

# **Eco-evolutionary dynamics of finite populations from first principles**

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by

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# Certificate

This is to certify that this dissertation entitled **Eco-evolutionary dynamics of finite populations from first principles** towards the partial fulfilment of the BS-MS dual degree programme at the Indian Institute of Science Education and Research, Pune represents study/work carried out by Ananda Shikhara Bhat at the Indian Institute of Science Education and Research, Pune, under the supervision of Vishwesha Guttal, Centre for Ecological Sciences, Indian Institute of Science with Rohini Balakrishnan, Centre for Ecological Sciences, Indian Institute of Science as a co-supervisor, during the academic year 2022-2023.

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This thesis is dedicated to ?



# Declaration

I hereby declare that the matter embodied in the report entitled **Eco-evolutionary dynamics of finite populations from first principles** are the results of the work carried out by me at the Centre for Ecological Sciences, Indian Institute of Science, under the supervision of Vishwesha Guttal with Rohini Balakrishnan as a co-supervisor, and the same has not been submitted elsewhere for any other degree.

Ananda Shikhara Bhat

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Rohini Balakrishnan



# Acknowledgments

Not more than 250 words



# Abstract

Some central questions of ecology and evolution ask how many distinct variants of an entity can emerge and coexist in sympatry. Examples include the study of standing genetic variation (alleles), polymorphisms (genotypes/phenotypes), and sympatric speciation (species). Historically, these questions have often been studied through phenomenological models formulated for infinitely large populations. Stochastic individual-based models (IbMs), where mechanistic rules are specified for each individual, are more realistic but are rarely studied analytically.

In this thesis, I show how ideas from statistical physics can be used to analytically formulate and study IbMs from biological first principles. Starting from a stochastic ‘birth-death process’, I show how density dependence of the population dynamics can be used to obtain a continuous approximation of the system as a stochastic differential equation (SDE). I show that well-known ‘fundamental theorems’ of evolution, such as the Price equation, are recovered in the infinite population limit. My stochastic formulation reveals a new directional evolutionary force in finite populations that lends itself to a simple biological interpretation and has no analogue in infinitely large populations. As an application, I show how this formalism can be used to study cooperation in finite populations. Finally, I extend this theory to study quantitative traits through a stochastic field equation, which can be thought of as an infinite-dimensional SDE. In the infinite population limit, I recover well-known frameworks such as Kimura’s continuum-of-alleles and adaptive dynamics. My work thus highlights the connections between various equations in ecology and evolution by revealing their common stochastic underpinnings.



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# Part I

# Background



# Chapter 1

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## Introduction

The epistemic aim of science is not truth, but understanding

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Angela Potochnik

More than 150 years have passed since Ernst Haeckel first coined the term ‘ecology’ in 1866. Today, ecology is incredibly interdisciplinary, borrowing techniques and ideas from diverse fields such as computer science, statistics, economics, dynamical systems, physics, and information theory. With this development has come an array of tools intended to help the theoretician use abstract entities which only exist on paper to capture the essence of the real biological systems we see around us. Consequently, there has also been a boom in models that seek to explain natural phenomena using these tools. Despite the apparent overabundance of such seemingly disparate models in the literature, theoretical ecologists often think in terms of a few very general organizing principles which can be adapted in various ways to model specific biological systems (Vellend, 2016). There is thus value to formulating general, idealized models in abstract terms to underscore these organizing principles and better illustrate the fundamental processes that are required to capture the ‘essence’ of an ecological pattern. Such abstractions and idealizations are vital to model building and are useful in gaining insights into complex phenomena such as those that abound in ecology. However, it is important to remember that abstractions, are, ultimately, unrealistic by construction.

As such, it is important to investigate whether predictions of general abstract theories are robust to failure of some of the more unrealistic assumptions that they make. Some of the central questions of ecology boil down to the question of investigating the phenomenon of multiple interacting ‘eco-variants’ (ecologically relevant phenotypic variants: Some examples in section 1.2) coexisting in sympatry. In section 1.1, I reiterate some old arguments about the utility and pitfalls of general idealized models in ecology and evolution. In section 1.2, I highlight diverse ecologically important contexts in which the coexistence of multiple discrete ‘eco-variants’ is relevant. One general class of models, called ‘adaptive diversification’, has gained immense popularity in trying to answer such questions of coexisting phenotypic variants. Chapter 2 introduces this research program. I summarize three distinct modelling approaches to adaptive diversification in section 2.1 that differ in their simplifying assumptions and present some important general predictions of these models in sections 2.3 and 2.2. I identify a problematic idealization within these existing models, and outline my goal of addressing this shortcoming for my thesis in section 2.4. Chapter 3 develops stochastic models of eco-evolutionary population dynamics from first principles, and I show that various known models from evolutionary game theory, population genetics, quantitative dynamics, and adaptive dynamics arise as special cases in the deterministic limit. This section also highlights the connections between the three modelling paradigms of adaptive diversification mentioned in section 2.1 by explicitly deriving them. This modelling exercise results in a useful organizational framework for general population models in ecology and evolution and shows how tools from statistical physics and mathematics can be useful in analyzing the models. Some approximations derived in this chapter are used in Chapter 5 to analytically investigate adaptive diversification in finite populations.

## 1.1 Idealization and generality in ecology

The push and pull between the search for general patterns and the specification of minutiae has a long and torturous history in ecology (Kingsland, 1985). One of the first mathematical idealizations in ecology came in the form of the logistic equation formulated by Pearl and Verhulst, and shortly thereafter, equations for the populations of interacting predator and prey species, put forth independently by Lotka and Volterra. These models were immediately controversial, and for good reason: Many ecologists felt that they were overly idealistic and neglected many important truths about real biological populations (Kingsland, 1985). These models were nevertheless quite good at predicting the patterns of such populations,

and have proved valuable to the field of population ecology. Today, these models are viewed as ‘classical’ and are regularly used even by hard-line empiricists, not because we believe them to be true in all their gory biological details, but because we recognize that they can be *useful* despite being blatantly false generalizations. This is a single instance of a more general philosophical idea concerning the goals and ideals of science. As suggested by the epigraph at the beginning of the chapter, philosophers of science (Potochnik, 2018) have recently argued that science does not seek truth, but instead seeks understanding. The fact that idealization is part and parcel of science is clear if one looks at the actual practice, be it theorists making unrealistic assumptions on paper to model specific phenomena or experimentalists creating artificially controlled conditions in the laboratory to test specific hypotheses (Zuk and Travisano, 2018). Relatively simple models of complex eco-evolutionary processes are therefore desirable as a way to shine light on these phenomena. To reiterate once more, the goal of such simple models is not truth (whatever that is), predictive power (as with models in physics), or detailed description (as with detailed individual-based simulations, very flexible statistical models, or machine learning), but *understanding*. Since the world is complicated and humans are limited, such understanding inevitably comes at the cost of other desirable qualities such as the ability to make precise quantitative predictions. It is important to remember at the outset that the models I speak about in this thesis may seem to be over-idealized and too general, and will make only qualitative predictions. This is *by design*, in pursuit of general insight over precise quantitative prediction.

Vellend has recently argued that conceptual synthesis in community ecology requires “shifting the emphasis away from an organizational structure based on the useful lines of inquiry carved out by researchers, to one based on the fundamental processes that underlie community dynamics and patterns” (Vellend, 2016). Vellend’s assertion is based on the fact that population genetics has managed to come up with reasonably comprehensive theory due to its focus on the abstract ‘high-level’ processes of selection, mutation, drift, and gene flow instead of the myriad ‘low-level’ processes that may be responsible for generating them. In contrast, he believes that practitioners of community ecology often focus on specific ‘low-level’ processes such as predation rate, limiting resources ( $R^*$ ), storage effects, priority effects, senescence, and niche partitioning, leading to a plethora of models (see Table 5.1 in (Vellend, 2016) for an in-exhaustive list of 24 such models) and the conclusion that community ecology ‘is a mess’. Vellend proposes organizing ecological models according to the ‘high-level’ processes of selection, ecological drift (demographic stochasticity), dispersal, and speciation. Of course, no such general organization will be perfect or all-encompassing. As Robert

MacArthur once remarked, “general events are only seen by ecologists with rather blurred vision. The very sharp-sighted always find discrepancies and are able to see that there is no generality, only a spectrum of special cases” (Kingsland, 1985). However, I believe the act of looking past the myriad low-level processes present in biological systems and categorizing theories, models, and concepts in terms of a small number of general fundamental high-level processes provides a powerful unifying tool to organize concepts in biology. This is perhaps best exemplified by Darwin’s theory of natural selection as first proposed in *The Origin of Species*. Darwin famously painstakingly collected a series of ‘low-level’ facts and observations regarding breeds, wild populations, and the geographic record to support his hypothesis. However, ultimately, these observations culminated in a synthesis whereby they were all unified under a single, abstract, ‘high-level’ process, namely evolution by natural selection. In the spirit of this approach, the questions I seek to answer in this thesis are in terms of rather abstract sounding ‘high-level’ processes. In the next section, I survey some of the existing literature to provide concrete examples which motivate these general models.

## 1.2 Coexistence of eco-variants in diverse contexts

The phenomenon of coexistence of multiple phenotypically distinct, ecologically relevant variants of an organism in sympatry occurs in several different contexts in the natural world. This is best illustrated through examples, which I provide below.

### 1.2.1 Alternative Reproductive Tactics

Alternative reproductive tactics (ARTs) are discrete polymorphisms that occur in sympatry in one or both sexes of a species in response to intrasexual competition for mates. More precisely, two or more traits which are expressed in individuals of a given sex of a given species can be said to be ARTs if (Oliveira et al., 2008):

- (a) They are *alternative*, in the sense that a given individual can only express one of the behaviors at any given point in time.
- (b) They are *reproductive*, in the sense that the traits are directly relevant to the process of obtaining a mate and are intended to mitigate conspecific intrasexual competition.
- (c) They are *tactics*, in the sense of serving a well-defined adaptive function and thus having fitness consequences. Usually, different ARTs have different associated fitness

ARTs are widespread in the animal kingdom, and may be seen either in morphological traits, or as more complex behavioral polymorphisms (see (Oliveira et al., 2008) for an overview). Most (if not all) species which exhibit ARTs only show a small number of polymorphisms (usually 2-3, 5 in a handful of cases, and very rarely 7-8) - I can maybe make a table for this: Somehow wasn't able to find one in the literature. ARTs have obvious consequences for reproductive life history, and can strongly influence the ecology and evolutionary trajectory of organisms.

### 1.2.2 Trophic resource polymorphisms

Trophic resource polymorphism is defined as “the occurrence of discrete intraspecific morphs showing differential niche use, usually through differences in feeding biology and habitat use” (Skulason and Smith, 1995). Species which exhibit trophic resource polymorphisms often show marked, discontinuous morphological variations adapted for specific niche usage. For example, arctic charr and african cichlid fishes both often exhibit discrete trophic polymorphisms in which different morphs (of the same species) are specialized for feeding at different strata of the lakes they live in (Recknagel, Hooker, et al., 2017). Such polymorphisms also generally occur in relatively small numbers in sympatry (see Table 1 in (Smith and Skúlason, 1996)). They are relatively widespread in vertebrates, and are thought to have important evolutionary consequences by acting as the ‘substrate’ for adaptive radiations (Smith and Skúlason, 1996).

### 1.2.3 Mating types in isogamous species

Isogamous organisms are sexual, but do not have gametes which can be classified into ‘male’ and ‘female’ based on size. Gametes of such species can, however, be divided into distinct ‘mating types’ according to chemical self-incompatibility. There is substantial variation in the number of mating types present in a given species: While most organisms have only two mating types, this is by no means the rule (Phadke and Zufall, 2009; Constable and Kokko, 2018), with a handful of organisms having 7-10 mating types, and one species of fungus (*Schizophyllum commune*) exhibiting over 23,000 mating types. The study of mating types in isogamous species is ecologically and evolutionarily relevant, not only due to the intrinsic importance of mating and self-incompatibility, but due to the fact that isogamy is

thought to be the evolutionary precursor to anisogamy: Thus, studying the factors governing the number of mating types in isogamous species may shed light on why anisogamous species have only two distinct types of gametes.

### 1.2.4 Phenotypic clustering and sympatric speciation

Write stuff about sympatric speciation, adaptive radiations, and phenotypic clustering.

In all these cases, we are interested in monitoring the changes in the number of distinct phenotypic entities, in a scenario in which the phenotype is ecologically relevant for fitness. Existing literature has tended to use the word ‘morph’ for this concept, and I will bow down to convention and do the same. However, it is important to remember that in this context, ‘morphs’ are only defined in terms of traits that *affect fitness*, in contrast to the more general use of the word in biology to mean any difference whatsoever (as in single nucleotide polymorphisms, for example). Note that in many of these cases, even though the emergent alternative morphs are discretely distributed, the underlying traits need not be, and indeed are often continuously varying, and only categorized into discrete bins by human experimentalists. Such discrete morphs are often persistent in phylogenetically similar lineages (Jamie and Meier, 2020), suggesting they are evolutionarily predictable to some degree, and are also thought to be important for very general evolutionary processes (West-Eberhard, 1986). Intraspecific variation also provides an important metric for the diversity harboured by populations and can have important ecological consequences. Two important questions immediately arise:

1. How does a population that is initially monomorphic for a (selectively non-neutral) trait evolve to become polymorphic for this trait in a seemingly discrete manner?
2. What governs the number of discrete morphs that co-occur in a population?

This very general setting motivates a view in which an ‘individual’ is simply characterized by its phenotype as a point in some abstract ‘trait space’. These questions then concern the distribution of points in this space (analogous to the frequency of each ‘type’ of individual) changes over evolutionary time due to ecological fitness determinants (through the traits that the individuals possess). More formally, we can visualize an abstract trait space  $\mathcal{T}$  which captures all possible phenotypes that an individual may exhibit. Any phenotype can then

be viewed as some point  $x \in \mathcal{T}$ . We are interested in the distribution of trait values in the population subject to some ecological and evolutionary rules, and a ‘morph’ or ‘eco-variant’ is just a cluster within this trait space (a mode in the distribution).



# Chapter 2

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## Adaptive diversification: a crash course

From so simple a beginning, endless forms most beautiful and wonderful have been, and are being, evolved

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Charles Darwin

### 2.1 Adaptive diversification

The questions proposed at the end of the previous chapter are best addressed by a modeling framework called ‘adaptive diversification’, where an initially monomorphic population evolves to become polymorphic due to (disruptive) frequency-dependent selection. The framework has been widely used in evolutionary ecology and evolutionary game theory, especially in the context of sympatric speciation (Dieckmann and Doebeli, 1999). Models of adaptive diversification can be broadly classified into three classes of models which differ starkly in their approach and assumptions (Doebeli, 2011). I introduce all three approaches below.

### 2.1.1 The ‘classic’ adaptive dynamics approach

The classic approach to modelling adaptive diversification was first articulated in the late 90s by J.J. Metz’s group (S. Geritz et al., 1998). The crux of the approach relies on the observation that evolutionary stability (in the ESS sense of evolutionary game theory) and asymptotic convergence stability (in the sense of dynamical systems) need not always coincide.

More concretely, consider an infinitely large asexual population that is monomorphic for some quantitative trait such that every individual of the population has the trait value  $x \in \mathcal{T} \subseteq \mathbb{R}^n$ . We are interested in the dynamics of  $x$  over evolutionary time. There is assumed to be a separation of timescales between ecology and evolution such that whenever we observe the population, it is at ecological equilibrium (This is equivalent to a strong-selection + weak-mutation setting). The evolutionary dynamics of the trait value in the population are modelled as following the equation:

$$\frac{dx}{dt} = g(x) = B(x) \left( \nabla_y f(y; x) \Big|_{y=x} \right) \quad (2.1)$$

Here,  $B(x)$  describes the mutational process of the trait and is intended to model mutational biases. For the sake of simplicity, I will assume that  $B(x) = 1$  below, but the essential results are not greatly changed by more complicated forms.  $f(y; x)$  is the *invasion fitness* function, and describes the expected fitness of a mutant type  $y$  appearing in a population that is monomorphic  $x$ -valued.  $x$  is sometimes called the ‘resident’ trait value. Thus, evolution is modelled as following the gradient  $\nabla_y f(y; x)$  of the invasion fitness, a quantity sometimes called the selection gradient. (2.1) can be interpreted to mean that at each time step, the population ‘samples’ all local mutations, and if a mutant can invade this resident population, then the trait rapidly spreads in the population, and by the time we next ‘observe’ it, the entire population has adopted this mutant trait. Equation (2.1) is called the *canonical equation of adaptive dynamics*. Fixed points for this equation, *i.e* points  $x^*$  for which  $g(x^*) = 0$ , are called *evolutionary singularities*. These singularities can be characterized by two different stability notions, as we will see below, and the difference between the two notions captures the important phenomenon of *evolutionary branching*, which we will encounter shortly.

**Definition.** (*Convergence stability*) A singularity  $x^*$  is said to be convergent stable (CS) if it is an asymptotically stable fixed point for equation (2.1).

Thus, singularities which are convergence stable are local attractors, in the sense that nearby populations will evolve towards this state.

**Definition.** (*Evolutionary stability*) A singularity  $x^*$  is said to be evolutionarily stable (ES) if it cannot be invaded by any nearby mutants.

In the one dimensional case, evolutionary stability requires that the invasion fitness be such that no mutant can invade the population. Since  $g(x^*) = \frac{\partial}{\partial y} f(y; x^*) = 0$  by definition at a singularity, the condition for evolutionary stability is controlled by the second derivative, and is given by:

$$\left. \frac{\partial^2}{\partial y^2} f(y; x) \right|_{y=x=x^*} < 0 \quad (2.2)$$

On the other hand, from elementary non-linear dynamics, we know that convergence stability requires  $\frac{dg}{dx} < 0$ , *i.e.*:

$$\left. \frac{\partial^2}{\partial x \partial y} f(y; x) \right|_{y=x=x^*} + \left. \frac{\partial^2}{\partial y^2} f(y; x) \right|_{y=x=x^*} < 0 \quad (2.3)$$

Note that neither (2.2) nor (2.3) imply the other, and thus, we arrive at the following classification of evolutionary singularities:

	ES	not ES
CS	(A)	(B)
not CS	(C)	(D)

Points which are not convergent stable are not of interest to us because populations can only attain such a state if they begin there. Thus, (C) and (D) can be ignored for our purposes.<sup>1</sup>

Points of type (A) are both evolutionarily stable and convergent stable. Such points represent ‘endpoints’ for evolution, since populations are attracted to such points and also cannot

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<sup>1</sup>Singularities of type (C) are sometimes called ‘garden of Eden’ points, since a population that begins at such a point will remain there and cannot be invaded by nearby mutants, but if a population does not begin there (or is somehow driven out by external forces), it can never find its way back to the singularity.

evolve away from them since they cannot be invaded by any nearby mutants. Points of type (B) are CS but not ES. Populations are attracted to such points, but once they have arrived, they are susceptible to invasion by nearby mutants. Let  $x^*$  be such a point, and let  $x_1 < x^* < x_2$  be two points in the immediate vicinity of  $x^*$ .

**Claim.** (Protected Polymorphism) Each of  $x_1$  and  $x_2$  can invade the other

*Proof.* We can Taylor expand the invasion fitness function as

$$f(x_1; x_2) = \underbrace{f(x_2; x_2)}_{=0} + \underbrace{(x_1 - x_2)}_{<0} \underbrace{\frac{\partial f}{\partial x_1}(x_1; x_2)}_{=g(x_2)} \Big|_{x_1=x_2} + \frac{(x_1 - x_2)^2}{2} \underbrace{\frac{\partial^2 f}{\partial x_1^2}(x_1; x_2)}_{=0} \Big|_{x_1=x_2}$$

where we have neglected terms that are higher than second order. Since  $x^*$  is convergent stable,  $\frac{dg}{dx} \Big|_{x=x^*} < 0$  and we therefore see that  $g$  is a decreasing function of  $x$  in the immediate vicinity of  $x^*$ . Thus, since  $x_2 > x^*$ , we must have  $g(x_2) < g(x^*) = 0$ , and we can conclude that the second term in the RHS must be positive. Lastly, since  $x^*$  is evolutionarily unstable, we must have  $\frac{\partial^2 f}{\partial x_1^2}(x_1; x^*) \Big|_{x_1=x^*} > 0$  by the stability criterion. Thus, assuming  $f$  is smooth,

for  $x_2$  sufficiently close to  $x^*$ , it must be the case that  $\frac{\partial^2 f}{\partial x_1^2}(x_1; x_2) \Big|_{x_1=x_2} > 0$ . Thus, the third term of the RHS is also positive, meaning that  $f(x_1; x_2) > 0$ , and that  $x_1$  can thus invade  $x_2$ . An exactly analogous argument shows that  $f(x_2; x_1) > 0$ , thus completing the proof.  $\square$

Mutual invasibility of  $x_1$  and  $x_2$  results in a so-called ‘protected polymorphism’ in which the population harbours some members with trait value  $x_1$  and some members with trait value  $x_2$ . This can be shown in some cases to lead to further divergence where the polymorphisms grow further apart in trait space while both being maintained in the population. Thus, the population appears to have ‘branched’ from a monomorphic state to a dimorphic state in trait space. Due to this reason, points of type (B) are called *branching points*, and the population is said to have undergone *evolutionary branching* once it has gone from a monomorphism to a dimorphism. Note that once a population has branched, equation (2.1) no longer describes the population, since it is no longer monomorphic - We instead need a system of *two* equations, one for each morph.

In adaptive dynamics, the name of the game is thus formulating reasonable guesses for  $B(x)$  and  $f(y; x)$ . These are sometimes derived from more mechanistic processes (such as explic-

itly formulating birth/death functions), but the conceptual idea is the same regardless of how complicated these functions may be, and evolutionary branching easily arises in a very wide range of ecological scenarios as long as the frequency-dependence of the selective force is strong enough (Doebeli and Dieckmann, 2000; Doebeli, 2011).

### 2.1.2 The PDE approach

A slightly more general approach to adaptive diversification is to relax the assumption of separation of timescales while keeping the assumption of infinite population size. In this case, we instead wish to formulate an equation for the distribution  $\phi(u)$  of trait values in  $\mathcal{T}$ . We thus seek PDEs of the form:

$$\frac{\partial \phi(u)}{\partial t} = F(u, \phi(u), t)$$

In PDE models, diversification shows up as patterns (in the Turing sense), and the existence of a polymorphism corresponds to a multimodal solution for  $\phi(x)$ . The functional form of  $F$  is often formulated through biological principles. For example, in analogy to the logistic equation, one could postulate the continuous version:

$$\frac{\partial \phi(u)}{\partial t} = r\phi(u) \left( 1 - \frac{\phi(u)}{K(u)} \int_{\mathcal{T}} \alpha(u, v)\phi(v)dv \right) \quad (2.4)$$

where  $r$  is a growth rate,  $K(u)$  gives the carrying capacity of the environment for individuals with phenotype  $u$ , and  $\alpha(u, v)$  is a competition kernel which determines the effect of an individual with phenotype  $v$  on the growth of an individual with phenotype  $u$ , and the integral thus gives a measure of the effective density experienced by individuals with phenotype  $u$ .  $\alpha(u, v)$  is generally chosen such that strength of competition decreases with phenotypic distance (for example,  $\alpha(u, v) = \exp(|u - v|)$ ), in analogy with niche partitioning. Note that this is an integrodifferential equation, and as such, is usually not easy to solve for most functional forms of  $\alpha(u, v)$ . We thus need to resort to numerical methods to solve such equations.

PDE models can also incorporate space more easily than the classic adaptive dynamics approach. For example, Doebeli *et al.* propose a spatial model of resource competition in which we track the density  $\phi(x, u)$  of  $u$ -phenotype individuals at the location  $x$  given by the

PDE:

$$\frac{\partial \phi(x, u)}{\partial t} = r \left( \int_{\mathcal{T}} B(v) \phi(x, v) dv - \frac{\phi(x, u)}{K(x, u)} \int_{\mathcal{S}} \int_{\mathcal{T}} \alpha_p(u, v) \alpha_s(x, y) \phi(y, v) dv dy \right) + m \left( \int_{\mathcal{S}} D(x, y) \phi(y, u) dy - \phi(x, u) \right) \quad (2.5)$$

where  $B(v)$  is a birth kernel that specifies births and mutations,  $K(x, u)$  is a carrying capacity function that varies with both phenotype and geographic location,  $\alpha_p(u, v)$  describes how strength of competition varies with phenotypic distance,  $\alpha_s(x, y)$  describes how strength of competition varies with spatial (geographic) distance,  $m$  is a migration rate, and  $D(x, y)$  is a dispersion kernel that describes the probability that an individual at location  $y$  will migrate into location  $x$ .

PDE models sacrifice interpretability for increased generality. While these models can include space as well as incorporate polymorphic populations more easily, the equations themselves generally have to be solved numerically, and it is more difficult to gain understanding as to why a certain behavior is observed. Nevertheless, mathematically sophisticated techniques have shown that multimodality remains a robust phenomenon for a very wide class of PDE models (Elmhirst et al., 2008; Doebeli, 2011).

