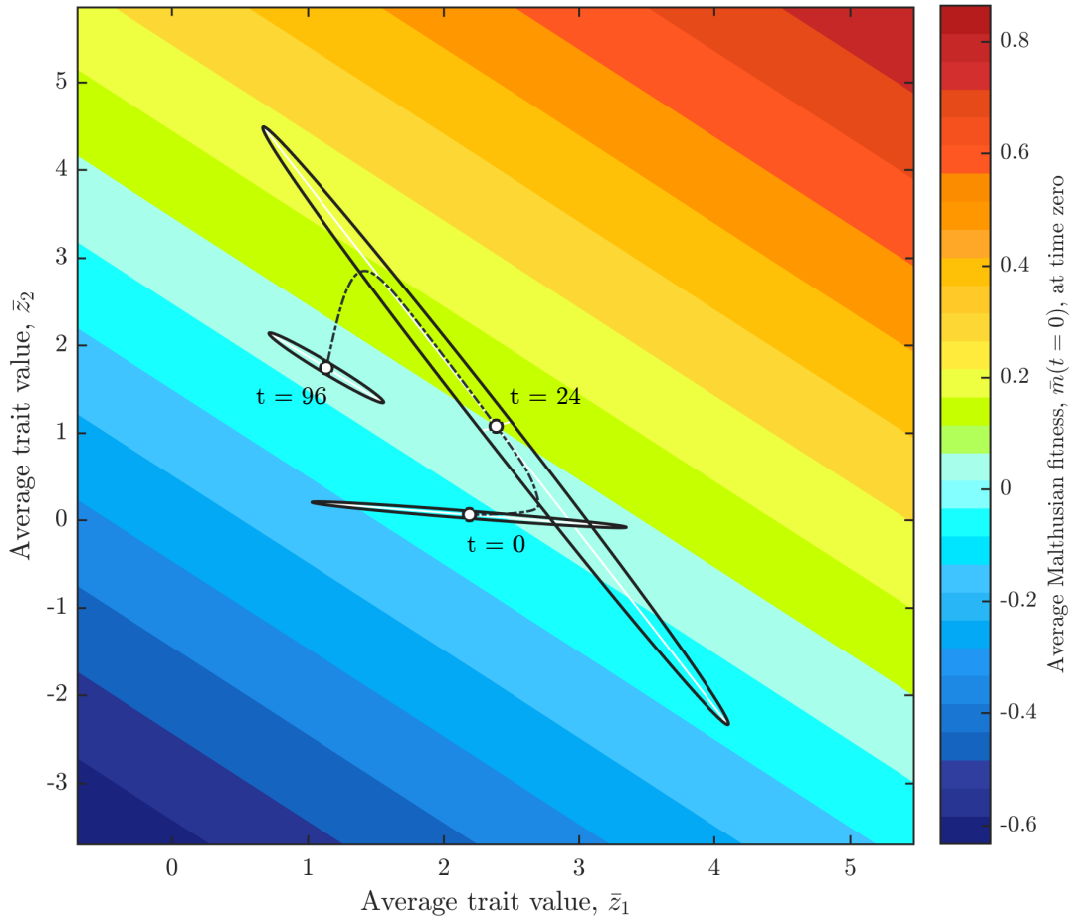


Figure 6.11: G-matrix evolution with mutation and phenotypic plasticity. The first order term of the linear approximation to the adaptive landscape at time $t = 0$ is illustrated by the contour map (which is represented as a plane in 2-dimensional trait space). The population average trait values, $\bar{\boldsymbol{z}}$ at time $t = 0$ (light grey) and time $t = 96$ (dark grey) are plotted as circles on the landscape, and the **G**-matrix of additive genetic variance is represented at time $t = 0$ and $t = 96$ as an ellipse centred at the average trait values. The change in population average trait values over time is indicated by a trajectory represented by a dashed black line. Parameters used in the model were: $\rho = 1/2$, $\varsigma = 1/4$, $K = 1 \times 10^8$, $\varphi = 5/K$, $\mu = 0.001$, and $\zeta = 0.01$.

After a period of time the trajectory of the population diverges from its previous path, taking the population seemingly away from the direction of steepest ascent on the landscape. What happens in this model is that the second loss-of-function mutant genotype responds to the growth of the wild-type genotype by increasing the expression of its second trait, giving it a higher overall phenotypic value than the wild-type. The increased expression of the trait gives the mutant a higher Malthusian fitness than the wild-type, resulting in its increase in frequency in the population due to selection. Yet the corresponding decrease in frequency of the wild-type causes the mutant to lower the expression of its second trait.

The effect of phenotypic plasticity in this context is therefore first to increase the average Malthusian fitness in the population and then to lower it. Phenotypic plasticity initially amplifies the creation of genetic variance (as can be seen from the size of the ellipse representing the $\mathbf{G}$-matrix), but ultimately causes a dramatic loss of genetic variance later when selection acts on this variance. Overall we see that the inclusion of phenotypic plasticity can both increase and decrease genetic variation in populations by favouring previously unfavourable genotypes.

