Modeling Adaptive and Non-adaptive Responses of Populations to Environmental Change

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Manuscript elements: Table 1, Table 2, Figure 1, figure 2, figure 3, figure 4, figure 5, online supplementary information (including figure S1, figure S2 and figure S3). All figures are to print in color.

Keywords: Population dynamics, evolutionary genetics, structured models, environmental change.

Abstract

Understanding how the natural world will be impacted by environmental change is one of the most pressing challenges facing humanity. Addressing this challenge is difficult because environmental change can generate both population level plastic and evolutionary responses, with plastic responses being either adaptive or non-adaptive. We develop an approach that links mechanistic quantitative genetic theory with data-driven structured models to allow prediction of population responses to environmental change via plasticity and adaptive evolution. After introducing general new theory, we construct a number of examples models to demonstrate that evolutionary responses to environmental change will be considerably slower than plastic responses, that adaptive plasticity can accelerate population recovery to environmental change but that it slows the rate of adaptation to the new environment. Parameterization of the models we develop requires information on genetic and phenotypic variation and demography which will not always be available. We consequently develop a method based on the statistical analysis of temporal trends in model parameter values of examining whether the full machinery of the evolutionarily explicit models we develop will be needed to predict responses to environmental change, or whether simpler non-evolutionary models that are now widely constructed may be sufficient.

Introduction

Ecosystems from the deep ocean to the high arctic, from deserts to tropical forests are responding to environmental change. Understanding and predicting these responses is one of the most pressing issues currently facing humanity. For this reason, in the last quarter of a century, there has been considerable interest in developing ways to understand how the natural world will be affected by environmental change (Bossdorf et al., 2008; Dawson et al., 2011; Gilbert and Epel, 2009; Hoffmann and Sgrò, 2011; Ives, 1995; Lavergne et al., 2010; Wiens et al., 2009). We introduce a new, general approach combining insights from structured population modeling and evolutionary genetics that allows us to examine how adaptive evolution and plasticity contribute to the way that populations, and consequently the ecosystems in which they are embedded, respond to environmental change.

Environment change alters the expected demographic rates of individuals within a population (Chevin et al., 2010). For example, if environmental change reduced the probability of survival of all individuals within a population without impacting recruitment, then population size would decline (Caswell, 2001). Predicting the way populations will respond to environmental change consequently requires understanding how such change impacts demographic rates (Coulson et al., 2001). Individual differences in expected demographic rates within a population are ubiquitous, with some individuals having a greater propensity to survive or reproduce than others (Link et al., 2002). This heterogeneity across individuals is determined by phenotypic variation (Wilson and Nussey, 2010). For example, large individuals often have higher survival and recruitment rates compared to their smaller counterparts (e.g. Festa-Bianchet et al., 1998; Sedinger et al., 1995). To understand how environmental change influences demographic rates at the population level it is consequently necessary to know (i) the distribution of phenotypes within the population and (ii) their expected demographic rates in different environments (Ozgul et al., 2010).

Dynamic models of population responses to environmental change need to incorporate information not only on the associations between phenotypic traits and expected survival and reproduction in different environments, but also on the way that environmental variation influences phenotypic

development within individuals as they age, and the distribution of phenotypes among new born individuals recruiting to the population (Rees et al., 2014). As well as environmental variation, genes also influences the way that phenotypes develop within individuals (Cheverud et al., 1983), as can an individual's current phenotypic state (Badyaev and Martin, 2000; Easterling et al., 2000). Parental phenotypes, parental genotypes and environmental variation can all influence the distribution of offspring phenotypes as can mating patterns (Baldwin, 1896; Charlesworth, 1994; Gavrilets and Scheiner, 1993; Lynch and Walsh, 1998; Monaghan, 2008). This complexity makes predicting population responses to environmental change challenging.

Adaptive evolution in response to environmental change occurs when selection – the association between phenotypes and expected survival and reproduction – results in a change in allele frequencies. Such genetic change can lead to change in the distribution of the phenotypes that influence survival and reproduction. However, phenotype distributions can respond to environmental change in the absence of adaptive evolution via plasticity. The ability for phenotype distributions to change in the absence of adaptive evolution is often genetically determined. Individuals can modify their own phenotypes, or those of their offspring, by altering their physiology, metabolism or behavior (Aubin-Horth and Renn, 2009; Richards, 2006). This is achieved by altering gene expression patterns by up and down regulating expression of particular genes, or even turning some genes off and others on (Snell-Rood et al., 2010). These genetic effects that are not encoded in DNA are termed epigenetic effects.

Epigenetic responses to environmental change occur at the level of the individual. For them to leave a signature at the population level in the distribution of phenotypes, multiple individuals need to exhibit similar epigenetic responses to environmental change (Lande, 2009). When this happens, populations are said to exhibit plastic responses. We distinguish between two types of plastic response – phenotypic plasticity (Scheiner, 1993) and epigenetic inheritance (Richards, 2006). Phenotypic plasticity occurs when phenotype distributions change within surviving individuals due to epigenetic responses to a changing environmental. In contrast, epigenetic inheritance occurs when a change in the environment impacts the phenotype of offspring recruiting to the pop-

ulation (Blake and Watson, 2016). Epigenetic inheritance can be influenced by the environment the offspring find themselves when they become independent, or by their parents. For example, parents may provision developing offspring (seeds or foetuses) with different resources or hormone levels as a function of their own phenotypes (Love et al., 2005). We refer to this environment as the developmental environment. Alternatively, once independent from their parents, offspring development may be determined by the ecological environment they experience (Johan Solberg et al., 2004). In germinating seeds, the ecological environment could be determined by light, water and nutrient availability.

Any general framework that can be used to predict how environmental change will impact populations consequently needs to incorporate how plasticity and genetic variation generates phenotypic variation, and how phenotypic variation impacts expected demography. We show how evolutionarily explicit integral projection models (IPMs) (Barfield et al., 2011; Childs et al., 2016; Coulson et al., 2011) provide a powerful framework within which to do this.

IPMs are a very flexible structured modeling tool. They project the dynamics of phenotype distributions as a function of expected survival and reproduction, the way the phenotype develops and the distribution of offspring phenotypes (Coulson, 2012; Easterling et al., 2000; Merow et al., 2014). Because IPMs track the dynamics of the entire distribution of phenotypic traits, numerous quantities of interest to ecologists and evolutionary biologists describing life history, population dynamic and phenotypic traits can be calculated from them (Childs et al., 2003; Coulson et al., 2011, 2010; Ellner and Rees, 2006; Rees et al., 2014; Steiner et al., 2014, 2012; Vindenes and Langangen, 2015). They consequently offer great potential to study eco-evolutionary feedbacks and dynamics (Coulson et al., 2011). However, most IPMs to date have been restricted to phenotypic variation in that they do not include genotype-phenotype maps (Merow et al., 2014). A small number of evolutionarily explicit IPMs have been developed. Coulson et al. (2011) used IPMs to track the distribution of body size and coat color in wolves, where coat color was determined by genotype at a single bi-allelic locus. They showed how environmental change would impact genotype frequencies at this locus. Barfield et al. (2011) and Childs et al. (2016) developed IPMs

of quantitative characters determined by a large number of unlinked loci of small effect. However, none of these models incorporates plasticity, nor different genetic influences on the phenotype at different ages, and these omissions limit their utility in predicting how populations will be influenced by environmental change (Chevin, 2015).

Environmental change can be biotic or abiotic. Climate change is an example of abiotic change while change in the size or structure of a prey, competitor or predator population, or the arrival of a new species within the ecosystem, provide examples of biotic environmental change. Abiotic and biotic changes can interact. For example, a changing climate can alter the strength of intra-specific density-dependence and species interactions. IPMs have been extended to incorporate biotic and abiotic environmental change and their interaction (Adler et al., 2010; Bassar et al., 2016; Childs et al., 2003; Rees and Ellner, 2009), which makes them very flexible tools to simultaneously explore impacts of such changes on the dynamics of phenotypes, life history and populations. This flexibility makes them a potentially powerful tool to investigate how adaptive evolution and plasticity can contribute to population responses to environmental change.

The aim of this paper is to introduce the general framework. We do this by (i) introducing two sex IPMs of phenotypic traits (Schindler et al., 2015, 2013; Traill et al., 2014*a*) that are not evolutionarily explicit, (ii) extending these models to include flexible genotype-phenotype maps that allow the role of adaptive evolution and plastic responses to environmental change to be examined, (iii) develop simple models to illustrate the framework. These models provide new results on the role of plasticity on evolutionary trajectories yet also allow us to retrieve key insights from evolutionary genetics.

Methods and Results

We start this section by introducing our general modelling approach. Our models consist of combinations of functions, so we start by focusing on the biological processes these functions capture, and the way they combine to project the dynamics of phenotypic trait distributions. Our start-

ing point is a model of the entire phenotype that we then extend to capture the dynamics of a phenotype consisting of genetic and environmentally determined components (Falconer, 1960). In order to construct models within our approach it is necessary to select forms for each function so we next turn our attention to this challenge. In the next sections we consider appropriate forms for functions that describe the dynamics of first the genetic component of the phenotype and second its environmental component. Next, we combine insights from these two sections to consider the dynamics of phenotypes consisting of both a genetic and environmental component. Finally, we consider how to identify circumstances when the full machinery of evolutionarily explicit IPMs are required, and when purely phenotypic ones will likely suffice.

Modeling approach

We use the term mechanistic to refer to functional forms that are derived from a mechanistic understanding of a process. For example, Mendelian inheritance rules that are central to quantitative and population genetics are mechanistic in that the distribution of offspring genotypes or breeding values is known *a priori* from the parental genotypes or breeding values and the mating system (Barfield et al., 2011; Charlesworth, 1994). The term phenomenological is used to refer to functional forms that are identified from the statistical analysis of data (Crawley, 2007). We refer to functions, be they mechanistic or phenomenological, as $f(\dots)$ where the dots inside parentheses define the variables the function f operates on. Parameters of a function are referenced by the same letter as the function, with subscripts defining the variable they influence. For example, a parameter $f_{\mathcal{Z}}$ represents a parameter of function f that operates on variable $\mathcal{Z}$. We reserve I for the intercept of functions and a for age. Age is only included in models for species with overlapping generations. We use primes ($'$) to represent a possible change in trait value from one time step to the next, either among surviving individuals, or between parents and their offspring. The notation we use is the standard notation used for Integral Projection Models (IPMs) Coulson (2012); Merow et al. (2014); Rees et al. (2014). Notation is provided in Table 1. We now turn to our approach.

Selection is the underpinning of adaptive evolution. It operates on the phenotype, and de-

pending upon the genotype-phenotype map, can result in some genotypes having greater fitness than others. Under some circumstances such variation in genotype fitness can result in evolution defined as a change in allele frequencies. However, in other circumstances, for example when phenotypes determined by heterozygote genotypes have greater fitness than phenotypes determined by homozygote genotypes, variation in genotype fitness does not necessarily result in allele frequency change (Charlesworth, 1994; Fisher, 1930).

In order to predict evolution and population dynamics it is necessary to understand: (i) the genotype-phenotype map at birth, (ii) how the phenotype develops, (iii) how the phenotype influences survival at each developmental stage, (iv) the species' mating system and (v) patterns of mate choice based on the phenotype, as well as how these mate choice patterns influence (vi) reproductive success, (vii) the distribution of genotypes among offspring and (viii) how all these processes result in change in allele frequency from one generation to the next. Processes (i) to (vi) (and consequently also (viii)) can be influenced by environmental variation. Dispersal can also be an important driver of evolution. It can be added into the models we develop relatively easily, but is not considered further here.

Our starting point is a phenotypic modeling approach that captures all demographic processes that can contribute to the dynamics of phenotypes – survival, recruitment, development, inheritance, and mating patterns. Two sex phenotypic integral projection models (IPMs) (Coulson et al., 2011; Schindler et al., 2015, 2013; Traill et al., 2014*a*) capture processes (ii) to (vi) listed above but they do not include genotypes, or consequently a genotype-phenotype map. Instead they include a function that maps parental phenotype at time t to the phenotypes of recruiting offspring at time $t + 1$ (Easterling et al., 2000). These functions are phenomenological in that no genetic mechanisms of inheritance are included (Coulson et al., 2010; Smallegange and Coulson, 2013). Having introduced these models we then extend them to include genotype-phenotype maps.

The model consists of two equations – one for females and one for males – with each equation consisting of two additive components (Schindler et al., 2013). The first component deals with survival and development of individuals already within the population, the second component deals

with reproduction and the generation of phenotypes among newborns entering the population,

$$
\begin{aligned}
N_f(\mathcal{Z}', t+1) &= \int [D_f(\mathcal{Z}'|\mathcal{Z}, \theta, t) S_f(\mathcal{Z}, \theta, t) N_f(\mathcal{Z}, t)] d\mathcal{Z} + \\
&+ sC_{N_f N_m} \iint [H_f(\mathcal{Z}'|\mathcal{Z}_m, \mathcal{Z}_f, \theta, t) M(\mathcal{Z}_m, \mathcal{Z}_f, t) \dots \\
&\dots N_f(\mathcal{Z}_f, t) N_m(\mathcal{Z}_m, t) R(\mathcal{Z}_f, \mathcal{Z}_m, \theta, t)] d\mathcal{Z}_m d\mathcal{Z}_f \\
N_m(\mathcal{Z}', t+1) &= \int [D_m(\mathcal{Z}'|\mathcal{Z}, \theta, t) S_m(\mathcal{Z}, \theta, t) N_m(\mathcal{Z}, t)] d\mathcal{Z} + \\
&+ (1-s) C_{N_f N_m} \iint [H_m(\mathcal{Z}'|\mathcal{Z}_m, \mathcal{Z}_f, \theta, t) M(\mathcal{Z}_m, \mathcal{Z}_f, t) \dots \\
&\dots N_f(\mathcal{Z}_f, t) N_m(\mathcal{Z}_m, t) R(\mathcal{Z}_f, \mathcal{Z}_m, \theta, t)] d\mathcal{Z}_m d\mathcal{Z}_f
\end{aligned} \tag{1}
$$

$N_f(\mathcal{Z}', t+1)$ and $N_m(\mathcal{Z}', t+1)$ are distributions of phenotypes $\mathcal{Z}'$ in respectively females and males at time $t+1$; $D_f(\mathcal{Z}'|\mathcal{Z}, \theta, t)$ and $D_m(\mathcal{Z}'|\mathcal{Z}, \theta, t)$ are the probability of the phenotype developing from $\mathcal{Z}$ to $\mathcal{Z}'$ in respectively females and males between t and $t+1$ as a function of environmental drivers θ; $S_f(\mathcal{Z}, \theta, t)$ and $S_m(\mathcal{Z}, \theta, t)$ are survival functions for females and males from t to $t+1$ including effects of phenotype and environmental drivers θ; s is the birth sex ratio measured as the proportion of female offspring produced; and $C_{N_f N_m}$ is a normalisation constant; $H_f(\mathcal{Z}'|\mathcal{Z}_m, \mathcal{Z}_f, \theta, t)$ and $H_m(\mathcal{Z}'|\mathcal{Z}_m, \mathcal{Z}_f, \theta, t)$ describe the probabilities of parents with phenotypes $\mathcal{Z}_m$ and $\mathcal{Z}_f$ respectively producing male and female offspring with phenotype $\mathcal{Z}'$ as a function of environmental drivers θ at time t; $M(\mathcal{Z}_m, \mathcal{Z}_f, t)$ captures the rate of mating between a male with phenotype $\mathcal{Z}_m$ and a female with phenotype $\mathcal{Z}_f$; $R(\mathcal{Z}_f, \mathcal{Z}_m, \theta, t)$ describes the expected litter size given a mating between a male and a female with phenotypes $\mathcal{Z}_m$ and $\mathcal{Z}_f$ in environment θ at time t. The survival, mating and litter size functions determine the strength of selection on $\mathcal{Z}$ (Schindler et al., 2015).