### 2.1.3 Stochastic individual-based models

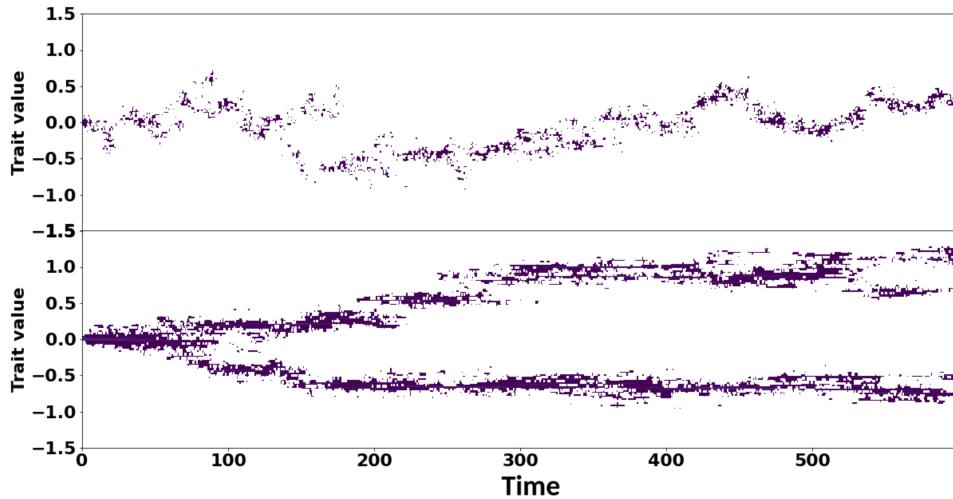
The most general approach to modelling adaptive diversification is through individual-based models. In such models, birth rates, death rates, and interaction rules are specified for each individual, and system-level properties are observed by letting the system change according to these rules. These models can be shown to be more general, biologically explicit versions of both PDE models and adaptive dynamics models, as will be discussed in section 2.2.

## 2.2 Demographic stochasticity and stochastic models

The probabilistic origins of adaptive diversification were first noted by Dieckmann and Law, who used a stochastic individual-based model in which ecological rules at the level of the individual led to the population evolving as a Markov chain in trait space in a ‘quasi-

monomorphic' manner (Dieckmann and Law, 1996). This stochastic process was shown to yield the canonical equation of adaptive dynamics (2.1) as a first order deterministic approximation, thus establishing a connection between stochastic individual-based rules (microscopic dynamics) and deterministic evolution via adaptive dynamics (macroscopic approximations). Champagnat *et al.* have since used more sophisticated mathematical tools (measure-valued processes and their infinitesimal generators) to extend such models to include polymorphic populations, and have arrived at similar results (Champagnat et al., 2006; Champagnat et al., 2008). These latter studies were able to show convergence of the expected paths of the stochastic process to both PDE models such as (2.4) and the canonical equation (2.1) based on the approximations used and the limits taken (large population size, weak mutation, separation of ecological and evolutionary timescales, etc), thus uniting the three modelling approaches introduced in section 2.1. However, despite this explicit recognition of the probabilistic roots that unify adaptive diversification, the effects of demographic stochasticity on the process of diversification are relatively poorly studied.

The effects of demographic stochasticity on evolutionary branching were first studied by Claessen *et al.*, first for asexual populations (Claessen, Andersson, Persson, and A.M.d. Roos, 2007) and later for sexual populations (Claessen, Andersson, Persson, and A.M. d. Roos, 2008). Both studies used a two-patch resource competition models, and broadly first formulated deterministic adaptive dynamics for the system, and then used computational individual-based simulations in which the total population size is capped in order to study the effects of demographic stochasticity. Both studies found that smaller populations have longer waiting times to reach evolutionary branching, and found that below a critical threshold population size, populations did not branch and remained monomorphic. The sexual model (Claessen, Andersson, Persson, and A.M. d. Roos, 2008) was also empirically tested using data on resource polymorphism in populations of arctic charr fishes, where lake size acts as a proxy for the maximum allowed population size, and the authors indeed found that populations living in larger lakes tended to exhibit more polymorphism.



**Figure 2.1: Effect of population size on evolutionary branching.** Two different realizations of a stochastic individual-based model of resource competition in one dimension where individuals compete according to a continuous version of the logistic equation, written in Python. The infinite population limit of this equation is given by (2.4) with  $\sigma_K = 1.9$ ,  $\sigma_\alpha = 0.7$ . The PDE model (infinite population limit) predicts evolutionary branching for these parameter values. Each point represents an individual. The model on top has a population of around 1000 individuals and remains monomorphic. The model on the bottom has a population of around 10000 individuals and exhibits evolutionary branching, where an initially monomorphic population evolves to become dimorphic.

On the mathematical front, Wakano and Iwasa first provided analytical support for the phenomenon of delayed evolutionary branching in small monomorphic populations using a moment-based approach in a Wright-Fisher model where evolutionary branching was identified by an ‘explosion’ in the variance of the trait distribution in the population (Wakano and Iwasa, 2013). These authors identified two different regimes of branching, which they call ‘deterministic branching’ (meaning branching is guaranteed) and ‘stochastic branching’ (meaning branches have a propensity to recombine soon after branching) based on population size and selection strength. They too found that polymorphism is more likely in larger populations, and that monomorphism is virtually guaranteed if the population size is small enough. Importantly, since their model was in a Wright-Fisher framework, the total population size was assumed to be fixed. Debarre and Otto have recently extended these results to cases in which population sizes are allowed to vary using a similar moment-based approach (Débarre and Otto, 2016). These latter authors were able to further decompose

the regimes of selection strength (and population size) identified by Wakano and Iwasa. Within Wakano and Iwasa's 'stochastic branching' regime, Debarre and Otto identify a 'no branching' regime, an 'intermittent branching' regime, and a 'branched' regime. The first and last of these are characterized by branching events that are either extremely infrequent or extremely frequent, leading to predictable dynamics. Only in the smaller intermediate range was branching 'truly' unpredictable over biologically relevant timescales. In this intermediate regime, populations undergo repeated cycles of branching and collapse, and hence the number of polymorphisms in the population varies with time.

## 2.3 Diversity in multi-dimensional trait space

Organisms rarely (if ever) vary along a single independent phenotypic axis. However, adaptive dynamics in multi-dimensional trait space is not very easy to deal with due to mathematical technicalities that arise with identifying necessary and sufficient criteria for evolutionary singularities to be branching points (Doebeli, 2011; Leimar, 2009). As such, adaptive diversification in multi-dimensional trait spaces is usually studied through PDE models or individual-based models (I. Ispolatov et al., 2016). As usual, all models discussed in this section operate in the (infinitely) large population limit. Surprisingly, while the question of saturating levels of diversity in adaptive diversification has not been extensively studied in either one dimensional models or explicit spatial models, it *has* been examined in the context of the dependence on the dimensionality of the trait space. The motivation for these studies arises from the classic notions of competitive exclusion and limiting similarity, with position in trait space being thought of as analogous to the (Hutchinsonian) ecological niche.

Broadly, the results of these studies align with intuitive expectations: As the dimensionality of the trait space increases, expected diversity increases. For one-dimensional adaptive diversification, strong frequency-dependence is needed to ensure coexistence of multiple morphs/branches at equilibrium. Using the continuous logistic equation (2.4) with Gaussian forms of  $K(x)$  and  $\alpha(x, y)$ , Doebeli and Ispolatov have shown that as the dimensionality of the trait space increases, progressively weaker frequency dependence is sufficient to maintain multiple morphs at equilibrium (Doebeli and I. Ispolatov, 2010). Furthermore, they have also shown that for a fixed level of frequency-dependence, the probability of having multiple morphs at equilibrium increases as the dimensionality of the trait space increases. Other

authors have since arrived at broadly similar conclusions in more general settings (Débarre, Nuismer, et al., 2014; Svardal et al., 2014). While these studies say that coexistence is *easier* in higher dimensions, they do not comment on how many morphs are expected to coexist at equilibrium. This has only been addressed by a recent study (Doebeli and I. Ispolatov, 2017) which used adaptive dynamics for a continuous analogue of the Lotka-Volterra competition equations to attack the question. They find that all else being equal, the number of coexisting morphs should increase exponentially with the dimensionality of the trait space that the organisms compete in. These authors also repeat this analysis using PDE models (Equation (2.4) in particular) and computational individual-based simulations in place of adaptive dynamics and claim to find the same broad results.

## 2.4 The importance of being finite (and stochastic)

The previous sections paint an intriguing picture of the state of adaptive diversification as an explanatory paradigm. Distinct modeling approaches (adaptive dynamics, PDE models, and stochastic IbMs) have been proposed to model adaptive diversification, and all predict that diversification is a robust phenomenon (Doebeli, 2011). However, theory predicts an exponential increase in the number of coexisting eco-variants as the dimensionality of the trait space increases. Since organisms generally live in rather high-dimensional trait spaces, if we were to buy into the theory, we would expect extremely high diversity of eco-variants to be the norm in nature. However, empirical literature (see section 1.2) suggests that this is not the case. What, then, may explain this apparent disagreement of theory with the real world, and how may we remedy it?

I posit here that the culprit is the assumption of infinite population size. Indeed, we have seen that theoretical studies predict that when demographic stochasticity is taken into account, waiting time to branching increases, and below a threshold population size, the system fails to diversify. Though this is only an indirect measure of the expected number of coexisting eco-variants, it is nevertheless rather suggestive. Furthermore, empirical literature also suggests that population size can have important effects on the diversity of eco-variants that a population can harbour: In several species of lake fish known to harbour adaptive phenotypic polymorphisms, studies (Claessen, Andersson, Persson, and A.M. d. Roos, 2008; Recknagel, Elmer, et al., 2014; Recknagel, Hooker, et al., 2017) show that population size is positively correlated lake size, and that larger lakes harbour more intraspecific polymorphism. However, since larger lakes also present more ecological opportunity in the form of

resource niches, it is important to remember that population size is not the only factor at play here. Studies have also shown that higher population density is positively correlated with color polymorphism in African land snails (Owen, 1963) and the occurrence of a discrete dimorphism in forcep size in European earwigs (Tomkins and Brown, 2004).

Intuitively, larger demographic stochasticity can lead to lower diversity due to the stochastic elimination of rare mutants regardless of their fitness advantage, in stark contrast to the ‘invasion implies fixation’ paradigm of deterministic models such as adaptive dynamics. Larger demographic stochasticity also leaves populations with less ‘access’ to mutations per unit time, which may explain why studies have consistently observed a larger wait time to diversification. Lastly, theories such as adaptive dynamics require the population to be exactly located at evolutionary singularities, whereas with finite, stochastic populations, we observe a spread around these singularities, further hindering diversification.

In this thesis, I will directly use stochastic birth-death derived from first principles to investigate the expected number of distinct eco-variants that can be harboured in a system. In the process, we will develop a general organizational paradigm for developing stochastic individual-level population models from first principles, and show that many well-known models from population genetics arise as special cases in the infinite population size limit. Using certain approximation schemes, we will arrive at a tractable approximate process that describes how weak stochastic fluctuations drive populations away from deterministic expectations.



# **Part II**

## **Theory & Applications**



# Chapter 3

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## Population dynamics from stochastic first principles

Somewhere [ ... ] between the specific that has no meaning and the general that has no content there must be, for each purpose and at each level of abstraction, an optimum degree of generality

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Kenneth Boulding

### 3.1 Background and motivation

Raymond Pearl, one of the pioneers of mathematical ecology as a discipline, wrote in 1927 that “What we want to know is how the biological forces of natality and mortality are so integrated and correlated in their action as to lead to a final result in size of population which follows this particular curve rather than some other one” (Pearl and Slobodkin, 1976). Pearl realized 95 years ago that population dynamics must be ultimately explained by the mechanistic processes of birth and death. Today, there are mounting calls for more mechanistic models of evolution that are grounded in these fundamental processes of birth and

death (S.A.H. Geritz and Kisdi, 2012; Doebeli, Y. Ispolatov, et al., 2017). Ecologists also increasingly recognize that incorporating stochasticity is vital to developing more realistic ecological models (Hastings, 2004; Coulson et al., 2004; Boettiger, 2018; Shoemaker et al., 2020; Schreiber et al., 2022) and does more than ‘add noise’ to deterministic expectations. Individual-based models, where ecological rules are specified at the level of the individual, are a powerful mathematical tool for mechanistic descriptions of stochastic population dynamics (Black and McKane, 2012). Birth-death processes are a very general class of stochastic processes that can be used to capture a wide range of eco-evolutionary processes. ‘System-size expansions’ and their subsequent analysis using the ‘weak noise approximation’ are common tools for analyzing stochastic birth-death processes that are well-known in the statistical physics and applied mathematics communities (Gardiner, 2009). However, these tools remain relatively underappreciated in ecology, despite being relatively easy to understand and extremely well-motivated in scenarios germane to ecology and evolution. Here, I present a formulation of population dynamics constructed from first principles grounded in birth-death processes. To facilitate readership by a broad audience, only passing familiarity with calculus (derivatives, integrals, Taylor expansions) and probability are assumed. Familiarity with stochastic calculus is helpful for some sections but is not required, and I provide a brief introduction below. I begin by introducing birth-death processes, SDEs, and the Fokker-Planck equation in a non-technical manner, and providing the intuition for system-size expansions and weak noise analysis in ecological systems. In section 3.2, I show how fluctuating population size of populations of identical individuals can be tracked through a one-dimensional birth-death process. I introduce a description of the system via a ‘master equation’, and then conduct a ‘system-size expansion’ to obtain a Fokker-Planck equation for the system. Finally, I conduct a weak noise approximation to arrive at a linear Fokker-Planck equation which can be solved exactly using some stochastic calculus to arrive at a closed-form solution given by a time-dependent Ornstein-Uhlenbeck process. As an example, I illustrate the complete process for a stochastic version of the logistic equation. In section 3.3, I present a multivariate process to describe the evolution of discretely varying traits, and, as before, illustrate the system size expansion and the weak noise approximation. Under mild assumptions, we show that the deterministic limit of this process is the well-known replicator-mutator equation (or equivalently, Eigen’s quasispecies equation), thus establishing the microscopic basis of well-known equations in evolutionary game theory. I also show that the mean value of the trait in the population changes according to the Price equation in the deterministic limit. Chapter 4 introduces a function-valued process to model the evo-

lution of quantitative traits such as body size, which can take on uncountably many values. This function-valued process can then also be analyzed via a system-size approximation to arrive at a ‘functional’ Fokker-Planck equation, in terms of functional derivatives. Under mild assumptions, we show that classic equations such as Kimura’s infinite alleles model and the canonical equation of adaptive dynamics can be derived as the deterministic limits of this stochastic process. We also conduct a weak noise approximation to arrive at a linear functional Fokker-Planck equation. Sections 3.2 and 3.3 apply techniques that are well-known in physics, as applied to population biology. In contrast, chapter 4, to the best of my knowledge, is entirely original. Chapter 4 also presents a simple heuristic derivation of quantitative genetics models and adaptive dynamics from stochastic first principles that is much simpler than the rigorous mathematical derivations grounded in measure theory and martingale/markov theory that are currently standard reference in theoretical ecology (Champagnat et al., 2008). I illustrate the utility of all this abstract formalism through examples in Chapter 5.

### 3.1.1 Birth-death processes

Mathematically, a birth-death process is a so-called ‘continuous-time Markov chain’ in which only transitions between local states are allowed. In other words, a birth-death process is a stochastic process unfolding in continuous time such that

- The process is ‘Markov’, meaning that the future is statistically independent of the past given the present. In more mathematical terms, if the value of the stochastic process at time  $t$  is given by  $X_t$ ,  $\mathbb{P}(\cdot|E)$  denotes probability conditioned on  $E$ , and  $u < s \leq t$ , then

$$\mathbb{P}(X_t|X_s, X_u) = \mathbb{P}(X_t|X_s)$$

- Direct transitions must be ‘local’. Mathematicians usually reserve the phrase ‘birth-death process’ to processes that take values in the non-negative integers  $\{0, 1, 2, 3, 4, \dots\}$ . In this case, only direct transitions from  $n$  to  $n \pm 1$  are allowed to occur. Biologically, this is saying that we observe the population on a fine enough timescale that the probability of two or more births/deaths occurring at the exact same time is very low and we can disallow it entirely in our models. The conditions for higher dimensional birth-death processes look similar.

Since these processes unfold in continuous time, they are characterized not by transition probabilities but by transition *rates*, which can be thought of as the probability of transition ‘per unit time’. The quantity of interest is usually the probability of being in a particular state at a given point in time. The entire birth-death process can be described in terms of such a quantity, through a so-called ‘Master equation’. The master equation is a partial differential equation (PDE) for the probability of being in a given state at a given time, However, in all but the simplest cases, we can’t actually solve this PDE, because it is simply too hard. The primary source of difficulty is non-linearity in the transition rates and the fact that transitions occur in discrete, discontinuous ‘jumps’. It is much easier to describe and analyze systems by using tools from stochastic calculus and partial differential equations, as we describe below.

### 3.1.2 SDEs and the Fokker-Planck equation

Stochastic systems which change continuously (in the state space) can be described in terms of a ‘stochastic differential equation’ (SDE), which here is interchangeable with the phrase ‘Itô process’. An SDE for a stochastic process  $\{X_t\}_{t \geq 0}$  is an equation of the form

$$X_t = \int_0^t F(s, X_s) ds + \int_0^t G(s, X_s) dB_s \quad (3.1)$$

where  $F(t, x)$  and  $G(t, x)$  are ‘nice’ functions<sup>1</sup> In the physics literature,  $F$  and  $G$  are often called the ‘drift’ and ‘diffusion’ of the process respectively. However, we will not use this terminology here due to potential confusion with genetic drift (which actually corresponds to the ‘diffusion’ in the physics terminology).  $B_t$  is the so-called ‘standard Brownian motion’. Named after the botanist Robert Brown (who was looking at the random erratic motion of pollen grains in water under a microscope),  $\{B_t\}_{t \geq 0}$  is a stochastic process that is supposed to model ‘random noise’ or ‘undirected diffusion’ of a particle. If one imagines  $B_t$  as recording the position of a small pollen grain at time  $t$ , then  $B_t$  can be formally thought of as a process that has the following properties:

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<sup>1</sup>For the mathematically oriented reader, there are two requirements: Firstly, we require the functions to have ‘linear growth’, meaning that we can find a constant  $C > 0$  such that  $\|F(t, x)\| + \|G(t, x)\| \leq C(1 + \|x\|)$  for every  $x \in \mathbb{R}^d$  and  $t > 0$ . We also require ‘Lipschitz continuity’, which means that we can find a constant  $L > 0$  such that  $\|F(t, x) - F(t, y)\| + \|G(t, x) - G(t, y)\| \leq L\|x - y\|$  for every pair  $x, y \in \mathbb{R}^d$  and  $t > 0$ . Here,  $\|\cdot\|$  denotes the natural norm on the space under consideration and for our cases will usually be the Euclidean norm. For biological systems, both of these conditions will usually be satisfied, and so we assume going further that all our SDEs are always well-defined and admit solutions.

- It starts at the origin, *i.e.*  $B_0 = 0$ . This is a harmless assumption made for convenience and amounts to a choice of coordinate system.
- It moves continuously, without sudden jumps across regions of space, *i.e.* the map  $t \rightarrow B_t$  is continuous. This simply says that our pollen grain moves short distances in short intervals of time.
- The future movement is independent of past history. That is, given times  $u < s < t$ , the displacement  $B_t - B_s$  is independent of the past position  $B_u$ .
- The movement is directionless and random, and displacement is normally distributed. More precisely, given two times  $s < t$ , the displacement  $B_t - B_s$  follows a normal distribution with a mean of 0 (this is the ‘directionless’ part) and a variance of  $t - s$  (this is the ‘random’ part).

It can then be shown that since the motion is equally likely to be in any direction, the expected position at any point of time is the same as the initial position, *i.e.*  $\mathbb{E}[B_t | B_0] = B_0 = 0$ .

The second integral in equation (3.1) is Itô’s ‘stochastic integral’, and is to be interpreted in the following sense: Fix a time  $T > 0$ . Partition the interval  $[0, T]$  into  $n$  intervals of the form  $[t_i, t_{i+1}]$  such that  $0 = t_0 < t_1 < t_2 < \dots < t_n = T$ . Then, the (Itô) stochastic integral from 0 to  $T$  can be thought of as:

$$\int_0^T G(s, X_s) dB_s := \lim_{n \rightarrow \infty} \sum_{i=1}^n G(t_i, X_{t_i})(B_{t_{i+1}} - B_{t_i})$$

That is to say, it is obtained by making successively finer partitions of the form  $[t_i, t_{i+1}]$ , and then computing the ‘area of the rectangle’ formed with  $B_{t_{i+1}} - B_{t_i}$  and  $G(t_i, X_{t_i})$  as sides. This should look similar to the classic Riemann integral, with the uniform width  $t_{i+1} - t_i$  of the Riemann integral replaced by a random width corresponding to the random displacement of a Brownian particle during the uniform time interval  $[t_i, t_{i+1}]$ .

Equation (3.1) is often represented in the compact form:

$$dX_t = F(t, X_t)dt + G(t, X_t)dB_t \quad (3.2)$$

. The physics literature also often uses the ‘Langevin form’:

$$\frac{dx}{dt} = F(t, x) + G(t, x)\eta(t) \quad (3.3)$$

where  $\eta(t)$  is supposed to be ‘Gaussian white noise’, defined indirectly such that  $\int_0^t G(s, x)\eta(s)ds$  behaves the same as  $\int_0^t G(s, X_s)dB_s$ . However, it is important to remember that these are both purely formal expressions - Equation (3.2) is meaningless on its own and is really just shorthand for equation (3.1), which is well-defined as explained above; Equation (3.3) is even worse, because the Brownian motion is known to be non-differentiable, and as such,  $\eta(t)$  cannot really exist - Both equations are thus to be interpreted as shorthand for equation (3.1), which formally ‘makes sense’. SDEs are convenient because they satisfy several ‘nice’ analytical properties. For example, using the fact that the Brownian motion has no expected change in value (*i.e.*  $\mathbb{E}[B_t|B_0] = B_0 = 0$ ), it can be shown<sup>2</sup> that the stochastic integral also has an expectation value of 0 for all  $t$ , *i.e.*:

$$\mathbb{E} \left[ \int_0^t G(s, X_s)dB_s \middle| X_0 \right] = 0$$

Using this, and the fact that the future path of the Brownian motion itself is independent of its history, one can derive the following ‘notational algebra table’ for manipulating products of formal expressions of the form (3.2):

	$dt$	$dB_t$
$dt$	0	0
$dB_t$	0	$dt$

which becomes very useful for formal manipulation. Using this property, one can show using some simple algebra that if a process  $X_t$  taking values in  $\mathbb{R}$  satisfies the SDE (3.2), then the

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<sup>2</sup>We can actually prove something stronger: We can show under rather mild regularity assumptions on  $X_t$  and  $G(t, x)$  that the stochastic integral is a continuous square-integrable martingale starting at the origin - This means that the map  $t \rightarrow \int_0^t G(s, X_s)dB_s$  is continuous, starts at the origin, and always has an expectation value of 0.

probability density  $P(x, t)$  of finding the process in a state  $x \in \mathbb{R}$  at time  $t$  satisfies the PDE

$$\frac{\partial P}{\partial t}(x, t) = -\frac{\partial}{\partial x}\{F(t, x)P(x, t)\} + \frac{1}{2}\frac{\partial^2}{\partial x^2}\{(G(t, x))^2P(x, t)\} \quad (3.4)$$

. I present a simple informal derivation in Appendix A. Equation (3.4) is called the ‘Fokker-Planck equation’ in the physics and applied mathematics literature (Gardiner, 2009) and is often called the ‘Kolmogorov forward equation’ in the population genetics (Ewens, 2004) and pure mathematics (Øksendal, 1998) literature. If the function  $G$  is independent of  $x$ , then it comes out of the derivatives in equation (3.4), and the resultant Fokker-Planck equation is said to be ‘linear’ (and is much easier to solve). This link between SDEs and Fokker-Planck equations goes both ways: One can show that every stochastic process with a probability density described by a Fokker-Planck equation of the form (3.4) corresponds to the solution of an SDE of the form (3.2), though the proof is much more technical and will not be discussed here. This two-way correspondence proves to be extremely useful, as one approach often works for applications in which the other fails. This correspondence makes it greatly desirable to be able to describe our stochastic process of interest as either the solution to an Itô SDE of the form (3.2) or as the solution to a Fokker-Planck equation of the form (3.4). System-size expansions facilitate such a description for birth-death processes.