6.4 Concluding remarks

To summarise, in this chapter we have seen that the abstract form of the dynamical systems theory can be readily applied to specific problems of interest by formulating simplifying assumptions and applying these in the form of constraints on the complexity of the systems being studied. We have studied two examples designed to highlight the practicalities of applying these constraints. In the first example, we have shown that processes like horizontal gene transfer and phenotypic plasticity can easily be incorporated into models by following the mathematical framework of the dynamical systems theory, and studied from ecological, genotypic and phenotypic perspectives simultaneously using the theory laid out in Chapter 2. In the second example, we have shown that genetic details about epsitasis and mutation can also easily be incorporated into models by following the mathematical framework of the dynamical systems theory, and studied from the adaptive landscape perspective using the theory laid out in Chapter 3. Along the way we have noted several potentially interesting results that warrant further investigation. These include the role that phenotypic plasticity plays in driving populations toward stable mixed equillibria, the role that natural selection plays in driving the spread of horizontal gene transfer, and how epistatic mutations and phenotypic plasticity can interact to give rise to the creation or destruction of genetic variance in populations. To

understand these processes better there are numerous avenues for future research that must be considered. Certainly one would ideally integrate these models with data from real microbial systems, but there are also more sophisticated mathematical tools available from the theory of differential equations that can be brought to bare on these systems to compliment the relatively straightforward numerical analysis we have explored here.

Chapter 7

Discussion

7.1 Overview

In this chapter, I summarise the main results of the thesis and consider avenues for further research. To recap, in this thesis I was motivated by ongoing debates in evolutionary theory about the generality and equivalence of a number of theoretical frameworks. My primary aim was to provide the formal foundations of a 'dynamical systems theory of natural selection', and to use the principles that embody evolution by natural selection to formally link several presently disconnected frameworks in evolutionary theory. Accordingly, the main results in this thesis are as follows:

In Chapter 2, we developed the foundations for our dynamical systems approach. First, we returned to the underpinning mathematics of population ecology and population genetics and reinterpreted these in terms of the abstract principles of natural selection. We then used these foundations to derive a dynamical law, the Malthusian selection equation (2.28), that gave rise to three complementary perspectives on the dynamics of natural selection: *i*) *ecological*—in terms of changes in the population composition and the population size; *ii*) *genotypic*—in terms of changes in the relative frequency of genotypes in the population; *iii*) *phenotypic*—in terms of changes in the summary statistics of phenotypic traits in the population. This allowed me to provide unifying links between the foundations of population ecology, the foundations of population genetics, evolutionary dynamics, and the Price equation. Moreover, the approach identified a general route through which the Malthusian fitness of individuals can be calculated, one that is somewhat different from the general approaches given by Fisher (1930), and Price (1995), but related to those advocated by Kimura (1958) and Charlesworth (1970).

In Chapter 3, we extended the dynamical systems framework to study the dynamics

of the evolutionary response to natural selection, by incorporating the key principles of evolutionary genetics into the selection equations obtained in Chapter 2. In particular, we derived a method of population-weighted least-squares linear regression that can be applied to populations defined by a dynamical system. We then studied the evolutionary response to natural selection from several perspectives, including Robertson's (1966) secondary theorem of natural selection, Fisher's (1930) fundamental theorem of natural selection, and several alternative perspectives on the multivariate breeder's equation (3.2) (Lande, 1979; Lande and Arnold, 1983) and Simpson's (1944) adaptive landscape. We therefore demonstrated how theorists can study the evolution of the $\mathbf{G}$-matrix as it changes through time to constrain and shape adaptive evolutionary change, a key challenge in quantitative genetic theory (Arnold et al., 2008).

In Chapter 4, we extended this quantitative genetic view of the dynamics of natural selection to study the dynamics of social evolution resulting from kin selection. In particular, by using the quantitative genetic approaches we derive in Chapter 3 we formulated a partition of the Malthusian fitness of entities into its neighbour-modulated fitness form (Queller, 1992a,b; Frank, 1997; Gardner et al., 2011)., and then used this to derive a univariate and multivariate form of Hamilton's rule in continuous time (Hamilton, 1964, 1970).

In Chapter 5, we extended the dynamical systems framework to incorporate a form of interdemic group selection. In particular, we derived the Malthusian interdemic group selection equation (5.21) which gave rise to three complementary perspectives on the dynamics of interdemic group selection: *i*) ecological—in terms of the changing frequencies of different types of groups and changes in the overall group-population size; *ii*) genotypic—in terms of changes in the relative frequencies of groups of different compositions in the group population; and *iii*) phenotypic—in terms of the changes in the average group trait values in the group-population.