$C_{N_f N_m}$ can be used to capture a range of mating systems. For example, if we follow Schindler et al. (2013) and write,

$$
C_{N_f N_m} = \frac{\int_{\mathcal{Z}_{f(\min)}}^{\infty} N_f(\mathcal{Z}_f, t) d\mathcal{Z}_f}{\int_0^{\infty} M(\mathcal{Z}_m, \mathcal{Z}_f, t) N_m(\mathcal{Z}_m, t) N_f(\mathcal{Z}_f, t) d\mathcal{Z}_m d\mathcal{Z}_f} \tag{2}
$$

this adds a minimum size at which females can reproduce $\mathcal{Z}_{f(\min)}$. Depending on the mating behavior of the species, $C_{N_f N_m}$ can be modified in various ways. For example, it can easily be altered

such that the number of birth events is determined by the number of the rarer sex, as in monogamous species. Mate choice can be influenced by specifying different functions for $M(\mathcal{Z}_m, \mathcal{Z}_f, t)$. Schindler et al. (2013) demonstrate how it can be specified for random mating, assortative mating, disassortative mating and size-selective mating.

In phenotypic IPMs, the phenotypic development functions are usually Gaussian probability functions (Easterling et al., 2000), e.g.:

$$D(\mathcal{Z}'|\mathcal{Z}, \theta, t) = \frac{1}{V^D(\mathcal{Z}, \theta, t)\sqrt{2\pi}} e^{-\frac{(\mathcal{Z}' - \mu^D(\mathcal{Z}, \theta, t))^2}{2V^D(\mathcal{Z}, \theta, t)^2}}. \tag{3}$$

The functions $\mu^D(\mathcal{Z}, \theta, t)$ and $V^D(\mathcal{Z}, \theta, t)$ respectively describe the expected value of $\mathcal{Z}'$ given $\mathcal{Z}$ and θ at time t and the variance around $\mu^D(\mathcal{Z}, \theta, t)$. The Gaussian form can also be used for development functions $H(\mathcal{Z}'|\mathcal{Z}, \theta, t)$ with functions $\mu^H(\dots)$ and $V^H(\dots)$.

We extend the two sex phenotypic IPM in equation (1) to include genotypes by writing the phenotype as a function $\mathcal{Z} = z(\mathcal{G}, \mathcal{E})$. We assume that $\mathcal{Z}$ is a quantitative phenotype (i.e. measured in integer or real values). The genotypic value $\mathcal{G}$ and environmental value $\mathcal{E}$ describe the numerical contributions of the genetic and environmental components of the phenotype to an individual's phenotypic trait value. A simple map can consequently be written $\mathcal{Z} = \mathcal{G} + \mathcal{E}$ (Falconer, 1960).

$\mathcal{G}$ is determined by genotype, g. When the map between g and $\mathcal{G}$ is additive, the dynamics of g and $\mathcal{G}$ are identical. In contrast, when alleles interact, either at a locus (dominance) or across loci (epistasis) the map between g and $\mathcal{G}$ is not additive, and the dynamics of $\mathcal{G}$ are not identical to the dynamics of g (Fisher, 1930). In classical quantitative genetics it is assumed that the map between g and $\mathcal{G}$ is additive (Falconer, 1960). Under these assumptions, it is not necessary to track the dynamics of g but evolution can be investigated by modeling the dynamics of just $\mathcal{G}$. When the map is additive we refer to the genetic component of the phenotype as a breeding value and denote it $\mathcal{A}$.

In classical population genetics, when the contribution of dominance and epistasis to evolution are often a key focus, it is necessary to track the dynamics of g and calculate $\mathcal{G}$ from each g. The map between $\mathcal{G}$ and the phenotype $\mathcal{Z}$ is often assumed to be one-to-one (Hartl et al., 1997). In other

words, the dynamics of $\mathcal{G}$ and $\mathcal{Z}$ are identical. In contrast, in quantitative genetics, the environment can influence the map between $\mathcal{A}$ and $\mathcal{Z}$ by influencing the value of the environmental component of the phenotype, $\mathcal{E}$ (Falconer, 1960). $\mathcal{E}$ can take different values in different individuals and can vary within individuals throughout life. The dynamics of the phenotype may not consequently represent the dynamics of the genotypic value $\mathcal{A}$. Statistical quantitative genetics is concerned with estimating moments of $\mathcal{A}$ from $\mathcal{Z}$ by correcting for environmental and individual variables that determine $\mathcal{E}$ (Kruuk et al., 2008).

The genotype-phenotype map for phenotypic traits measured by biologists in free living populations is rarely known, and quantitative genetic assumptions are widely adopted (Kruuk et al., 2008). In particular, the infinitesimal model is assumed in which $\mathcal{A}$ is determined by a large number of unlinked loci of small, additive, effect (Fisher, 1930). Until we have a better understanding of the genetic architecture of complex traits, this approach is the most powerful available to investigate evolution in the wild (Kruuk et al., 2008). We consequently adopt it here.

We track the joint distribution of the two components $N(\mathcal{A}, \mathcal{E}, t)$. The utility of this is we can write expressions to describe the dynamics of each of the components separately, if necessary, before easily combining them to retrieve the dynamics of the phenotype. For $\mathcal{Z} = \mathcal{A} + \mathcal{E}$ we can use a convolution (represented by the mathematical operator $*$) between the two components of the phenotype to construct the phenotype (Barfield et al., 2011).

Phenotypic plasticity and epigenetic inheritance are captured in the dynamics of $\mathcal{E}$. In previous quantitative genetic IPMs $\mathcal{E}$ is a randomly distributed variable that captures developmental noise (Barfield et al., 2011; Childs et al., 2016). A key contribution of this paper is to show how $\mathcal{E}$ can be extended to also capture the biotic or abiotic environment as well as signatures of parental $\mathcal{A}$s and $\mathcal{E}$s. $\mathcal{E}$ is consequently defined as function of these drivers. There are various notations we could use to capture this. To be consistent with previous integral projection model formulations (Coulson, 2012; Merow et al., 2014; Rees et al., 2014) we write $\mathcal{E}'|\mathcal{E}, \mathcal{A}, \theta, t$ to capture the effects of $\mathcal{E}$, $\mathcal{A}$ and the environment θ at time t on $\mathcal{E}'$.

We now expand terms in our two-sex phenotypic IPM to include the genotype-phenotype map

$\mathcal{Z} = z(\mathcal{A}, \mathcal{E})$. We start by considering the dynamics of $\mathcal{A}$ and $\mathcal{E}$ among females that are already within the population. The same logic extends to males. We then develop general expressions for mating and inheritance of $\mathcal{A}$ and $\mathcal{E}$.

We start with the bivariate distribution of $\mathcal{A}$ and $\mathcal{E}$ at time t among females that are already within the population at time t: $N_f(\mathcal{A}, \mathcal{E}, t)$. Viability selection now operates on this distribution. Viability selection is a simple multiplicative process describing the expected survival from t to $t+1$ as a function of the phenotype. We can consequently write,

$$N_f^s(\mathcal{A}, \mathcal{E}, t) = S_f(z(\mathcal{A}, \mathcal{E}), \theta, t) N_f(\mathcal{A}, \mathcal{E}, t). \tag{4}$$

When it comes to development, the genotype does not develop but remains fixed for life. However, $\mathcal{A}$ can vary with age if different genes contribute to the phenotype at different ages (Wilson et al., 2005). In the section §**Adaptive Evolution** we consider the dynamics of age-structured breeding values. We focus here on the case where $\mathcal{A}$ remains fixed for life but the environmental component may vary,

$$N_f^s(\mathcal{A}, \mathcal{E}', t+1) = \int D_f(\mathcal{E}' | (\mathcal{E}, \mathcal{A}, \theta), t) N_f^s(\mathcal{A}, \mathcal{E}, t) d\mathcal{E}. \tag{5}$$

Recruitment is dealt with in a similar way to survival in that it is a multiplicative process,

$$\begin{aligned} N^r((\mathcal{A}_m, \mathcal{E}_m), (\mathcal{A}_f, \mathcal{E}_f), t) &= M((\mathcal{A}_m, \mathcal{E}_m), (\mathcal{A}_f, \mathcal{E}_f), t) N(\mathcal{A}_m, \mathcal{E}_m, t) \ldots \\ &\ldots \; N(\mathcal{A}_f, \mathcal{E}_f, t) R(z(\mathcal{A}_m, \mathcal{E}_m), (z\mathcal{A}_f, \mathcal{E}_f), \theta, t). \end{aligned}$$

Note this is a recruitment related term of both male and female offspring that is not yet scaled by the normalization factor $C_{N_f N_m}$.

As with development, inheritance of the genetic and environmental components of the phenotype operates in different ways. For example, once mating pairs have formed and the number of offspring from each mating has been determined, the distribution of offspring genotypes is predictable. We can write the inheritance function for the genetic and environmental components of the phenotype as,

$$
\begin{aligned}
N_f^r(\mathcal{A}', \mathcal{E}', t+1) &= sC_{N_f N_m} \iiiint H_f(\mathcal{A}'|(\mathcal{A}_m, \mathcal{A}_f), \mathcal{E}'|(\mathcal{E}_m, \mathcal{E}_f, \theta, t)) \dots \\
&\dots \quad N^r((\mathcal{A}_m, \mathcal{E}_m), (\mathcal{A}_f, \mathcal{E}_f), t) d\mathcal{A}_m d\mathcal{E}_m d\mathcal{A}_f d\mathcal{E}_f
\end{aligned} \tag{6}
$$

then,

$$
N_f(\mathcal{A}', \mathcal{E}', t+1) = N_f^r(\mathcal{A}', \mathcal{E}', t+1) + N_f^s(\mathcal{A}, \mathcal{E}', t+1). \tag{7}
$$

The same logic applies to the production of male offspring.

We can construct the phenotype from the two components $\mathcal{A}'$ and $\mathcal{E}'$, e.g.

$$
N_f(\mathcal{Z}', t+1) = \int_{\Omega_{\mathcal{Z}'}} N_f^r(\mathcal{A}', \mathcal{E}', t+1) d\mathcal{E}' d\mathcal{A}' + \int_{\Omega_{\mathcal{Z}'}} N_f^s(\mathcal{A}, \mathcal{E}', t+1) d\mathcal{E}' \tag{8}
$$

where $\Omega_{\mathcal{Z}'}$ is the set of $(\mathcal{A}', \mathcal{E}')$ values satisfying $z(\mathcal{A}', \mathcal{E}') = \mathcal{Z}'$. For the second integral in equation (8) we have $z(\mathcal{A}, \mathcal{E}') = \mathcal{Z}'$ as the $\mathcal{A}$ does not change within individuals and consequently has no prime.

The additivity assumption means that models of clonal inheritance can generate very similar predictions to models of two sexes, particularly if both males and females have similar demography. However, clonal models are simpler than two sex models (Lande, 1982). We utilize this consequence of the additivity assumption and initially work with clonal reproduction to examine how the dynamics of $\mathcal{A}$ and $\mathcal{E}$ influence population and phenotypic trait dynamics and adaptive evolution. We can write a clonal model,

$$
\begin{aligned}
N(\mathcal{A}, \mathcal{E}', t+1) &= \int [D(\mathcal{E}'|\mathcal{E}, \mathcal{A}, \theta, t) S(z(\mathcal{A}, \mathcal{E}), \theta, t) + H(\mathcal{E}'|\mathcal{E}, \mathcal{A}, \theta, t) \dots \\
&\dots \quad R(z(\mathcal{A}, \mathcal{E}), \theta, t)] N(\mathcal{A}, \mathcal{E}, t) d\mathcal{E}
\end{aligned} \tag{9}
$$

and

$$
N(\mathcal{Z}', t+1) = \int_{\omega'_{\mathcal{Z}}} N(\mathcal{A}, \mathcal{E}', t+1) d\mathcal{E}'. \tag{10}
$$

Functional Forms

In order to construct models it is necessary to identify forms for each of the functions described in the section above. These forms can differ for development and inheritance of $\mathcal{A}$ and $\mathcal{E}$. To illustrate this we construct models for two limits. At one limit, all phenotypic variation is attributable to individual differences in $\mathcal{A}$. At the other limit, all individuals are genetically identical: they have the same $\mathcal{A}$ and all individual variation is attributable to $\mathcal{E}$. This captures plasticity defined as the same genotype expressing different phenotypes in different environments. Having considered functional forms for these two limits we combine insights to construct models for phenotypes that are determined by $\mathcal{A}$ and $\mathcal{E}$.

We primarily focus on linear functions for three reasons. First, they are easier to interpret and analyze than non-linear or non-additive forms. Second, when the environment changes impacting populations, responses, at least in the short term, can be well described with linear or linearized additive models (Cooch et al., 2001). Third, selection, the underpinning of evolution, is often directional and well described with linear or linearized associations between phenotypic traits and components of fitness (Kingsolver et al., 2001). Parameters used for all models are provided in the Supplementary Information (SI §1.1), as are expressions to calculate key statistics used to show ecological and evolutionary change from model outputs (SI §1.2). Code to produce each figure is available on GitHub – https://github.com/tncoulson/QG-meets-IPM-figure-code/tree/master.

The environmental drivers θ, t can be both abiotic and biotic. We focus primarily on a biotic driver, population density. However, abiotic drivers have been incorporated into phenotypic IPMs (Simmonds and Coulson, 2015), as have a number of other biotic drivers including frequency dependence (Bassar et al., 2016; Coulson et al., 2011), and species interactions (Adler et al., 2010). Our approach can be extended to capture these biotic drivers using these insights if desired.

Adaptive Evolution

In this section we start with a simple clonal model of a univariate distribution of $\mathcal{A}$. We go on to show how genetic constraints can be imposed to slow, or stop, evolution. We then extend this clonal

model in two ways: first, to include a multivariate, age-structured, distribution of $\boldsymbol{\mathcal{A}}$, and second we relax the clonality assumption and compare the dynamics of clonal and sexual models. Finally, we introduce a new functional form to describe sexual reproduction and compare its performance with our initial approach.

Genotypes (and hence $\mathcal{A}$) are determined at birth and remain fixed throughout life; neither are influenced by the environment. A consequence of this is the development function simplifies to a one-to-one map and can be removed from equations (4) and (8). We also start by considering clonal reproduction, which means that the inheritance function can also be removed as offspring genotype is identical to parental genotype. The dynamics of $\mathcal{A}$ are consequently determined by the survival and reproduction functions – selection. In these models, as long as there is genetic variation within a population, and fitness is a monotonic function of genotype, evolution, defined as $\mathbb{E}(\mathcal{A}, t+1) = \mathbb{E}_R(\mathcal{A}, t) \neq \mathbb{E}(\mathcal{A}, t)$ (where $\mathbb{E}$ represents expectations) will occur.

In our first models we assume non-overlapping generations,

$$N(\mathcal{A}, t+1) = R(\mathcal{A}, t)N(\mathcal{A}, t).$$

and a linear reproduction function $R(\mathcal{A}, t) = R_I + R_{\mathcal{A}}\mathcal{A}$ with expected fitness increasing with the value of $\mathcal{A}$. Over the course of a simulation of 30 generations (SI §1.1 Model A), the population never achieves an equilibrium structure or growth rate; it grows hyper-exponentially (Figure 1(a), black line) and the shape of the breeding value distribution continually changes location (Figure 3(b), black line) and shape (Figure 1(b,d, black lines)). Linear selection only slowly erodes the genetic variance and skew (Figure 1(c,d)) and these changes lead to a slight slowing of the rate of change in the mean breeding value (Figure 1(b)) and the population growth rate (Figure 1(a)) each generation (the black lines are not linear).