### 3.1.3 Density-dependence and the intuition for system-size expansions in ecology

The fundamental idea behind the system-size expansion relates to the nature of the jumps between successive states of a birth-death process. In most situations in ecology, at an individual level, births and deaths of individuals are affected by local population density and not directly by the total population size. Despite this, the jumps themselves occur in terms of the addition (birth) or removal (death) of a *single individual* from the population. If there are many individuals, each individual contributes a negligible amount to the density, and thus, the discontinuous jumps due to individual-level births or deaths can look like a small, *continuous* change in population density. This is the essential idea behind the system-size expansion. The name derives from the formalization of this idea as a change of variable from the discrete values  $\{0, 1, 2, \dots, n-1, n, n+1, \dots\}$  to the approximately continuous values  $\{0, 1/K, 2/K, \dots, x-1/K, x, x+1/K, \dots\}$  by the introduction of a ‘system size parameter’  $K$ . In ecology, this parameter will be some fundamental limit on resources, such as habitat size or carrying capacity. In physics and chemistry, it is usually the total volume of a

container in which physical or chemical reactions take place. When  $K$  is large, the fact that transitions occur in units of a small value  $1/K$  can be exploited via a Taylor expansion of the transition rates in the Master equation, which then yields a Fokker-Planck equation upon neglecting higher order terms. A similar approximation is well-known (ever since Fisher) in theoretical population genetics (Ewens, 2004), where it goes by the name of the ‘diffusion approximation’, and has been heavily used by Kimura (Crow and Kimura, 1970) in his stochastic models. However, the population genetics version of the approximation often lacks an explicit system size parameter (in physics parlance (Gardiner, 2009), it is closer to a Kramers-Moyal expansion than a Van Kampen expansion) and is thus often somewhat ad-hoc.

### **3.1.4 The intuition for the weak noise approximation in ecology**

If the parameter  $K$  is sufficiently large, then the Fokker-Planck equation obtained via the system-size expansion can be further simplified to obtain a linear Fokker-Planck equation. This is accomplished by viewing the stochastic dynamics as fluctuating about a deterministic trajectory (obtained by letting  $K \rightarrow \infty$ ) and only works if  $K$  is large enough to be able to neglect all but the highest-order terms. This is usually an excellent approximation for populations in which the deterministic trajectory has already reached an attractor (stable fixed point, stable limit cycle, etc.). Since many deterministic eco-evolutionary models are expected to relax to such attractors, such an approximation is a useful first step in increasing the generality of existing models (which are usually studied only in the equilibrium regime) to incorporate the dynamics of finite populations. Importantly, this approximation *only* works if we can discard all but highest-order terms of  $K$ : Including higher-order terms leads to equations that do not form Fokker-Planck equations and do not even describe probability densities. As such, this approximation is best suited to describe populations that are ‘medium sized’ - small enough that they cannot be assumed to be infinitely large, yet large enough that stochasticity is rather weak and the deterministic limit is somewhat predictive - A situation that occurs frequently in ecology and evolution.

## 3.2 Warm up: One-dimensional processes for population size

The simplest birth-death processes are those in which the state at any time can be characterized by a single number. Populations of identical individuals are an obvious example of such a system. The mathematics below are adapted from sections 6.3 and 7.2 of (Gardiner, 2009).

### 3.2.1 Description of the process and the Master Equation

Consider a population of identical individuals subject to some ecological rules that affect individuals' birth and death rates. Since all individuals are identical, we can only really track the population size through time. The population as a whole at any time  $t$  can thus be characterized by a single number - its population size (Figure 3.1). Imagine further that if a population has  $n$  identical individuals, then, from the ecological rules, we can determine a *birth rate*  $b(n)$ , which gives us a measure of the probability that a new individual will be born and the population size becomes  $n + 1$  'per unit time'. One must be slightly precise about what exactly they mean when they say 'per unit time' since there are no discrete 'time steps' for individuals to be born. Here, by 'birth rate', we mean the probability that there will be a birth (and no death) per an *infinitesimal* amount of time. More formally, letting  $N_t$  denote the random variable representing the population size at time  $t$  and letting  $\mathbb{P}(E)$  denote the probability (in the common-sense usage) of an event  $E$ , the birth rate  $b(n)$  of a population with population size  $n$  is the quantity

$$b(n) := \lim_{\epsilon \rightarrow 0} \frac{1}{\epsilon} \mathbb{P}(N_{t+\epsilon} = n + 1 | N_t = n) \quad (3.5)$$

Exactly analogously, we also assume we can define a *death rate*  $d(n)$  of a population of  $n$  individuals as the quantity

$$d(n) := \lim_{\epsilon \rightarrow 0} \frac{1}{\epsilon} \mathbb{P}(N_{t+\epsilon} = n - 1 | N_t = n) \quad (3.6)$$

An alternative, perhaps more intuitive characterization, of these same quantities is the following: If we have a population of size  $n$ , and we know that *either a birth or a death* has

just occurred, then, the probability that the event that occurred is a birth is

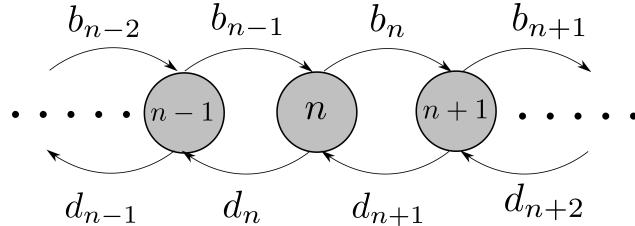
$$\mathbb{P}[\text{ birth } | \text{ something happened }] = \frac{b(n)}{b(n) + d(n)}$$

and the probability that the event was instead a death is given by

$$\mathbb{P}[\text{ death } | \text{ something happened }] = \frac{d(n)}{b(n) + d(n)}$$

**Example 1.** Consider the case where the per-capita birth rate is a constant  $\lambda > 0$ , *i.e.*,  $b(n) = \lambda n$ , and the per-capita death rate has the linear density-dependence  $d(n) = (\mu + (\lambda - \mu)\frac{n}{K})n$ , where  $\mu$  and  $K$  are positive constants. Taking the difference between the birth and death rates, we obtain  $b(n) - d(n) = (\lambda - \mu)n(1 - \frac{n}{K})$ , where, identifying  $r = \lambda - \mu$ , we obtain the familiar logistic equation on the RHS. Note, however, that the population itself is stochastic, whereas the logistic equation is a deterministic description.

Now, let  $P(n, t)$  be the probability that the population size is  $n$  at time  $t$ . We wish to have an equation to describe how  $P(n, t)$  changes with time - this will provide a probabilistic description of how we expect the population size to change over time.



**Figure 3.1: Schematic description of a one-dimensional birth-death process.** Consider a population of identical individuals. The state of the system can be described by a single number, in this case, the population size. Births and deaths result in changes in the total population size, and the birth and death rates are dependent on the current population size.

To do this, we imagine a large ensemble of populations. In a large ensemble of copies evolving independently, a fraction  $P(n, t)$  will have population size  $n$  at time  $t$  by definition of

probability. We can now simply measure the ‘inflow’ and ‘outflow’ of copies of the population from each state. If a population has  $n$  individuals, it could either have gotten there from a population of  $n + 1$  individuals, with a death rate of  $d(n + 1)$ , or from a population of  $n - 1$  individuals, with a birth rate of  $b(n - 1)$ . Thus, the rate of ‘inflow’ to the state  $n$  is given by

$$R_{\text{in}}(n, t) = b(n - 1)P(n - 1, t) + d(n + 1)P(n + 1, t) \quad (3.7)$$

Similarly, if the population has  $n$  individuals, it could obtain a different state in two ways: With rate  $b(n)$ , the population witnesses a birth, and with rate  $d(n)$ , it witnesses a death. Thus, the rate of ‘outflow’ is given by

$$R_{\text{out}}(n, t) = b(n)P(n, t) + d(n)P(n, t) \quad (3.8)$$

The rate of change of the probability of the system being in state  $n$  is given by the rate of inflow minus the rate of outflow. Thus, we have

$$\begin{aligned} \frac{\partial P}{\partial t}(n, t) &= R_{\text{in}}(n, t) - R_{\text{out}}(n, t) \\ &= b(n - 1)P(n - 1, t) + d(n + 1)P(n + 1, t) - b(n)P(n, t) - d(n)P(n, t) \end{aligned} \quad (3.9)$$

For convenience, let us define two ‘step operators’  $\mathcal{E}^\pm$ , which act on any functions of populations to their right by either adding or removing an individual, *i.e.*

$$\mathcal{E}^\pm f(n, t) = f(n \pm 1, t)$$

Rearranging the RHS of (3.9) to write in terms of these step operators, we obtain the compact expression

$$\frac{\partial P}{\partial t}(n, t) = (\mathcal{E}^- - 1)b(n)P(n, t) + (\mathcal{E}^+ - 1)d(n)P(n, t) \quad (3.10)$$

This is the so-called ‘master equation’, and completely describes our system. However, in general,  $b(n)$  and  $d(n)$  may be rather complicated, in which case it may not be possible to solve (3.10) directly.

### 3.2.2 The system-size expansion

The system-size expansion arises from noting that in many systems, the interactions are governed not by population size, but by population *density*. However, the population jumps

themselves are discretized at the scale of the individual, which becomes negligibly small if we have a large population density. Thus, we assume that there exists a system-size parameter  $K > 0$  such that the discrete jumps between states happen in units of  $1/K$ , and we make the substitutions

$$\begin{aligned}x &= \frac{n}{K} \\b_K(x) &= \frac{1}{K}b(n) \\d_K(x) &= \frac{1}{K}d(n)\end{aligned}$$

As  $K$  grows very large, the discontinuous jumps in  $n$  thus appear like ‘continuous’ transitions in our new variable  $x$ , which can be thought of as the ‘density’ of organisms. A system-size parameter  $K$  often naturally emerges in ecological systems through resource-limiting factors such as habitat size or carrying capacity. Under these substitutions, equation (3.10) becomes

$$\frac{\partial P}{\partial t}(x, t) = (\Delta^- - 1)Kb_K(x)P(x, t) + (\Delta^+ - 1)Kd_K(x)P(x, t) \quad (3.11)$$

where we now have the new step operators

$$\Delta^\pm f(x, t) = f\left(x \pm \frac{1}{K}, t\right) \quad (3.12)$$

If  $K$  is large, then we can now taylor-expand the action of these step operators as:

$$\Delta^\pm f(x, t) = f\left(x \pm \frac{1}{K}, t\right) = f(x, t) \pm \frac{1}{K} \frac{\partial f}{\partial x}(x, t) + \frac{1}{2K^2} \frac{\partial^2 f}{\partial x^2}(x, t) + \mathcal{O}(K^{-3})$$

Substituting these expansions into (3.11) and neglecting terms of  $\mathcal{O}(K^{-3})$  and higher, we obtain

$$\frac{\partial P}{\partial t}(x, t) = -\frac{\partial}{\partial x}\{A^-(x)P(x, t)\} + \frac{1}{2K} \frac{\partial^2}{\partial x^2}\{A^+(x)P(x, t)\} \quad (3.13)$$

where

$$A^\pm(x) = b_K(x) \pm d_K(x)$$

Equation (3.13) has the form of a so-called ‘Fokker-Planck equation’, and corresponds to the SDE:

$$dX_t = A^-(X_t)dt + \sqrt{\frac{A^+(X_t)}{K}}dB_t \quad (3.14)$$

interpreted in the Itô sense. Note that the deterministic component of this process depends on the difference between birth and death rates (a mechanistic measure of Malthusian fitness), whereas the stochastic part depends on their sum and scales inversely with  $\sqrt{K}$ .

### 3.2.3 Stochastic fluctuations and the weak noise approximation

If we assume the noise is *weak*, then we can go still further with analytic techniques by measuring fluctuations from the deterministic expectations, albeit with some slightly cumbersome calculations to arrive at the final expressions. We will grit our teeth and get through the algebra below, with my promise that the final answer is neat and easy to handle. It is clear that as  $K \rightarrow \infty$ , equation (3.14) describes a deterministic process, obtained as the solution to

$$\frac{dx}{dt} = A^-(x) = b_K(x) - d_K(x) \quad (3.15)$$

This is a very intuitive equation, saying that the rate of change of the population is equal to the birth rate minus the death rate. Let the solution of this equation be given by  $\alpha(t)$ , so that  $\frac{d\alpha}{dt}(t) = A^-(\alpha(t))$ .

We can now measure (scaled) fluctuations from the deterministic solution  $\alpha$  through a new variable  $y = \sqrt{K}(x - \alpha(t))$ . For notational clarity, we will also introduce a new time variable  $s = t$  which is equal to the original time variable (this is just so the equations look clearer). Let the probability density function of this new variable be given by  $\tilde{P}(y, s)$ . In summary, we have introduced the variables:

$$\begin{aligned} y &= \sqrt{K}(x - \alpha(t)) \\ s &= t \\ \tilde{P}(y, s) &= \frac{1}{\sqrt{K}}P(x, t) \end{aligned}$$

Note that by ordinary rules of variable substitution, we have:

$$\begin{aligned} \frac{\partial \tilde{P}}{\partial t} &= \frac{\partial \tilde{P}}{\partial y} \frac{\partial y}{\partial t} + \frac{\partial \tilde{P}}{\partial s} \frac{\partial s}{\partial t} \\ &= \frac{\partial \tilde{P}}{\partial y} \left( -\sqrt{K} \frac{d\alpha}{dt} \right) + \frac{\partial \tilde{P}}{\partial s} \\ &= -\sqrt{K} A^-(\alpha(s)) \frac{\partial \tilde{P}}{\partial y} + \frac{\partial \tilde{P}}{\partial s} \end{aligned} \quad (3.16)$$

and

$$\frac{\partial}{\partial y} = \frac{1}{\sqrt{K}} \frac{\partial}{\partial x} \quad (3.17)$$

Reformulating (3.13) in terms of  $y, s$  and  $\tilde{P}$  and substituting (3.16) and (3.17) yields:

$$\begin{aligned} -A^-(\alpha) \frac{\partial \tilde{P}}{\partial x} + \frac{\partial \tilde{P}}{\partial s} &= -\sqrt{K} \frac{\partial}{\partial y} \left( A^-(\alpha + \frac{y}{\sqrt{K}}) \tilde{P} \right) + \frac{1}{2} \frac{\partial^2}{\partial y^2} \left( A^+(\alpha + \frac{y}{\sqrt{K}}) \tilde{P} \right) \\ \Rightarrow \frac{\partial \tilde{P}}{\partial s} &= -\frac{\partial}{\partial y} \left[ \sqrt{K} \left( A^-(\alpha + \frac{y}{\sqrt{K}}) - A^-(\alpha) \right) \tilde{P} \right] + \frac{1}{2} \frac{\partial^2}{\partial y^2} \left( A^+(\alpha + \frac{y}{\sqrt{K}}) \tilde{P} \right) \end{aligned} \quad (3.18)$$

We are now ready to make a weak noise ‘expansion’. We do so by assuming that  $\tilde{P}, A^-(\alpha + \frac{y}{\sqrt{K}})$ , and  $A^+(\alpha + \frac{y}{\sqrt{K}})$  can be approximated by series expansions in  $\frac{1}{\sqrt{K}}$  of the form:

$$\begin{aligned} \tilde{P} &= \sum_{n=0}^{\infty} \tilde{P}_n \left( \frac{1}{\sqrt{K}} \right)^n \\ A^- \left( \alpha(s) + \frac{y}{\sqrt{K}} \right) &= \sum_{n=0}^{\infty} A_n^-(s) \left( \frac{y}{\sqrt{K}} \right)^n \\ A^+ \left( \alpha(s) + \frac{y}{\sqrt{K}} \right) &= \sum_{n=0}^{\infty} A_n^+(s) \left( \frac{y}{\sqrt{K}} \right)^n \end{aligned}$$

with  $A_0^-(s) = A^-(\alpha(s)), A_0^+(s) = A^+(\alpha(s))$ . These could be Taylor expansions, for example, but the exact form of the coefficients is irrelevant as long as it is known to us, so any expansion will work. We can now substitute these series expansions into (3.18) to obtain:

$$\begin{aligned} \sum_{n=0}^{\infty} \left( \frac{1}{\sqrt{K}} \right)^n \frac{\partial \tilde{P}_n}{\partial s} &= -\frac{\partial}{\partial y} \left[ \sqrt{K} \left( \sum_{n=1}^{\infty} A_n^-(s) \left( \frac{y}{\sqrt{K}} \right)^n \right) \left( \sum_{m=0}^{\infty} \tilde{P}_m \left( \frac{1}{\sqrt{K}} \right)^m \right) \right] \\ &\quad + \frac{1}{2} \frac{\partial^2}{\partial y^2} \left[ \left( \sum_{n=0}^{\infty} A_n^+(s) \left( \frac{y}{\sqrt{K}} \right)^n \right) \left( \sum_{m=0}^{\infty} \tilde{P}_m \left( \frac{1}{\sqrt{K}} \right)^m \right) \right] \end{aligned} \quad (3.19)$$

We can now compare the coefficients of  $K^{-n/2}$  for each  $n$  in order to arrive at approximations in the series expansion, the idea being that you neglect all terms which are of order greater than  $\mathcal{O}(K^{-m/2})$  for some  $m$  according to the desired precision.

We observe that for any fixed  $r$ , the coefficient of  $K^{-r/2}$  on the LHS is  $\frac{\partial \tilde{P}_r}{\partial s}$ . On the RHS, the coefficients of  $K^{-r/2}$  in the second term have the form  $\tilde{P}_m A_n^+ y^n$ , subject to the constraint that  $m+n=r$ . Furthermore, all such terms (and only such terms) are coefficients of  $K^{-r/2}$ .

Thus, after grouping, the coefficient of  $K^{-r/2}$  from the second terms of the RHS of (3.19) is precisely

$$\frac{1}{2} \frac{\partial^2}{\partial y^2} \sum_{m=0}^r \tilde{P}_m A_{r-m}^+ y^{r-m}$$

Exactly analogous reasoning reveals that the contribution of the first term of the RHS is:

$$-\frac{\partial}{\partial y} \sum_{m=0}^r \tilde{P}_m A_{r-m+1}^- y^{r-m+1}$$

Thus, we find that the  $r$ th term of the expansion satisfies:

$$\frac{\partial \tilde{P}_r}{\partial s} = -\frac{\partial}{\partial y} \left( \sum_{m=0}^r \tilde{P}_m A_{r-m+1}^- y^{r-m+1} \right) + \frac{1}{2} \frac{\partial^2}{\partial y^2} \left( \sum_{m=0}^r \tilde{P}_m A_{r-m}^+ y^{r-m} \right) \quad (3.20)$$

If we assume we can obtain a reasonable approximation by retaining only the first term of the expansion and neglecting all higher-order terms<sup>3</sup>, we are left with the expression:

$$\frac{\partial \tilde{P}_0}{\partial s} = -A_1^-(s) \frac{\partial}{\partial y} (y \tilde{P}_0) + \frac{A_0^+(s)}{2} \frac{\partial^2 \tilde{P}_0}{\partial y^2} \quad (3.21)$$

which is simply the Fokker-Planck equation for the Itô process

$$dY_t = A_1^-(t) Y_t dt + \sqrt{A_0^+(t)} dB_t$$

This equation describes a so-called ‘Ornstein-Uhlenbeck process’, and is easily solved by using  $\exp(-\int A_1^-(s)ds)$  as an ‘integrating factor’. In particular, multiplying both sides by  $\exp(-\int A_1^-(s)ds)$  yields

$$\begin{aligned} \exp \left( - \int_0^t A_1^-(s) ds \right) dY_t - Y_t A_1^-(t) \exp \left( - \int_0^t A_1^-(s) ds \right) dt &= \sqrt{A_0^+(t)} \exp \left( - \int_0^t A_1^-(s) ds \right) dB_t \\ \Rightarrow d \left( \exp \left( - \int_0^t A_1^-(s) ds \right) Y_t \right) &= \sqrt{A_0^+(t)} \exp \left( - \int_0^t A_1^-(s) ds \right) dB_t \end{aligned}$$

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<sup>3</sup>For example, if the deterministic trajectory is at a stable fixed point and subject to weak fluctuations

Integrating both sides and noting that  $A_0^+(s) = A^+(\alpha(s))$ , we thus obtain the final expression

$$Y_t = Y_0 \exp \left( \int_0^t A_1^-(s) ds \right) + \int_0^t \exp \left( - \int_s^t A_1^-(v) dv \right) \sqrt{A^+(\alpha(s))} dB_s \quad (3.22)$$

as the zeroth-order weak noise approximation for stochastic fluctuations from the deterministic trajectory due to demographic noise. Note that this is an exact equation, and one can get many insights from it. For example, if  $Y_0 = 0$  (*i.e.* we start at the deterministic steady state, a natural assumption for measuring fluctuations from it), then we can show by taking expectations in (3.22) and using results presented in 3.1.2 that we must have  $\mathbb{E}[Y_t|Y_0] = 0$ . In other words, the fluctuations have zero expectation and are expected to occur symmetrically about  $\alpha(t)$ , with no bias. The variance (spread) of the fluctuations  $Y_t$ , as well as higher moments, can also be exactly calculated from (3.22) using some tools from stochastic calculus, but we will not demonstrate this here.

Importantly, higher order terms do not form FPEs, and in general,  $\tilde{P}_r$  for  $r > 0$  may be negative and therefore does not even describe a probability. As such, formulating the solution as the solution to an SDE only works for  $\tilde{P}_0$ . If noise is large enough that it is not well-approximated by  $\tilde{P}_0$ , this method is not very useful.

### 3.3 Multi-dimensional processes for discrete traits

Let us now consider a slightly more complicated scenario. Assume that our population is *not* composed of identical organisms, but instead can contain up to  $m$  different kinds of organisms - For example, individuals may come in one of  $m$  colors, or a gene may have  $m$  different alleles. The formalism we have developed in the previous section carries out essentially unchanged in this case.

#### 3.3.1 Description of the process and the Master Equation

Given a population that can contain up to  $m$  different (fixed) kinds of organisms, it can be entirely characterized by specifying the number of organisms of each type (Figure 3.2A). Thus, the state of the population at a given time  $t$  is an  $m$ -dimensional *vector* of the form  $\mathbf{v} = [v_1(t), v_2(t), \dots, v_m(t)]$ , where  $v_i(t)$  is the number of individuals of type  $i$ .

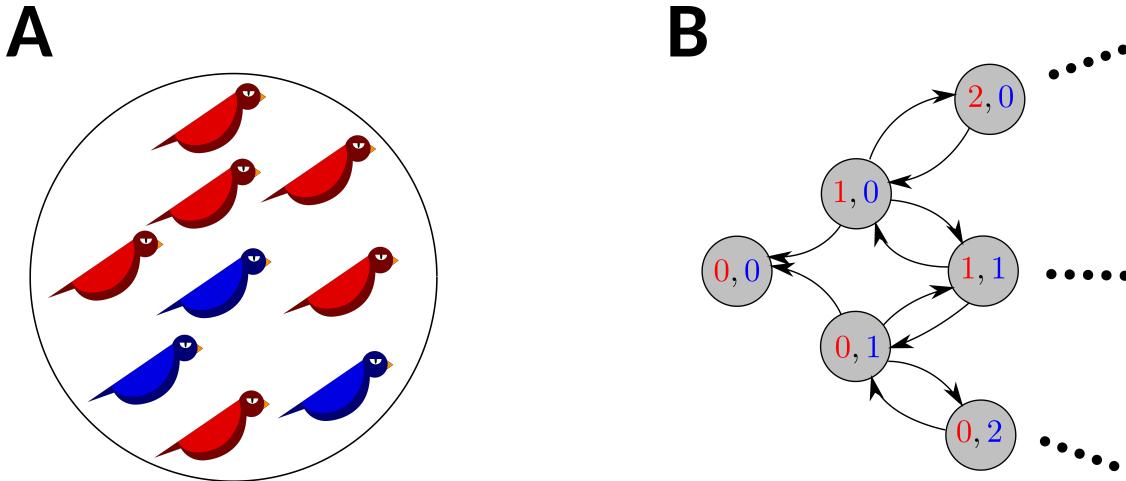
Given a state  $\mathbf{v}(t)$ , we also need to describe how this vector can change over time due to

births and deaths (ecology). In this case, a birth or death could result in an individual belonging to one of  $m$  different types. Thus, whereas before we had two functions  $b(n)$  and  $d(n)$  which take in a number as an input, we now require  $2m$  functions that take in a vector as an input (Figure 3.2B). In other words, for each type  $i \in \{1, 2, \dots, m\}$ , we must specify a birth rate  $b_i(\mathbf{v})$  and a death rate  $d_i(\mathbf{v})$ . By ‘rates’, we mean that if we know that *either a birth or a death* occurs, then the probability that this event is the birth of an individual of type  $i$  is given by

$$\mathbb{P}[\text{ Birth of a type } i \text{ individual} | \text{ something happened}] = \frac{b_i(\mathbf{v})}{\sum_{j=1}^m (b_j(\mathbf{v}) + d_j(\mathbf{v}))}$$

and the probability that the event is the death of an individual of type  $i$  is

$$\mathbb{P}[\text{ Death of a type } i \text{ individual} | \text{ something happened}] = \frac{d_i(\mathbf{v})}{\sum_{j=1}^m (b_j(\mathbf{v}) + d_j(\mathbf{v}))}$$



**Figure 3.2:** (A) Consider a population of birds in which individuals are either red or blue. In this case, we have  $m = 2$ , since there are two types of individuals in the population. (B) The state of the system can be described by a vector containing the number of individuals of each discrete type (in this case, the number of red and blue birds in the population). Births and deaths result in changes in the elements of the state vector.