Finally, in Chapter 6, we have seen that the abstract form of the dynamical systems theory can be readily applied to specific problems of interest by formulating simplifying assumptions and applying these in the form of constraints on the complexity of the systems being studied. In particular, we developed several toy models corresponding to populations of asexually reproducing microbes.

7.2 Further work

In this thesis we have therefore seen that the traditional frameworks in evolutionary theory can be incorporated into a general dynamical systems theory of natural selection. There are, however, a number of areas for further work. Since the dynamical systems theory of natural selection has been developed using the abstract principles of natural selection, rather than the formulation of a model based on a particular biological system, it has a certain generality that permits applications to a broad range of biological systems. Yet in taking this general approach there a number of potentially important features of the biological world that we have left out.

7.2.1 The dynamics of intrademic group selection

Evolutionary theorists typically describe two types of group selection (Reeve and Keller, 1999; West et al., 2007c): *i*) *intrademic* group selection, which rests upon the differential survival and reproduction of different types of individuals in a population that happens to be group-structured; and *ii*) *interdemic* group selection, which rests upon the differential survival and reproduction of groups of different compositions *and* the differential survival and reproduction of different types of individuals within groups. The distinction between interdemic and intrademic group selection is not, however, always clear. Consider, for instance, one of the first descriptions of group selection given by Darwin (1871)—in the *Descent of Man*, he wrote, 'there can be no doubt that a tribe including many members who ... were always ready to give aid to each other and to sacrifice themselves for the common good, would be victorious over other tribes; and this would be natural selection'. On the one hand, Darwin (1871) seems to be trying to explain the preponderance of an individual-level character, namely, cooperative behaviour (intrademic), but on the other he is describing the differential survival and reproduction of tribes with different properties (interdemic).

In Chapter 5, we extended the dynamical systems framework to incorporate the dynamics of interdemic group selection. In this section we present the main results of preliminary work already undertaken on the intrademic form of group selection. Since the work is still in its early stages, however, it also represents a significant area for further research. The main point resulting from this preliminary work is that interdemic and intrademic group selection are the same process that can be viewed from different perspectives. To illustrate this, we make no additional biological assumptions about the dynamics of

selection we studied in Chapter 5, but recast the dynamics in an intrademic form first popularised by Price (1972a).

Working with the same system as we did in Chapter 5, the abundance of i-genotype individuals in the global-population (consisting of all individuals in all groups) can be found by taking into account the group density θ at each point $\boldsymbol{n}$, and the abundance of i-genotype individuals n_i at that point. This gives us a quantity $\pi_i = \int_\Omega \theta n_i \; d\Omega$. The abundance of all genotypes in the global-population is then given by a vector $\boldsymbol{\pi} = (\pi_1, \ldots, \pi_{|\mathbb{G}|}) \in \mathbb{R}_+^{|\mathbb{G}|}$. We can also calculate the size of the global-population at any time t by simply summing over the abundance of each genotype to give: $\Pi = \sum_{i=1}^{|\mathbb{G}|} \pi_i = \sum_{i=1}^{|\mathbb{G}|} \int_\Omega \theta n_i \; d\Omega = \int_\Omega \theta N \; d\Omega$. In terms of the dynamics, firstly, we identify a selection equation that describes the instantaneous rate of change of the abundance of i-genotype individuals in the global-population. This is given by

$$\dot{\pi}_i = \int_\Omega \theta n_i \left(\mathcal{M} + \mathcal{B} \frac{\Delta n_i}{n_i} + \frac{v_i}{n_i} \right) \; d\Omega, \tag{7.1}$$

where we recall that $\mathcal{B}$ are the reproduction rate and $\mathcal{M}$ and Malthusian fitness of $\boldsymbol{n}$-composition groups, respectively, and v_i/n_i represents the ratio of the rate of change of the abundance i-genotype entities within a group (given by the Malthusian selection equation (2.28) from Chapter 2) and the abundance of those entities. This result is not particularly remarkable, but we will see in a moment that this 'Malthusian intrademic selection equation' gives rise to an important intuitive notion of fitness from an intrademic perspective. To see this, we first need to describe the growth rate of the global-population, which we find by summing over all genotypes in equation (7.1) to be given by

$$\dot{\Pi} = \Pi \sum_{i=1}^{|\mathbb{G}|} \int_\Omega \psi_i \left(\mathcal{M} + \mathcal{B} \frac{\Delta n_i}{n_i} + \frac{v_i}{n_i} \right) \; d\Omega, \tag{7.2}$$

where $\psi_i = \theta n_i / \Pi$ is the *relative* abundance of i-genotype individuals within $\boldsymbol{n}$-composition groups in the global-population. However, we can make a subtle change here in re-write this as

$$\dot{\Pi} = \Pi \sum_{i=1}^{|\mathbb{G}|} \int_\Omega \psi_i \left(\mathcal{M} + \mathcal{B} \frac{\Delta n_i}{n_i} + m_i \right) \; d\Omega, \tag{7.3}$$