In this model there are two ways to prevent the fitness function from generating change in the location of the distribution. First, the fitness function can take unimodal non-linear forms such as $R(\mathcal{A}, t) = R_I + R_{\mathcal{A}}\mathcal{A} + R_{\mathcal{A}^2}\mathcal{A}^2$ with $R_{\mathcal{A}^2} < 0$ and $R(\mathcal{A}, t)$ constrained to non-negative values. This generates stabilizing selection, with the mean breeding value being maintained at the value that

maximizes fitness. Eventually, in this model, the breeding value distribution will achieve a trivial equilibrium – a Dirac delta function at this value. Second, continual change in the location of the distribution can be prevented by defining a maximum possible value for $\mathcal{A}$ that cannot be exceeded. This captures a genetic constraint in the maximum possible character value – i.e. evolution has not evolved a genetic solution to creating a larger breeding value. In our models, this process can be captured by setting the abundance of $N(\mathcal{A} > x, 1) = 0$ where x is the maximum possible trait value that evolution can achieve. Selection now pushes the breeding value distribution up to x, again eventually achieving a trivial equilibrium captured by a Dirac delta function where all mass of the distribution is at $\mathcal{A} = x$.

Genetic constraints can also impact the transient dynamics of the breeding value distribution (Figure 1(a-d, red lines)). When we impose a genetic constraint (SI §1.1 model A with $x = 11.5$), the genetic variance and skew evolve faster than when no genetic constraint is in place (Figure 1(c) and (d)). These more rapid changes result in a slowing in the evolution of the mean breeding value (Figure 1(b)), and of the population growth rate (Figure 1(a)).

Genetic covariances between traits can also capture genetic constraints and can also influence the outcome of evolution. We demonstrate this by developing an age-structured model. $\mathcal{A}$ now becomes age-structured but is still inherited at birth. We construct a multivariate character $\boldsymbol{\mathcal{A}}$ describing the breeding values that influence a character at each age (e.g. $\mathcal{A}1, \mathcal{A}2, \ldots, \mathcal{A}n$ for breeding values at ages $a = 1, 2, \ldots, n$). If some of the same loci contribute to the genetic components of the character at different ages there is a genetic covariation across ages. The genetic variances within each age, and the covariances between ages, can be used to construct a $\mathbf{G}$ matrix (Lande, 1979). Such age-structured $\mathbf{G}$ matrices underpin the character-state approach of quantitative genetics (Lynch and Walsh, 1998). As we demonstrate, IPMs of multivariate characters can be used to study the dynamics of genetic covariances, as well as of genetic variances. In the age-structured model that follows, we define a bivariate normal distribution with a known variance-covariance structure as our starting point and iterate this forwards (SI §1.1 models B-D). We consider a simple case: a monocarpic biennial life cycle where individuals in their first year of life do not reproduce and all

age 2 individuals die after reproduction. As with our model for a species with non-overlapping generations we assume clonal inheritance,

$$N(\mathcal{A}1, 1, t+1) = R(\mathcal{A}2, 2, t)N(\mathcal{A}2, 2, t)$$
$$N(\mathcal{A}2, 2, t+1) = S(\mathcal{A}1, 1, t)N(\mathcal{A}1, 1, t), \tag{11}$$

where survival from age 1 to age 2 is specified as

$$S(\mathcal{A}1, 1, t) = \frac{1}{1 + e^{-(S_{I,1} + S_{\mathcal{A}1,1}\mathcal{A}1)}} \tag{12}$$

with expected survival to age 2 being highest for larger values of $\mathcal{A}1$. Although $\mathcal{A}2$ is not under direct selection, its distribution is modified by its covariance with $\mathcal{A}1$.

$\mathcal{A}2$, the genotype at age 2, determines expected reproduction,

$$R(\mathcal{A}2, 2, t) = e^{(R_{I,2} + R_{\mathcal{A}2}\mathcal{A}2)}. \tag{13}$$

Although $\mathcal{A}1$ does not directly influence reproduction, there is an association between it and reproduction via its covariance with $\mathcal{A}2$. All age 2 individuals die following reproduction in this model, although it is possible to extend our approach to any arbitrary number of ages.

The evolutionary dynamics that particular parameterizations of the fitness functions $S(\mathcal{A}1, 1, t)$ and $R(\mathcal{A}2, 2, t)$ generate are dependent upon (i) the initial covariance between the characters and (ii) the fitness functions (SI §1.1 models B-D). Many parameterizations and initial covariances are likely to generate evolutionary dynamics that may be biologically unrealistic. We demonstrate this with three contrasting parameterizations, considering size as our trait (Figure 1(e)-(g)). In the first example, (Figure 1(e) SI §1.1 model B), the two characters positively covary and experience selection in the same direction. Over the course of the simulation the average developmental trajectory has evolved with $\mathcal{A}1$ evolving to be 1.76 times larger and $\mathcal{A}2$ evolving to be 1.52 times larger. For a trait like body size, such a proportional change at different ages may be appropriate. In examples (Figure 1(f and g), SI §1.1 models C and D) the bivariate character evolves in contrasting ways. In (F), $\mathcal{A}2$ evolves much faster than $\mathcal{A}1$ while in (G) $\mathcal{A}1$ evolves to be larger, while $\mathcal{A}2$ evolves to be

smaller. These simulations demonstrate that only a constrained set of fitness functions and genetic covariances will give biologically realistic evolutionary trajectories for the size-related traits that biologists often study.

We now return to a univariate model and examine the clonality assumption. How can the clonality assumption be relaxed, and what are the consequences? In sexually reproducing species, offspring inherit a mix of their parent's genomes. However, genetic segregation means that full siblings do not have the same genotype. When additivity is assumed, the breeding value of offspring is expected to be midway between parental breeding values. However, to obtain the distribution of offspring genotypes, the contribution of genetic segregation to variation among offspring needs to be taken into account. In two sex models, three steps are required to generate the distribution of offspring genotypes or breeding values given parental values. First, a distribution of mating pairs needs to be constructed. Second, the distribution of midpoint parental genotypes or breeding values given the distribution of mating pairs needs to be constructed. Third, segregation variance needs to be added to the distribution (Feldman and Cavalli-Sforza, 1979; Felsenstein, 1981; Turelli and Barton, 1994). The mating system and the segregation variance are related: when mating is assortative with respect to genotype, the segregation variance is small and siblings closely resemble one another and their parents. In contrast, when mating is disassortative with respect to genotype, siblings can differ markedly from one another, and the segregation variance is large.

Expressions have been derived for the segregation variance for the infinitesimal model where it is assumed that traits are determined by a very large number of unlinked loci of small additive effects and mating is random (Fisher, 1930). The infinitesimal model is assumed in most empirical quantitative genetic analyses (Kruuk et al., 2008) and in our initial model. For random mating where both sexes have identical demographies, the distribution of offspring breeding values given parental breeding values is (Barfield et al., 2011):

$$N(\mathcal{A}, t+1) = \left(\frac{N_R(\cdot, t)}{2} * \frac{N_R(\cdot, t)}{2} * \phi\left(\cdot, \frac{\sigma_R^2(\mathcal{A}, t)}{2}\right)\right)(\mathcal{A}), \tag{14}$$

where $*$ represents convolution and $\phi(\mathcal{A}, \sigma^2) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left[-\frac{\mathcal{A}^2}{\sigma^2}\right]$ is a Gaussian function with mean

zero and variance σ^2 representing the segregation variance.

If males and females have different demographies then they will have different distributions of genetic values after selection; we represent these as $N_R^{(M)}(\mathcal{A},t)$ and $N_R^{(F)}(\mathcal{A},t)$, respectively. In this case, eq. (14) is replaced by

$$N(\mathcal{A},t+1) = \left(\frac{N_R^{(M)}(\cdot,t)}{2} * \frac{N_R^{(F)}(\cdot,t)}{2} * \phi\left(\cdot, \frac{\sigma^2_{R^{(M)}}(\mathcal{A},t) + \sigma^2_{R^{(F)}}(\mathcal{A},t)}{2} \right) \right)(\mathcal{A}), \tag{15}$$

where $\sigma^2_{R^{(M)}}(\mathcal{A},t)$ and $\sigma^2_{R^{(F)}}(\mathcal{A},t)$ are the post-recruitment-selection genetic value variances of males and females, respectively.

The first two terms on the right hand side of equation (15) generates the distribution of expected parental midpoint values; it ensures that the mean breeding value among offspring is midway between the two parental breeding values. However, because the parental distributions are halved, the variance of this distribution is half that of the parental distributions. The third term on the right hand side of equation (15) adds the segregation variance. For random mating, the variance is assumed to be normally distributed with a mean of 0 and a variance of half the additive genetic variance among the entire population when the population is at linkage equilibrium (Felsenstein, 1981). We approximate this variance as half the additive genetic variance in the parental distribution (Feldman and Cavalli-Sforza, 1979). This approach has already been incorporated into IPMs (Barfield et al., 2011; Childs et al., 2016).

We now run two simulations (Figure 2(a)-(d)) to examine differences in the predictions of clonal and sexual models. The first model assumes clonal inheritance and the second the convolution in Equation (15), with both models assuming a linear function $R(\mathcal{Z},t)$ (SI §1.1 model E). The two models predict slightly divergent dynamics. The reason for this is that equation (15) results in the skew and kurtosis in $N_R(\mathcal{A},t)$ is reduced at each time step in the sexual model compared to in the clonal model. If selection is exponential (and the starting distribution proportional to a Gaussian distribution) then there will be no difference between the two approaches. This is because a normal distribution multiplied by an exponential fitness function results in a normal distribution with an unchanged variance (Diaconis et al., 1979). These results suggest that insights from clonal models

will approximate those from sexual models reasonably well, at least when males and females have similar demography.

Some authors have queried the use of Equation (3) as an approximation in IPMs to the inheritance convolution in Equation (15) used in models of sexually reproducing species (Chevin et al., 2010; Janeiro et al., in press). However, being able to construct inheritance functions for $\mathcal{A}$ that are of the form of equation (3) would be useful as it would permit methods developed for two sex phenotypic IPMs to be applied to evolutionarily explicit IPMs (e.g. Schindler et al., 2015). Given Gaussian approximations frequently perform well in models of evolution (Turelli and Barton, 1994) we hypothesize that Gaussian inheritance functions may perform well in evolutionarily explicit IPMs. We consequently constructed a Gaussian inheritance function and compared results with those obtained from the convolution.

Equation (15) results in the mean and variance of the parental and offspring breeding value being the same. We can approximate this by ensuring that the function $\mu^H(\mathcal{A}, t)$ passes through the coordinate $x = \mathbb{E}(N_R(\mathcal{A}, t)), y = \mathbb{E}(N_R(\mathcal{A}, t))$ and that the variance $V^H(\mathcal{A}, t) = \sigma^2(N_R(\mathcal{A}, t))$. When both sexes have the same demography, we can write,

$$\begin{aligned} \mu^H(\mathcal{A}, t) &= (1-\eta)\mathbb{E}_R(N_R(\mathcal{A}, t)) + \eta\mathcal{A} \\ V^H(\mathcal{A}, t) &= (1-\eta)^2\sigma^2(N_R(\mathcal{A}, t)) \end{aligned} \tag{16}$$

where $\mathbb{E}$ and σ^2 represent expectations and variances respectively and η represents the degree of assortative mating. When $\eta = 1$ mating is entirely assortative, when $\theta = 0.5$ mating is random and when $\eta = 0$ mating is completely disassortative. An equation for the case when males and females have different demographies is provided in the SI §1.3. The approximation in Equation (16) will increase in accuracy as the distribution of mid-point parental breeding values becomes more Gaussian.

When we compared predictions from equations (15) and (16) with $\eta = 0.5$ using the same model used to compare clonal and sexual life histories, results were indistinguishable (Figure 2(a)-(d). This reveals that, for linear selection, Gaussian inheritance functions for $\mathcal{A}$ perform remarkably well.

Our approximation can be used to examine the dynamical contributions of non-additive genetic processes to population responses to environmental change in a phenomenological manner. Fisher (1930) demonstrated that dominance variance can be treated as an offset, and in our models this would lower the intercept of the function $\mu^H(\mathcal{G}, t)$ in equation (16). A consequence of this is that the mean of the offspring genotype is no longer equal to the mean of parental genotype and the dynamics of genotypes no longer exactly match the dynamics of alleles. We demonstrate this with a single locus-two allele model. When the effects of alleles are additive, the dynamics of the genotype captures the dynamics of alleles (Figure 2(e)). In contrast, when the heterozygote has higher fitness, allele frequencies do not change once the equilibrium is achieved. However, selection and inheritance alter genotype frequencies (Figure 2(f)). This effect of dominance variance can be phenomenologically capturing within an IPM by setting the intercept of the inheritance function for the genetic component of the phenotype to be less than $\frac{\mathbb{E}_R(N_R\mathcal{A},t)}{2}$ – this imposes an offset that can reverse gains made by selection (Figure 2(g)). Because this offset is negative when dominance variance is operating, dominance variance will slow, or prevent, rates of evolutionary change. We could easily phenomenologically explore how a particular value of this offset impacts predicted dynamics, however, further work is required to relate different levels of dominance variance to specific values of the offset in our models.

Having shown how IPMs can be formulated to project forwards the dynamics of the genetic component of the phenotype under a wide range of circumstances, we now turn our attention to the dynamics of the environmental component of the phenotype.

Plasticity

Plasticity is determined by the dynamics of $\mathcal{E}$ and in particular in how $\mathcal{E}$ is influenced by the ecological environment θ. For this, we require a probability density function. We show in this section how different forms of plasticity can be incorporated into evolutionarily explicit IPMs, and explore the dynamics of some simple cases.

To capture plasticity in IPMs we need to model the probability of transition from $\mathcal{E}$ at time

t to $\mathcal{E}'$ at time $t+1$ as a function of the environment θ. For most plastic traits we have a poor mechanistic understanding of development and inheritance patterns, and for that reason we use the Gaussian probability density function in Equation (3).

In quantitative genetics it is often assumed that the mean of $\mathbb{E}(\mathcal{E}, t) = 0$ and any individual departures are purely random (Falconer, 1960). In equation 3 this requires the intercepts and slopes of the functions $\mu^D(\dots)$ and $\mu^H(\dots)$ to take the following values: $\mu_I^H = 0$, $\mu_I^D = 0$, $\mu_{\mathcal{E}}^H = 1$ and $\mu_{\mathcal{E}}^D = 1$. We relax this assumption and allow the mean (and variance) of $\mathcal{E}$ to vary with time as θ varies by specifying particular forms for development and inheritance functions of $\mathcal{E}$.

Gaussian transition functions (equation 3) can be formulated to predictably modify moments of the distribution of $\mathcal{E}$ from time t to time $t+1$. For example, careful choice of intercepts and slopes of $\mu^D\mathcal{E}, t$, $\mu^H\mathcal{E}, t$, $V^D\mathcal{E}, t$ and $V^H\mathcal{E}, t$ can be used to predictable grow, or shrink, the variance of $\mathcal{E}$ via either development or inheritance (SI §1.4). In addition, specific biological processes can be easily incorporated into the dynamics of $\mathcal{E}$: if the slopes $\mu_{\mathcal{E}}^D \neq 0$ or $\mu_{\mathcal{E}}^H \neq 0$ then there will be temporal autocorrelation in the value of $\mathcal{E}$ among individuals, and between parents and their offspring. For example, if $\mu_{\mathcal{E}}^D > 0$ then individuals with a relatively large value of $\mathcal{E}$ at time t will be expected to have a relatively large value of $\mathcal{E}'$ at time $t+1$. This property of development functions is useful as it allows some memory of $\mathcal{E}$ across ages: if an individual has benefited from a particularly good set of circumstances at one age, any phenotypic consequences can persist to older ages. In a similar vein, if $\mu_{\mathcal{E}}^H > 0$ then a parent with a relatively large $\mathcal{E}$ at time t will produce offspring with relatively large $\mathcal{E}'$s at time $t+1$, a form of parental environmental effect (Nussey et al., 2007).