As before, we can describe the rate of change of  $P(\mathbf{v}, t)$ , the probability of finding the

population in a state  $\mathbf{v}$  at time  $t$ , by measuring the inflow and outflow rates. Given a population  $\mathbf{v} = [v_1, \dots, v_m]$ , the ‘inflow’ is from all populations of the form  $[v_1, \dots, v_i - 1, \dots, v_m]$  through a birth of a type  $i$  individual, and from all populations of the form  $[v_1, \dots, v_i + 1, \dots, v_m]$  through the death of a type  $i$  individual. Thus, we have the inflow rate

$$\begin{aligned} R_{\text{in}}(\mathbf{v}, t) &= \sum_{j=1}^m b_j([v_1, \dots, v_j - 1, \dots, v_m]) P([v_1, \dots, v_j - 1, \dots, v_m], t) \\ &\quad + \sum_{j=1}^m d_j([v_1, \dots, v_j + 1, \dots, v_m]) P([v_1, \dots, v_j + 1, \dots, v_m], t) \end{aligned} \quad (3.23)$$

Outflow is through births and deaths of individuals in the population  $\mathbf{v}$  itself, and thus we have:

$$R_{\text{out}}(\mathbf{v}, t) = \sum_{j=1}^m b_j(\mathbf{v}) P(\mathbf{v}, t) + \sum_{j=1}^m d_j(\mathbf{v}) P(\mathbf{v}, t) \quad (3.24)$$

As before, we now define step operators, both for notational ease and in anticipation of the system size expansion. Note that now, we need  $2m$  step operators. For each  $i \in \{1, \dots, m\}$ , let us define two step operators  $\mathcal{E}_i^\pm$  by their action on any function  $f([v_1, \dots, v_m], t)$  as:

$$\mathcal{E}_i^\pm f([v_1, \dots, v_m], t) = f([v_1, \dots, v_i \pm 1, \dots, v_m], t) \quad (3.25)$$

In other words,  $\mathcal{E}_i^\pm$  just changes the population through the addition or removal of one type  $i$  individual. We can now the rate of change of  $P(\mathbf{v}, t)$  as

$$\frac{\partial P}{\partial t}(\mathbf{v}, t) = R_{\text{in}}(\mathbf{v}, t) - R_{\text{out}}(\mathbf{v}, t) \quad (3.26)$$

Substituting (3.23), (3.24), and (3.25), we obtain:

$$\frac{\partial P}{\partial t}(\mathbf{v}, t) = \sum_{j=1}^m [(\mathcal{E}_j^- - 1)b_j(\mathbf{v})P(\mathbf{v}, t) + (\mathcal{E}_j^+ - 1)d_j(\mathbf{v})P(\mathbf{v}, t)] \quad (3.27)$$

This is the master equation of our  $m$ -dimensional process.

### 3.3.2 The system-size expansion

As before, we now assume we can find a system size parameter  $K > 0$  such that we can make the substitutions

$$\begin{aligned}\mathbf{x} &= \frac{\mathbf{v}}{K} \\ b_i^{(K)}(\mathbf{x}) &= \frac{1}{K}b_i(\mathbf{v}) \\ d_i^{(K)}(\mathbf{x}) &= \frac{1}{K}d_i(\mathbf{v})\end{aligned}$$

and define new step operators  $\Delta_i^\pm$  by their action on any real-valued function  $f(\mathbf{x}, t)$  as

$$\Delta_i^\pm f([x_1, \dots, x_m], t) = f([x_1, \dots, x_i \pm \frac{1}{K}, \dots, x_m], t) \quad (3.28)$$

In terms of these new variables, (3.27) becomes

$$\frac{\partial P}{\partial t}(\mathbf{x}, t) = K \sum_{j=1}^m \left[ (\Delta_j^- - 1)b_j^{(K)}(\mathbf{x})P(\mathbf{x}, t) + (\Delta_j^+ - 1)d_j^{(K)}(\mathbf{x})P(\mathbf{x}, t) \right] \quad (3.29)$$

If  $K$  is large, we can once again Taylor expand the action of the step operators as

$$f([x_1, \dots, x_i \pm \frac{1}{K}, \dots, x_m], t) = f(\mathbf{x}, t) \pm \frac{1}{K} \frac{\partial f}{\partial x_i}(\mathbf{x}, t) + \frac{1}{2K^2} \frac{\partial^2 f}{\partial x_i^2}(\mathbf{x}, t) + \mathcal{O}(K^{-3})$$

which, after substituting into (3.29), yields the equation

$$\frac{\partial P}{\partial t}(\mathbf{x}, t) = \sum_{j=1}^m \left[ -\frac{\partial}{\partial x_j} \{A_j^-(\mathbf{x})P(\mathbf{x}, t)\} + \frac{1}{2K} \frac{\partial^2}{\partial x_j^2} \{A_j^+(\mathbf{x})P(\mathbf{x}, t)\} \right] \quad (3.30)$$

where

$$A_i^\pm(\mathbf{x}) = b_i^{(K)}(\mathbf{x}) \pm d_i^{(K)}(\mathbf{x})$$

Equation (3.30) is an  $m$ -dimensional Fokker-Planck equation, and corresponds to the  $m$ -dimensional Itô process

$$d\mathbf{X}_t = \mathbf{A}^-(\mathbf{X}_t)dt + \frac{1}{\sqrt{K}}\mathbf{D}(\mathbf{X}_t)d\mathbf{B}_t \quad (3.31)$$

where  $\mathbf{A}^-(\mathbf{X}_t)$  is the  $m$  dimensional ‘drift vector’ with  $i^{\text{th}}$  element =  $A_i^-(\mathbf{X}_t)$ .  $\mathbf{D}(\mathbf{X}_t)$  is the  $m \times m$  ‘diffusion matrix’ with  $ij^{\text{th}}$  element  $(\mathbf{D}(\mathbf{X}_t))_{ij} = \delta_{ij} (A_i^+ A_j^+)^{\frac{1}{4}}$ , where  $\delta_{ij}$  is the Kronecker delta symbol, defined by

$$\delta_{ij} = \begin{cases} 1 & i = j \\ 0 & i \neq j \end{cases}$$

Finally,  $\mathbf{B}_t$  is the  $m$ -dimensional Brownian motion and can be thought of as a vector of independent one-dimensional Brownian motions (which have been defined in 3.1.2). This is the ‘mesoscopic’ description of our process.

### 3.3.3 The deterministic limit

Once again, we can take  $K \rightarrow \infty$  in (3.31) to obtain a deterministic expression. Here, the expression reads

$$\frac{d\mathbf{x}}{dt} = \mathbf{A}^-(\mathbf{x}) = \mathbf{b}^{(K)}(\mathbf{x}) - \mathbf{d}^{(K)}(\mathbf{x}) \quad (3.32)$$

where the  $m$ -dimensional vector-valued functions  $\mathbf{b}^{(K)}(\mathbf{x})$  and  $\mathbf{d}^{(K)}(\mathbf{x})$  on the RHS are defined as having  $i^{\text{th}}$  element  $b_i^{(K)}(\mathbf{x})$  and  $d_i^{(K)}(\mathbf{x})$  respectively. This deterministic limit is sometimes called the ‘macroscopic’ description.

#### Some familiar faces: Replicator-mutator, quasispecies equation, and the Price equation

In this multi-dimensional case, the macroscopic description amounts to a description of evolutionary game theory under mild assumptions on the birth and death rate vectors. We show this below, using methods first outlined by (Page and Nowak, 2002). Let us assume that we can write the birth and death rate vectors as

$$\begin{aligned} b_i^{(K)}(\mathbf{x}) &= \mu Q_i(\mathbf{x}) + b_i^{(\text{ind})}(\mathbf{x})x_i \\ d_i^{(K)}(\mathbf{x}) &= d_i^{(\text{ind})}(\mathbf{x})x_i \end{aligned} \quad (3.33)$$

where  $\mu \geq 0$  is a constant describing the mutation rate,  $Q_i(\mathbf{x})$  is a real-valued function that describes the birth rate of type  $i$  individuals due to mutations in the population  $\mathbf{x}$ , and  $b_i^{(\text{ind})}(\mathbf{x})$  and  $d_i^{(\text{ind})}(\mathbf{x})$  are real-valued functions that respectively describe the per-capita birth and death rate of type  $i$  individuals. Our assumptions of the functional forms (3.33)

thus amount to saying that birth and death rates can be separated into mutational and non-mutational components, and furthermore that the density dependence of the birth and death rates due to non-mutational effects is in a form that allows us to write down per-capita birth and death rates. Plugging these definitions into (3.32) and writing it down component-wise, we obtain the equation

$$\frac{dx_i}{dt} = w_i(\mathbf{x})x_i + \mu Q_i(\mathbf{x}) \quad (3.34)$$

Where for each  $i$ , we have defined the real-valued function  $w_i(\mathbf{x}) := b_i^{(\text{int})}(\mathbf{x}) - d_i^{(\text{int})}(\mathbf{x})$ . Setting the mutation rate  $\mu \rightarrow 0$  in equation (3.34) makes it clear that the quantity  $w_i(\mathbf{x})x_i$  describes the growth rate of type  $i$  individuals in the population due to all processes other than mutation. The quantity  $w_i(\mathbf{x})$  thus describes the per-capita growth rate of type  $i$  individuals in a population  $\mathbf{x}$ , and is sometimes called the ‘Malthusian fitness’ of type  $i$ . Ecologists often denote this quantity by the symbol  $r_i$  and simply call it the (exponential) growth rate of type  $i$ , but we will stick to  $w_i$  and ‘fitness’ here. It is notable that the fitness of a type depends on the state of the population as a whole (*i.e.*  $\mathbf{x}$ ) and is thus frequency-dependent.

Given a state  $\mathbf{x}(t)$ , we can now compute the total (scaled) population size and the frequency of each type in the population as:

$$\begin{aligned} N_K(t) &:= \sum_{i=1}^m x_i(t) \\ p_i(t) &:= \frac{x_i(t)}{N_K(t)} \end{aligned} \quad (3.35)$$

We can also calculate the statistical mean value of any type level quantity  $f$  in the population as

$$\bar{f}(t) := \sum_{i=1}^m f_i p_i(\mathbf{x}(t)) \quad (3.36)$$

, where  $f_i$  is the value of the quantity for the  $i$ th type.

We can now compute the rate of change of  $p_i$ , the proportion of type  $i$  individuals in the population:

$$\frac{dp_i}{dt} = \frac{1}{N_K(t)} \frac{dx_i}{dt} - \frac{x_i}{N_K^2(t)} \frac{dN_K}{dt}$$

$$= \frac{1}{N_K(t)} \frac{dx_i}{dt} - \frac{x_i}{N_K^2(t)} \sum_{j=1}^m \frac{dx_j}{dt} \quad (3.37)$$

Substituting (3.34) into (3.37), we now obtain

$$\begin{aligned} \frac{dp_i}{dt} &= \frac{1}{N_K(t)} [w_i(\mathbf{x})x_i + \mu Q_i(\mathbf{x})] - \frac{x_i}{N_K^2(t)} \sum_{j=1}^m [w_j(\mathbf{x})x_j + \mu Q_j(\mathbf{x})] \\ &= w_i(\mathbf{x})p_i + \frac{\mu}{N_K} Q_i(\mathbf{x}) - p_i \sum_{j=1}^m \left[ w_j(\mathbf{x})p_j + \frac{\mu}{N_K} Q_j(\mathbf{x}) \right] \end{aligned}$$

Where we have used the definition of  $p_i$  from (3.35). Now using the definition of mean fitness from (3.36) and rearranging terms, we obtain

$$\frac{dp_i}{dt} = (w_i(\mathbf{x}) - \bar{w})p_i + \mu \left[ Q_i(\mathbf{p}) - p_i \left( \sum_{j=1}^m Q_j(\mathbf{p}) \right) \right] \quad (3.38)$$

Where we have used the notation  $Q_i(\mathbf{p}) = Q_i(\mathbf{x})/N_K(t)$  for notational clarity. The first term of (3.38) describes changes due to faithful (non-mutational) replication, and the second describes changes due to mutation. For this reason, equation (3.38) is called the *replicator-mutator equation* in the evolutionary game theory literature, where the individual ‘types’ are interpreted to be pure strategies. If in addition, each  $w_i(\mathbf{x})$  is linear in  $\mathbf{x}$ , meaning we can write  $w_i(\mathbf{x}) = \sum_j a_{ij}x_j$  for some set of constants  $a_{ij}$ , then we get the replicator-mutator equation for matrix games, and the constants  $a_{ij}$  form the ‘payoff matrix’. As is well-known, the replicator equation (without mutation) for matrix games with  $m$  pure strategies is equivalent to the generalized Lotka-Volterra equations for a community with  $m-1$  species(Hofbauer and Sigmund, 1998), providing the connection to community ecology. Equation (3.38) is also equivalent to Eigen’s *quasispecies equation* from molecular evolution if each ‘type’ is interpreted as a genetic sequence and each  $w_i(\mathbf{x})$  is a constant function<sup>4</sup>. We can now calculate how the mean of any ‘type level’ quantity  $f$ , defined as  $f_i$  for the  $i^{\text{th}}$  type, changes in the population (For example, if each type is a phenotype for a trait such

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<sup>4</sup>Mutational effects are often additionally assumed to act through direct ‘transmission probabilities’ of mutating from one type to another. This means that we can write  $Q_i(\mathbf{p}) = \sum_{j \neq i} Q_{ij}p_j$ , where  $Q_{ij} \geq 0$  is

a constant describing the probability of a  $j \rightarrow i$  mutation (conditioned on the occurrence of a mutation). Substituting this into (3.38) yields an equation in terms of ‘ $Q$ -matrices’ or ‘mutation matrices’ that may be more familiar to some biologists.

as height, which can be assigned a numerical value, then setting  $f_i = \text{value of } i^{\text{th}} \text{ phenotype}$  gives us the mean trait value in the population). Multiplying both sides of equation (3.38) by  $f_i$  and summing over all  $i$ , we obtain

$$\begin{aligned} \frac{d}{dt} \left( \sum_{i=1}^m f_i p_i \right) &= \sum_{i=1}^m f_i w_i(\mathbf{x}) p_i - \bar{w} \sum_{i=1}^m f_i p_i + \mu \left[ \sum_{i=1}^m Q_i(\mathbf{p}) f_i - \left( \sum_{j=1}^m Q_j(\mathbf{p}) \sum_{i=1}^m p_i f_i \right) \right] \\ \Rightarrow \frac{d\bar{f}}{dt} &= \bar{w}\bar{f} - (\bar{w})(\bar{f}) + \mu \left[ \sum_{i=1}^m Q_i(\mathbf{p}) f_i - \left( \sum_{j=1}^m Q_j(\mathbf{p}) \right) \bar{f} \right] \end{aligned}$$

Using the definition of statistical covariance of two variables  $X$  and  $Y$  as  $\text{Cov}(X, Y) = \overline{XY} - (\overline{X})(\overline{Y})$ , we obtain

$$\frac{d\bar{f}}{dt} = \text{Cov}(w, f) + \mu \left[ \sum_{i=1}^m Q_i(\mathbf{p}) f_i - \left( \sum_{j=1}^m Q_j(\mathbf{p}) \right) \bar{f} \right] \quad (3.39)$$

The first term of the RHS describes the statistical covariance between the quantity  $f$  and the fitness  $w$ . The second term describes ‘transmission bias’ due to mutational effects - The first summation is the ‘inflow’ of  $f$  due to mutations, and the second is the ‘outflow’. Equation (3.39) is thus a version of the Price equation.

### 3.3.4 Stochastic trait frequency dynamics for finite populations

Following ideas similar in spirit to (McLeod and Day, 2019), we can also use (3.31) to write down stochastic equations for  $p_i(t)$ , the frequency of type  $i$  individuals in the population to contrast with the replicator-mutator equation (3.38) derived above. In appendix B, we show that we can use Itô’s formula to write down a general stochastic equation for the frequencies of each type in the population. Unlike (McLeod and Day, 2019), we make no assumptions about the separation of ecological and evolutionary time scales or the strength of selection and are able to present an entirely general calculation. Letting  $\tau_i(\mathbf{x}) = b_i^{(\text{ind})}(\mathbf{x}) + d_i^{(\text{ind})}(\mathbf{x})$  be the *per-capita turnover rate* of the  $i^{\text{th}}$  type and denoting  $\bar{\tau} = \sum_i p_i \tau_i$ , we show in appendix B that when the birth and death rates are defined by (3.33), then the frequency of the  $i^{\text{th}}$

type in the population  $\mathbf{X}_t$ , changes according to the equation:

$$\begin{aligned} dp_i(t) = & \left[ (w_i(\mathbf{x}) - \bar{w})p_i + \mu \left\{ Q_i(\mathbf{p}) - p_i \left( \sum_{j=1}^m Q_j(\mathbf{p}) \right) \right\} \right] dt \\ & - \frac{1}{K} \frac{1}{N_K(t)} \left[ (\tau_i(\mathbf{x}) - \bar{\tau})p_i + \mu \left\{ Q_i(\mathbf{p}) - p_i \left( \sum_{j=1}^m Q_j(\mathbf{p}) \right) \right\} \right] dt \\ & + \frac{1}{\sqrt{K}} \left[ (A_i^+)^{1/2} dB_t^{(i)} - p_i \sum_{j=1}^m (A_j^+)^{1/2} dB_t^{(j)} \right] \end{aligned} \quad (3.40)$$

where  $B_t^{(1)}, B_t^{(2)}, \dots, B_t^{(m)}$  are  $m$  independent one-dimensional standard Brownian motion processes. The first term in this expression is the same as equation (3.38) and describes directional changes in the population composition due to ‘classical’ evolutionary forces such as selection and mutation. We saw in the previous section that the replicator-mutator equation is generically satisfied in the infinite population limit for all birth-death processes that are in the (very general) functional forms (3.33), a result that is made explicit in (3.40) (just take  $K \rightarrow \infty$  to convince yourself). The second term is an additional directional force on population composition that is only seen in finite populations and can be thought of as a biasing ‘selection’ for reduced turnover rate due to an effect similar to gambler’s ruin in probability theory. The consequences of this term, along with the connection to previous studies and standard infinite population models, are discussed in chapter 6. Finally, the last term of equation (3.40) describes non-directional stochastic effects due to fluctuations and has a ‘spreading effect’. To the highest order in  $\sqrt{K}$ , the effect of these fluctuations can be described through the weak noise approximation, as we explain below. However, the  $1/K$  factor in the second term of (3.40) means that the effect of differential turnover rates disappears in this weak noise regime (and also in other such approximate treatments, such as the Chemical Langevin equation).

### 3.3.5 Stochastic fluctuations and the weak noise approximation

If the noise is *weak*, we can go a little further, as in the one-dimensional case. Let the deterministic trajectory obtained by solving (3.32) be given by  $\mathbf{a}(t)$ . We can once again track

stochastic fluctuations from the deterministic trajectory by introducing the new variables

$$\begin{aligned} \mathbf{y} &= \sqrt{K}(\mathbf{x} - \mathbf{a}(t)) \\ s &= t \\ \tilde{P}(\mathbf{y}, s) &= \frac{1}{\sqrt{K}} P(\mathbf{x}, t) \end{aligned} \quad (3.41)$$

Then, after some algebra that follows the exact same steps as in section 3.2.3 and retaining only the highest order terms in  $\sqrt{K}$ , we obtain the equation:

$$\frac{\partial \tilde{P}_0}{\partial s}(\mathbf{y}, s) = \sum_{j=1}^m \left( -\frac{\partial}{\partial y_j} \left\{ (A_j^-)_1(s) \tilde{P}_0(\mathbf{y}, s) \right\} + \frac{1}{2} A_j^+(\mathbf{a}(s)) \frac{\partial^2}{\partial y_j^2} \{\tilde{P}_0(\mathbf{y}, s)\} \right) \quad (3.42)$$

where  $(A_j^-)_1(s)$  is the  $\mathcal{O}(1/\sqrt{K})$  term of the power series expansion

$$A_j^-(\mathbf{a} + \frac{\mathbf{y}}{\sqrt{K}}) = \sum_{n=1}^{\infty} (A_j^-)_n(s) \left( \frac{\mathbf{y}}{\sqrt{K}} \right)^n$$

In the case where the series expansion is a Taylor expansion, then the first-order term of this expansion is given by

$$(A_j^-)_1(s) = \sum_{i=1}^m y_i \left( \frac{\partial A_j^-(\mathbf{x})}{\partial x_i} \Big|_{\mathbf{x}=\mathbf{a}(s)} \right) \quad (3.43)$$

In multi-variable calculus, the directional derivative<sup>5</sup>  $D_{\mathbf{v}}(f(\mathbf{x}))$  of a multidimensional function  $f : \mathbb{R}^n \rightarrow \mathbb{R}$  along a vector  $\mathbf{v}$  is the function defined by:

$$D_{\mathbf{v}}(f(\mathbf{x})) := \sum_{i=1}^n \left( \frac{\partial f(\mathbf{x})}{\partial x_i} \right) v_i = \lim_{h \rightarrow 0} \frac{f(\mathbf{x} + h\mathbf{v}) - f(\mathbf{x})}{h} \quad (3.44)$$

Comparing with (3.43), we see that the weak-noise approximation of our process is:

$$\frac{\partial P}{\partial t}(\mathbf{y}, t) = \sum_{j=1}^m \left( -\frac{\partial}{\partial y_j} \left\{ D_{\mathbf{y}}(A_j^-(\mathbf{a}))(t) P(\mathbf{y}, t) \right\} + \frac{1}{2} A_j^+(\mathbf{a}(t)) \frac{\partial^2}{\partial y_j^2} \{P(\mathbf{y}, t)\} \right) \quad (3.45)$$

where we have dropped the tildes and gone back from  $s$  to  $t$  for notational clarity. The directional derivative of the population turnover rate  $A_j^-$  ‘in the direction’ of the stochastic fluctuation  $\mathbf{y}$  at the deterministic point  $\mathbf{a}(s)$  here is the multidimensional analogue of the

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<sup>5</sup>Physicists sometimes use the notation  $\partial_{\mathbf{v}} f(\mathbf{x})$  or  $\mathbf{v} \cdot \nabla f(\mathbf{x})$  for this object.

derivative we had in (3.21). The meaning of equation (3.45) is clearer if we compute how the moments of the fluctuation  $y_i$  in the density of type  $i$  individuals (for some  $i$ ) change over time. Let  $n > 0$ . We have:

$$\frac{d}{dt} \mathbb{E}[y_i^n] = \frac{d}{dt} \int_{\mathbb{R}^m} y_i^n P(\mathbf{y}, t) d\mathbf{y} \quad (3.46)$$

$$= \int_{\mathbb{R}^m} y_i^n \frac{\partial P}{\partial t}(\mathbf{y}, t) d\mathbf{y} \quad (3.47)$$

where we have assumed that  $y_i^n$  and  $P(\mathbf{y}, t)$  vary sufficiently smoothly to allow us to interchange the order of derivatives and integrals and used the shorthand  $\int_{\mathbb{R}^m} f(\mathbf{y}) d\mathbf{y} = \int_{\mathbb{R}} \int_{\mathbb{R}} \dots \int_{\mathbb{R}} f(\mathbf{y}) dy_1 dy_2 \dots dy_m$ . The one-dimensional integrals are over the entire real line and not just over  $[0, \infty)$  because fluctuations can be either positive (greater than  $\mathbf{a}(t)$ ) or negative (lesser than  $\mathbf{a}(t)$ ). For notational brevity, let us use the shorthand  $D_j = D_{\mathbf{y}}(A_j^-(\mathbf{a}))(t)$ . We can now substitute (3.45) into (3.47) to obtain

$$\frac{d}{dt} \mathbb{E}[y_i^n] = \int_{\mathbb{R}^m} y_i^n \left( \sum_{j=1}^m \left( -\frac{\partial}{\partial y_j} \{D_j P(\mathbf{y}, t)\} + \frac{1}{2} A_j^+(\mathbf{a}(t)) \frac{\partial^2}{\partial y_j^2} \{P(\mathbf{y}, t)\} \right) \right) d\mathbf{y} \quad (3.48)$$

$$= \sum_{j=1}^m \left[ - \int_{\mathbb{R}^m} y_i^n \frac{\partial}{\partial y_j} \{D_j P(\mathbf{y}, t)\} d\mathbf{y} + \frac{A_j^+(\mathbf{a}(t))}{2} \int_{\mathbb{R}^m} y_i^n \frac{\partial^2}{\partial y_j^2} \{P(\mathbf{y}, t)\} d\mathbf{y} \right] \quad (3.49)$$