where we recall that m_i is the Malthusian fitness of an i-genotype entity within the $\boldsymbol{n}$-composition group it occupies. It is important to note that we are not saying that $m_i = v_i/n_i$ here. Instead, the claim is that the *sum* over these two quantities when they are multiplied by n_i are equal. Indeed, we have already seen this to be the case in Chapter 2, when we discussed how the Malthusian fitness of individuals, m_i, should be defined. The reason for making this change will be come clear shortly. For now, we see from equation (7.3) that the quantity $\sum_{i=1}^{|\mathbb{G}|} \int_{\Omega} \psi_i \left(\mathcal{M} + \mathcal{B}\frac{\Delta n_i}{n_i} + m_i \right) \, d\Omega$ gives us an instantaneous measure of the exponential growth-rate of the global-population.

The primary utility of equation (7.3) is therefore that it gives us a definition for the Malthusian 'global' fitness of an i-genotype individual within the global-population, which we denote by $\phi_i := \phi_i(\boldsymbol{n}, t) \in \mathbb{R}$. Recall from Chapter 2 our discussion of how Kimura (1958) redefined Malthusian fitness to be the 'the net reproductive rate of [a] genotype m_i such that [its] contribution to the rate of increase of the population number N is $n_i m_i$' (where n_i is the number of i genotypes). From this definition, we can see that the Malthusian 'global' fitness of an i-genotype individual residing in an $\boldsymbol{n}$-composition group is given by

$$\phi_i = \mathcal{M} + \mathcal{B}\frac{\Delta n_i}{n_i} + m_i. \tag{7.4}$$

Remarkably, we see that an i-genotype individual's Malthusian global fitness is just the sum of its Malthusian fitness within the $\boldsymbol{n}$-composition group it occupies, m_i, the Malthusian group fitness of its group within the group-population, $\mathcal{M}$, and some other less familiar term $\mathcal{B}\Delta n_i/n_i$.

This less familiar term is interesting. The component $\Delta n_i = n_i' - n_i$ represents the difference between the expected abundance of i-genotype individuals in the typical group descendants of the group the i-genotype individual resides in at time t. If there are relatively more i-genotype individuals in group descendants than in the existing ancestral group, then this term will be positive. This term therefore represents a measure of the likelihood that i-genotype individuals are 'fairly' represented in group descendants when groups reproduce. That is, it takes into account the fact that the reproduction of the group an individual resides in may do little for its fitness in the global population if an individual does not transmit copies of its genotype to group descendants.

Malthusian global fitness therefore shares similar properties to Hamilton's (1964; 1970) notion of 'inclusive fitness' that we discussed in Chapter 4, in that it is partitioned into components that have direct (m_i) and indirect ($\mathcal{M} + \mathcal{B}\Delta n_i/n_i$) fitness effects. Let

us give a couple of examples to make this more concrete. Firstly, consider the slime mould *Dictyostilium discoidium*. When resources becomes scarce, single-celled amoebae aggregate to form a stalk with an explosive spore that can redistribute some of the cells to new, ideally resource plentiful, pastures (Strassmann et al., 2000). To do well in the global population of all amoebae, an individual cell therefore has to maximise three things: *i*) firstly it has to be successful at surviving and reproducing within a group compared to cells of different genotypes (due to m_i); *ii*) secondly, it has to be a member of an aggregate of cells that are good at surviving (as a group) long enough to form a stalk and distribute cells to new pastures (due to $\mathcal{M}$); and *iii*) finally, it has to make sure it has a reasonable chance of being part of the subset of cells distributed from the spore (due to $\mathcal{B}\Delta n_i/n_i$). What is interesting about this view is that it suggests that 'cheats' can emerge that are just as likely to survive and reproduce in the amoebic population, but which can increase their chances of making it into the spore (Ghoul et al., 2014). This simple theoretical prediction follows directly from the definition of fitness without even forming a model, but there is ample evidence to suggest that such cheats do indeed exist in natural populations (Strassmann et al., 2000; Foster et al., 2004; West et al., 2007a).

For another example, consider the dynamics of cancer. Cancer is increasingly viewed as an evolutionary process whereby the inevitable mutations that occur during growth and development generate somatic cell lineages that differ in their propensity to survive and reproduce in a manner that is both irregular and harmful to organismal function (Leroi et al., 2003; Crespi and Summers, 2005; Merlo et al., 2006; Greaves and Maley, 2012). In contrast to our description of cancer in terms of a two-level selection process from an interdemic group selection perspective in Chapter 5, we can now describe cancer in terms of a single-level process from an intrademic group selection perspective. Cancer cell dynamics in a population of multi-cellular organisms depend on three key rates: *i*) the relative survival and reproduction abilities of cancer cells to healthy somatic cells within organisms (due to m_i); *ii*) the relative survival and reproduction abilities of organisms containing cancer cells to survive and reproduce (due to $\mathcal{M}$); and *iii*) the relative ability of cancer cells to make it into the germ line and be passed on to the descendants of organisms (due to $\mathcal{B}\Delta n_i/n_i$). Thus, although cancer cells are very good at survival and reproduction within a host organism (Hanahan and Weinberg, 2000, 2011), they are extremely unlikely to spread among the global-population of all somatic cells (among all multi-cellular organisms). There are two obvious reasons for this: *i*) cancer cells ultimately reduce the Malthusian fitness of the multi-cellular organisms they reside in; and *ii*) cancer cells are unlikely to feature among the genotypes that are passed on to offspring (an interesting exception to this rule are the 'transmissible cancers' (Dingli and Nowak, 2006)).