Deterministic IPMs incorporate probabilistic transitions when $V^H(\mathcal{E}'|\mathcal{E}, \mathcal{A}, t) = 0$ and $V^D(\mathcal{E}'|\mathcal{E}, \mathcal{A}, t) = 0$. These probabilities do not vary from one time step to the next. In stochastic models these functions can include terms for an environmental driver θ, such that the variation in trajectories changes with the environment. In evolutionarily explicit models, the variance in transition rates among different values of $\mathcal{E}$ can be made to depend upon θ, $\mathcal{A}$ and their interaction (if desired). This means that individuals with specific values of $\mathcal{A}$ can produce offspring with more variable values of $\mathcal{E}$ (and

consequently $\mathcal{Z}$) in particular environments than individuals with other values of $\mathcal{A}$. This is an example of bet-hedging (Childs et al., 2010). We do not provide examples of bet-hedging in this paper, but instead focus on the incorporation of θ into $\mu^H(\mathcal{E}'|\mathcal{E}, \mathcal{A}, \theta, t)$ and $\mu^D(\mathcal{E}'|\mathcal{E}, \mathcal{A}, \theta, t)$.

Different formulations of $\mu^H(\dots)$ and $\mu^D(\dots)$ can be used to capture a variety of different forms of plasticity (Table 2). When θ is incorporated as an additive effect, it acts to shift the intercept of these functions as t changes. This means that the environment influences all values of $\mathcal{A}$ in the same manner. If $\mathcal{Z} = \mathcal{A} + \mathcal{E}$ then $\mathcal{Z}$ changes as a function of how θ influences $\mathcal{E}$ if $\mathcal{A}$ remains constant. $\mathcal{A}$ remains constant when it does not vary within individuals as they age, or if $\mathcal{A}'$ in offspring is the same as $\mathcal{A}$ in parents.

Interactions between $\mathcal{E}$, $\mathcal{A}$ and θ are listed in Table 2. Each form describes a different type of reaction norm (Gavrilets and Scheiner, 1993). These forms allow $\mathcal{E}$ to develop among individuals (phenotypic plasticity) or be inherited (epigenetic inheritance) as a function of an individual's breeding value $\mathcal{A}$ and the environment θ as well as the value of $\mathcal{E}$ at time t.

Plasticity can be either adaptive or non-adaptive (Ghalambor et al., 2015), and both forms can be captured into our models. Adaptive plasticity enables populations to rapidly respond to an environmental change. For example, if environmental change reduces population size, then adaptive plasticity would result in a change to the mean of the phenotype via either phenotypic plasticity (the development function) or epigenetic inheritance (the inheritance function) that leads to an increase in survival or recruitment rates. In contrast, non-adaptive plasticity does the opposite, potentially exacerbating the detrimental effects of environmental change.

We demonstrate this with an example of a simple IPM of a species with non-overlapping generations: $N(\mathcal{E}', t+1) = \int H(\mathcal{E}'|\mathcal{E}, \theta, t) R(\mathcal{E}, t) N(\mathcal{E}, t) d\mathcal{E}$. Because plasticity is defined as different breeding values $\mathcal{A}$ or genotypes expressing a different phenotype $\mathcal{Z}$ in different environments, our models assume all individuals have the same $\mathcal{A}$ but that $\mathcal{E}$, and consequently $\mathcal{Z}$, is a function of the environment θ. This means we can remove $\mathcal{A}$ from the model. We assume a linear fitness function

and a Gaussian inheritance function,

$$
\begin{aligned}
R(\mathcal{E},t) &= R_I + R_{\mathcal{E}}\mathcal{E} + R_\theta\theta \\
\mu^H(\mathcal{E},t) &= \mu_I^H + \mu_{\mathcal{E}}^H\mathcal{E} + \mu_\theta^H\theta \\
V^H(\mathcal{E},t) &= V_I^H
\end{aligned}
$$

Next, we assume that the phenotypic trait is positively associated with expected recruitment such that $R_{\mathcal{E}} > 0$. We also assume that the environmental driver is positively associated with expected recruitment such that as θ increases in value, fitness increases ($R_\theta > 0$). This means that the population growth rate (in a density-independent model) or population size (in a density-dependent model) also increases with θ. Now assume that a negative environmental perturbation decreases θ such that fitness decreases. For adaptive plasticity to counter this, the effect of the decrease in θ on epigenetic inheritance must increase the expected value of $\mathcal{E}$. In our simple model, this can only occur if $\mu_\theta^H < 0$. Then, as θ declines, $\mu_\theta^H\theta$ becomes less, and the value of $\mu_I^H + \mu_\theta^H\theta$ becomes larger, increasing the mean of $\mathcal{E}$ and fitness. In general, in additive linear models like this, if $R_{\mathcal{E}}$ and μ_θ^H take opposing signs then plasticity will be adaptive.

We develop three density-dependent models of a phenotype in a species with non-overlapping generations. In all models we define the fitness function to be $R(\mathcal{E},t) = R_I + R_{\mathcal{E}}\mathcal{E} + R_{n(t)}n(t)$ where $n(t) = \int N(\mathcal{E},t)d\mathcal{E}$ and where $R_{n(t)} < 0$. In each model we define $\mu^H(\mathcal{E},t) = \mu_I^H + \mu_{\mathcal{E}}^H\mathcal{E} + \mu_{n(t)}^H n(t)$. We set in model (F) $\mu_{n(t)}^H = 0$; in model (G) $\mu_{n(t)}^H < 0$; and in model (H) $\mu_{n(t)}^H > 0$ (SI §1.1).

The first model (F) does not include plasticity ($\mu_{n(t)}^H = 0$), the second (G) captures adaptive plasticity ($\mu_{n(t)}^H < 0$ and $R_{\mathcal{E}} > 0$), and the third (H) captures non-adaptive plasticity ($\mu_{n(t)}^H > 0$ and $R_{\mathcal{E}} > 0$). Because the models are not age-structured and do not include development, plasticity operates via epigenetic inheritance (e.g. maternal environmental effects). The same logic can be extended to the development function in age-structured populations. In our examples, parameterizations are chosen so all models converge to the same value of carrying capacity, K. Once all three models have converged, we initially impose a one off perturbation. Model (G) regains the equilibrium first, followed by model (F), and then model (H) (Figure 3(a)) showing that adaptive

plasticity allows the population to recover from a one off environmental perturbation much faster than when there is no plasticity, or plasticity is non-adaptive. Non-adaptivity plasticity significantly slows the rate at which the population can recover from a perturbation, with the initial population size pre-perturbation only re-attained after 80 generations.

Adaptive and non-adaptive plasticity also impact the way populations respond to permanent environmental change. We demonstrate this by running the same models (F), (G) and (H), except now we impose a constant change in fitness by permanently changing the intercept of the fitness function R_I. When we do this, the three models attain different equilibria population sizes (Figure 3(b)) and different mean phenotypes (Figure 3(c)). Model (G) achieves a larger population size than the two other models. This buffering of the population against environmental change happens because adaptive phenotypic plasticity results in a change in the mean phenotype (Figure 2(c)) that increases the expected recruitment rate and asymptotic population size (Figure 2(b)). In contrast, non-adaptive plasticity exacerbates the consequences via a change in the mean phenotype that decreases fitness.

In contrast to our example models in the §**Adaptive Evolution**, the IPMs we have developed in this section, and indeed all non-genetic IPMs so far published, achieve an asymptotic population growth rate or equilibrium population size and a stable population structure. These IPMs have monotonically increasing or decreasing fitness functions: an increase in the character results in an increase in expected fitness. A consequence of this is that in these models the recruitment function acts to alter the location of the character distribution, and often also alter its shape (Wallace et al., 2013). In other words, $N_R(\mathcal{E},t)-N(\mathcal{E},t) \neq 0$. In models of species with non-overlapping generations at equilibrium like those above, the inheritance function for $\mathcal{E}$ must exactly reverse the changes to the character distribution generated by the fitness function. This means, for deterministic models, that

$$N_R(\mathcal{E},t) - N(\mathcal{E},t) = N(\mathcal{E}',t+1) - N_R(\mathcal{E},t). \tag{17}$$

This equality requires moments of parental and offspring characters to differ from one another if $N_R(\mathcal{E},t) - N(\mathcal{E},t) \neq 0$. When there is a correlation between parental and offspring traits in the

inheritance function for $\mathcal{E}$ as in our models, the intercept of the inheritance function must take a value such that offspring characters are smaller than their parent's were at the same age (Coulson and Tuljapurkar, 2008).

IPMs for species with overlapping generations include development functions $D(\mathcal{E}'|\mathcal{E}, a, t)$. These functions can alter the size and distribution of the character distribution as individuals age. When generations are overlapping, and at equilibrium, changes to the location of the character distribution via survival, recruitment and development are all exactly countered by the inheritance functions $H(\mathcal{X}'|\mathcal{X}, a, t)$.

Coulson and Tuljapurkar (2008) showed that in red deer age-specific effects meant that young and old parents were incapable of producing offspring that had the same body weight as they did at birth. This mechanism reversed the effects of viability selection removing small individuals from the population early in life. The same process was observed in marmots (Ozgul et al., 2010) and Soay sheep (Ozgul et al., 2009) and may be general for body size in mammals.

We have now developed IPMs for (i) $\mathcal{A}$ where we assumed all individuals had the same, constant, $\mathcal{E}$ and (ii) $\mathcal{E}$ where we assumed all individuals had the same, constant, $\mathcal{A}$. We have shown how IPMs can capture a wide range of biological processes including adaptive and non-adaptive plasticity and correlated characters, and the circumstances when equilibria are achieved. We now link together these advances into models of the joint dynamics of the bivariate distribution $N(\mathcal{A}, \mathcal{E}, t)$.

Models for the phenotype consisting of genetic and environmental components

In the section we construct models where the character can be determined by a mixture of the genetic and environmental components. These models allow us to explore how adaptive evolution is influenced by plasticity.

We first develop a dynamic univariate version of the Breeders equation (Falconer, 1960) for a species with non-overlapping generations in a constant environment. In this case, the environmental component of the phenotype is assumed to be a consequence of developmental noise: individuals achieve their genetic potential, plus or minus a departure. At each generation within each breeding

value, the distribution of the environmental component of the phenotype is assumed to be Gaussian with a mean of 0 and a constant variance (SI §1.1 Model I).

Our initial conditions are a bivariate Gaussian distribution of $\mathcal{A}$ and $\mathcal{E}$ which we iterate forwards for 300 time steps. Over time, the mean of the genetic component of the phenotype increases. In contrast, the mean of the environmental component is constant. The population grows hyper-exponentially (Figure 4(a)), the mean of the phenotype increases in value due to evolution (Figure 4(a,d)) and the additive genetic variance is slowly eroded (Figure S2). Because the additive genetic variance is eroded, while the phenotypic variance remains constant, the heritability declines over time (Figure S2).

Our second model (SI §1.1 model J) has a negative density-dependent term in the fitness function. The phenotype evolves faster in this model than in our density-independent model (Figure 4(b)). Population size grows nearly linearly in this model (Figure 4(d)), although the rate of increase does slow slightly each generation as genetic variation is eroded. The difference between the hyper-exponential and nearly linear increases in population size between the density independent and density-dependent models explain the difference in the rates of evolution. This is because the selection differential that determines the rate of evolution (an emergent property from our model (Wallace et al., 2013)) has the population growth rate in its denominator. The population growth rate is smaller in the density-dependent model (just above unity) than in our density-independent one (it increases with time), and this leads to an increase in the strength of selection and the rate of evolution (see also Pelletier and Coulson, 2012). A consequence of this is that the additive genetic variation and heritability tend towards zero faster the in density-dependent model than in the density-independent one (Figure S2).

In our third model (SI §1.1 model K), negative density-dependence is included in the inheritance function for the environmental component of the phenotype as well as in the fitness function. This captures adaptive phenotypic plasticity. This results in a negative change in the mean of the environmental component of the phenotype with time (Figure 4(c)). This decrease is reflected in a change in the mean of the phenotype itself. Adaptive phenotypic plasticity leads to a decline in

the population growth rate which results in a slight increase in the rate of evolution compared to the density-dependent model with no plasticity. However, the effect is not large and is only just distinguishable when comparing Figures 4(b) and (c).

In our final models (SI §1.1 models L to N) we examine how a one off perturbation influences the mean of the phenotype, its components and the population growth rate (Figure 4(g)-(l)) when there is no plasticity, adaptive plasticity and non-adaptive plasticity. We set the variance in the genetic and environmental component of the phenotype to be equal, giving an initial heritability of $h^2 = 0.5$. In each model we allow the population to achieve the same equilibrium population size in the absence of selection ($R_{\mathcal{Z}} = 0$). We then impose a one off mortality event when 99% of individuals above the mean of the phenotype are killed off. At this point we also impose selection ($R_{\mathcal{Z}} = 0.1$). In all three models the mortality event results in a small change in the mean value of the phenotype (SI §1.5 for an explanation) (Figure 4(g)-(i), red lines) but a halving of population size (Figure 4(j)-(l)). Adaptive plasticity results in the environmental component of the phenotype returning to its pre-perturbation value very quickly (Figure 4(g)-(i) blue lines). In contrast, although the perturbation causes a modest change in the mean of the genetic component of the phenotype, it takes > 10 generations for evolution to reverse the change (Figure 4(g)-(i), black lines). This demonstrates that a strong selective effect can leave a large population dynamic impact, but leave only a small initial signature in the phenotype even when the trait is highly heritable.

Over the longer term, the dynamics of the all components of the phenotype, the phenotype itself and the population dynamics all depend upon whether plasticity is adaptive or non-adaptive. Adaptive plasticity allows the population size to initially recover from the perturbation more quickly than when plasticity is absent or non-adaptive (Figure 4(j)-(l)). However, over a longer time period, non-adaptive plasticity results in the population achieving a larger size than when plasticity is absent or adaptive. These differences in population growth rate impact rates of evolution: immediately following the perturbation, the rate of evolution is greatest when plasticity is non-adaptive. However, the rate of evolution then increases when plasticity is adaptive (Figures S2 and S3). As with our previous models, the effects of adaptive and non-adaptive plasticity on rates of

evolution are relatively small, but our results demonstrate how the two processes can interact.

Signatures of evolution in phenomenological descriptions of mechanistic processes

The models in the previous section are quite complex. Do we always need to construct such evolutionarily explicit IPMs to predict population responses to environmental change, or can we rely on simpler, phenotypic IPMs? There are two reasons why it may be preferable to not construct evolutionarily explicit models. First, evolutionarily explicit IPMs are more complicated to construct than those that do not include genotypes or breeding values. Second, when data are unavailable to explicitly include breeding values into models (Traill et al., 2014*b*), the effects of evolution on predicted dynamics can still be explored by examining the consequences of perturbing parameter values (Traill et al., 2014*a*).

When evolution occurs within a system we would expect parameters in phenomenological inheritance and development functions that are fitted to data to change with time. We can see this in Figure 1(e)-(g)). In these age-structured evolutionarily explicit models, the bivariate breeding value distribution (black contours) changes location as evolution occurs. We have fitted Gaussian development functions to these bivariate distributions at the beginning of each simulation and at the end (coloured image plots). The parameters that determine these developments functions have clearly changed as the location of the functions have changed. A similar process occurs for inheritance functions (not shown).