We will evaluate the integrals on the RHS of (3.49) using integration by parts. Recall that for any two functions  $u$  and  $v$  defined on a domain  $\Omega$ , the general formula for integration by parts is given by:

$$\int_{\Omega} \frac{\partial u}{\partial x_i} v d\mathbf{x} = - \int_{\Omega} u \frac{\partial v}{\partial x_i} d\mathbf{x} + \int_{\partial\Omega} uv \gamma_i dS(\mathbf{x}) \quad (3.50)$$

where  $\partial\Omega$  is the boundary of  $\Omega$ ,  $dS$  is the surface element of this boundary, and  $\gamma_i$  is the  $i^{\text{th}}$  component of the unit outward normal to the boundary. In our case, we have  $\Omega = \mathbb{R}^m$ , and thus the boundary conditions are evaluated as  $\|\mathbf{y}\| \rightarrow \infty$ . We assume that the magnitude of stochastic fluctuations is bounded, and therefore impose the condition  $\lim_{\|\mathbf{y}\| \rightarrow \infty} P(\mathbf{y}, t) = 0$ . Further, we assume that this decay is fast enough that  $\lim_{\|\mathbf{y}\| \rightarrow \infty} D_j P(\mathbf{y}, t) = 0 \forall j$ . Under these conditions, we can evaluate the two integrals in the RHS of (3.49) by using integration by

parts and discarding the boundary term (The second term on the RHS of (3.50)). Note that since the  $y_i$ s are orthogonal to each other, we have the relation:

$$\frac{\partial y_i^n}{\partial y_j} = \delta_{ij} n y_i^{n-1}$$

Using this relation and then using integration by parts on the RHS of (3.49) (once for the first term and twice for the second term), we obtain the considerably simpler expression

$$\frac{d}{dt} \mathbb{E}[y_i^n] = n \int_{\mathbb{R}^m} y_i^{n-1} D_i P(\mathbf{y}, t) d\mathbf{y} + \frac{n(n-1)}{2} A_i^+(\mathbf{a}(t)) \int_{\mathbb{R}^m} y_i^{n-2} P(\mathbf{y}, t) d\mathbf{y} \quad (3.51)$$

$$\Rightarrow \frac{d}{dt} \mathbb{E}[y_i^n] = n \mathbb{E}[y_i^{n-1} D_i] + \frac{n(n-1)}{2} A_i^+(\mathbf{a}(t)) \mathbb{E}[y_i^{n-2}] \quad (3.52)$$

Of particular interest are the cases  $n = 1$  (corresponding to the expected value of  $y_i$ ) and  $n = 2$  (which can be used along with the expected value to compute the variance of  $y_i$ ). We have:

$$\frac{d}{dt} \mathbb{E}[y_i] = \mathbb{E}[D_i] \quad (3.53)$$

$$\frac{d}{dt} \mathbb{E}[y_i^2] = 2\mathbb{E}[y_i D_i] + A_i^+(\mathbf{a}(t)) = 2\text{Cov}(y_i, D_i) + 2\mathbb{E}[y_i] \mathbb{E}[D_i] + A_i^+(\mathbf{a}(t)) \quad (3.54)$$

Thus, whether stochastic fluctuations are expected to grow or decay is controlled by  $D_i$ , a measure of how the growth rate ( $b_i - d_i$ ) changes along the direction of the fluctuation, whereas the spread of the fluctuations (the variance) has contributions from the net turnover rate ( $A_i^+ = b_i + d_i$ ) and the covariance between the fluctuation and  $D_i$ . Note that unlike in the Price equation (3.39), this is a true *probability* covariance (as opposed to a statistical covariance between two deterministic quantities). In the case of the functional forms given by (3.33), we have:

$$A_i^-(\mathbf{x}) = w_i(\mathbf{x})x_i + \mu Q_i(\mathbf{x}) \quad (3.55)$$

and thus, from (3.43), we can calculate the directional derivative  $D_i$  as

$$D_i = \sum_{k=1}^m y_k \left( \frac{\partial A_i^-(\mathbf{x})}{\partial x_k} \Big|_{\mathbf{x}=\mathbf{a}(t)} \right) \quad (3.56)$$

$$= \sum_{k=1}^m y_k \left( \frac{\partial}{\partial x_k} (w_i(\mathbf{x})x_i + \mu Q_i(\mathbf{x})) \Big|_{\mathbf{x}=\mathbf{a}(t)} \right) \quad (3.57)$$

$$= \sum_{k=1}^m y_k \left( a_i \frac{\partial w_i}{\partial x_k} \Big|_{\mathbf{x}=\mathbf{a}(t)} \right) + y_i w_i(\mathbf{a}) + \mu \sum_{k=1}^m y_k \left( \frac{\partial Q_i}{\partial x_k}(\mathbf{x}) \Big|_{\mathbf{x}=\mathbf{a}(t)} \right) \quad (3.58)$$

$$= y_i w_i(\mathbf{a}) + a_i D_{\mathbf{y}}(w_i(\mathbf{a})) + \mu D_{\mathbf{y}}(Q_i(\mathbf{a})) \quad (3.59)$$

Using this in (3.53), we see that the expected change of a fluctuation in the density of type  $i$  individuals evolves as:

$$\frac{d}{dt} \mathbb{E}[y_i] = \underbrace{w_i(\mathbf{a}) \mathbb{E}[y_i]}_{\substack{\text{Current fitness of type } i \\ \text{at deterministic trajectory } \mathbf{a} \\ (\text{scaled by expected density } \mathbb{E}[y_i])}} + \underbrace{a_i \mathbb{E}[D_{\mathbf{y}}(w_i(\mathbf{a}))]}_{\substack{\text{Expected change in fitness} \\ \text{of type } i \text{ in going from } \mathbf{a} \text{ to } \mathbf{y} \\ (\text{scaled by deterministic density } a_i)}} + \underbrace{\mu \mathbb{E}[D_{\mathbf{y}}(Q_i(\mathbf{a}))]}_{\substack{\text{Expected effect of} \\ \text{mutations}}} \quad (3.60)$$

# Chapter 4

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## Stochastic field equations for the evolution of quantitative traits

The result has been forty years of bewilderment about what he meant, whereas if he had been willing to make a slight sacrifice of strict mathematical propriety (as I have done) he could have expressed himself in a way that everyone would have understood

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George Price (speaking about Fisher)

So far, we have dealt with populations in which individuals come in countably many different kinds. While developing these models, we have been on mathematically solid ground that is well understood by statistical physicists and mathematicians. However, things become more complicated when we deal with ‘quantitative’ traits. Traits like body size, body weight, or beak length, often take on uncountably many values (say, all values in the interval  $[0, 1]$ , for example). In this case, we cannot describe the population using a vector as we did before, but instead require a function. More precisely, if the set of all possible trait values is  $\mathcal{T}$ , we will characterize the population using a special kind of function  $\phi^{(t)}$  such that the quantity  $\int_A \phi^{(t)}(x)dx$  gives us the number of individuals that are in any ‘nice’ region  $A \subset \mathcal{T}$

of the possible trait space<sup>1</sup>. The state space of the stochastic process thus becomes infinite-dimensional, which complicates matters slightly. The principal objects of interest here are *functionals*  $F[x, \phi^{(t)}]$  which take in a scalar  $x$  representing the trait value of interest, and a function  $\phi^{(t)}$  representing the population at time  $t$ . Thus, whereas in the previous section we were interested in how a function  $f(x(t))$  changes based on the change in an input variable  $x(t)$  (the population), we are now interested in how a functional  $F[\phi^{(t)}]$  changes with the change in an input function  $\phi^{(t)}$ . The mathematics for these sorts of processes is an active area of research and is comparatively far from well developed. The mathematically rigorous formulation of the kinds of processes we study here falls in the realm of measure-valued branching processes, and is highly technical and rather inaccessible unless one is already comfortable with advanced measure-theoretic notions (Champagnat et al., 2006; Champagnat et al., 2008). This means that the existing formalism, while admirable in its generality and mathematical rigor, is rather unusable for most biologists, who do not have formal training in analysis. One can, however, make progress if they are willing to take some mathematical leaps of faith and sacrifice rigor for the sake of accessibility and heuristic understanding. I will shamelessly adopt this attitude below and hope that any questions of rigor, well-posedness, existence, etc. will be sorted out by some clever mathematicians in the future. Physicists use the term ‘field’ for functions of the form  $f(x, t) : \mathbb{R}^n \times [0, \infty) \rightarrow \mathbb{R}^m$ , where  $\mathbb{R}^n$  represents space and  $[0, \infty)$  represents time. They then call models which describe such functions ‘field theories’. In physics jargon, the stochastic process we will formulate  $\{\phi^{(t)}\}_{t \geq 0}$  when viewed as a sequence of functions  $\{\phi^{(t)}(y)\}_{t \geq 0}$  thus describes a (scalar) ‘stochastic field’, and the formalism we will develop below is a ‘stochastic field theory’ of evolution, where physical space has been replaced by an abstract trait space. This is closely related to the area of physics called ‘statistical field theory’, the analog of quantum field theory for systems with a large number of classical particles. Stochastic field theories over physical space have recently been used in biology to model brain function (Bressloff, 2010) and collective motion (Ó Laighléis et al., 2018). In the following sections, I will rely

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<sup>1</sup>The mathematically informed reader may notice that this sounds like I am trying to dance around the word ‘measure’. Indeed, we are really looking to construct branching processes that take values in some nice space of measures that can be endowed with sufficient mathematical structure for notions like convergence and integration to make sense. All the Dirac deltas that will turn up shortly are ‘properly’ viewed as measures, and integrals with Dirac deltas in the integrand are to be interpreted as integration with respect to the Dirac measure. If one tries to be careful about these things, they will quickly find themselves drowning in a quagmire of mathematical formalism. If you know and care about enough mathematics for this to really bother you, see (Champagnat et al., 2006) for a much more rigorous treatment that avoids using informal tools such as functional derivatives and functional equivalents of Fokker-Planck equations in favor of a probabilistic approach grounded in (measure-theoretic) Markov and martingale theory.

heavily on a heuristic object called the functional derivative  $\delta F/\delta\phi$ . The functional derivative is an *ad hoc*, somewhat informal notion, defined indirectly as the unique object that obeys, for any ‘nice’ function  $\rho$

$$\int \frac{\delta F}{\delta\phi(x)} \rho(x) dx = \lim_{h \rightarrow 0} \frac{F[\phi + h\rho] - F[\phi]}{h} \quad (4.1)$$

This definition is formulated in analogy to directional derivatives in multi-variable calculus: Noting that a function can be thought of as an infinite-dimensional vector, informally ‘taking the limit’  $n \rightarrow \infty$  in (3.44) yields (4.1).

## 4.1 Description of the process and the Master Equation

We envision a population of individuals with a ‘trait’ that takes values in some one-dimensional set  $\mathcal{T} \subseteq \mathbb{R}$ . Since the trait of any given individual is fixed, and since each individual can only have one exact trait value, an individual with a trait value  $x \in \mathcal{T}$  can be characterized as a Dirac delta mass centered at  $x$ , defined indirectly as the object which satisfies, for any one-dimensional function  $f$ ,

$$\int_A f(y) \delta_{x_i} dy = \begin{cases} f(x_i) & x_i \in A \\ 0 & x_i \notin A \end{cases}$$

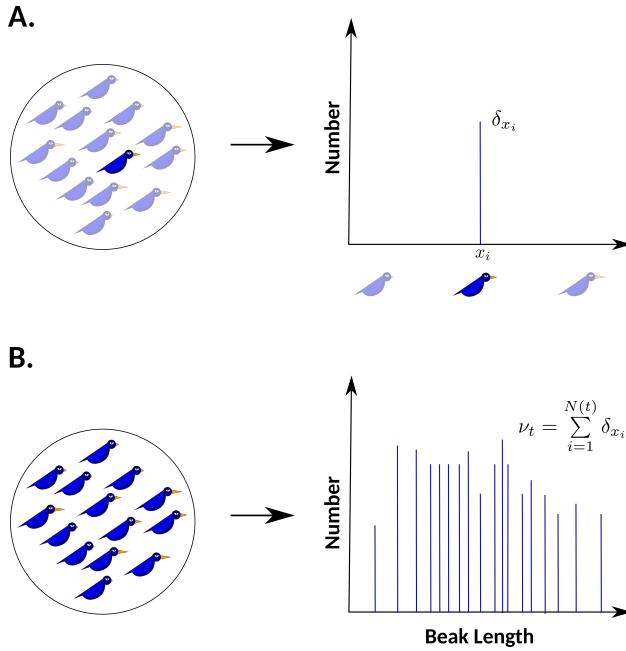
for every ‘nice’ subset  $A \subset \mathcal{T}$ . Physicists often write  $\delta_{x_i} = \delta(y - x_i)$  as a ‘function’ of a dummy variable  $y$  (which will be integrated over). I will stick to the notation  $\delta_{x_i}$  because it emphasizes that the object is meant to represent an individual with a trait value of  $x_i$  (the dummy variable  $y$  can be confusing in this regard). Note that by choosing  $f(x) \equiv 1$ , we get an ‘indicator’ that is 1 if the individual is within the set  $A$  and 0 otherwise. Thus, if the population at any time  $t$  consists of  $N(t)$  individuals with trait values  $\{x_1, x_2, \dots, x_{N(t)}\}$ , then it can be completely characterized (Figure 4.1) by the ‘distribution’

$$\nu^{(t)} = \sum_{i=1}^{N(t)} \delta_{x_i}$$

which in physics notation would be a function  $\nu^{(t)}(y) = \sum_i^{N(t)} \delta(y - x_i)$ . Thus, the state space of our process is

$$\mathcal{M} = \left\{ \sum_{i=1}^n \delta_{x_i} \mid n \in \mathbb{N}, x_i \in \mathcal{T} \right\}$$

Note that for any set  $A \subset \mathcal{T}$ ,  $\int_A \nu^{(t)} dx$  gives the number of individuals that have trait values that lie within the set  $A$  and that integrating over  $\mathcal{T}$  gives the population size  $N(t)$  at time  $t$ . Given the population  $\nu^{(t)} = \sum_{i=1}^{N(t)} \delta_{x_i}$  and a real function  $f(x)$ , we have  $\int_{\mathcal{T}} f(y) \nu^{(t)} dy = \sum_{i=1}^{N(t)} f(x_i)$ .



**Figure 4.1: Schematic description of a function valued birth-death process.** Consider a population of birds in which individuals have varying beak lengths. **(A)** Each individual in the population can be described as a Dirac delta mass centered at its beak length. This is because each individual has exactly one fixed beak length, and therefore, can be thought of as a distribution centered at that particular beak length and with zero spread. **(B)** The population as a whole is thus described as a sum of Dirac masses.  $N(t)$  here is the size of the population at time  $t$ . Birth and death of individuals would correspond to the addition and removal of Dirac masses respectively. Note that if we had a large number of individuals, this distribution begins to look like a continuous distribution.

Now that we have described the population, we must define the rules for how it changes. We assume that there exist non-negative functionals  $b(x|\nu)$  and  $d(x|\nu)$  which describe the

rate at which individuals with trait value  $x$  are born and die respectively in a population  $\nu$ . Again, we must be careful about what exactly we mean when we speak about ‘rates’. In this case, we mean that if we know that the population is currently described by the function  $\nu$ , and we know that *either a birth or a death* occurs, then the probability that this event is the birth of an individual whose phenotype is within the set  $A \subset \mathcal{T}$  is given by

$$\mathbb{P}[\text{Birth with offspring in } A | \text{something happened}] = \frac{1}{\mathcal{N}} \int_A b(x|\nu) dx$$

and the probability that the event is the death of an individual whose phenotype is within the set  $A$  is

$$\mathbb{P}[\text{Death of an individual in } A | \text{something happened}] = \frac{1}{\mathcal{N}} \int_A d(x|\nu) dx$$

where  $\mathcal{N} = \int_{\mathcal{T}} b(x|\nu) + d(x|\nu) dx$  is the normalizing constant in both cases. Note that we assume  $\mathcal{N}$  is always finite and non-zero.

**Example 2.** Consider the birth and death functionals:

$$\begin{aligned} b(x|\nu) &= r \int_{\mathcal{T}} m(x,y)\nu(y) dy; \quad m(x,y) = \exp\left(\frac{-(x-y)^2}{\sigma_m^2}\right) \\ d(x|\nu) &= \frac{\nu(x)}{Kn(x)} \int_{\mathcal{T}} \alpha(x,y)\nu(y) dy; \quad \alpha(x,y) = \exp\left(\frac{-(x-y)^2}{\sigma_{\alpha}^2}\right) \end{aligned} \tag{4.2}$$

This choice corresponds to an asexual population having a constant (per-capita) birth rate  $r$ . Birth is sometimes with mutation, and the extent of the mutations is controlled by a Gaussian kernel  $m(x,y)$ . The death rate is density-dependent, mediated by a Gaussian competition kernel  $\alpha(x,y)$ , and also contains a phenotype-dependent carrying capacity controlled by  $n(x)$ , scaled by a constant  $K$ . The biological interpretation of the death rate is through ecological specialization for limiting resources - Individuals have different intrinsic advantages (controlled by  $n(x)$ ), and experience greater competition from conspecifics that are closer to them in phenotype space (controlled by  $\alpha(x,y)$ ).

Let us now define, for each  $x \in \mathcal{T}$ , two *step operators*  $\mathcal{E}_x^{\pm}$  that satisfy

$$\mathcal{E}_x^{\pm}[f(y,\nu)] = f(y, \nu \pm \delta_x)$$

In other words, the step operators  $\mathcal{E}_x^\pm$  simply describe the effect of adding or removing a single individual with trait value  $x$  from the population. It is known (only for one-dimensional traits) that we can find a density function  $P(\nu, t)$  such that the probability that the process takes value  $\nu^{(t)}$  at time  $t$  is given by  $\int_{\mathcal{T}} P(\nu, t) dx$ .

We can now use the same trick as earlier and obtain a master equation by counting inflow and outflow of states. Any change to a state must be through the addition or subtraction of a single Dirac delta mass. For any state  $\nu \in \mathcal{M}$ , the transition rate from  $\nu - \delta_x$  to  $\nu$  is simply  $\mathcal{E}_x^- b(x|\nu)$ , and similarly, the transition rate from  $\nu + \delta_x$  to  $\nu$  is  $\mathcal{E}_x^+ d(x|\nu)$ . The transition rate out of  $\nu$  to a state  $\nu + \delta_x$  is just  $b(x|\nu)$ , and transition out to a state  $\nu - \delta_x$  is just  $d(x|\nu)$ . Thus, integrating over all possible  $x$  to obtain the total inflow and outflow rate for a state  $\nu$ , we see that  $P(\nu, t)$  must satisfy:

$$\frac{\partial P}{\partial t}(\nu, t) = \int_{\mathcal{T}} [(\mathcal{E}_x^- - 1)b(x|\nu)P(\nu, t) + (\mathcal{E}_x^+ - 1)d(x|\nu)P(\nu, t)] dx \quad (4.3)$$

This is the ‘Master equation’ of our process.

## 4.2 The functional system-size expansion

To proceed, as before, we assume that there exists a system-size parameter  $K > 0$  to obtain a new process  $\{\phi^{(t)}\}_{t \geq 0}$  such that for any set  $A \subset \mathcal{T}$ ,  $\int_A \phi^{(t)} dx$  gives the ‘density’ of individuals that have trait values that lie within the set  $A$ . Note that we expect this stochastic process to evolve continuously if  $K$  is large since the contribution of each individual is negligible. Specifically, we assume that there exists a  $K > 0$  such that we can make the substitutions:

$$\begin{aligned}\phi^{(t)} &= \frac{1}{K} \nu^{(t)} = \frac{1}{K} \sum_{i=1}^{N(t)} \delta_{x_i} \\ b_K(x|\phi^{(t)}) &= \frac{1}{K} b(x|\nu^{(t)}) \\ d_K(x|\phi^{(t)}) &= \frac{1}{K} d(x|\nu^{(t)})\end{aligned}$$

$\{\phi^{(t)}\}_{t \geq 0}$  takes values in

$$\mathcal{M}_K = \left\{ \frac{1}{K} \sum_{i=1}^n \delta_{x_i} \mid n \in \mathbb{N}, x_i \in \mathcal{T} \right\}$$

In terms of these new variables, we obtain the master equation:

$$\frac{\partial P}{\partial t}(\phi, t) = K \int_{\mathcal{T}} [(\Delta_x^- - 1)b_K(x|\phi)P(\phi, t) + (\Delta_x^+ - 1)d_K(x|\phi)P(\phi, t)] dx \quad (4.4)$$

where we have introduced new step operators  $\Delta_x^\pm$  that satisfy:

$$\Delta_x^\pm[F(y, \phi)] = F\left(y, \phi \pm \frac{1}{K}\delta_x\right)$$

We can now conduct a system-size expansion as before by using a functional ‘Taylor expansion’ of the step operators. Recall that the functional version of the Taylor expansion of a functional  $F[\rho]$  about a function  $\rho_0$  defined on a domain  $\Omega \subseteq \mathbb{R}$  is given by:

$$F[\rho_0 + \rho] = F[\rho_0] + \int_{\Omega} \rho(x) \frac{\delta F}{\delta \rho_0(x)} dx + \frac{1}{2!} \int_{\Omega} \int_{\Omega} \rho(x) \rho(y) \frac{\delta^2 F}{\delta \rho_0(x) \delta \rho_0(y)} dx dy + \dots$$

Since  $\Delta_x^\pm[F[\phi]] = F[\phi \pm \delta_x/K]$ , we can Taylor expand the RHS to see that our step operators obey

$$\begin{aligned} \Delta_x^\pm[F[\phi]] &= F[\phi] \pm \frac{1}{K} \int_{\mathcal{T}} \frac{\delta F}{\delta \phi(y)} \delta_x dy + \frac{1}{2K^2} \int_{\mathcal{T}} \int_{\mathcal{T}} \frac{\delta^2 F}{\delta \phi(y) \delta \phi(z)} \delta_x dy \delta_x dz + \mathcal{O}(K^{-3}) \\ &= F[\phi] \pm \frac{1}{K} \frac{\delta F}{\delta \phi(x)} + \frac{1}{2K^2} \frac{\delta^2 F}{\delta \phi(x)^2} + \mathcal{O}(K^{-3}) \end{aligned} \quad (4.5)$$

Neglecting terms of  $\mathcal{O}(K^{-3})$ , we can now substitute (4.5) into (4.4) to obtain:

$$\begin{aligned} \frac{\partial P}{\partial t}(\phi, t) &= K \int_{\mathcal{T}} \left[ \left( -\frac{1}{K} \frac{\delta}{\delta \phi(x)} + \frac{1}{2K^2} \frac{\delta^2}{\delta \phi(x)^2} \right) \{b_K(x|\phi)P(\phi, t)\} \right] dx \\ &\quad + K \int_{\mathcal{T}} \left[ \left( \frac{1}{K} \frac{\delta}{\delta \phi(x)} + \frac{1}{2K^2} \frac{\delta^2}{\delta \phi^2(x)} \right) \{d_K(x|\phi)P(\phi, t)\} \right] dx \end{aligned}$$

Rearranging these terms, we obtain a ‘functional Fokker-Planck equation’:

$$\boxed{\frac{\partial P}{\partial t}(\phi, t) = \int_{\mathcal{T}} \left[ -\frac{\delta}{\delta\phi(x)} \{ \mathcal{A}^-(x|\phi) P(\phi, t) \} + \frac{1}{2K} \frac{\delta^2}{\delta\phi(x)^2} \{ \mathcal{A}^+(x|\phi) P(\phi, t) \} \right] dx} \quad (4.6)$$

where

$$\mathcal{A}^\pm(x|\phi) = b_K(x|\phi) \pm d_K(x|\phi) = \frac{1}{K} (b(x|\nu) \pm d(x|\nu))$$

This constitutes the ‘mesoscopic’ description. For large (but finite)  $K$ , equation (4.6) can be analyzed using a weak noise approximation as before.

### 4.3 The deterministic limit

We can once again appeal to the link between Fokker-Planck equations and Langevins (Lafuerza and McKane, 2016) to say that (4.6) corresponds to the Langevin equation:

$$\frac{\partial \phi}{\partial t}(x, t) = \mathcal{A}^-(x|\phi) + \frac{1}{\sqrt{K}} \eta(x, t) \quad (4.7)$$

where  $\eta(x, t)$  is the ‘Gaussian spacetime white noise’ with zero mean and autocovariance function

$$\mathbb{E}[\eta(x, t)\eta(x', t')] = \sqrt{\mathcal{A}^+(x|\phi)\mathcal{A}^+(x'|\phi)} \delta(x - x')\delta(t - t')$$

Taking  $K \rightarrow \infty$  in equation (4.7) then yields a PDE:

$$\frac{\partial \psi}{\partial t}(x, t) = \mathcal{A}^-(x|\psi) = b_K(x|\psi) - d_K(x|\psi) \quad (4.8)$$

where we have used a different symbol  $\psi$  simply to highlight that  $\psi(x, t)$  as the solution to equation (4.8) is a deterministic function, whereas  $\phi(x, t)$  as defined in equation (4.7) is really a stochastic process  $\{\phi^{(t)}\}_{t \geq 0}$ . Equation (4.8) simply says that in the absence of stochasticity, the change in the density of individuals with trait values  $x$  is given by the difference between the birth and death rates of these individuals in the population. Models of this form are precisely the ‘PDE’ models discussed in chapter 2. They are also equivalent to the ‘oligomorphic dynamics’ of (Sasaki and Dieckmann, 2011) if one assumes the population

is composed of a small number of ‘morphs’, *i.e.*  $\psi(x, t) = \sum_{k=1}^S n_k \psi_k(x, t)$ , where  $\psi_k(x, t)$  is the phenotypic distribution of the  $k$ th morph (often assumed a normal distribution with narrow variance) and  $S$  is the number of distinct morphs in the population. Equation (4.8) also appears in models of intraspecific trait variation in community ecology, such as the ‘trait space equations’ of (Wickman et al., 2022) in their framework for eco-evolutionary community dynamics.