7.2.1.1 Malthusian intrademic Price equation

To understand phenotypic dynamics from an intrademic group selection perspective, we must think more closely about what a phenotypic trait now represents, given that we must now 'ignore' group-level traits. We now need to identify the measurable properties of an i-genotype individual, given that it resides at a point $\boldsymbol{n}$ in the composition space Ω. We can think of this point as setting the 'environmental context' that helps in determining an individual's phenotype. We can still measure all the original traits from the genotype-phenotype map, $\mathbf{Z}$, at that point, to obtain the individual's phenotype within its group, $\boldsymbol{z}_{i\bullet}$, but we can now also measure the traits associated with the group at that point as well, which are given by $\boldsymbol{\mathcal{Z}}$. We can think of the group traits as being 'contextual traits' associated with each individual in that group (Damuth and Heisler, 1988; Goodnight et al., 1992). That is, an i-genotype individual has the 'observable characteristic' of residing in a group with a given group phenotype. Based on this contextual definition of phenotypes, and that of Malthusian global fitness given by equation (7.4), we can write a version of the Price-Hamilton formalism of group selection, that which Okasha (2006, p. 65) refers to as the 'Price approach to MLS1', for the total change in average trait values of individuals within the global-population:

$$\begin{bmatrix} \dot{\mathrm{E}}_{\boldsymbol{n}\in\Omega}(z_{i1}) \\ \vdots \\ \dot{\mathrm{E}}_{\boldsymbol{n}\in\Omega}(z_{i|\mathbb{P}|}) \end{bmatrix} = \begin{bmatrix} \mathrm{Cov}_{\boldsymbol{n}\in\Omega}(\bar{\phi},\bar{z}_1) \\ \vdots \\ \mathrm{Cov}_{\boldsymbol{n}\in\Omega}(\bar{\phi},\bar{z}_{|\mathbb{P}|}) \end{bmatrix} + \begin{bmatrix} \mathrm{E}_{\boldsymbol{n}\in\Omega}\left(\mathcal{B}\frac{[(N\bar{z}_1)'-N'\bar{z}_1]}{N}\right) \\ \vdots \\ \mathrm{E}_{\boldsymbol{n}\in\Omega}\left(\mathcal{B}\frac{\left[(N\bar{z}_{|\mathbb{P}|})'-N'\bar{z}_{|\mathbb{P}|}\right]}{N}\right) \end{bmatrix} + \begin{bmatrix} \mathrm{E}_{\boldsymbol{n}\in\Omega}(N\dot{\bar{z}}_1) \\ \vdots \\ \mathrm{E}_{\boldsymbol{n}\in\Omega}(N\dot{\bar{z}}_{|\mathbb{P}|}) \end{bmatrix}. \tag{7.5}$$

This equation expresses the total instantaneous change in the average trait values of individuals in the *global*-population, $\mathrm{E}_{\boldsymbol{n}\in\Omega}(z_{ik})$, as the sum of three components.

The first term, $\mathrm{Cov}_{\boldsymbol{n}\in\Omega}(\bar{\phi},\bar{z}_k)$, represents the covariance between the within-group average of Malthusian global fitness of individuals, $\bar{\phi}$, and the within-group average of the kth phenotypic trait held by individuals over all groups. Using (Okasha, 2006, p. 65) convention, we may interpret this as the impact of group selection toward the differential contribution of groups to the global-population of individuals some instantaneous moment in time later. Since a group's fitness is interpreted as the average of the Malthusian global fitness of individuals it is comprised of, group selection can happen because a group itself reproduces or because individuals within the group themselves reproduce. Note that this is a very different definition of group selection to the one we described in Chapter 5 from an interdemic perspective.

The second term, $\mathrm{E}_{\boldsymbol{n}\in\Omega}(\mathcal{B}\left[(N\bar{z}_1)' - N'\bar{z}_1\right]/N)$, represents the expected value of the quantity $\mathcal{B}\left[(N\bar{z}_1)' - N'\bar{z}_1\right]/N$ over all groups. The difference between the quantities $(N\bar{z}_k)'$ and $N'\bar{z}_k$ accounts for two different sources of transmission biases in the phenotypes of individuals when groups reproduce. First, offspring groups might have different sizes to their parents, even if their relative composition of individuals is the same. Second, offspring groups might have different genotypic compositions to their parents, even if they are of the same size.