Numerous authors have previously noted this phenomenon in models of evolution. For example, in population genetic (Charlesworth, 1994) and eco-evolutionary models (Coulson et al., 2011; Yoshida et al., 2003) when genotype frequencies change with time, macroscopic, population level quantities like mean survival and recruitment also change; in adaptive dynamic models, as one strategy invades another, population level parameters inevitably change with strategy frequency over time (Metz et al., 1996); in quantitative genetic predator-prey models population level parameters of both predators and prey vary over time leading to persistence of the interaction (Doebeli,

1997); and in evolutionarily explicit IPMs parameters in inheritance functions have been shown to change with time as evolution progresses (Rees and Ellner, 2016). These insights are useful because if evolution is occurring within a system, then temporal trends in statistical estimates of model parameters would be expected – in other words, the effect of time, either additively or in an interaction with other parameters, would be expected in $\mu^H(\mathcal{Z}, t)$, $\mu^H(\mathcal{Z}, a, t)$ or $\mu^D(\mathcal{Z}, t)$. If significant temporal trends are observed in parameters in development and inheritance functions that cannot be attributed to a changing environmental driver, then evolutionarily explicit IPMs may required.

What about parameters in fitness functions $S(\mathcal{Z}, t)$ and $R(\mathcal{Z}, t)$? Can any inferences from temporal trends in these parameters be made? In our approach, evolution of a focal trait would not be expected to alter statistical estimates of the fitness functions. In our models, evolution simply moves the location and shape of the phenotype distribution, but not its association with survival or recruitment.

We have identified one circumstance where evolution will leave a signature in the dynamics of fitness function parameters. Parameters in these functions can evolve in the presence of a genetically unmeasured correlated character that is also evolving. To demonstrate this we construct a model of a bivariate character, examine the dynamics it predicts, before exploring the consequences of failing to measure one of the characters.

We assume clonal inheritance such that dynamics of the characters are solely determined by a bivariate fitness function,

$$R(\boldsymbol{\mathcal{A}}, t) = R_I - R_{\mathcal{A}1}\mathcal{A}1 + R_{\mathcal{A}2}\mathcal{A}2 \tag{18}$$

The dynamics this model predicts depend upon the initial covariance between the two characters in a similar way to our age-structured model (equation 11). In our first example the two characters negatively covary, while in the second they positively covary (SI §1.1 for model parameterizations). The initial negative covariation allows rapid evolution, with population growth (Figure 5(a)), the mean of the characters (Figure 5(b)), their variances (Figure 5(c))) and the covariance between them (Figure 5(d)) evolving relatively quickly. In contrast, when the two characters positively

covary, evolution is much slower, with the character means, variances and covariance changing much more slowly, even though the fitness functions are identical in each model (Figure 5(e)-(h)).

We now construct a fitness function for $\mathcal{A}1$ when $\mathcal{A}2$ is not measured. We start by defining mean fitness, an observable, as $\mathbb{E}(R.t) = \mathbb{E}(R(\boldsymbol{\mathcal{A}}, t))$. The slope $\hat{R}_{\mathcal{A}1,t}$ is given by,

$$\hat{R}_{\mathcal{A}1,t} = R_{\mathcal{A}1} + \frac{\sigma(\mathcal{A}1, \mathcal{A}2, t)}{\sigma^2(\mathcal{A}1, t)} R_{\mathcal{A}2}. \tag{19}$$

The intercept can be calculated in the usual manner by estimating the means of fitness and $\mathcal{A}1$

$$\hat{R}_{I,t} = \mathbb{E}(R, t) - \hat{R}_{\mathcal{A}1,t}\mathbb{E}(\mathcal{A}1, t), \tag{20}$$

giving,

$$R(\boldsymbol{\mathcal{A}}, t) = \hat{R}_{I,t} + \hat{R}_{\mathcal{A}1,t}\mathcal{A}1. \tag{21}$$

Equation (21) is what would be estimated from data if $\mathcal{A}2$ were not measured and included in analyses (Kendall, 2015; Söderström and Stoica, 2002). It will correctly describe the consequences of selection on $\mathcal{A}1$ even though $\mathcal{A}2$ could be correlated with it. This is because the unmeasured correlated character impacts fitness whether it is measured or not, and consequently impacts the association between the focal character and fitness in its absence (Lande and Arnold, 1983). However, the fitness function cannot provide accurate predictions over multiple generations when it is assumed that the fitness function is constant.

Over multiple generations the existence of unmeasured correlated characters will alter parameters in the fitness function in Equation (21) if selection alters genetic variances and covariances of measured and unmeasured correlated characters (Figure 5(i)-(j)). This is because $\hat{R}_{I,t}$ and $\hat{R}_{\mathcal{A}1,t}$ are both functions of the covariance between the two characters (equations 19-21). If selection alters this covariance, parameters $\hat{R}_{I,t}$ and $\hat{R}_{\mathcal{A}1,t}$ will evolve with time. It is also why parameters we use the subscript t for $\hat{R}_{I,t}$ and $\hat{R}_{\mathcal{A}1,t}$. Evidence of correlated characters under selection can consequently be inferred if parameters in fitness functions are observed to change with time in a system in the absence of a changing environmental driver. Note that a non-stationary unmeasured environmental driver could also generate trends in parameter values in fitness functions in phenomenological IPMs.

Discussion

In this paper we develop an approach that allows prediction of how populations respond to environmental change via adaptive evolution and plasticity. We do this by incorporating mechanistic insights from evolutionary genetics into data-driven structured population models. Our approach is to split the phenotype into its genetic and environmental components and to model the dynamics of the genetic component with functions based on mechanistic understanding. In contrast, the dynamics of the environmental component of the phenotype, where mechanistic insight is lacking, are modeled with phenomenological functions that can be identified from the analysis of data. Our approach is appropriate for sexually reproducing or clonal species with either overlapping or non-overlapping generations.

Evolutionarily explicit structured models

Integral projection models (IPMs) are now a widely used tool in ecology and evolution because of their versatility and the ease with which they can be parameterized (Merow et al., 2014). All key statistics routinely estimated in population ecology, quantitative genetics, population genetics and life history describe some aspect of a character distribution or its dynamics (Coulson et al., 2010). IPMs are so versatile because they describe the dynamics of these distributions. Characterization of the determinants of these statistics gained via sensitivity or elasticity analysis of models have provided insight into how ecological and evolutionary quantities that interest biologists are linked (Coulson et al., 2011). Although this logic was developed several years ago, there has recently been criticism that IPMs cannot be used to track the dynamics of multivariate breeding values expressed at different ages (Chevin, 2015; Janeiro et al., in press). Our paper addresses this criticism head-on—we show how IPMs can be formulated to capture such mechanistic complexity. In demonstrating this we develop a general modeling approach to capture population responses to environmental change. Having done this, we are now in a position to construct IPMs of quantitative characters and examine how perturbing the environment will influence not only the dynamics

of the phenotype and its genetic and environmental components, but also the life history (Steiner et al., 2014, 2012) and population dynamics (Easterling et al., 2000).

The work we present here adds to a growing literature that explicitly incorporates evolution into structured models, and integral projection models in particular. Within the population genetics paradigm, Charlesworth (1994) developed structured models with a one-to-one map between genotype and phenotype in age-structured populations. Building on this work, Coulson et al. (2011) showed how simple genetic architectures can be incorporated into IPMs, developing a model to explore how evolution at a single locus would occur simultaneously with phenotypic change of discrete and continuous characters, life history and population dynamics.

Working in the quantitative genetic paradigm, Lande (1982) derived age-structured models that tracked the dynamics of the mean of the additive genetic component of the phenotype ($\mathbb{E}(\mathcal{A})$ in our notation) and the mean of the phenotype itself ($\mathbb{E}(\mathcal{Z})$). He assumed a constant genetic-variance covariance matrix and consequently weak selection and normally distributed character values—assumptions we relax. Barfield et al. (2011) extended Lande (1982)'s approach to track the dynamics of the entire character distribution and to stage-structured populations. In doing so, they developed a general, flexible approach to track the entire distributions of $\mathcal{A}$ and $\mathcal{Z}$. Childs et al. (2016) extended this approach to two sexes. Because $\mathcal{A}$ is inherited with mechanistic rules that are not impacted by the environment, while inheritance and development of $\mathcal{E}$ are plastic and can be impacted by the ecological environment (Falconer, 1960), it is difficult to incorporate the effects of the environment on the dynamics of the phenotype by focusing on $\mathcal{A}$ and $\mathcal{Z}$ as Lande (1982), Barfield et al. (2011) and Childs et al. (2016) have done. In contrast, our approach (which otherwise has a similar logic to Barfield et al. (2011) and Childs et al. (2016)) tracks the dynamics of $\mathcal{E}$ and $\mathcal{A}$ (or $\mathcal{G}$—the full genotypic value, including non-additive components—if desired), making incorporation of environmental drivers that influence inheritance and development of $[\mathcal{E}]$ more straightforward. We show that it is possible to have selection operating on the phenotype while incorporating mechanistic insights into the dynamics of the genetic component of the phenotype and phenomenological insight into the role of the ecological environment on the dynamics of the

environmental component of the phenotype. By doing this, we show how population responses to environmental change via adaptive evolution, phenotypic plasticity and epigenetic inheritance can be simultaneously explored. This opens up the way to provide novel insights into the circumstances when each process is expected to contribute to population responses to environmental change.

Population responses to environmental change

Unlike previous evolutionarily explicit IPMs (Barfield et al., 2011; Childs et al., 2016; Rees and Ellner, 2016), our approach requires explicit consideration of the inheritance and development of $\mathcal{E}$, the environmental component of the phenotype. This allows our models to capture a range of plastic responses to environmental change along with adaptive ones. What do our findings say about the contributions of plasticity, evolution, and their interaction to population responses to environmental change?

Detrimental environmental change often causes a decline in population size. When there is an association between a phenotypic trait and survival and recruitment rates, phenotypic change can lead to increased survival and recruitment rates (Ozgul et al., 2010) and consequently an increase in population growth rate and size. Two processes can lead to phenotypic change – plasticity and adaptive evolution. There has been considerable discussion about the relative roles of each in allowing populations to respond to change (e.g. Bonduriansky et al., 2012; Chevin et al., 2010).

Genotypes and breeding values remain fixed within individuals throughout life which means that differential survival and recruitment rates are the processes that alter these distributions and underpin evolution. The strength of differential survival and recruitment can be impacted by environmental variation generating fluctuating selection (Lande, 2007). Environmental variation does not influence genetic inheritance: once mating pairs are formed, inheritance of breeding values, $\mathcal{A}$, does not alter the mean or variance of breeding value distributions (Fisher, 1930). In contrast, distributions of the environmental component of the phenotype can be altered via survival, recruitment, development and inheritance with each process potentially impacted by environmental variation (Reed et al., 2010). Given these differences between the dynamics of $\mathcal{A}$ and $\mathcal{E}$ plasticity

can lead to more rapid change than evolution in our models (e.g. Figure 4). This is because more biological processes can directly alter the distribution of plastic characters than can impact distributions of breeding values. These results are consistent with those of other authors, including Lande (2009) and Chevin et al. (2010), who also concluded that plastic change should be faster than evolutionary change. But how quickly will evolution alter phenotypic trait distributions?

Our results on the speed of evolution suggest that claims of detectable rapid evolution in quantitative phenotypes is likely to take a few tens of generations. For example, environmental change increases mortality leading to a decline in population size, but for mortality selection to lead to evolutionary change over the course of a generation, a large proportion of the population needs to be selectively removed and the phenotype needs to be highly heritable. This is seen in our model results (Figure 4(g)-(i)) and with a simple numerical example: when all individuals above the mean of a normally distributed character are removed from the population and the trait has a heritable of $h^2 = 0.5$, population size halves in a single time step but the mean of the character will only shift from the 50th percentile to the 37.5^{th} percentile. For a standard normal distribution with a mean of 0 and a standard deviation of unity, this means the mean would only shift by 0.319 – i.e. less than $\frac{1}{3}^{\text{rd}}$ of a standard deviation – i.e. a long way from statistical significance. This is an extreme example – environmental change rarely leads to such a rapid population decline, extreme truncation selection, and traits that are selectively targeted have heritabilities substantially lower than 0.5 (Kruuk et al., 2008). In reality, mortality selection resulting from environmental change will likely result in a change to the mean of the distribution that is only a fraction of a standard deviation compared to our example. Given this, reports of rapid evolution due to environmental change increasing mortality selection over a small number of generations (e.g. Coltman et al., 2003) should be treated with caution; the statistical analyses on which such conclusions are based are likely suspect. It is much more likely that change is a consequence of phenotypic plasticity. Over multiple generations, recruitment selection can also contribute to evolutionary change and our approach allows the role of this to be investigated. However, unless reproduction is restricted to individuals with extreme phenotypic trait values in both sexes, it seems unlikely that evolution

can generate statistically demonstrable evolutionary change over a small number of generations (Coulson et al., in revision). This is not to say that evolution is not important over longer time scales. Over tens of generations evolution can shift phenotypic trait means to a greater extent that phenotypic plasticity (Figure 4(g)-(i) blue versus black lines).

In order for plasticity to allow populations to rapidly respond to environmental change, a large proportion of individuals within the population must exhibit the same plastic response. A good example of such a dynamic is for size-related traits that are determined by resource availability, particularly when scramble competition is operating. When resources becoming limiting, all individuals will be unable to develop as rapidly as when resources are more common. A consequence of this is that individuals that developed in cohorts when resource were sparse will exhibit smaller body sizes compared to individuals in those cohorts that developed when resources were more abundant. We can capture this form of plasticity in our framework with an additive effect of density in the inheritance or development function for $\mathcal{E}$ (e.g. Figure 3). In contrast, when contest competition operates, larger individuals would acquire more resources than those that are smaller, and would develop faster. We can capture this in our models with interactions between density, $\mathcal{E}$ and $\mathcal{A}$ in either the inheritance or development functions for $\mathcal{E}$.

The above discussion demonstrates how our approach can be used to capture different forms of plasticity. However, for plasticity to help populations respond to environmental change it must be adaptive: plasticity must change the mean trait value in a way that increases fitness (Ghalambor et al., 2007). We demonstrate that for additive, linear models, adaptive and non-adaptive plasticity can be specified by altering the sign for the effect of the environment in the function specifying the mean dynamics of the inheritance or development functions (Figure 3). When interactions are included in these functions specifying general rules for whether plasticity is adaptive or non-adaptive will likely be more challenging. However, our approach provides a way in which to investigate when plasticity is adaptive or non-adaptive, and how different types of plasticity will influence population responses to environmental change.

Our results also show how plasticity can influence evolutionary rates. Plasticity, operating via

development and inheritance functions for the environmental component of the phenotype, alters the distribution of the phenotype, and this can alter the strength of selection, which can then influence the dynamics of the genetic component of the phenotype (evolution). The effects of plasticity on selection and evolution can be surprisingly complex. We only examined the evolutionary consequences of plasticity following an environmental shock that influenced all individuals in the same way, but even in this simple case we found that adaptive plasticity initially slowed the rate of evolution compared to non-adaptive plasticity, before increasing it (Figure 5 and SI). In general in order to understand how plasticity will influence selection, it is necessary to understand how it influences both the numerator and denominator of the selection differential that underpins evolution (Pelletier and Coulson, 2012). The numerator is the covariance between the phenotype and absolute fitness (Falconer, 1960) and the denominator is mean fitness. In our models of species with non-overlapping generations this is mean recruitment – the population growth rate (Fisher, 1930). Selection is linear in our models where plasticity influences all individuals in the same way via an additive effect of density on inheritance of the environmental component of the phenotype (figure 5), and this means that plasticity influences the population growth rate rather than the numerator of the selection differential. A consequence of this is that it is differences in the population growth rate that generates the differences in evolutionary rates between models when plasticity is adaptive and non-adaptive. In more complex cases when plasticity influences the covariance between the phenotype and fitness via genotype-phenotype interactions within a generation, to understand how selection influences evolution it is necessary to understand how plasticity not only influences mean fitness, but also how it generates differences between the covariance between the genetic component of the phenotype and fitness and the covariance between the phenotype itself and fitness. Because the components of the selection differential can be calculated from IPMs (Coulson et al., 2010; Wallace et al., 2013) the approach we develop here provides a flexible way to examine how different types of plasticity can influence evolution following environmental change. But in order to explore such dynamics in real systems it will be necessary to parameterize our models for real systems.