If one wishes to be mathematically careful, the connection between (4.6) and (4.7) becomes somewhat tenuous. In particular, while the equivalence between Fokker-Planck equations and SDEs (Langevin equations) for finite-dimensional stochastic processes is part of the standard mathematical canon, the corresponding equivalence is much less well understood for the infinite-dimensional function-valued processes that we are dealing with, and the interpretation of any formal ‘Langevin equation’ (corresponding now to a stochastic partial differential equation, or SPDE) that we write down is unclear. Nevertheless, we will pretend all is well and assume that one can do this, bolstered by the fact that we can recover some well-known deterministic equations from equation (4.8), as we show below.

### 4.3.1 Some familiar faces: Kimura-Crow and adaptive dynamics

The ‘macroscopic’ version of our function-valued process corresponds to quantitative genetics and adaptive dynamics (which is a generalization of evolutionary game theory for quantitative traits). We begin with the deterministic process given by (4.8). We assume that the birth and death functions take the form:

$$\begin{aligned} b_K(x|\psi) &= \mu b_{\text{mut}}(x|\psi) + b_{\text{ind}}(x|\psi)\psi(x, t) \\ d_K(x|\psi) &= d_{\text{ind}}(x|\psi)\psi(x, t) \end{aligned} \tag{4.9}$$

Here,  $b_{\text{mut}}(x|\psi)$  describes birth due to mutations, and  $\mu \geq 0$  is a mutation rate. The functions  $b_{\text{ind}}(x|\psi)$  and  $d_{\text{ind}}(x|\psi)$  describe the per-capita birth rate and death rate of type  $x$  in a population  $\psi$ . For example,  $b_{\text{ind}}(x|\psi)$  may incorporate the effects of mate choice in the sexual case or intrinsic duplication rate in the asexual case, and  $d_{\text{int}}(x|\psi)$  may model death due to intraspecific competition for resources. Substituting equation (4.9) into (4.8), we obtain

$$\frac{\partial \psi}{\partial t}(x, t) = w(x|\psi)\psi(x, t) + \mu b_{\text{mut}}(x|\psi) \tag{4.10}$$

where we have defined  $w(x|\psi) := b_{\text{int}}(x|\psi) - d_{\text{int}}(x|\psi)$ , which can be thought of as the (Malthusian) ‘fitness’ of the phenotype  $x$ . To track population numbers and trait frequencies, we follow the approach of (Week et al., 2021) and define

$$\begin{aligned} N_K(t) &:= \int_{\mathcal{T}} \psi(x, t) dx \\ p(x, t) &:= \frac{\psi(x, t)}{N_K(t)} \end{aligned} \quad (4.11)$$

We can also define the population mean fitness as:

$$\bar{w}(t) = \int_{\mathcal{T}} w(x|\psi)p(x, t) dx \quad (4.12)$$

Using the chain rule in the definition of  $p(x, t)$ , we can calculate:

$$\begin{aligned} \frac{\partial p}{\partial t} &= \frac{1}{N_K(t)} \frac{\partial \psi}{\partial t}(x, t) - \frac{\psi(x, t)}{N_K^2(t)} \frac{dN_K}{dt} \\ &= \frac{1}{N_K(t)} \frac{\partial \psi}{\partial t}(x, t) - \frac{\psi(x, t)}{N_K^2(t)} \int_{\mathcal{T}} \frac{\partial \psi}{\partial t}(y, t) dy \end{aligned}$$

Where we have used the definition of  $N_K(t)$  and assumed that integrals and derivatives commute in the second line. Substituting (4.10), we now obtain

$$\begin{aligned} \frac{\partial p}{\partial t} &= \frac{1}{N_K(t)} [w(x|\psi)\psi(x, t) + \mu b_{\text{mut}}(x|\psi)] - \frac{\psi(x, t)}{N_K^2(t)} \int_{\mathcal{T}} w(y|\psi)\psi(y, t) + \mu b_{\text{mut}}(y|\psi) dy \\ &= w(x|\psi)p(x, t) + \frac{\mu}{N_K(t)} b_{\text{mut}}(x|\psi) - p(x, t) \left( \int_{\mathcal{T}} w(y|\psi)p(y, t) dy + \frac{\mu}{N_K(t)} \int_{\mathcal{T}} b_{\text{mut}}(y|\psi) dy \right) \end{aligned}$$

where we have used the definition of  $p(x, t)$  in the second line. Using (4.12) and rearranging the terms gives us:

$$\frac{\partial p}{\partial t}(x, t) = [w(x|\psi) - \bar{w}(t)] p(x, t) + \frac{\mu}{N_K(t)} \left[ b_{\text{mut}}(x|\psi) - p(x, t) \int_{\mathcal{T}} b_{\text{mut}}(y|\psi) dy \right] \quad (4.13)$$

This is a continuous version of the replicator-mutator equation when each  $x$  is viewed as a strategy. It also yields Kimura's continuum-of-alleles model when each  $x$  is viewed as an allele,  $b_{\text{mut}}(x|\psi)$  takes the form of a convolution of  $\psi(x,t)$  with a mutation kernel, and the trait space is the entire real line, *i.e.*  $\mathcal{T} = \mathbb{R}$ . To see this, let  $b_{\text{mut}}(y|\psi) = \int_{\mathbb{R}} m(y-z)\psi(z,t)dz$ , where  $m(x)$  is a mutation kernel, which by definition is normalized such that  $\int_{\mathbb{R}} m(x)dx = 1$ . Let us further note that we have implicitly been assuming that the total number of individuals (scaled by  $K$ ) remains finite at all times, *i.e.*  $N_K(t) = \int_{\mathbb{R}} \psi(x,t)dx < \infty \forall t$ . Thus,  $m(x)\psi(y,t) \in \mathcal{L}^1(\mathbb{R} \times \mathbb{R}) \forall t$  and we can use the Fubini-Tonnelli theorem to interchange the order of integration of iterated integrals of  $m(y-z)\psi(z,t)$ . We are now ready to evaluate the rightmost integral of (4.13).

We have:

$$\begin{aligned}
\int_{\mathbb{R}} b_{\text{mut}}(y|\psi)dy &= \int_{\mathbb{R}} \int_{\mathbb{R}} m(y-z)\psi(z,t)dz dy \\
&= \int_{\mathbb{R}} \int_{\mathbb{R}} m(y-z)\psi(z,t)dy dz \\
&= \int_{\mathbb{R}} \psi(z,t) \left( \int_{\mathbb{R}} m(y-z)dy \right) dz \\
&= \int_{\mathbb{R}} \psi(z,t) \int_{\mathbb{R}} m(u)dudz \\
&= \int_{\mathbb{R}} \psi(z,t) dz \int_{\mathbb{R}} m(u)du \\
&= N_K(t) \int_{\mathbb{R}} m(u)du
\end{aligned} \tag{4.14}$$

where we have used the Fubini-Tonnelli theorem to go from the first step to the second, and have made the substitution  $u = y - z$  to go from the third to the fourth step. We then note that since  $m$  is a kernel, it satisfies  $\int_{\mathbb{R}} m(u)du = 1$ , and (4.14) therefore becomes  $\int_{\mathbb{R}} b_{\text{mut}}(y|\psi)dy = N_K(t)$ . Substituting this in (4.13), we have

$$\frac{\partial p}{\partial t}(x,t) = [w(x|\psi) - \bar{w}(t)] p(x,t) + \frac{\mu}{N_K(t)} \left[ \int_{\mathbb{R}} m(x-z)\psi(z,t)dz - p(x,t)N_K(t) \right]$$

Substituting our definition  $p(z, t) = \psi(z, t)/N_K(t)$  now yields

$$\boxed{\frac{\partial p}{\partial t}(x, t) = [w(x|\psi) - \bar{w}(t)] p(x, t) + \mu \left[ \int_{\mathbb{R}} m(x-z)p(z, t)dz - p(x, t) \right]} \quad (4.15)$$

which is Kimura's continuum of alleles model.

Note that if we define the mean trait value as

$$\bar{x}(t) = \int_{\mathcal{T}} xp(x, t)dx$$

then, by multiplying both sides of equation (4.13) by  $x$  and integrating over the trait space, we obtain

$$\begin{aligned} \frac{d\bar{x}}{dt} &= \int_{\mathcal{T}} xw(x|\psi)p(x, t)dx - \bar{w}(t) \int_{\mathcal{T}} xp(x, t)dx + \frac{\mu}{N_K(t)} \int_{\mathcal{T}} x \left[ b_{\text{mut}}(x|\psi) - p(x, t) \int_{\mathcal{T}} b_{\text{mut}}(y|\psi)dy \right] dx \\ &= \bar{x}\bar{w} - \bar{w} \cdot \bar{x} + \frac{\mu}{N_K(t)} \int_{\mathcal{T}} x \left[ b_{\text{mut}}(x|\psi) - p(x, t) \int_{\mathcal{T}} b_{\text{mut}}(y|\psi)dy \right] dx \end{aligned} \quad (4.16)$$

We now observe that

$$\text{Cov}(x, w(x|\psi)) = \bar{x}\bar{w} - \bar{x} \cdot \bar{w} \quad (4.17)$$

is the statistical covariance of the trait value with the Malthusian fitness function (Importantly, just like in the Price equation, this is an *analogy* - Everything here is deterministic). The second term, which we will denote by

$$M(x|\psi) := \frac{\mu}{N_K(t)} \left[ \int_{\mathcal{T}} xb_{\text{mut}}(x|\psi)dx - \left( \bar{x} \int_{\mathcal{T}} b_{\text{mut}}(x|\psi)dx \right) \right] \quad (4.18)$$

reflects the transmission bias of mutations. Thus, we see that equation (4.16) reads

$$\boxed{\frac{d\bar{x}}{dt} = \text{Cov}(x, w(x|\psi)) + M(x|\psi)} \quad (4.19)$$

from which it is clear that we have obtained a version of the Price equation for quantitative traits. Adaptive dynamics is recovered under the following additional assumptions:

- Rare mutations, *i.e.*  $\mu \rightarrow 0$ .
- Small mutational effects with ‘almost faithful’ reproduction, meaning  $b_{\text{mut}}(x|\psi) \rightarrow 0$ , and the distribution  $\psi(x,t)$  tends to stay very ‘sharp’ (*i.e* strongly peaked about its mean value).
- Separation of ecological and evolutionary timescales, meaning that the system is always at ecological equilibrium. Thus, the expected rate of change of resident numbers in a resident population is 0, and we have  $w(y|\delta_{y(t)}) = 0$ .

The first two assumptions are sometimes called the ‘weak mutation’ limit, and the last is sometimes called the ‘strong selection’ limit, both for obvious reasons. Under these assumptions, if we supply an initial condition  $\psi(x,0) = N_K(0)\delta_{y_0}$  for some constants  $N_K(0) > 0$  and  $y_0 \in \mathcal{T}$  (meaning we start with a completely monomorphic population of size  $N_K(0)$  in which all individuals have trait value  $y_0$ ), then it is reasonable to assume that the population remains sufficiently clustered for some (possibly small) time  $t > 0$  that we can continue to approximate the distribution  $\psi(x,t)$  as a Dirac Delta mass  $N_K(t)\delta_{y(t)}$  that is moving across the trait space in a deterministic manner dictated by a function  $y(t)$  (*to be found*). Note that we have  $p(x,t) = \delta_{y(t)}$ ,  $\bar{x}(t) = y(t)$ , and  $\bar{w}(t) = 0$ . Thus, from equation (4.19), we have

$$\begin{aligned} \frac{d\bar{x}}{dt} &= \int_{\mathcal{T}} (x - \bar{x}(t))(w(x|\psi) - \bar{w}(t))p(x,t)dx \\ \Rightarrow \frac{dy}{dt} &= \int_{\mathcal{T}} (x - \bar{x}(t))w(x|N_K\delta_{y(t)})\delta_{y(t)}dx \end{aligned} \quad (4.20)$$

Our ‘weak mutation’ assumptions imply that the population will be concentrated in an infinitesimal neighborhood around the mean value  $y(t)$  (*i.e* that the distribution of traits in the population is sharply peaked). We can thus Taylor expand  $w(x|N_K\delta_{y(t)})$  about  $y(t)$  as:

$$w(x|N_K\delta_{y(t)}) = \underbrace{w(y|N_K\delta_{y(t)})}_{=0} + (x - y(t)) \frac{d}{dz} w(z|N_K\delta_{y(t)}) \Big|_{z=y} + \dots$$

Thus, substituting in (4.20), to first order, we obtain

$$\frac{dy}{dt} = \left( \int_{\mathcal{T}} (x - \bar{x}(t))^2 p(x,t) dx \right) \frac{d}{dz} w(z|N_K\delta_{y(t)}) \Big|_{z=y}$$

where we have used  $\bar{x}(t) = y(t)$ . We can define the shorthand  $B(y) = \int_{\mathcal{T}} (x - y(t))^2 p(x, t) dx = \int_{\mathcal{T}} (x - \bar{x}(t))^2 p(x, t) dx$  to obtain:

$$\boxed{\frac{dy}{dt} = B(y) \left( \frac{d}{dz} w(z|N_K \delta_{y(t)}) \Big|_{z=y} \right)} \quad (4.21)$$

Note that by definition,  $B(y(t))$  is the variance of the trait in the population at time  $t$ . The term  $w(z|N_K \delta_{y(t)})$  is the expected growth rate of an individual with trait value  $z$  in a population of size  $N_K$  in which (almost) every individual has trait value  $y$ . This quantity is referred to as the ‘invasion fitness’ of a ‘mutant’ trait  $z$  in a population of ‘resident’  $y$  individuals. Comparing with (2.1), we can see that we have thus derived the canonical equation of adaptive dynamics. Note that strictly speaking, if  $\psi(x, t) = \delta_{y(t)}$  exactly, then  $B(y) \equiv 0$ . This just reflects our assumption that mutations are sampled from infinitesimally close to the resident value. More detailed mathematical arguments are required to ensure that this convergence ‘makes sense’ and that  $B(y)$  does not actually equal 0. This has been proved using much more sophisticated mathematical tools in (Champagnat et al., 2006), which is where we refer the interested reader. An alternative heuristic argument is also provided in the classic article by (Dieckmann and Law, 1996).

## 4.4 Stochastic fluctuations and the weak noise approximation

We can now formally carry out a functional analogue of the weak noise expansion. Assume that  $\psi(x, t)$  is the deterministic trajectory obtained as the solution to (4.8). We introduce a new process  $\{\zeta^{(s)}\}_{s \geq 0}$  which measures the fluctuations of  $\phi^{(t)}$  from the deterministic trajectory  $\psi(x, t)$ . More precisely, we introduce the new variables:

$$\begin{aligned} \zeta^{(s)}(x) &= \sqrt{K}(\phi^{(t)}(x) - \psi(x, t)) \\ s &= t \\ \tilde{P}(\zeta, s) &= \frac{1}{\sqrt{K}} P(\phi, t) \end{aligned} \quad (4.22)$$

Note that the following relations hold:

$$\frac{\delta F[\zeta]}{\delta \phi(x)} = \int_{\mathcal{T}} \frac{\delta F[\zeta]}{\delta \zeta(y)} \frac{\delta \zeta(y)}{\delta \phi(x)} dy = \sqrt{K} \frac{\delta F[\zeta]}{\delta \zeta(x)} \quad (4.23)$$

$$\frac{\partial}{\partial s} = \frac{\partial}{\partial t} \quad (4.24)$$

Furthermore, for any  $\zeta \in \mathcal{M}_K$ , we have:

$$\begin{aligned} \frac{\partial \tilde{P}}{\partial t}(\zeta, s) &= \frac{\delta \tilde{P}}{\delta \zeta} \frac{\partial \zeta}{\partial t} + \frac{\partial \tilde{P}}{\partial s} \frac{\partial s}{\partial t} \\ &= \frac{\delta \tilde{P}}{\delta \zeta} \left( -\sqrt{K} \frac{\partial \psi}{\partial t} \right) + \frac{\partial \tilde{P}}{\partial s} \\ &= -\sqrt{K} \frac{\delta}{\delta \zeta} \{ \mathcal{A}^-(x|\psi) \tilde{P}(\zeta, s) \} + \frac{\partial \tilde{P}}{\partial s} \end{aligned} \quad (4.25)$$

Reformulating equation (4.6) in terms of the new variables (4.22) and using the relations (4.23), (4.24) and (4.25), we obtain:

$$\begin{aligned} -\sqrt{K} \frac{\delta}{\delta \zeta(x)} \{ \mathcal{A}^-(x|\psi) \tilde{P}(\zeta, s) \} + \frac{\partial \tilde{P}}{\partial s} &= \int_{\mathcal{T}} \left[ - \left( \sqrt{K} \frac{\delta}{\delta \zeta(x)} \right) \{ \mathcal{A}^- \left( x \middle| \psi + \frac{\zeta}{\sqrt{K}} \right) \tilde{P}(\zeta, s) \} \right] dx \\ &\quad + \int_{\mathcal{T}} \left[ \frac{1}{2K} \left( K \frac{\delta^2}{\delta \zeta(x)^2} \right) \{ \mathcal{A}^+ \left( x \middle| \psi + \frac{\zeta}{\sqrt{K}} \right) \tilde{P}(\zeta, s) \} \right] dx \end{aligned}$$

and rearranging gives us:

$$\begin{aligned} \frac{\partial \tilde{P}}{\partial s} &= -\sqrt{K} \int_{\mathcal{T}} \frac{\delta}{\delta \zeta(x)} \left\{ \left( \mathcal{A}^- \left( x \middle| \psi + \frac{\zeta}{\sqrt{K}} \right) - \mathcal{A}^-(x|\psi) \right) \tilde{P}(\zeta, s) \right\} dx \\ &\quad + \frac{1}{2} \int_{\mathcal{T}} \frac{\delta^2}{\delta \zeta(x)^2} \{ \mathcal{A}^+ \left( x \middle| \psi + \frac{\zeta}{\sqrt{K}} \right) \tilde{P}(\zeta, s) \} dx \end{aligned} \quad (4.26)$$

We will now Taylor expand our functionals about  $\psi$  (we assume that this is possible). Thus, we have the expansions:

$$\mathcal{A}^- \left( x \middle| \psi + \frac{\zeta}{\sqrt{K}} \right) = \mathcal{A}^- (x|\psi) + \frac{1}{\sqrt{K}} \int_{\mathcal{T}} \zeta(y) \frac{\delta}{\delta \psi(y)} \{ \mathcal{A}^-(y|\psi) \} dy + \dots$$

$$\mathcal{A}^+ \left( x \middle| \psi + \frac{\zeta}{\sqrt{K}} \right) = \mathcal{A}^+ (x|\psi) + \frac{1}{\sqrt{K}} \int_{\mathcal{T}} \zeta(y) \frac{\delta}{\delta \psi(y)} \{ \mathcal{A}^+(y|\psi) \} dy + \dots$$

We also assume that  $\tilde{P}$  can be expanded as

$$\tilde{P} = \sum_{n=0}^{\infty} \tilde{P}_n \left( \frac{1}{\sqrt{K}} \right)^n$$

substituting these expansions into equation (4.26) and equating coefficients of powers of  $K$ , we see that upto leading order in  $K$  (corresponding to the zeroth order terms of  $\tilde{P}$  and  $\mathcal{A}^+ \left( x \middle| \psi + \frac{\zeta}{\sqrt{K}} \right)$ , and the first order term of  $\mathcal{A}^- \left( x \middle| \psi + \frac{\zeta}{\sqrt{K}} \right)$ ) we have:

$$\frac{\partial \tilde{P}_0}{\partial s}(\zeta, s) = \int_{\mathcal{T}} \left[ -\frac{\delta}{\delta \zeta(x)} \left\{ \int_{\mathcal{T}} \zeta(y) \frac{\delta}{\delta \psi(y)} \{ \mathcal{A}^-(y|\psi) \} dy \tilde{P}_0(\zeta, s) \right\} + \frac{1}{2} \mathcal{A}^+(x|\psi) \frac{\delta^2}{\delta \zeta(x)^2} \{ \tilde{P}_0(\zeta, s) \} \right] dx$$

We thus arrive at the functional Fokker-Planck equation:

$$\frac{\partial \tilde{P}_0}{\partial s}(\zeta, s) = \int_{\mathcal{T}} \left( -\frac{\delta}{\delta \zeta(x)} \left\{ \mathcal{D}_{\zeta}[\mathcal{A}^-](x) \tilde{P}_0(\zeta, s) \right\} + \frac{1}{2} \mathcal{A}^+(x|\psi) \frac{\delta^2}{\delta \zeta(x)^2} \{ \tilde{P}_0(\zeta, s) \} \right) dx \quad (4.27)$$

where

$$\mathcal{D}_{\zeta}[\mathcal{A}^-](x) = \int_{\mathcal{T}} \zeta(y) \frac{\delta}{\delta \psi(y)} \{ \mathcal{A}^-(y|\psi) \} dy = \frac{d}{d\epsilon} \mathcal{A}^-(x|\psi + \epsilon \zeta) \Big|_{\epsilon=0}$$

can be thought of now as the functional analogue of a directional derivative of  $\mathcal{A}^-(x|\psi)$  in the direction of the function  $\zeta$ .

# Chapter 5

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## Examples and Applications

Our future advances will not be concerned with universal laws, but instead with universal approaches to tackling particular problems

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Peter Kareiva

In the previous chapter, we used various tools and arguments to illustrate how to obtain approximate equations for very general stochastic birth-death processes. In this chapter, we put this theory into use through examples to study extinction and diversity in finite populations.

### 5.1 Example in one dimension: The stochastic logistic equation

Consider the functional forms of example 1, given by

$$\begin{aligned} b(n) &= \lambda n \\ d(n) &= \left( \mu + (\lambda - \mu) \frac{n}{K} \right) n \end{aligned} \tag{5.1}$$

Here,  $K$  is the system-size parameter. Introducing the new variable  $x = n/K$ , we obtain

$$\begin{aligned} b_K(x) &= \frac{1}{K}b(n) = \frac{1}{K}\lambda Kx \\ d_K(x) &= \frac{1}{K}d(n) = \frac{1}{K}\left(\mu + (\lambda - \mu)\frac{Kx}{K}\right)Kx \end{aligned}$$

Thus, we have

$$A^\pm(x) = b_K(x) \pm d_K(x) = x(\lambda \pm ((\mu + (\lambda - \mu)x)))$$

Defining  $r = \lambda - \mu$  and  $v = \lambda + \mu$  and using equation (3.14), we see that the ‘mesoscopic view’ of the system is given by the solution of the SDE

$$dX_t = rX_t(1 - X_t)dt + \sqrt{\frac{X_t(v + rX_t)}{K}}dB_t \quad (5.2)$$

From equation (3.15), we see that the deterministic dynamics are

$$\frac{dx}{dt} = A^-(x) = rx(1 - x) \quad (5.3)$$

showing that in the infinite population limit, we obtain the logistic equation. Letting  $\alpha(t)$  be the solution of the logistic equation (5.3), We can Taylor expand  $A^\pm(x)$  for the weak noise approximation, and we find:

$$\begin{aligned} A_1^-(x) &= \frac{d}{dx}(rx(1 - x)) \Big|_{x=\alpha} = r(1 - 2\alpha(t)) \\ A_0^+(x) &= \alpha(t)(v + r\alpha(t)) \end{aligned}$$

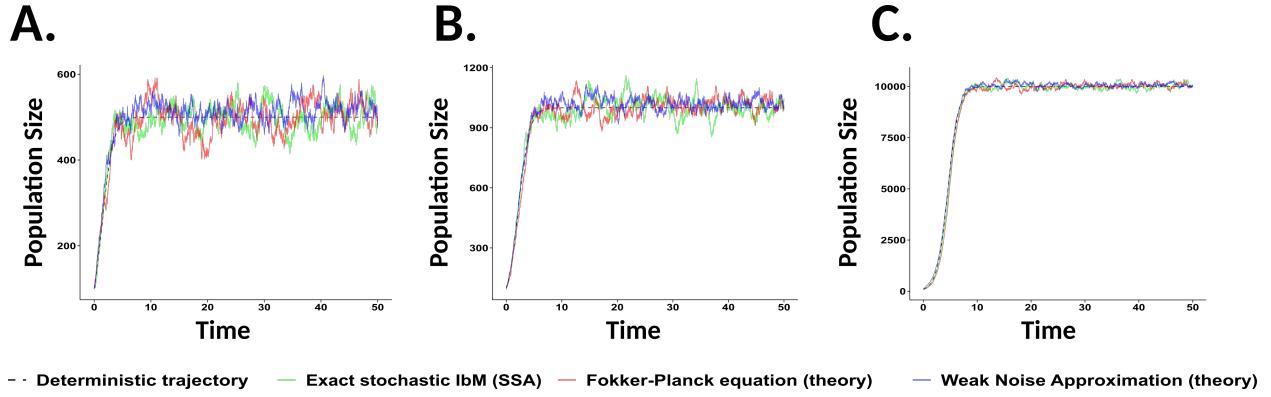
Thus, the weak noise approximation of 5.1 is given by

$$X_t = \alpha(t) + \frac{1}{\sqrt{K}}Y_t \quad (5.4)$$

where the stochastic process  $Y_t$  is an Ornstein-Uhlenbeck process given by the solution to the linear SDE

$$\begin{aligned} dY_t &= A_1^-(t)Y_tdt + \sqrt{A_0^+(t)}dB_t \\ \Rightarrow dY_t &= r(1 - 2\alpha(t))Y_tdt + \sqrt{\alpha(t)(v + r\alpha(t))}dB_t \end{aligned} \quad (5.5)$$

The time series predicted by these three processes look qualitatively similar and all seem to fluctuate about the deterministic steady state (Figure 5.1).