The third term, $\mathrm{E}_{\boldsymbol{n}\in\Omega}(N\dot{\bar{z}}_k)$, represents the expected value of the quantity $N\dot{\bar{z}}_k$. To understand what this term represents, note that $\dot{\bar{z}}_k$ is the equivalent variable as that from the Malthusian Price equation (2.49) from Chapter 2. That is, this term simply accounts for an expected value over all groups of the group-size-weighted expected change in average trait values in a group due to within-group dynamics. Indeed, substituting for $\dot{\bar{z}}_k$ for the Malthusian Price equation (2.49) from Chapter 2, we can expand equation (7.5) to give

$$\begin{bmatrix} \dot{\mathrm{E}}_{\boldsymbol{n}\in\Omega}(z_{i1}) \\ \vdots \\ \dot{\mathrm{E}}_{\boldsymbol{n}\in\Omega}(z_{i|\mathbb{P}|}) \end{bmatrix} = \begin{bmatrix} \mathrm{Cov}_{\boldsymbol{n}\in\Omega}(\bar{\phi}, \bar{z}_1) \\ \vdots \\ \mathrm{Cov}_{\boldsymbol{n}\in\Omega}(\bar{\phi}, \bar{z}_{|\mathbb{P}|}) \end{bmatrix} + \begin{bmatrix} \mathrm{E}_{\boldsymbol{n}\in\Omega}\left(\mathcal{B}\frac{[(N\bar{z}_1)' - N'\bar{z}_1]}{N}\right) \\ \vdots \\ \mathrm{E}_{\boldsymbol{n}\in\Omega}\left(\mathcal{B}\frac{\left[(N\bar{z}_{|\mathbb{P}|})' - N'\bar{z}_{|\mathbb{P}|}\right]}{N}\right) \end{bmatrix} \tag{7.6}$$

$$+ \begin{bmatrix} \mathrm{E}_{\boldsymbol{n}\in\Omega}(N\left[\mathrm{Cov}_{i\in\mathbb{G}}(m_i, z_{i1}) + \mathrm{E}_{i\in\mathbb{G}}(b_i\Delta z_{i1}) + \mathrm{E}_{i\in\mathbb{G}}(\dot{z}_{i1})\right]) \\ \vdots \\ \mathrm{E}_{\boldsymbol{n}\in\Omega}(N\left[\mathrm{Cov}_{i\in\mathbb{G}}(m_i, z_{i|\mathbb{P}|}) + \mathrm{E}_{i\in\mathbb{G}}(b_i\Delta z_{i|\mathbb{P}|}) + \mathrm{E}_{i\in\mathbb{G}}(\dot{z}_{i|\mathbb{P}|})\right]) \end{bmatrix}.$$

Recall that $\mathrm{Cov}_{i\in\mathbb{G}}(m_i, z_{ik}) + \mathrm{E}_{i\in\mathbb{G}}(b_i\Delta z_{ik}) + \mathrm{E}_{i\in\mathbb{G}}(\dot{z}_{ik})$ gives the total change in the average trait values of individuals within $\boldsymbol{n}$-composition groups, so that the third term is the group-sized weighted expected value over all groups of the within-group phenotypic selection dynamics. The utility of this form of Price equation, made popular the work of Price (1972a), Hamilton (1975) and Wilson (1975), is that it can be used to compare and contrast selection dynamics across what might seem to be very different evolutionary contexts. Thus, as Reeve and Keller (1999) argue, one of the virtues of intrademic group selection models is that they 'provide a simple, standardised means of unveiling the structure of selection working simultaneously at different hierarchical levels.'

It is important to stress, therefore, that no new biological assumptions have been made in formulating the Malthusian intrademic Price equation (7.5) here as compared to the

Malthusian interdemic Price equation (5.38) from Chapter 5. They both describe phenotypic dynamics, they just describing evolutionary change in phenotypic summary statistics using a different accounting method. Thus, although (Okasha, 2006, pg. 65) argues that MLS-1 and MLS-2 are distinct types of process that occur in nature, saying, 'whether either occurs in particular case is a matter of objective fact', our analysis suggests this is not necessarily true. Both the Malthusian interdemic Price equation (5.38) and the Malthusian intrademic Price equation (7.5) emerge from the same dynamical system.

Another important corollary of this result is that it suggest the dynamics of both interdemic and intrademic group selection can be recast in terms of analogous kin selection dynamics. The idea that kin selection and group selection are the same process dates back to a result obtained by Queller (1992b). Yet there continues to be equivocation about this result. In particular, many authors consider Queller's result to be a special case that holds only under certain conditions. In particular, some authors have questioned whether kin and group selection are the same processes if one uses a dynamical systems approach to modelling, rather than a static approach based on discrete-generation versions of the Price equation. For instance, consider recent statements by Simon et al. (2013) who say, 'the claim that models of group selection can always be recast as an analogous kin selection model (Queller, 1992b) cannot be properly stated, let alone proved, in our framework, and in general the claim is simply false', and Simon (2014) who concludes that 'real-world examples of group selection are outside the domain of the Price equation.' Thus, the demonstration that group and kin selection models are formally equivalent in a dynamical setting represents a major area for future work.