Parameterizing and analyzing evolutionarily explicit IPMs

Large literatures exist on how to statistically parameterize IPMs (Easterling et al., 2000; Merow et al., 2014; Rees et al., 2014). The vast majority of IPMs have been constructed phenomenologically, using statistical descriptions of observational data. Several authors have shown how fixed and random effects incorporated into these statistical functions can be formulated within IPMs (Childs et al., 2003; Coulson, 2012; Rees and Ellner, 2009), but additional statistical estimation is required to parameterize the evolutionarily explicit IPMs we have developed.

Fitness functions in evolutionarily explicit IPMs can be parameterized using standard general, generalized and additive regression methods that are routinely used to parameterize phenomenological IPMs (Rees and Ellner, 2009). If relatedness information is available and the infinitesimal model is assumed, genetic and phenotypic variances and covariances can be estimated using the animal model (Lynch and Walsh, 1998). These quantities can be used to construct the initial distributions of the genetic and environmental components of the phenotype. Parameter estimates of ecological drivers fitted as fixed or random effects in the animal model can be used to parameterize inheritance and development functions for the environmental component of the phenotype. It is consequently possible to parameterize models using our approach with existing methods.

There is also a large literature on how to analyze IPMs (Ellner and Rees, 2006; Steiner et al., 2014, 2012). The majority of these tools, including sensitivity and elasticity analysis of model predictions to transition rates and function parameters (Coulson et al., 2011, 2010; Ellner and Rees, 2006; Steiner et al., 2014, 2012), are likely sufficiently general to be applicable to evolutionarily explicit IPMs. In future work we plan to parameterize models for bird, mammal and fish species with overlapping generations and to analyze them with existing methods. Once evolutionarily explicit IPMs have been parameterized and analyzed we will be able to explore how populations, phenotypic characters and life histories are predicted to respond to a range of environmental changes via plasticity and adaptation.

When should evolutionarily explicit IPMs be used to predict population responses to environmental change?

Chevin (2015) and Janeiro et al. (in press) speculated that published IPMs that did not include explicit evolutionary processes could provide spurious insight. Three strands of evidence suggest this speculation may often be unwarranted.

First, the signature of evolutionary change in model predictions is a function of the heritability of the trait: when the phenotypic variance is dominated by the environmental component of the phenotype then the dynamics of that component will dominate model predictions. Most IPMs to date have been constructed for body weight (Merow et al., 2014), a trait that often has a heritability of less than 0.2 in vertebrates (e.g., blue tits; Garnett, 1981) and often around 0.1 (e.g., bighorn sheep; Wilson et al., 2005). This means that model predictions will be dominated by the dynamics of the environmental component of the phenotype and that a phenomenological statistical approach to parameterising these models has the potential to capture observed dynamics well.

Second, even when phenotypic traits are heritable, they rarely evolve in the wild as predicted: evolutionary stasis of heritable phenotypic traits in the presence of directional selection is frequently observed in nature (Merilä et al., 2001). When fitness functions are monotonic in the phenotypic value and selection is directional (which is typical for body size (Kingsolver et al., 2001)), then in order to maintain an equilibrium trait distribution the inheritance function must reverse the phenotypic changes caused by selection. Coulson and Tuljapurkar (2008) showed this for the mean phenotypic trait; equation (17) demonstrates that this must apply to all moments of the phenotype distribution. However, when the genotype-phenotype map is additive and there is additive genetic variance for the trait, directional selection is expected to result in evolutionary change and the inheritance function for the genetic component of the phenotype can not reverse genetic changes attributable to selection. Unmeasured genetically correlated characters can prevent evolutionary change in these circumstances, although the cases when this is likely to prevent evolution are restrictive, and evidence for such characters playing a major role in limiting evolution in the wild is lacking (Agrawal and Stinchcombe, 2009). Assuming selection on the phenotype has been measured ap-

propriately and is directional, this suggests that the assumption of an additive genotype-phenotype map may be violated, and the mean of the parental and offspring breeding value distributions may not be equal. A mechanism such as over-dominance can achieve this (Fisher, 1930). Our approach allows the effects of relaxing assumptions of quantitative genetics on evolutionary change to be approximated through the use of phenomenological inheritance functions for the genetic component of the phenotype.

Third, because evolutionary change is rarely observed in the wild when it is predicted, observed phenotype change in natural populations is usually attributable to plasticity (e.g. Ozgul et al., 2010, 2009). In these cases, standard, non-evolutionarily explicit, IPMs have accurately captured observed dynamics (Childs et al., 2003; Merow et al., 2014; Ozgul et al., 2010).

These three strands of evidence suggest that evolutionarily explicit IPMs may frequently not be required to gain useful insight into population responses to environmental change. If there is no statistical evidence of temporal trends in inheritance, development or fitness function parameters once variation in the ecological environment has been corrected for, then the use of evolutionarily explicit IPMs may result in the construction of unnecessarily complex models. There is often a temptation to include ever more complexity into models, but this comes at the cost of analytical tractability: as more mechanisms or processes are incorporated into models, understanding why a model produces the predictions it does becomes increasingly challenging. However, when evolutionary change is convincingly documented (e.g. Reznick et al., 1997) or is proposed to be a possible mechanism generating rapid phenotypic change (Coltman et al., 2003), the construction of evolutionarily explicit IPMs is advised as the models allow separation of the roles of adaptive and plastic responses to environmental change.

We have shown how evolutionarily explicit IPMs can be constructed, invalidating the criticisms of Chevin (2015) and Janeiro et al. (in press) that IPMs have not been developed to incorporate the character-state approach of quantitative genetics. IPMs that are not evolutionarily explicit have been used to address many questions in ecology and their application has proven insightful (Merow et al., 2014). They are likely to remain widely used and we expect this use to result in important

new insights. However, we have extended their utility to cases where evolutionary processes are known, or proposed, to be drivers of phenotypic change.

Conclusions

In this paper we have developed a theoretical modeling approach that links demography and quantitative genetics to explore how populations will respond to environmental change. The approach is general, providing formal links between ecology and evolution. Our work builds upon a growing literature of developing evolutionarily explicit structured population models. This body of literature shows how flexible IPMs are. They provide a powerful tool with the potential to unify ecology and evolution.

Acknowledgements

Bernt-Erik Saether, Luis-Miguel Chevin and Michael Morrissey participated in useful discussion and provided comments on an earlier version of the manuscript. Stephen Proulx, Thomas Reed, and two anonymous reviewers provided critical feedback that greatly improved the first submitted version of the paper. TC greatly acknowledges the support of Centre for Advanced Study in Oslo, Norway, that funded and hosted our research project (Climate effects on harvested large mammal populations) during the Academic year of 2015/16.

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Table 1: Notation used in the paper.

Notation	Definition
$\mathcal{Z}$	An individual's phenotypic trait value. $\mathcal{Z}$ can be anything that can be measured on an organism when it is captured or observed. $\mathcal{Z}$ cannot be a life history quantity (like life expectancy) which are emergent properties of the dynamics of $\mathcal{Z}$.
$\mathcal{G}$	The genetic component of the phenotype defined as the total genotypic contribution of an individual's genotype to $\mathcal{Z}$. $\mathcal{G}$ can be calculated across multiple loci and can be decomposed into contributions from epistasis, dominance, and additive genetic effects.
$\mathcal{A}$	The additive genetic component (breeding value) of $\mathcal{G}$. Change in the distribution of $\mathcal{A}$ reflects change in allele frequencies and consequently evolution.
$\mathcal{E}$	The environmental component of the phenotype defined as phenotypic variation not attributable to genetic contributions. Determined by gene expression patterns or developmental noise. Nutrient or energy availability may influence gene expression meaning $\mathcal{E}$ may be correlated with environmental drivers θ.
θ	An environmental driver
$\mathcal{X}$	$\mathcal{X} \in \{\mathcal{Z}, \mathcal{G}, \mathcal{A}, \mathcal{E}\}$
$N(\mathcal{X}, t)$	The distribution of $\mathcal{X}$ at time t
$S(\mathcal{X}, t)$	Survival function: describes the expected association between $\mathcal{X}$ and survival between t and t+1. Only used in age-structured models.
$R(\mathcal{X}, t)$	Recruitment function: describes the expected association between $\mathcal{X}$ and the number of offspring produced between t and $t+1$ that survive to recruit into the population at time $t+1$.
$H(\mathcal{X}'\|\mathcal{X}, t)$	Inheritance function: describes the expected probability of a reproducing individual with character value $\mathcal{X}$ at t producing an offspring with character value $\mathcal{X}'$ at $t+1$ when it recruits to the population.

$D(\mathcal{X}'\|\mathcal{X}, t)$	Development function: describes expected probability of a surviving individual with character value $\mathcal{X}$ at t expressing character value $\mathcal{X}'$ at $t+1$. Only used in age-structured models.

Table 2: Different forms of plasticity and their incorporation into IPMs. Each term in the table below can be included in the functions $\mu^H(\mathcal{E}, t)$, $\mu^H(\mathcal{E}, a, t)$ or $\mu^D(\mathcal{E}, a, t)$. Similar terms could be included in $V^H(\mathcal{E}, t)$, $V^H(\mathcal{E}, a, t)$ or $V^D(\mathcal{E}, a, t)$ if the variance in inheritance or development varied for specific values of $\mathcal{E}$ in predictable ways. This would capture different forms of bet-hedging.

Term	Biological interpretation	Type of plasticity
μ_I^H		No plasticity.
$+\mu_{\mathcal{E}'}^H \mathcal{E}'$	Temporal autocorrelation in $\mathcal{E}$	No plasticity.
$+\mu_\theta^H \theta$	Ecological environment influences all values of $\mathcal{E}$ in the same way.	Additive plasticity generated by temporal variation in the ecological environment.
$+\mu_{\theta,\mathcal{E}}^H \theta\mathcal{E}$	Temporal autocorrelation in $\mathcal{E}$ depends upon the ecological environment.	Non-additive plasticity generated by temporal and spatial variation in the ecological environment.
$+\mu_{\mathcal{A}}^H \mathcal{A}$	Value of $\mathcal{E}$ depends upon $\mathcal{E}$.	No plasticity unless $\mathcal{E}$ also depends upon θ.
$+\mu_{\theta,\mathcal{A}}^H \theta\mathcal{A}$	Value of the $\mathcal{E}$ depends upon an interaction between $\mathcal{A}$ and the ecological environment.	Genotype by environment interaction.
$+\mu_{\mathcal{A},\mathcal{E}'}^H \mathcal{A}\mathcal{E}'$	Temporal autocorrelation in $\mathcal{E}$ depends upon the $\mathcal{A}$.	Genotype by environment interaction.

Figure legends

Figure 1. The role of selection on the dynamics of $\mathcal{A}$. Dynamics of univariate $\mathcal{A}$ subject to linear selection and clonal inheritance (a)-(d) (SI §1.1 Model A). The population does not reach

an equilibrium, with (a) population growth, and the (b) mean, (c) variance and (d) skew of the character continually evolving. Imposing a maximum possible character value constrains change (red lines versus black lines (a)-(d)). In the age-structured case we track the dynamics of a bivariate character distribution (e)-(g) (SI §1.1 models B, C and D). The models in (e) and (f) (SI Models B and C) are identical except the starting distribution at time $t = 1$ has a covariance of -0.2 in (f) compared to 0.7 in (e). The parameterisation in (g) is chosen to demonstrate a case where the two traits evolve in different directions. The coloured image plots in figures (e)-(g) represent Gaussian development functions $D(\mathcal{Z}'|\mathcal{Z}, t)$ fitted to the bivariate distributions of $\boldsymbol{\mathcal{A}}$ at the beginning and end of the simulation. Evolution of the bivariate character has resulted in different parameterisations of these phenomenological functions. The lighter the shading, the greater the probability of a transition from character value $\mathcal{Z}$ at age 1 and to $\mathcal{Z}'$ age 2.

Figure 2. The dynamics of inheritance (SI Model E). The dynamics of (a) population growth rate ($R0$), the (b) mean and (c) variance of $\mathcal{A}$ vary between models with clonal inheritance (black line), the convolution in equation (15) (red line) and the Gaussian inheritance function in equation (16) (blue line). Dynamics predicted from the convolution and the Gaussian inheritance function are indistinguishable in this model. (d) the temporal dynamics of the clonal model versus the other models. The initial distribution at $t = 1$ is Gaussian. After 100 generations the character distributions predicted by the clonal and sexual models have only diverged slightly. The infinitesimal model of quantitative genetics assumes that the dynamics of alleles can be inferred from the dynamics of genotypes. Under this assumption (e) selection alters genotype and allele frequencies, while inheritance does not. In contrast, (f) when dominance variance operates, both selection and inheritance alter genotype frequency while neither alter allele frequencies. For a Gaussian distributed character, (g) dominance variance acts as an offset, reducing the intercept of a Gaussian inheritance function.

Figure 3. Dynamics of $\mathcal{E}$ and plasticity. (a) Return times to equilibrium for three inheritance functions (SI §1.1 models F-H) following a one off perturbation (see main text). There is no plasticity incorporated into model F (black line). Model G (red line) and model H (blue line)

respectively incorporate adaptive and non-adaptive phenotypic plasticity. In (b) and (c) we imposed a permanent environmental change by reducing the intercept of the fitness function. (c) Represents the mean phenotype.

Figure 4. A dynamic version of the Breeders Equation. The dynamics of the phenotype (red lines) and its genetic (black lines) and environmental (blue lines) components (a)-(c) and (g)-(i), and the dynamics of the population (d)-(f) and (j)-(l). In the first model (a) and (d), both fitness and inheritance of the environmental component of the phenotype are independent of density (SI §1.1 model I). In the second model (b) and (e) fitness is negatively density-dependent and inheritance of the environmental component of the phenotype is density-independent (SI §1.1 model J). In the third model, both fitness and inheritance of the environmental component of the phenotype are negative density-dependent (SI §1.1 Model K). The treatment of plasticity can dramatically influence the dynamics of the phenotype and population size (SI §1.1 models L-N). Adaptive phenotypic plasticity (h) and (k) leads to the population size and phenotype recovering from a perturbation much faster than non-adaptive plasticity (i)-(l). The absence of a plastic response (g) and (j) results in the population recovering from a perturbation at an intermediate rate between cases where adaptive and non-adaptive plasticity are operating.

Figure 5. Dynamics of bivariate characters and evolution of fitness functions in the presence of an unmeasured, genetically correlated character (SI §1.1 model P and Q). We construct a simple model with clonal inheritance of two correlated characters that both influence fitness. We explore two initial starting conditions that only differ in their genetic covariance (SI §1.1 models P and Q). In (a)-(d) the covariance accelerates the rate of evolution compared to (e)-(h). The dynamics of the fitness function for each character when the other character is not measured (i) and (j). Regardless of the covariance between characters, the fitness functions evolve during the course of 120 time step simulation.