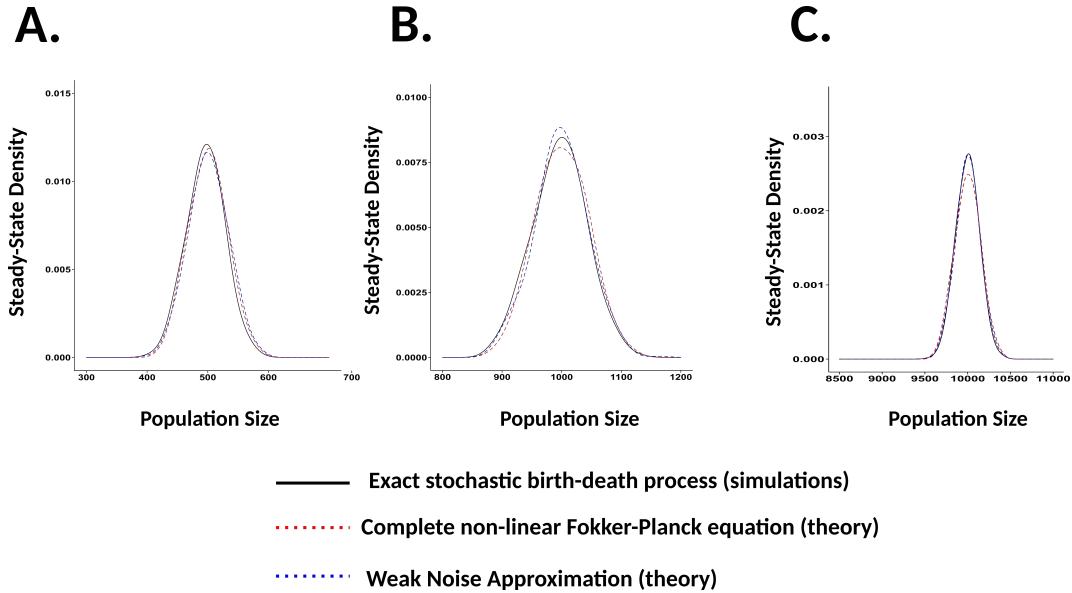


**Figure 5.1:** Comparison of a single realization of the exact birth-death process (5.1), the deterministic trajectory (5.3), the non-linear Fokker-Planck equation (5.2), and the weak noise approximation (5.5) for (A)  $K = 500$ , (B)  $K = 1000$ , and (C)  $K = 10000$ .  $\lambda = 2$ ,  $\mu = 1$  for all thee cases.

The deterministic trajectory (5.3) has two fixed points, one at  $x = 0$  (extinction) and one at  $x = 1$  (corresponding to a population size of  $n = K$ ). For  $r > 0$ ,  $x = 0$  is unstable and  $x = 1$  is a global attractor, meaning in the deterministic limit, when  $r > 0$ , all populations end up at  $x = 1$  given enough time. The stochastic dynamics (5.2) and (5.5) depend not only on  $r$ , but also on  $v$ , the sum of the birth and death rates. It has been proven that  $X_t = 0$  is the only recurrent state for the full stochastic dynamics (5.2), meaning that every population is guaranteed to go extinct<sup>1</sup> given enough time (Nåsell, 2001), thus illustrating an important difference between finite and infinite populations.  $X_t = 0$  is also an ‘absorbing’ state since once a population goes extinct, it has no way of being revived in this model. However, if  $K$  is large enough, the eventual extinction of the population may take a very long time. In fact, we can make the expected time to extinction arbitrarily long by making  $K$  sufficiently large. Thus, for moderately large values of  $K$ , it is biologically meaningful only to look at a weaker version of the steady state distribution by imposing the condition that the population does not go extinct and looking at the ‘transient’ dynamics (Hastings, 2004). Conditioned on non-extinction, the solution to (5.2) has a ‘quasistationary’ distribution about the deterministic attractor  $X_t = 1$ , with some variance reflecting the effect of noise-induced fluctuations in

<sup>1</sup>This can be proven using tools from Markov chain theory. For those interested, the proof uses ergodicity to arrive at a contradiction if any state other than 0 exhibits a non-zero density at steady state.

population size (Nåsell, 2001) due to the finite size of the population. The weak-noise approximation (5.5) implicitly assumes non-extinction by only measuring small fluctuations from the deterministic solution to (5.3) and thus, at steady state, naturally describes a quasistationary distribution centered about  $X_t = 1$ . The steady-state density (probability density function as  $t \rightarrow \infty$ ) of the exact birth-death process (5.1) is compared with that predicted by (5.2) and (5.5) for various values of  $K$  in figure 5.2.



**Figure 5.2:** Comparison of the steady-state densities given by (5.1), (5.2), and (5.5) for (A)  $K = 500$ , (B)  $K = 1000$ , and (C)  $K = 10000$ .  $\lambda = 2, \mu = 1$  for all thee cases. Each curve was obtained using 1000 independent realizations.

## 5.2 Example for discrete traits: Lotka-Volterra and matrix games in finite populations

The methods outlined in the above section have recently been used to study the population dynamics of a finite population playing a so-called ‘matrix game’ (An evolutionary game for which you can write down a payoff matrix) with 2 pure strategies (Tao and Cressman, 2007). Based on the interpretation of what each type represents, this is mathematically equivalent to studying frequency-dependent selection on a one-locus two-allele gene (with a bijective genotype-phenotype map and no mutations) or studying two-species competitive Lotka-Volterra dynamics, as we will show below. The stochastic Lotka-Volterra competition

model shown below has also been proved to be equivalent to an  $m$ -allele Moran model under certain limits (Constable and McKane, 2017).

Let us imagine a population with  $m$  types of individuals that are competing for resources. Let the state of the population be characterized by the vector  $\mathbf{v}(t) = [v_1(t), v_2(t), \dots, v_m(t)]$ , where  $v_i(t)$  is the number of type  $i$  individuals at time  $t$ . Let the birth and death rates of the  $i$ th type be given by:

$$\begin{aligned} b_i(\mathbf{v}) &= \lambda v_i \\ d_i(\mathbf{v}) &= \left( \mu + \frac{1}{K} \left( \sum_{j=1}^m M_{ij} v_j \right) \right) v_i \end{aligned} \quad (5.6)$$

where  $K > 0$  is our system size parameter (and represents a global carrying capacity across all types),  $\lambda > 0$  and  $\mu > 0$  are suitable positive constants representing the baseline natality and mortality common to all types, and  $M_{ij} \geq 0$  is a non-negative constant describing the effect of type  $j$  individuals on the death rate of type  $i$  individuals due to competition. We assume that  $M_{ij} \ll K$ . The values  $M_{ij}$  are often collected in an  $m \times m$  matrix  $\mathbf{M}$ . The negative of this matrix,  $-\mathbf{M}$ , is called the ‘payoff matrix’ (in evolutionary game theory) or ‘interaction matrix’ (in Lotka-Volterra models), which is why the infinite population analogues of such models are called ‘matrix games’ in the evolutionary game theory literature. Lotka-Volterra models also frequently assume that the diagonal elements  $M_{ii}$  are all equal, though we will not make that assumption here.

Going from population numbers  $\mathbf{v}$  to densities  $\mathbf{x} = \mathbf{v}/K$ , we obtain the birth and death rates:

$$\begin{aligned} b_i^{(K)}(\mathbf{x}) &= \lambda x_i \\ d_i^{(K)}(\mathbf{x}) &= \left( \mu + \sum_{j=1}^m M_{ij} x_j \right) x_i \end{aligned} \quad (5.7)$$

Thus, we have

$$A_i^\pm = x_i \left( \lambda \pm \left( \mu + \sum_{j=1}^m M_{ij} x_j \right) \right)$$

Defining  $r = \lambda - \mu$  and  $v = \lambda + \mu$ , we see from equation (3.31) that the mesoscopic view is the  $m$  dimensional SDE given by

$$d\mathbf{X}_t = \mathbf{A}^-(\mathbf{X}_t)dt + \frac{1}{\sqrt{K}}\mathbf{D}(\mathbf{X}_t)d\mathbf{B}_t \quad (5.8)$$

where

$$\mathbf{A}^-_i = (\mathbf{X}_t)_i(r - \sum_{j=1}^m M_{ij}(\mathbf{X}_t)_j)$$

and

$$(\mathbf{DD}^T)_i = (\mathbf{X}_t)_i(v + \sum_{j=1}^m M_{ij}(\mathbf{X}_t)_j)$$

From (3.32), we see that the deterministic limit is a set of  $m$  coupled ODEs given by

$$\frac{dx_i}{dt} = x_i \left( r - \sum_{j=1}^m M_{ij}x_j \right) \quad (5.9)$$

These are precisely the competitive Lotka-Volterra equations for a system of  $m$  species. By matching the terms of (5.7) with those of (3.33), we can identify that we have  $\mu = 0$  and

$$\begin{aligned} b_i^{(\text{int})}(\mathbf{x}) &= \lambda \\ d_i^{(\text{int})}(\mathbf{x}) &= \mu + \sum_{j=1}^m M_{ij}x_j \\ w_i(\mathbf{x}) &= r - \sum_{j=1}^m M_{ij}x_j \end{aligned} \quad (5.10)$$

If  $p_i(t)$  is the frequency of type  $i$  individuals in the population at time  $t$  and  $N_K(t) = \sum_i x_i(t)$ , then the mean fitness is given by

$$\bar{w}(t) = \sum_{i=1}^m w_i p_i \quad (5.11)$$

$$= \sum_{i=1}^m \left( r - \sum_{j=1}^m M_{ij}x_j \right) p_i \quad (5.12)$$

$$= r - \sum_{i=1}^m p_i \left( \sum_{j=1}^m M_{ij}x_j \right) \quad (5.13)$$

where we have used the fact that  $\sum_i p_i = 1$  in the last line. Using (3.38) to write down the equations for the frequencies  $p_i$ , we obtain

$$\frac{dp_i}{dt} = \left[ \sum_{i=1}^m p_i \left( \sum_{j=1}^m M_{ij} x_j \right) - \sum_{j=1}^m M_{ij} x_j \right] p_i \quad (5.14)$$

Let us define the payoff matrix  $\mathbf{B} = -\mathbf{M}$ . Then, the dynamics are

$$\frac{1}{N_K(t)} \frac{dp_i}{dt} = [(\mathbf{B}\mathbf{p})_i - \mathbf{p} \cdot \mathbf{B}\mathbf{p}] p_i \quad (5.15)$$

which is the familiar version of the replicator equation seen in most textbooks, with an extra  $N_K(t)$  factor to account for the fact that  $\sum_i x_i$  is allowed to fluctuate in our model. If instead  $N_K$  was a constant for all time, it could simply be absorbed into the definition of the payoff matrix  $B$  to obtain exactly the replicator equation as presented in most ecology/evolution textbooks. We briefly note here that if  $m$  is large, then both the stochastic dynamics (5.8) and the deterministic limit (5.9) can be simplified from an  $m$  dimensional system to an  $m-1$  dimensional system by a coordinate transformation. If we go from the variables  $x_1, \dots, x_m$  to the variables  $p_1, \dots, p_{m-1}, N_K$ , then, we can exploit the fact that  $N_K$  varies much less than the  $p_i$  terms to project the system onto a ‘slow manifold’ in which  $N_K$  is approximately constant, thus obtaining an  $m-1$  dimensional system of equations and recovering the relation between the Lotka-Volterra equations for  $m$  species and the replicator equation for  $m-1$  tactics (Constable and McKane, 2017; Parsons and Rogers, 2017). However, we will not explore this further in this manuscript, and refer the reader to (Constable, McKane, and Rogers, 2013) and (Parsons and Rogers, 2017) for a review of the ideas of (stochastic) dynamics on slow manifolds.

Let the solution to the equations (5.9) be given by  $\mathbf{a}(t) = [a_1(t), \dots, a_m(t)]$ . For the weak noise approximation, we can Taylor expand  $A_i^\pm$  and use (3.59) to compute the directional derivative as:

$$D_i = y_i w_i(\mathbf{a}) + a_i \sum_{k=1}^m y_k \left( \frac{\partial w_i}{\partial x_k} \Big|_{\mathbf{x}=\mathbf{a}(t)} \right) \quad (5.16)$$

$$= y_i w_i(\mathbf{a}) + a_i \sum_{k=1}^m y_k \left( \frac{\partial}{\partial x_k} \left( r + \sum_{j=1}^m B_{ij} x_j \right) \Big|_{\mathbf{x}=\mathbf{a}(t)} \right) \quad (5.17)$$

$$= y_i w_i(\mathbf{a}) + a_i \sum_{k=1}^m y_k B_{ik} \quad (5.18)$$

$$\Rightarrow D_i = y_i w_i(\mathbf{a}) + a_i w_i(\mathbf{y}) - r a_i \quad (5.19)$$

where we have used the fact that  $w_i(\mathbf{y}) = r + \sum_{k=1}^m y_k B_{ik}$  (from (5.10)) in the last step. Thus, in the weak noise approximation of our process, the dynamics are given by

$$\mathbf{x}(t) = \mathbf{a}(t) + \frac{1}{\sqrt{K}} \mathbf{y}(t) \quad (5.20)$$

where the stochastic fluctuations  $\mathbf{y}(t)$  satisfy the linear Fokker-Planck equation

$$\frac{\partial P}{\partial t}(\mathbf{y}, t) = \sum_{i=1}^m \left( -\frac{\partial}{\partial y_i} \{(y_i w_i(\mathbf{a}) + a_i w_i(\mathbf{y}) - r a_i) P(\mathbf{y}, t)\} + \frac{1}{2} \left( a_i \left( v - \sum_{j=1}^m B_{ij} a_j \right) \right) \frac{\partial^2}{\partial y_i^2} P(\mathbf{y}, t) \right) \quad (5.21)$$

Using (5.19) in (3.53), we see that the fluctuations are expected to evolve as:

$$\frac{d}{dt} \mathbb{E}[y_i] = w_i(\mathbf{a}) \mathbb{E}[y_i] + a_i \sum_{k=1}^m B_{ik} \mathbb{E}[y_k] \quad (5.22)$$

or, in matrix form:

$$\frac{d}{dt} \begin{bmatrix} \mathbb{E}[y_1] \\ \mathbb{E}[y_2] \\ \vdots \\ \mathbb{E}[y_i] \\ \vdots \\ \mathbb{E}[y_m] \end{bmatrix} = \begin{bmatrix} (r + \sum_{j=1}^m B_{1j} a_j + a_1 B_{11}) & a_1 B_{12} & a_1 B_{13} & \dots & \dots & a_1 B_{1m} \\ a_2 B_{21} & (r + \sum_{j=1}^m B_{2j} a_j + a_2 B_{22}) & a_2 B_{23} & \dots & \dots & a_2 B_{2m} \\ \vdots & \ddots & \ddots & & & \vdots \\ a_i B_{i1} & a_i B_{i2} & a_i B_{i3} & \dots & (r + \sum_{j=1}^m B_{ij} a_j + a_i B_{ii}) & a_i B_{im} \\ \vdots & & & & \ddots & \vdots \\ a_m B_{m1} & a_m B_{m2} & a_m B_{m3} & \dots & \dots & (r + \sum_{j=1}^m B_{mj} a_j + a_m B_{mm}) \end{bmatrix} \begin{bmatrix} \mathbb{E}[y_1] \\ \mathbb{E}[y_2] \\ \vdots \\ \mathbb{E}[y_i] \\ \vdots \\ \mathbb{E}[y_m] \end{bmatrix} \quad (5.23)$$

The eigenvalues of the first matrix on the RHS will tell us whether the fixed point  $\mathbb{E}[y_i] = 0 \forall i$  (the only fixed point of this system) is stable, or whether fluctuations are expected to grow (up to the point where the fluctuations are so large that the WNA is no longer valid). can compare time series or something here if we think it is helpful. Visualization may be little hard though, because we always have  $\geq 3$  dimensions ( $m, + 1$  additional for time)

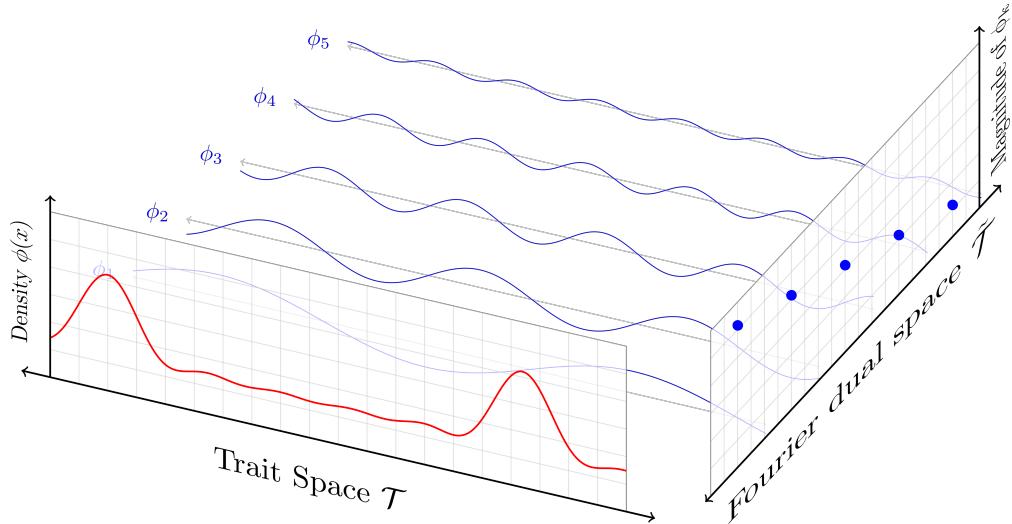
## 5.3 Example for quantitative traits

### 5.3.1 Interlude: Detecting clusters through Fourier analysis

In Chapter 4, we used various approximations to arrive at the linear functional Fokker-Planck equation

$$\frac{\partial P}{\partial t}(\zeta, t) = \int \left( -\frac{\delta}{\delta \zeta(x)} \{ \mathcal{D}_\zeta[\mathcal{A}^-](x)P(\zeta, t) \} + \frac{1}{2}\mathcal{A}^+(x|\psi) \frac{\delta^2}{\delta \zeta(x)^2} \{ P(\zeta, t) \} \right) dx \quad (5.24)$$

for describing stochastic fluctuations  $\zeta$  from the deterministic solution obtained by solving (4.8). Our goal is now to find a method to effectively detect and describe evolutionary branches (modes in trait space, corresponding to individual morphs) for this process. We will do this by measuring the autocorrelation of the distribution of the population over trait space.



**Figure 5.3: Schematic description of Fourier analysis.** A function  $\phi(x)$  (shown in red) over the trait space can be decomposed as the sum of infinitely many Fourier modes (shown in blue)  $\phi_k$ . In the Fourier dual space, we can look at the peaks of each of these Fourier modes: The magnitude of  $\phi_k$  tells us how much it contributes to the actual function of interest  $\phi$ .

A convenient theorem due to Weiner and Khinchin relates the autocorrelation of a probability distribution to its power spectral density via Fourier transformation. This has been

extensively used in spatial ecology, and we too will make use of it here. Specifically, we will carry out a basis expansion of our functions in the Fourier basis  $\{e^{ikx}\}_{k \in \mathbb{Z}}$ . If  $\mathcal{D}_\zeta[\mathcal{A}^-]$  is a translation-invariant<sup>2</sup> linear operator, then  $\exp(ikx)$  acts as an eigenfunction, significantly simplifying the calculations. We therefore assume this below.

Assume that  $\mathcal{D}_\zeta[\mathcal{A}^-]$  takes the form:

$$\mathcal{D}_\zeta[\mathcal{A}^-](x, t) = L[\zeta(x, t)]$$

for a translation-invariant linear operator  $L$  that only depends on  $x$  and  $t$ . The presence of phenotypic clustering and polymorphisms can be analyzed by examining the power spectrum of  $\tilde{P}_0(\zeta, s)$  over the trait space.

We assume that  $\zeta$ , and  $\mathcal{A}^+(x|\psi)$  admit the Fourier basis representations:

$$\begin{aligned} \zeta(x, t) &= \sum_{k=-\infty}^{\infty} e^{ikx} \zeta_k(t) \quad ; \quad \zeta_k(t) = \int_{\mathcal{T}} \zeta(x, t) e^{-ikx} dx \\ \mathcal{A}^+(x|\psi) &= \sum_{k=-\infty}^{\infty} e^{ikx} A_k(t) \quad ; \quad A_k(t) = \int_{\mathcal{T}} \mathcal{A}^+(x|\psi) e^{-ikx} dx \end{aligned} \tag{5.25}$$

In this case, the functional derivative operator obeys:

$$\frac{\delta}{\delta \zeta(x)} = \sum_{k=-\infty}^{\infty} e^{-ikx} \frac{\partial}{\partial \zeta_k} \tag{5.26}$$

and since  $L$  is linear and translation-invariant, we also have the relation<sup>3</sup>:

$$L[\zeta] = \sum_{k=-\infty}^{\infty} L_k \zeta_k e^{ikx} \tag{5.27}$$

---

<sup>2</sup>This is horrible nomenclature by the mathematicians. Though ‘invariant’ is the conventional name for this concept, the intended meaning is not really invariant but ‘equivariant’. Formally, let  $\mathcal{F}$  be a suitable function space of real valued functions. For any  $c \in \mathbb{R}$ , let  $T_c : \mathcal{F} \rightarrow \mathcal{F}$  be the translation operator on this space, defined by  $T_c[f(x)] = f(x + c)$ . An operator  $L : \mathcal{F} \rightarrow \mathcal{F}$  is said to be translation-invariant if it commutes with  $T_c$  for every  $c \in \mathbb{R}$ , i.e.  $T_c[L[f]] = L[T_c[f]] \forall f \in \mathcal{F} \forall c \in \mathbb{R}$

<sup>3</sup>This is because  $\exp(ikx)$  acts as an eigenfunction for translation invariant linear operators, and therefore, for any function  $\varphi = \sum \varphi_k \exp(ikx)$ , we have the relation  $L[\varphi] = L[\sum \varphi_k \exp(ikx)] = \sum \varphi_k L[\exp(ikx)] = \sum \varphi_k L_k \exp(ikx)$ , where  $L_k$  is the eigenvalue of  $L$  associated with the eigenfunction  $\exp(ikx)$ . It is helpful to draw the analogy with eigenvectors of matrices and view  $L_k \varphi_k$  as the projection of  $L[\varphi]$  along the  $k$ th eigenvector  $e_k = \exp(ikx)$ .

where

$$L_k = e^{-ikx} L[e^{ikx}]$$

Lastly, by definition of Fourier modes, we have, for any differentiable real function  $F$  and any fixed time  $t > 0$ :

$$\frac{\partial}{\partial \zeta_j(t)} F(\zeta_i(t)) = \delta_{ij} F'(\zeta_j(t)) \quad (5.28)$$

where  $\delta_{ij}$  is the Kronecker delta symbol. Using (5.25), (5.26), and (5.27) in (4.27), we get, for the first term of the RHS:

$$\begin{aligned} & - \int_{\mathcal{T}} \frac{\delta}{\delta \zeta(x)} \{L[\zeta(x, t)]P(\zeta, t)\} dx \\ &= - \int_{\mathcal{T}} \sum_k e^{-ikx} \frac{\partial}{\partial \zeta_k} \left\{ \sum_n e^{inx} L_n \zeta_n P \right\} dx \\ &= - \int_{\mathcal{T}} \sum_k \sum_n e^{-i(k-n)x} \frac{\partial}{\partial \zeta_k} \{L_n \zeta_n P\} dx \\ &= -2\pi \sum_k L_k \frac{\partial}{\partial \zeta_k} \{\zeta_k P\} \end{aligned} \quad (5.29)$$

and for the second:

$$\begin{aligned} & \int_{\mathcal{T}} \sum_k e^{ikx} A_k \left( \sum_m \sum_n e^{-i(m+n)x} \frac{\partial}{\partial \zeta_m} \frac{\partial}{\partial \zeta_n} P \right) dx \\ &= \int_{\mathcal{T}} \sum_k \sum_m \sum_n e^{i(k-m-n)x} A_k \frac{\partial}{\partial \zeta_m} \frac{\partial}{\partial \zeta_n} \{P\} dx \\ &= 2\pi \sum_m \sum_n A_{m+n} \frac{\partial}{\partial \zeta_m} \frac{\partial}{\partial \zeta_n} \{P\} \end{aligned} \quad (5.30)$$