7.2.2 The dynamics of selection in class-structured populations

One of the main simplifications we have employed in this thesis has been to assume that all individuals of a given genotype were, in some sense, the same. In particular, we assumed they had the same phenotype and the same Malthusian fitness[a]. Of course, in real systems individuals of the same genotype are not all the same. One way to deal with this within-genotype variation is to assign individuals to different classes. Populations defined by individuals of different classes are said to be 'class-structured' Taylor (1990).

For example, the study of caste differentiation in social insects is often treated in a class-structured way. This is because whether or not an individual is a member of one caste

[a]Chapter 5 represented a departure in this respect because individuals of different genotypes were also defined by their group membership, and could therefore have different phenotypes as a result of this membership.

or another generally depends upon a complicated interaction between genetic and environmental effects (Schwander et al., 2010). In these cases disentangling the selective and non-selective forces that generate variation in the abundances of different types of individual is a difficult task that will typically need special attention in models. The dynamical systems theory presented here already accounts for cases in which caste differentiation is controlled by a genetic or epigenetic mechanism (for instance, see Vaiserman (2014) and Simola et al. (2016)), but there may be scenarios in which environmental effects are the primary driver of caste variation which the dynamical systems theory does not yet cover. This is a significant area for future research.

As another example, the study of altruism directed towards relatives can also usefully be treated as a class-structured problem. This is because some relatives have greater 'value' to a focal actor than others for reasons other than their genetic relatedness. In particular, a focal actor would not typically be expected to gain the same level of indirect reproductive benefits from directing altruism towards a grandparent as it would from directing altruism towards a sibling because of the differences in these recipients in terms of their potential for contributing future offspring to the population. In these kind of cases the two potential recipients can be thought of as members of two different types of class with different types of 'reproductive value' (Fisher, 1930; Price and Smith, 1972; Grafen, 2006b; Barton and Etheridge, 2011). Understanding how a theory of reproductive value consistent with the dynamical systems theory can also be developed will also represent another significant area for future research.

7.2.3 The dynamics of selection in age-structured populations

Possibly the most important feature we have neglected in the work presented in this thesis is age-structure in the population. Without age-structure, all the individuals in the populations we have studied have been ageless. That is, they have not aged with time and consequently have not undergone a process of *development* or differed in their propensities to survive and reproduce at different ages. These rates will, of course, be crucial for a truly general treatment of the dynamics of natural selection. Early work in this area started, of course, with Fisher (1930). In *The Genetical Theory of Natural Selection* he introduced the concept of *reproductive value* as a fitness-like measure of the how much individuals of a given age, let us use y, contribute descendants to the population in the future. Other notable contributions have since been given by Leslie (1945, 1948) and, particularly, Charlesworth (1970, 1994). The logic employed in this thesis to model population dynamics would, however, possibly lead us down a different route to modelling age-structured populations.

To understand how an age-structured population might be modelled within the context of the dynamical systems theory of natural selection, let $n_i := n_i(y,t) \in \mathbb{R}_+$ now denote the abundance of i-genotype individuals of a particular age y in the population at some time t. The composition of the population as a whole is still given by a vector $\boldsymbol{n} = (n_1, ..., n_{|\mathbb{G}|})^{\mathrm{T}} \in \mathbb{R}_+^{|\mathbb{G}|}$. The finite size of the population is now given by summing over all genotypes *and* integrating over all ages, giving $N = \int_0^\infty \sum_{i=1}^{|\mathbb{G}|} n_i \; dy$. In the absence of births and deaths of individuals, our starting point would be to define the conservation equations describe how all individuals age. That is, without births and deaths, both the population size, and the total abundance of individuals of each genotype would remain constant, all individuals would simply age at a constant rate towards an infinite age. This could be described by a system of hyperbolic PDEs of the form

$$\partial_t n_i = -\partial_y n_i. \tag{7.7}$$

This system conserves the total abundance of individuals, since there are no births and deaths. If we then want to incorporate these processes, we would need to add source and sink terms to the RHS of equation (7.7). Assuming that reproduction is clonal, so that progenitor genotypes give rise to descendant genotypes of the same genotype, such terms might look like

$$\partial_t n_i = \int_0^\infty \hat{n}_i \hat{b}_i \hat{h}_i(\hat{y}, y) \; d\hat{y} - n_i d_i - \partial_y n_i, \tag{7.8}$$

where $b_i := b_i(y,t) \in \mathbb{R}_+$ would represent the reproduction rate of i-genotype individuals of age y, $\hat{h}_i(\hat{y}, y)$ would represent the kernel of an integral transform dictating the age y at which the descendants emerge from the reproduction of progenitors aged $\hat{y}$ (typically we would assume this is at age 0, so that $\hat{h}_i(\hat{y}, y) = \delta(0 - y)$ i.e. the Dirac delta function centred at 0), and $d_i := d_i(y,t) \in \mathbb{R}_+$ would represent the death rate of i-genotype individuals of age y.