Figure 1

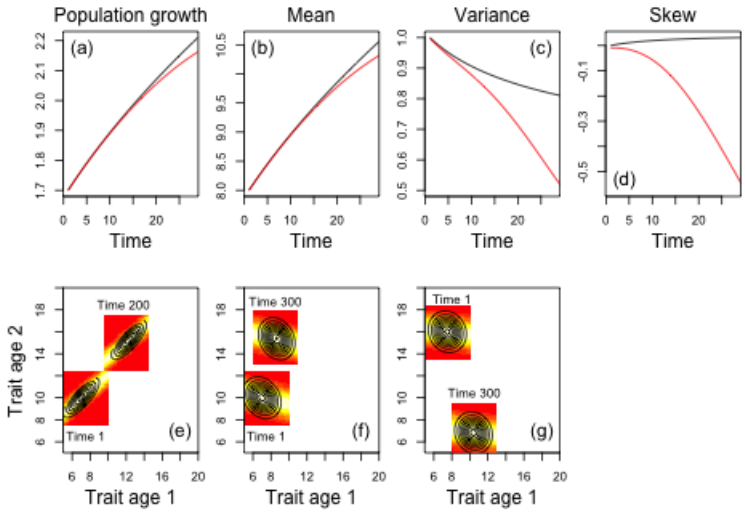

Population growth
Mean
Variance
Skew
(a)
(b)
(c)
(d)
Time
Trait age 1
Trait age 2
Time 200
Time 1
Time 300
(e)
(f)
(g)

Figure 2

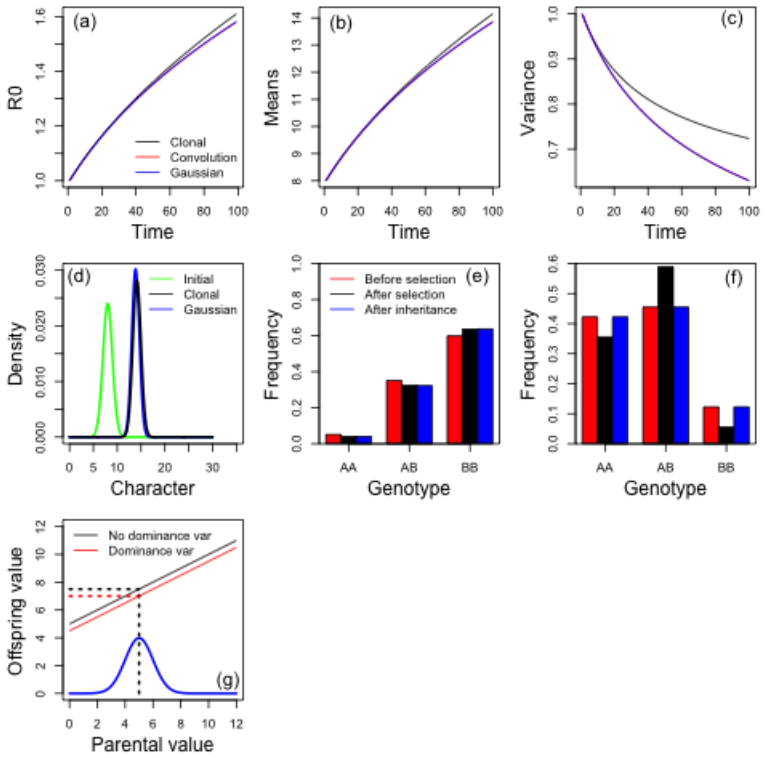

(a)
R0
Time
Clonal
Convolution
Gaussian
(b)
Means
Time
(c)
Variance
Time
(d)
Density
Character
Initial
Clonal
Gaussian
(e)
Frequency
Genotype
AA
AB
BB
Before selection
After selection
After inheritance
(f)
Frequency
Genotype
AA
AB
BB
(g)
Offspring value
Parental value
No dominance var
Dominance var

Figure 3

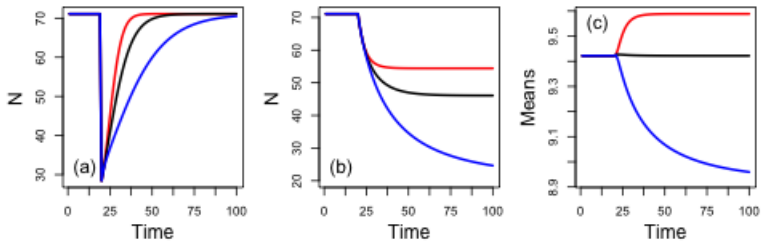


Figure 4

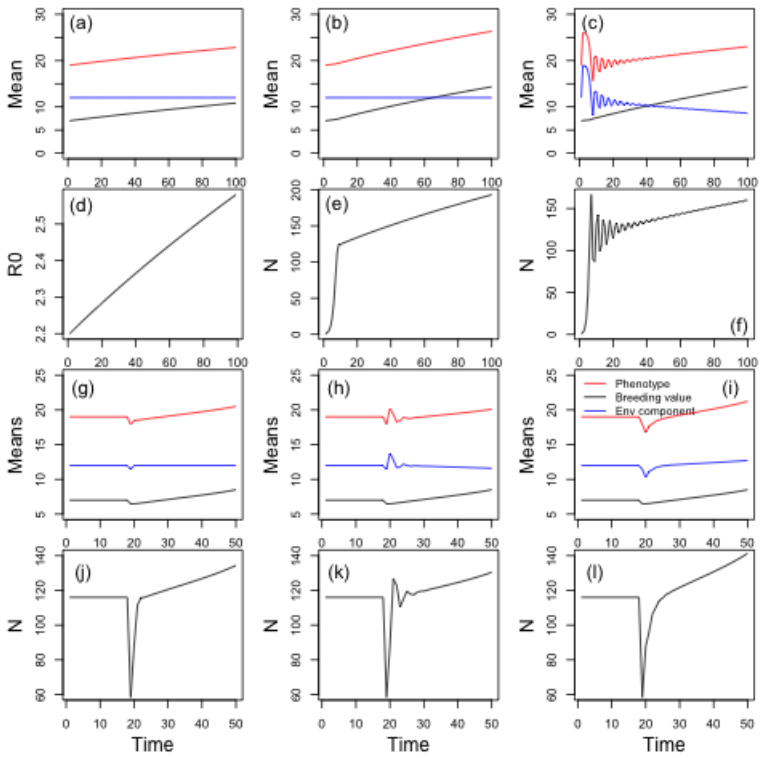
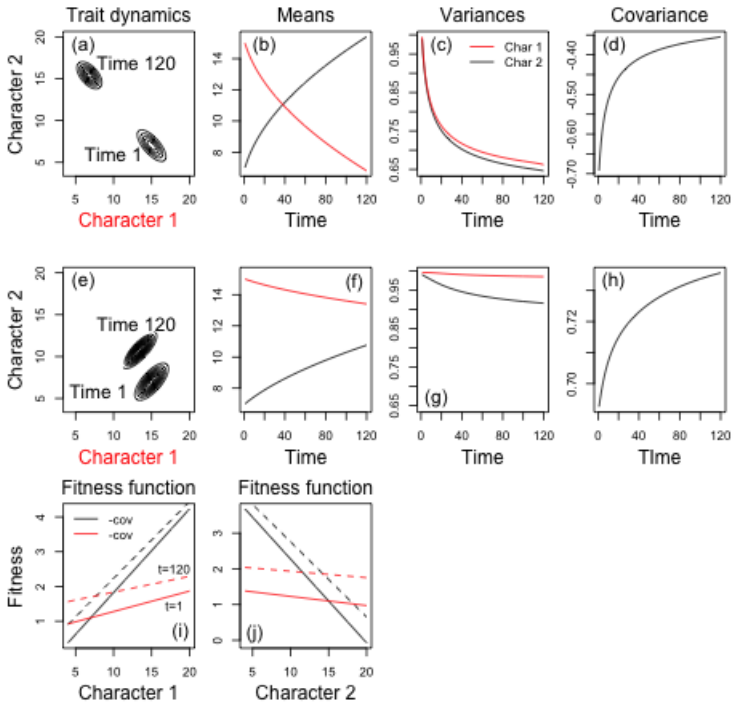

(a)
(b)
(c)
(d)
(e)
(f)
(g)
(h)
(i)
(j)
(k)
(l)
Mean
R0
N
Means
Time
Phenotype
Breeding value
Env component

Figure 5


Trait dynamics
Means
Variances
Covariance
(a)
Time 120
Time 1
Character 2
Character 1
(b)
Time
(c)
Char 1
Char 2
(d)
(e)
(f)
(g)
(h)
TIme
Fitness function
Fitness
-cov
-cov
t=120
t=1
(i)
(j)

Supplementary information

1.1 Model Parameterization

Model A:

$$
\begin{aligned}
N(\mathcal{A}, t=1) &= \phi(8,1) \\
R(\mathcal{A}, t) &= 0.1 + 0.2\mathcal{A} \\
\mu_H(\mathcal{A}, t) &= \mathcal{A} \\
V(\mathcal{A}, t) &= 0 \\
x &= \infty \text{ or } x = 11.5
\end{aligned}
$$

Models B and C:

$$
\begin{aligned}
S(\mathcal{A}1, 1, t) &= \frac{1}{1 + e^{-(0.1+0.03\mathcal{A})}} \\
S(\mathcal{A}2, 2, t) &= 0 \\
R(\mathcal{A}1, 1, t) &= 0 \\
R(\mathcal{A}2, 2, t) &= e^{0.01-0.075\mathcal{A}}.
\end{aligned}
$$

Starting conditions at time $t = 1$ are multivariate normal with the following parameters, **Model B**:

$$
\begin{aligned}
\mathbb{E}(\mathcal{A}1) &= 7 \\
\mathbb{E}(\mathcal{A}2) &= 10 \\
\sigma^2(\mathcal{A}1) &= 1 \\
\sigma^2(\mathcal{A}2) &= 0.8 \\
\sigma(\mathcal{A}1, \mathcal{A}2) &= -0.2
\end{aligned}
$$

Model C:

$$\begin{aligned}
\mathbb{E}(\mathcal{A}1) &= 7 \\
\mathbb{E}(\mathcal{A}2) &= 10 \\
\sigma^2(\mathcal{A}1) &= 1 \\
\sigma^2(\mathcal{A}2) &= 0.8 \\
\sigma(\mathcal{A}1, \mathcal{A}2) &= 0.2
\end{aligned}$$

Model D:

$$\begin{aligned}
S(\mathcal{A}, 1, t) &= \frac{1}{1 + e^{-(0.1+0.06\mathcal{A})}} \\
S(\mathcal{A}, 2, t) &= 0 \\
R(\mathcal{A}, 1, t) &= 0 \\
R(\mathcal{A}, 2, t) &= e^{0.01+0.05\mathcal{A}}.
\end{aligned}$$

Starting conditions at time $t = 1$ for **model D**:

$$\begin{aligned}
\mathbb{E}(\mathcal{A}1) &= 7.5 \\
\mathbb{E}(\mathcal{A}2) &= 16 \\
\sigma^2(\mathcal{A}1) &= 1 \\
\sigma^2(\mathcal{A}2) &= 0.8 \\
\sigma(\mathcal{A}1, \mathcal{A}2) &= -0.1
\end{aligned}$$

Model E:

$$R(\mathcal{A}, t) = 0.2 + 0.1\mathcal{A}. \tag{22}$$

Model F: no plasticity:

$$\begin{aligned}
R(\mathcal{E}, t) &= 0.2 + 0.1\mathcal{E} - 0.002n(t) \\
\mu_H(\mathcal{E}, t) &= 4.64 + 0.5\mathcal{E} \\
V_H(\mathcal{E}, t) &= 1
\end{aligned}$$

Model G: Adaptive phenotypic plasticity:

$$\begin{aligned} R(\mathcal{E},t) &= 0.2 + 0.1\mathcal{E} - 0.002n(t) \\ \mu_H(\mathcal{E},t) &= 5 + 0.5\mathcal{E} - 0.005n(t) \\ V_H(\mathcal{E},t) &= 1 \end{aligned}$$

Model H: Non-adaptive plasticity:

$$\begin{aligned} R(\mathcal{E},t) &= 0.2 + 0.1\mathcal{E} - 0.002n(t) \\ \mu_H(\mathcal{E},t) &= 4.29 + 0.5\mathcal{E} + 0.005n(t) \\ V_H(\mathcal{E},t) &= 1 \end{aligned}$$

Model I

$$\begin{aligned} w(\mathcal{Z},t) &= 0.3 + 0.1\mathcal{Z} \\ \mu^H(\mathcal{E},t) &= 0 \\ v^H(\mathcal{E},t) &= 1 \end{aligned}$$

Model J

$$\begin{aligned} w(\mathcal{Z},t) &= 0.3 + 0.1\mathcal{Z} - 0.01n(t) \\ \mu^H(\mathcal{E},t) &= 0 \\ v^H(\mathcal{E},t) &= 1 \end{aligned}$$

Model K

$$\begin{aligned} w(\mathcal{Z},t) &= 0.3 + 0.1\mathcal{Z} - 0.01n(t) \\ \mu^H(\mathcal{E},t) &= 19 - 0.065n(t) \\ v^H(\mathcal{E},t) &= 1 \end{aligned}$$

Initial starting conditions for $\mathcal{Z} = \mathcal{A} + \mathcal{E}$ for **models I to K**:

$$\begin{aligned}
\mathbb{E}(\mathcal{A}) &= 7 \\
\mathbb{E}(\mathcal{E}) &= 12 \\
\sigma^2(\mathcal{A}) &= 1 \\
\sigma^2(\mathcal{E}) &= 1 \\
\sigma(\mathcal{A}, \mathcal{E}) &= 0
\end{aligned}$$

Model L

$$\begin{aligned}
w(\mathcal{Z}, t) &= 0.3 + 0.1\mathcal{Z} - 0.01n(t) \\
\mu^H(\mathcal{E}, t) &= 12 \\
v^H(\mathcal{E}, t) &= 1
\end{aligned}$$

Model M

$$\begin{aligned}
w(\mathcal{Z}, t) &= 0.3 + 0.1\mathcal{Z} - 0.01n(t) \\
\mu^H(\mathcal{E}, t) &= 15.48 - 0.03n(t) \\
v^H(\mathcal{E}, t) &= 1
\end{aligned}$$

Model N

$$\begin{aligned}
w(\mathcal{Z}, t) &= 0.3 + 0.1\mathcal{Z} - 0.01n(t) \\
\mu^H(\mathcal{E}, t) &= 8.52 + 0.03n(t) \\
v^H(\mathcal{E}, t) &= 1
\end{aligned}$$

Initial starting conditions for $\mathcal{Z} = \mathcal{A} + \mathcal{E}$ for **models L to N**:

$$\begin{aligned}
\mathbb{E}(\mathcal{A}) &= 7 \\
\mathbb{E}(\mathcal{E}) &= 12 \\
\sigma^2(\mathcal{A}) &= 1 \\
\sigma^2(\mathcal{E}) &= 1 \\
\sigma(\mathcal{A}, \mathcal{E}) &= 0
\end{aligned}$$

Models P and Q:

$$\begin{aligned}
w(\boldsymbol{\mathcal{A}}, t) &= 2 - 0.13\mathcal{A}1 + 0.15\mathcal{A}2 \\
N(\boldsymbol{\mathcal{A}}', t+1) &= w(\boldsymbol{\mathcal{A}}, t) N(\boldsymbol{\mathcal{A}}, t)
\end{aligned}$$

Starting conditions at time $t+1$ for **model P**:

$$\begin{aligned}
\mathbb{E}(\mathcal{A}1) &= 7 \\
\mathbb{E}(\mathcal{A}2) &= 15 \\
\sigma^2(\mathcal{A}1) &= 1 \\
\sigma^2(\mathcal{A}2) &= 1 \\
\sigma(\mathcal{A}1, \mathcal{A}2) &= -0.7
\end{aligned}$$

Starting conditions at time $t+1$ for **model Q**:

$$\begin{aligned}
\mathbb{E}(\mathcal{A}1) &= 7 \\
\mathbb{E}(\mathcal{A}2) &= 15 \\
\sigma^2(\mathcal{A}1) &= 1 \\
\sigma^2(\mathcal{A}2) &= 1 \\
\sigma(\mathcal{A}1, \mathcal{A}2) &= 0.7
\end{aligned}$$

1.2 Calculating quantities from model outputs

The expectation of a distribution of $\mathcal{X} = (\mathcal{G}, \mathcal{A}, \mathcal{E}, \mathcal{Z})$ can be calculated as

$$\mathbb{E}(\mathcal{X}, t) = \frac{\int \mathcal{X} N(\mathcal{X}, t) d\mathcal{X}}{\int N(\mathcal{X}, t) d\mathcal{X}}, \tag{23}$$

The variance of a distribution can be calculated as

$$\sigma^2(\mathcal{X}, t) = \frac{\int \mathcal{X}\mathcal{X} N(\mathcal{X}, t) d\mathcal{X}}{\int N(\mathcal{X}, t) d\mathcal{X}} - \mathbb{E}(\mathcal{X}, t)^2. \tag{24}$$

For a bivariate distribution $\boldsymbol{\mathcal{X}}$ consisting of traits $\mathcal{X}1$ and $\mathcal{X}2$ then the covariance between these two traits will be,

$$\sigma(\mathcal{X}1, \mathcal{X}2, t) = \frac{\int \mathcal{X}1\mathcal{X}2 N(\boldsymbol{\mathcal{X}}, t) d\boldsymbol{\mathcal{X}}}{\int N(\boldsymbol{\mathcal{X}}, t) d\boldsymbol{\mathcal{X}}} - \mathbb{E}(\mathcal{X}1, t)\mathbb{E}(\mathcal{X}2, t). \tag{25}$$

The skew can be calculated as,

$$s^3(\mathcal{X}) = \frac{\int \mathcal{X}^3 N(\mathcal{X}, t) d\mathcal{X}}{\int N(\mathcal{X}, t) d\mathcal{X}} - 3\mathbb{E}(\mathcal{X}, t)\sigma^2(\mathcal{X}, t) - \frac{\mathbb{E}(\mathcal{X}, t)^3}{\sqrt{\sigma^2(\mathcal{X}, t)}^3}$$

The kurtosis can be calculated in the following way. First, we define the nth non-central moment of a distribution at time t as $m^n(\mathcal{X}, t) = \frac{\int \mathcal{X}^n N(\mathcal{X}, t) d\mathcal{X}}{\int N(\mathcal{X}, t) d\mathcal{X}}$, then,

$$k^4(\mathcal{X}) = \frac{\frac{\int \mathcal{X}^4 N(\mathcal{X}, t) d\mathcal{X}}{\int N(\mathcal{X}, t) d\mathcal{X}} - 4\mathbb{E}(\mathcal{X}, t) m^3(\mathcal{X}, t) + 6\mathbb{E}(\mathcal{X}, t)^2 m^2(\mathcal{X}) - 3\mathbb{E}(\mathcal{X}, t)^4}{\sigma^2(\mathcal{X}, t)} - 3$$

1.3 Gaussian inheritance function when demography differs between males and females

The distribution of mothers and fathers at time t is respectively defined as $N_R^f(\mathcal{A}, t)$ and $N_R^m(\mathcal{A}, t)$. These distributions are the same size.

We can write

$$N(\mathcal{A}, t+1) = \int H(\mathcal{A}' | \mathcal{A}_m, \mathcal{A}_f, t) N_R^m(\mathcal{A}, t) d\mathcal{A} \tag{26}$$

where the component functions of $H(\mathcal{A}' | \mathcal{A}_m, \mathcal{A}_f, t)$ are

$$\begin{aligned} \mu^H(\mathcal{A}, t) &= (1-\eta)\mathbb{E}(N_R^f(\mathcal{A}, t)) + \eta\mathcal{A} \\ V^H(\mathcal{A}, t) &= (1-\eta)^2 \sigma^2(N_R(\mathcal{A}, t)) \end{aligned} \tag{27}$$

and $\sigma^2(N_R(\mathcal{A},t))$ is the variance in $\mathcal{A}$ across all parents.

Alternatively,

$$N(\mathcal{A},t+1) = \int H(\mathcal{A}'|\mathcal{A}_m,\mathcal{A}_f,t)N_R^f(\mathcal{A},t)d\mathcal{A} \tag{28}$$

where the component functions of $H(\mathcal{A}'|\mathcal{A}_m,\mathcal{A}_f,t)$ are

$$\begin{aligned} \mu^H(\mathcal{A},t) &= (1-\eta)\mathbb{E}(N_R^m(\mathcal{A},t)) + \eta\mathcal{A} \\ V^H(\mathcal{A},t) &= (1-\eta)^2\sigma^2(N_R(\mathcal{A},t)). \end{aligned} \tag{29}$$

As the distributions $N_R^f(\mathcal{A},t)$ and $N_R^m(\mathcal{A},t)$ depart from normality, the approximations will predict dynamics that diverge from those predicted by the convolution.

1.4 How do different functions alter character distributions?

Assume $N(\mathcal{X},t)$ is proportional to a Gaussian distribution. The following parameterizations of a transition functions $H(\mathcal{X}|\mathcal{X}',t)$ in a model $N(\mathcal{X}',t+1) = \int H(\mathcal{X}'|\mathcal{X},t)N(\mathcal{X},t)$ will have no effect on the location or shape of the distribution such that $N(\mathcal{X},t) = N(\mathcal{X}',t+1)$,

$$\begin{aligned} \mu^H(\mathcal{X},t) &= (1-\beta)\mathbb{E}(\mathcal{X},t) + \beta\mathcal{X} \\ V^H(\mathcal{X},t) &= (1-\beta^2)\sigma^2(\mathcal{X},t). \end{aligned} \tag{30}$$

Note that in this model there is no fitness function and no selection.

When the intercept of $\mu^H(\mathcal{X},t)$ is less than $(1-\beta)\mathbb{E}(\mathcal{X},t)$ then $\mathbb{E}(\mathcal{X}',t+1) < \mathbb{E}(\mathcal{X}',t)$ and vice versa. A function $\mu^H(\mathcal{X},t)$ can consequently be parameterized to reduce the mean of a distribution across generations or time steps if desired.

The slope β will reduce $\sigma^2(\mathcal{X}',t+1)$ by β^2 compared to $\sigma^2(\mathcal{X},t)$. The intercept of $V^H(\mathcal{X},t)$ injects additional variation. If the intercept is larger than $(1-\beta^2)\sigma^2(\mathcal{X},t)$ then $\sigma^2(\mathcal{X}',t+1) > \sigma^2(\mathcal{X},t)$. Functions $\mu^H(\mathcal{X},t)$ and $V^H(\mathcal{X},t)$ can consequently be selected to alter the variance from one time step or age to the next.

The further the distribution $N(\mathcal{X},t)$ departs from normality, the more approximate these equalities will become. However, large departures from these equalities can be used to increase the mean or variance of any distribution in a desired direction.

In Figure S1 we show how $\mu^H(\mathcal{X}, t)$ and $V^H(\mathcal{X}, t)$ can be parameterized to modify the mean and variance of $N(\mathcal{X}, t)$ when it is proportional to a normal distribution.

1.5 mortality selection and changes in the mean phenotype

When a trait is normally distribution, selection needs to be strong in order to substantially shift the mean of a phenotype distribution. Such strong selection inevitably leads to a decrease in population size. In Figure S3 we show how killing 25% of the heaviest individuals has only a small effect on the mean for a distribution with a mean of 0 and a standard deviation of unity. The evolutionary response is even less if $\mathcal{E}$ and $\mathcal{G}$ are uncorrelated. For example, in the example in Figure S3, the evolutionary response would be half the phenotypic response for $h^{=}0.5$. In order to substantially shift the mean of the a normal distribution via mortality selection it is necessary for the majority of the population to die.

Supplementary Information Figure Legends

Figure S1. How parameterizations of transition functions for the environmental component of the phenotype $H(\mathcal{E}|\mathcal{E}', t)$ can be used to grow, maintain or shrink the mean and variance of $N(\mathcal{E}, t+1)$. We start with a normal distribution. The initial distribution is represented with a black line in the main figures. The inset figures in (a) to (c) shows the transition functions, with the black line representing the function that has no effect on the location or shape of $N(\mathcal{E}, t)$. (a) increasing or decreasing the intercept of $\mu^H(\mathcal{E}, t)$ influences the location, but not the shape of $N(\mathcal{E}, t)$. (b) How altering the slope of $\mu^H(\mathcal{E}, t)$ influences the shape of $N(\mathcal{E}, t)$. In this example the mean is unaffected as the function passes through the x, y co-ordinate $(\mathbb{E}(\mathcal{E}, t), \mathbb{E}(\mathcal{E}, t))$. (c) how altering the intercept of $V^H(\mathcal{E}, t)$ influences the variance. The transition functions in the insets of (b) and (c) generate distributions with the same means and variances (compare blue, red and black distributions in (b) and (c)). A change in variance between $N(\mathcal{E}, t)$ and $N(\mathcal{E}', t+1)$ achieved by altering the slope of $\mu^H(\mathcal{E}, t)$ or the intercept of $V^H(\mathcal{E}, t)$ generates different amounts of mixing. In (d) upper and lower $H(\mathcal{E}'|\mathcal{E}, t)$ functions impact the variance to the same extend (left hand figures) except the red

function simply spreads out the distribution without altering the relative rank of each individual. In contrast, the blue function changes relative ranks (right hand figures).

Figure S2. Dynamics of the additive genetic variance (a)-(c) and the heritability (d)-(f) in models I to K. Models of the additive genetic (back line) and environmental (red line) variance (g)-(i) and the heritability (j)-(l) in models L to N. See Figure 5 main paper for dynamics of means and population growth.

Figure S3. A normal distribution with mean 0 and standard deviation 1 prior to mortality selection (black line). Mortality occurs, killing off the top 25% of individuals (red distribution). The mean changes from 0 (vertical dashed line) to -0.0324. In other words, even a large highly selective mortality event has a relatively small effect on the mean of a normal distribution.

Figure S1

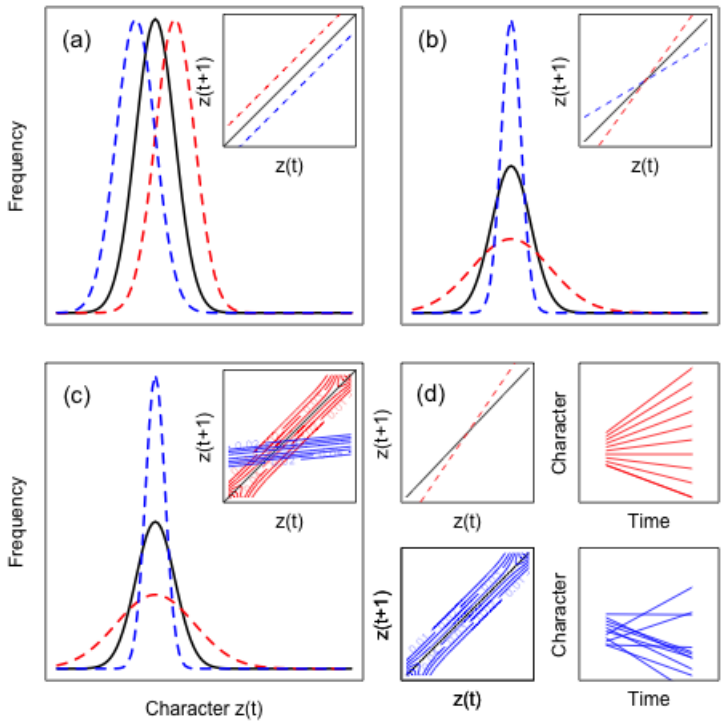


Figure S2

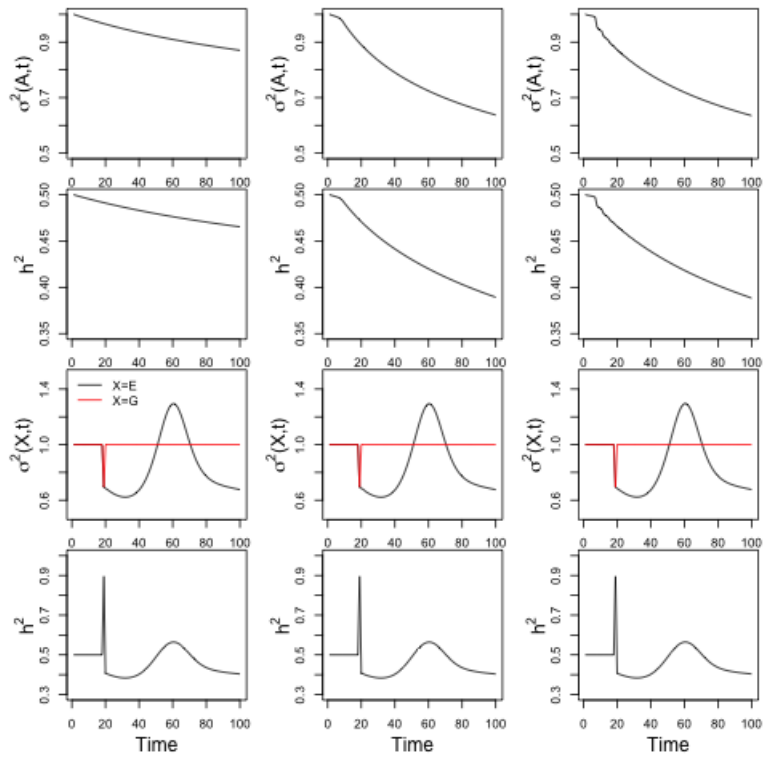
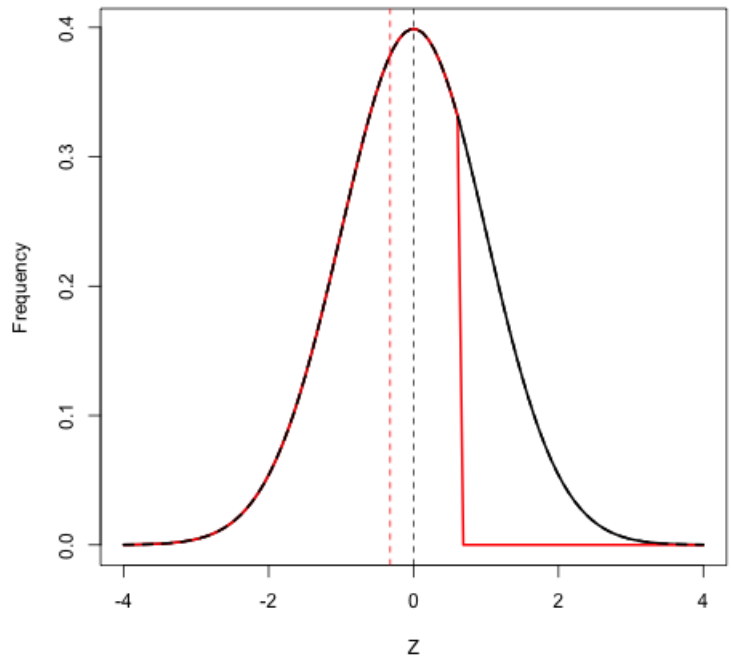



Figure S3