This would constitute a different approach to that taken by, for instance, Charlesworth (1970, 1994), whose equations are derived from knowing the probability of survival from age 0 to age y, and the probability of producing descendants *given* that an individual has reached age y. The reason for choosing these probabilistic functions with which to model age-structured populations is that these are measures for which we typically have real-world data on. Yet our approach would emphasise that these probabilities emerge from the dynamics of gain and loss of individuals of particular ages. That is, the probabilistic

rates of reproduction and survival at particular ages emerge from the functions b_i and d_i. Of course, this sort treatment of the problem is completely non-rigorous and much more work will be needed to determine what, if any, advantage there is to modelling the dynamics of age-structured populations in the way we have suggested. It would be interesting to see, for instance, how the dynamics of selection in an age-structured population would present themselves in terms of the covariance mathematics of Price (1970, 1972a).

7.2.4 The dynamics of selection in spatially-structured environments

Another important feature we have neglected in this thesis is spatial structure. Without spatial-structure, all the individuals in the populations we have studied have been, in some respect, well mixed. Although we allowed for non-random assortment of individuals in their interactions with one another, spatial structure adds a constraint on a system, since it generates not only non-random assortment, but also physical boundaries. Thus, in our framework it is perfectly possible for i-genotype individuals to interact only with other i-genotype individuals if that is a characteristic their phenotype represents. Providing there are partners in the population with whom to interact, the interactions *will* happen. This is not the case for a spatially structured population. There may be many potential partners with whom to interact, but the interactions will only happen if the spatial structure permits it.

Spatial structure is particularly important in social evolution theory (Rousset, 2013). In particular, it can increase the relatedness among individuals, since parents and offspring (who are more likely than not to share genes) can aggregate together in local patches. Thus, spatial structure can be favourable for the evolution of cooperative traits like altruism (Rousset, 2013). There is a long tradition of using differential equations to model spatial dependencies in populations. One of the best-known examples is Alan Turing's (1952) reaction-diffusion equations. An interesting avenue for future work might therefore be to explore extension of the Malthusian selection equation to spatial environments. One could then calculate the benefits, costs, and relatedness values of the continuous-time form of Hamilton's rule we derived in Chapter 4 as they vary over space.

7.2.5 The dynamics of genetic drift

An additional feature we have neglected in this thesis is the inherent stochasticity of real-world populations, which we know from population genetics can have a profound impact on the dynamics of natural selection. That is, the dynamical systems approach we have taken uses an inherent assumption that the populations we study are very large. When populations are small, however, genetic drift can significantly temper the strength of selection (Kimura, 1962). There are two directions we can take in response to this limitation. Firstly, we can say that the dynamical systems theory of natural selection is a theory developed for the purpose of studying the effects of selection not for studying the effects of drift. This might sound evasive, but we are interested in a theory that explains the appearance of adaptations in the natural world. We take it for granted that inherent randomness cannot be expected to lead organisms to appear designed as if to maximise anything. Secondly, we could make extensions to the dynamical systems theory of natural selection to account for drift, using, for instance, stochastic differential equations or other techniques that enable one to model the effects of noise on the long term steady-states of dynamical systems. One possibility is the stochastic dynamics framework increasingly used by those studying evolutionary dynamics (see, for example, Traulsen et al. (2006)).

7.3 Concluding remarks

Evolutionary theory is much more than a collection of ideas about particular biological phenomena; it has a meticulous underlying logic with a set of principles and rules that govern how natural selection brings about the appearance of design in the natural world (Gardner, 2009). By encoding this logic in the language of mathematics we can explore a world of evolutionary possibilities to better understand the world as it is today (May, 2004). Whilst Ariew and Lewontin (2004) have argued for the abandonment of an attempt to make a general quantitative dynamical model of evolutionary change, the work I have presented in this thesis suggests that this would constitute surrendering to the problem too soon.

The two main components of evolutionary theory are dynamics and adaptation, but the study of these two phenomena has become polarised in recent years. In this thesis I have taken frameworks that are typically used to study adaptation and applied them in a complementary fashion to frameworks that are typically used to study dynamics. Hence, in this thesis I have developed a conceptual and theoretical synthesis, a dynamical systems theory of natural selection, based on the abstract principles of evolution by

natural selection and using the tools of ordinary (ODEs) and partial differential equations (PDEs). Given the state of an existing biological system, and a set of assumptions about how individuals within the system interact, the job of the dynamical systems theory of natural selection is no less than to predict the future in its entirety.

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