Substituting (5.29) and (5.30) into (4.6), we see that the Fokker-Planck equation in Fourier space reads:

$$\frac{\partial P}{\partial t} = -2\pi \sum_k L_k \frac{\partial}{\partial \zeta_k} \{\zeta_k P\} + \pi \sum_m \sum_n A_{m+n} \frac{\partial}{\partial \zeta_m} \frac{\partial}{\partial \zeta_n} \{P\} \quad (5.31)$$

It is important to remember that since  $\zeta(x, t)$  is a stochastic process,  $\zeta_i$  is really a stochastic process and thus  $\zeta_i(t)$  is actually shorthand for the random variable  $(\zeta_i)_t(\omega)$ , where  $\omega$  is a sample path in the Fourier dual of our original probability space. Multiplying both sides of (5.31) by  $\zeta_r$  and integrating over the probability space to obtain expectation values, we see

that

$$\begin{aligned}
\frac{d}{dt} \mathbb{E}[\zeta_r] &= -2\pi \sum_k \int \zeta_r L_k \frac{\partial}{\partial \zeta_k} \{\zeta_k P\} d\omega + \pi \sum_m \sum_n A_{m+n} \int \zeta_r \frac{\partial}{\partial \zeta_m} \frac{\partial}{\partial \zeta_n} (P) d\omega \\
&= 2\pi \sum_k L_k \int \zeta_k \frac{\partial \zeta_r}{\partial \zeta_k} P d\omega + \pi \sum_m \sum_n A_{m+n} \int \frac{\partial^2 \zeta_r}{\partial \zeta_m \partial \zeta_n} P d\omega \\
&= 2\pi L_r \mathbb{E}[\zeta_r]
\end{aligned} \tag{5.32}$$

where we have used integration by parts and neglected the boundary term in the second step (assuming once again that  $P$  decays rapidly enough near the boundaries that this is doable), and then used (5.28) to arrive at the final expression. Similarly, multiplying (5.31) by  $\zeta_r \zeta_s$ , integrating over the probability space and using integration by parts, we get:

$$\begin{aligned}
\frac{d}{dt} \mathbb{E}[\zeta_r \zeta_s] &= 2\pi \sum_k L_k \int \zeta_k P \frac{\partial}{\partial \zeta_k} \{\zeta_r \zeta_s\} d\omega + \pi \sum_m \sum_n A_{m+n} \int_{-\infty}^{\infty} P \frac{\partial}{\partial \zeta_m} \frac{\partial}{\partial \zeta_n} \{\zeta_r \zeta_s\} d\omega \\
&= 2\pi(L_r + L_s) \mathbb{E}[\zeta_r \zeta_s] + \pi(A_{2r} + A_{2s})
\end{aligned} \tag{5.33}$$

At the stationary state, the LHS must be zero by definition, and we must therefore have, for every  $r, s \in \mathbb{Z}$ :

$$\mathbb{E}[\zeta_r \zeta_s] = -\frac{A_{2r} + A_{2s}}{2(L_r + L_s)} \tag{5.34}$$

Recall that the Fourier modes of any real function  $\varphi$  must satisfy  $\varphi_{-r} = \bar{\varphi}_r$ . Since  $\zeta$ ,  $A$  and  $L$  are all real, we can substitute  $s = -r$  in equation (5.34) to obtain the autocovariance relation:

$$\mathbb{E}[|\zeta_r|^2] = -\frac{\text{Re}(A_{2r})}{2\text{Re}(L_r)} \tag{5.35}$$

The presence of phenotypic clustering can be detected using the ‘spatial covariance’ of our original process  $\phi$ , defined as (Rogers, McKane, and Rossberg, 2012):

$$\Xi[x] = m(\mathcal{T}) \int_{\mathcal{T}} \mathbb{E}[\phi_{\infty}(x) \phi_{\infty}(y-x)] dy \tag{5.36}$$

where  $\phi_{\infty}$  is the stationary state distribution of  $\{\phi_t\}_t$  and  $m$  is the Lebesgue measure. We

can use a spatial analogue of the Wiener-Khinchin theorem to calculate:

$$\Xi[x] = m(\mathcal{T}) \left[ \int_{\mathcal{T}} \psi_{\infty}(x) \psi_{\infty}(y-x) dy + \frac{1}{K} \sum_{r=-\infty}^{\infty} \mathbb{E}[|\zeta_r|^2] e^{irx} \right] \quad (5.37)$$

where the expectations in the second term are for the stationary state. A flat  $\Xi[x]$  indicates that there are no clusters, and peaks indicate the presence of clusters.

### 5.3.2 An example: The quantitative logistic equation

Consider the birth and death functionals given by (4.2). In terms of the scaled variable  $\phi = K\nu$ , these functions read:

$$\begin{aligned} b_K(x|\phi) &= \frac{1}{K} b(x|\nu) = \frac{1}{K} \left( r \int_{\mathcal{T}} m(x,y) K\phi(y) dy \right) \\ d_K(x|\phi) &= \frac{1}{K} d(x|\nu) = \frac{1}{K} \left( \frac{K\phi(x)}{Kn(x)} \int_{\mathcal{T}} \alpha(x,y) K\phi(y) dy \right) \end{aligned} \quad (5.38)$$

Thus, using equation (4.8), the deterministic trajectory becomes:

$$\frac{\partial \psi}{\partial t}(x,t) = r \int_{\mathcal{T}} m(x,y) \psi(y,t) dy - \frac{1}{n(x)} \psi(x,t) \int_{\mathcal{T}} \alpha(x,y) \psi(y,t) dy \quad (5.39)$$

Note that if we employ the change of variables  $\Psi = K\psi$  to go back from  $\mathcal{M}_K$  (*i.e.*  $\phi^{(t)}$ ) to  $\mathcal{M}$  (*i.e.*  $\nu^{(t)}$ ), we recover the familiar continuous logistic equation (Equation (2.4)) as the deterministic limit:

$$\begin{aligned} \frac{\partial \Psi}{\partial t}(x,t) &= r \int_{\mathcal{T}} m(x,y) \Psi(y,t) dy - \frac{\Psi(x,t)}{Kn(x)} \int_{\mathcal{T}} \alpha(x,y) \Psi(y,t) dy \\ &\approx r\Psi(x,t) - \frac{\Psi(x,t)}{K(x)} \int_{\mathcal{T}} \alpha(x,y) \Psi(y,t) dy + D_m \nabla_x^2 \Psi(x,t) \end{aligned}$$

where  $K(x) = Kn(x)$  is the carrying capacity experienced by an individual of phenotype  $x$ , and  $D_m = r\sigma_m^2/2$  measures the ‘diffusion rate’ of the population in trait space. It is left as an exercise for the reader to verify by the same steps that if we instead have the birth

rate functional  $b(x|\phi) = \lambda \int m(x, y)\phi(y)dy$  (with  $m(x, y)$  as defined in (4.2)) and the death rate functional  $d(x|\phi) = \phi(x)(\mu + (\lambda - \mu)\phi(x)/K)$ , the macroscopic limit yields the famous Fisher-KPP equation with growth rate  $r = \lambda - \mu$  and diffusion constant  $D = \lambda\sigma_m^2/2$ .

In any case, for the system defined by (5.38), we can also calculate  $\mathcal{D}_\zeta[\mathcal{A}^-]$  as

$$\begin{aligned}\mathcal{D}_\zeta[\mathcal{A}^-] &= \frac{d}{d\epsilon} \left( r \int_{\mathcal{T}} m(x, y)(\psi(y) + \epsilon\zeta(y))dy - \frac{\psi(x) + \epsilon\zeta(x)}{n(x)} \int_{\mathcal{T}} \alpha(x, y)(\psi(y) + \epsilon\zeta(y))dy \right) \Big|_{\epsilon=0} \\ &= r \int_{\mathcal{T}} m(x, y)\zeta(y)dy - \frac{1}{n(x)} \left( \psi(x) \int_{\mathcal{T}} \alpha(x, y)\zeta(y)dy + \zeta(x) \int_{\mathcal{T}} \alpha(x, y)\psi(y)dy \right)\end{aligned}$$

# **Part III**

## **Discussion & Outlook**



# Chapter 6

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## A unified view of population dynamics

The grand aim of all science [is] to cover the greatest number of empirical facts by logical deduction from the smallest number of hypotheses or axioms

---

Albert Einstein

In this thesis, we have seen how stochastic birth-death processes can be used to construct and analyze mechanistic individual-based models for the dynamics of finite populations. In doing so, we have also seen that various well-known equations of evolutionary dynamics can be recovered in the infinite population size limit, sometimes also called the ‘macroscopic’ description. In the finite-dimensional case (corresponding to discrete trait variants), the macroscopic descriptions are the equations of population genetics and evolutionary game theory. In the infinite-dimensional case, they are the equations of quantitative genetics, and, in some further limits, adaptive dynamics. In both cases, the mean value of the trait in the population changes according to an equation resembling the Price equation. This highlights the natural connections between these various equations - For example, the same procedures that lead to the replicator-mutator equation in the case of discretely varying traits yield Kimura’s model in the quantitative case, underscoring the broad similarities between evolutionary game theory and quantitative genetics. The major formulations are summarized in Table 6.1.

Number of possible distinct trait variants ( $m$ )	State Space	Model parameters	Mesoscopic description	Infinite population limit
$m = 1$ (Identical individuals)	$[0, 1, 2, 3, \dots]$ (Population size)	Two real-valued functions, $b(N)$ and $d(N)$ , describing the birth and death rate of individuals when the population size is $N$	Univariate Fokker-Planck equation (one-dimensional SDEs)	Single species population dynamics
$1 < m < \infty$ (Discrete traits)	$[0, 1, 2, 3, \dots]^m$ (Number of individuals of each trait variant)	$2m$ real-valued functions, $b_i(\mathbf{v})$ and $d_i(\mathbf{v})$ (for $1 \leq i \leq m$ ) describing the birth and death rate of trait variant $i$ when the population is $\mathbf{v}$	Multivariate Fokker-Planck equation ( $m$ -dimensional SDEs)	Evolutionary game theory Lotka-Volterra competition Quasispecies equation Price equation (discrete traits)
$m = \infty$ (Quantitative traits)	$\left\{ \sum_{i=1}^n \delta_{x_i} \mid n \in \mathbb{N} \right\}$ (Each Dirac mass $\delta_{x_i}$ is an individual with trait value $x_i$ )	Two real-valued functionals $b(x \nu)$ and $d(x \nu)$ describing the birth and death rate of trait variant $x$ when the population is $\nu$	Functional Fokker-Planck equation (SPDEs/Field equations)	Kimura's continuum-of-alleles model Sasaki and Dieckmann, 2011's Oligomorphic Dynamics Wickman et al., 2022's Trait Space Equations for intraspecific trait variation Adaptive Dynamics Price equation (quantitative traits)

**Table 6.1:** Summary of the various birth-death processes studied in this chapter

Equation (3.40), which we derived in chapter 3, is a very general equation for how frequencies change over time in stochastic populations. To recap, we derived the equation:

$$\begin{aligned}
 dp_i(t) = & \underbrace{\left[ (w_i(\mathbf{x}) - \bar{w})p_i + \mu \left\{ Q_i(\mathbf{p}) - p_i \left( \sum_{j=1}^m Q_j(\mathbf{p}) \right) \right\} \right]}_{\text{Infinite population predictions}} dt \\
 & - \frac{1}{K} \underbrace{\frac{1}{N_K(t)} \left[ (\tau_i(\mathbf{x}) - \bar{\tau})p_i + \mu \left\{ Q_i(\mathbf{p}) - p_i \left( \sum_{j=1}^m Q_j(\mathbf{p}) \right) \right\} \right]}_{\text{Directional finite population effects}} dt \\
 & + \frac{1}{\sqrt{K}} \underbrace{\left[ (A_i^+)^{1/2} dB_t^{(i)} - p_i \sum_{j=1}^m (A_j^+)^{1/2} dB_t^{(j)} \right]}_{\text{Non-directional finite population effects}} \\
 & \quad \text{due to stochastic fluctuations}
 \end{aligned} \tag{6.1}$$

This equation is in ‘replicator-mutator’ form, and letting  $K \rightarrow \infty$  recovers the replicator-mutator equation. If we wish, we could also express the same equation in ‘Price’ form by calculating how the statistical mean value of a type level quantity changes over time. Let  $f$  be any type level quantity, with constant value  $f_i$  for the  $i^{\text{th}}$  type. By multiplying both sides of equation (6.1) by  $f_i$  and summing over all  $i$  (essentially the same steps as going from (3.38) to (3.39)), we see that the statistical mean  $\bar{f}$  of the quantity varies as:

$$\begin{aligned}
 d\bar{f} = & \text{Cov}(w, f)dt - \frac{1}{KN_K(t)} \text{Cov}(\tau, f)dt \\
 & + \mu \left( 1 - \frac{1}{KN_K(t)} \right) \left( \sum_{i=1}^m f_i Q_i(\mathbf{p}) - \bar{f} \sum_{i=1}^m Q_i(\mathbf{p}) \right) dt \\
 & + \frac{1}{\sqrt{K}} \left( \sum_{i=1}^m f_i \sqrt{A_i^+} dB_t^{(i)} - \bar{f} \sum_{i=1}^m \sqrt{A_i^+} dB_t^{(i)} \right)
 \end{aligned} \tag{6.2}$$

where all covariances are understood in the statistical sense (Note that since each  $w_i$ ,  $\tau_i$ ,  $\bar{w}$ , and  $\bar{\tau}$  are stochastic processes depending on  $\mathbf{p}$ , the terms  $\text{Cov}(w, f)$  and  $\text{Cov}(\tau, f)$  are themselves stochastic processes). Taking  $K \rightarrow \infty$  in equation (6.2) recovers the standard Price equation as the infinite population limit. In some sense, (6.1) and (6.2) are therefore ‘fundamental’ equations for the evolution of finite populations, with the replicator-mutator and Price equations as the infinite population limits respectively. In both equations, the first term represents the direct effects of forces captured in classic deterministic models -

the selection and mutation are partitioned into two terms in (6.2), but since mutation acts symmetrically in both the first and second term of (6.1), this has no major bearing on our interpretations. As is evident in both (6.1) and (6.2), finite populations experience a new directional force dependent on  $\tau_i = b_i^{(ind)} + d_i^{(ind)}$ , the per-capita turnover rate of type  $i$ , that cannot be captured in infinite population models. Remarkably, this term acts in a way that is mathematically exactly analogously to the classical evolutionary force of selection and mutation as captured by the first term in (6.1), but in the opposite direction - A higher relative  $\tau_i$  leads to a decrease in frequency (Notice the minus sign before the second term in (6.1)). Biologically, this term describes a biasing effect due to differential turnover rates and can intuitively be understood as being similar to the gambler's ruin through the following reasoning: If a type  $i$  has a higher  $\tau_i$ , it experiences greater turnover due to a generally higher birth and death rate and thus experience more births and deaths in a given time interval than an otherwise equivalent species with a lower  $\tau_i$ . More events mean greater demographic stochasticity, and types with a higher  $\tau_i$  thus tend to be eliminated by a stochastic analog of selection because they experience more chance events (births and deaths) in a given time period. This effect is less visible if the total population size is higher because larger populations generally experience less stochasticity, which is reflected in the  $1/N_K$  factor in this term. This stochastic analog of selection for reduced turnover rates, captured by the second term of equation (6.1), is the force responsible for the 'reversal of the direction of deterministic selection' induced by demographic noise in previous studies (Houchmandzadeh and Vallade, 2012; Houchmandzadeh, 2015; Constable, Rogers, et al., 2016; McLeod and Day, 2019). Note that types that tend to increase the *total* population size  $N_K(t)$  (such as altruists in evolutionary theory and mutualists in ecological communities) will reduce the magnitude of this effect compared to types that do not facilitate such an increase, such as cheaters and highly competitive species, which could explain why this effect preferentially favors the former types in reversing the direction of deterministic selection in finite population models (Houchmandzadeh, 2015; McLeod and Day, 2019). The fact that total population size controls the strength of the second term of (6.1) also explains why cooperation is favoured in the early transient period of population growth (Melbinger et al., 2010) when simulations are initiated from a small population size - In the early transient period,  $N_K(t)$  is small, and the biasing effect of differential turnover rates is stronger, thus favouring cooperation. More generally, selection for reduced turnover rate could explain why cooperation often persists for a long time in finite population IbMs (and the real world) despite infinite population models predicting their extinction. The fact that the entire term is multiplied by  $(KN_K(t))^{-1}$

suggests that the effect of this force is weak for medium to large populations, which explains why the persistence of cooperators is often only observed in restrictive sounding conditions such as quasi-neutrality, rapid attraction to a slow manifold, or a weak selection + weak mutation limit. In all three of these cases, the first term on the RHS of (3.40) becomes identically 0. It therefore no longer contributes to the total dynamics and allows us to see the contributions of the second term.

If the population is large (but finite) and the stochasticity is sufficiently weak, stochastic dynamics can be studied analytically using the weak noise approximation. Usually, this approximation is valid if we are studying a stochastic trajectory that is fluctuating about a point that is stable in the deterministic limit (Van Kampen, 1981). Such situations occur often, since many systems of the forms studied here quickly relax to stable equilibria.



# Chapter 7

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## Towards a stochastic evolutionary theory

Not only is algebraic reasoning exact; it imposes an exactness on the verbal postulates made before algebra can start which is usually lacking in the first verbal formulations of scientific principles.

---

J.B.S. Haldane

One striking feature that repeatedly shows up in our derivations is that finite populations exhibit phenomena that are not visible in infinite population models. Stochastic systems exhibit many interesting and biologically relevant phenomena which cannot be captured in the deterministic limit. For example, in both the stochastic logistic equation 5.1 and in two-strategy games with finite population sizes (Tao and Cressman, 2007), demographic noise ensures that all populations are guaranteed to go extinct given enough time, even if the deterministic limit predicts a stable state far from extinction. In the case of quantitative traits, demographic noise can hinder adaptive diversification by increasing the time before evolutionary branching occurs (Claessen, Andersson, Persson, and A.M.d. Roos, 2007; Wakano and Iwasa, 2013; Débarre and Otto, 2016), causing stochastic extinction of existing evolutionary branches (Rogers, McKane, and Rossberg, 2012; Johansson and Ripa,

2006), or preventing branching altogether if the population is too small (Rogers and McKane, 2015; Johnson et al., 2021). Stochastic systems also routinely exhibit evolution towards attractors that cannot be attained in the deterministic limit (DeLong and Cressler, 2023), sometimes even completely reversing the direction of evolution predicted by deterministic dynamics (Constable, Rogers, et al., 2016; McLeod and Day, 2019). Since real-life populations are stochastic and finite, it is thus imperative that modellers work with stochastic first-principles models instead of their deterministic limits, lest they risk missing important phenomena that are unique to stochastic systems (Black and McKane, 2012; Schreiber et al., 2022; Hastings, 2004; Shoemaker et al., 2020). In the context of our models, we have seen that if we observe the change in trait frequencies instead of the change in densities, finite populations are subject to an additional evolutionary force that vanishes in infinite population models.

# Appendix A

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## Deriving the Fokker-Planck equations for Itô SDEs

Here, I present a simple (informal) derivation of the Fokker-Planck equation (FPE) for a one-dimensional Itô process. The result for the multi-dimensional case follows from the same logic but is more notationally cumbersome.

Consider a one-dimensional real Itô process given by  $dX_t = \mu(X_t, t)dt + \sigma(X_t, t)dB_t$  on a filtered probability space  $\Omega \subseteq \mathbb{R}$  with probability measure  $\mathbb{P}$  such that  $\mathbb{P}(\cdot) \equiv 0$  on  $\partial\Omega$  and  $\mathbb{P} \ll m$ , where  $m$  is the Lebesgue measure. The latter requirement allows us to use the Radon-Nikodym theorem to write  $\int \cdot d\mathbb{P} = \int \cdot P(x, t)dx$ , where  $P(x, t)$  is a ‘probability density function’ defined at every point in  $\Omega \times [0, \infty)$ . Now, Let  $f : \mathbb{R} \rightarrow \mathbb{R}$  be an arbitrary  $C^2(\mathbb{R})$  function. By Itô’s lemma, we have:

$$df(X_t) = f'dX_t + \frac{1}{2}f''d\langle X \rangle_t$$

where  $\langle \cdot \rangle$  denotes the quadratic variation. For  $dX_t = \mu dt + \sigma dB_t$ , it is clear that  $d\langle X \rangle_t = \sigma^2 d\langle B \rangle_t = \sigma^2 dt$ , and thus, we obtain:

$$df(X_t) = \left( \mu f' + \frac{\sigma^2}{2} f'' \right) dt + \sigma f' dB_t$$

Writing this in integral form and taking expectations on both sides yields:

$$\mathbb{E}[f(X_t)] = \mathbb{E} \left[ \int_0^t \left( \mu f' + \frac{\sigma^2}{2} f'' \right) ds \right] + \mathbb{E} \left[ \int_0^t \sigma f' dB_s \right] \quad (\text{A.1})$$

Since the Brownian motion is a martingale, as long as  $X_t$  and  $\sigma(X_t, t)$  are reasonably ‘nice’<sup>1</sup>, the stochastic integral in the second term of the RHS of (A.1) will be a continuous  $L^2(\mathbb{P})$  martingale starting at the origin, and its expectation will therefore be 0. Using the definition of the expectation value, we are thus left with:

$$\int_{\Omega} f(X_t) P(x, t) dx = \int_{\Omega} \left( \int_0^t \mu f' + \frac{\sigma^2}{2} f'' ds \right) P(x, t) dx$$

Assuming derivatives and expectations commute, we can now differentiate with respect to time on both sides and use the fundamental theorem of calculus to write

$$\int_{\Omega} f(X_t) \frac{\partial P}{\partial t}(x, t) dx = \underbrace{\int_{\Omega} \mu f' P(x, t) dx}_{I(x, t)} + \underbrace{\int_{\Omega} \frac{\sigma^2}{2} f'' P(x, t) dx}_{J(x, t)} \quad (\text{A.2})$$

We will now use integration by parts to further evaluate  $I(x, t)$  and  $J(x, t)$ . Recall that the general formula for integration by parts is given by:

$$\int_{\Omega} u_{x_i} v dx = - \int_{\Omega} uv_{x_i} dx + \int_{\partial\Omega} uv \gamma_i dS(x)$$

where subscript indicates differentiation and  $\gamma$  is the unit outward normal. In our case, assuming that  $P(x, t) \equiv 0$  on  $\partial\Omega$ , the boundary term (second term of the RHS) vanishes and we can use integration by parts once on  $I(x, t)$  to obtain

$$I(x, t) = - \int_{\Omega} f(X_t) \left( \frac{\partial}{\partial x} \mu P(x, t) \right) dx \quad (\text{A.3})$$

---

<sup>1</sup>We require  $\sigma(X_t, t)f'(X_t) \in \mathcal{L}^*(B)$ , which is a highly technical condition. Since existence/uniqueness of solutions for the SDE already requires Lipschitz continuity of  $\sigma(X_t, t)$ , this seems like a reasonable assumption to make.

and twice on  $J(x, t)$  to obtain

$$\begin{aligned} J(x, t) &= -\frac{1}{2} \int_{\Omega} f'(X_t) \left( \frac{\partial}{\partial x} \sigma^2 P(x, t) \right) dx \\ &= \frac{1}{2} \int_{\Omega} f(X_t) \left( \frac{\partial^2}{\partial x^2} \sigma^2 P(x, t) \right) dx \end{aligned} \quad (\text{A.4})$$

Substituting (A.3) and (A.4) into (A.2) and collecting terms yields

$$\int_{\Omega} f(X_t) \frac{\partial P}{\partial t}(x, t) dx = \int_{\Omega} f(X_t) \left[ -\frac{\partial}{\partial x} (\mu P(x, t)) + \frac{1}{2} \frac{\partial^2}{\partial x^2} (\sigma^2 P(x, t)) \right] dx$$

Since this is true for an arbitrary choice of  $f(x)$  (as long as  $f$  is  $C^2$ ), we are thus led to conclude that the density function  $P(x, t)$  must satisfy:

$$\frac{\partial P}{\partial t}(x, t) = -\frac{\partial}{\partial x} (\mu(x, t)P(x, t)) + \frac{1}{2} \frac{\partial^2}{\partial x^2} ((\sigma(x, t))^2 P(x, t)) \quad (\text{A.5})$$

Equation (A.5) is the Fokker-Planck equation in one dimension. Using the exact same strategy, the multidimensional Fokker-Planck equation for the  $n$  dimensional Itô Process  $d\mathbf{X}_t = \mu(\mathbf{X}_t, t)dt + \sigma(\mathbf{X}_t, t)dB_t$  is found to be:

$$\frac{\partial P}{\partial t}(\mathbf{x}, t) = -\sum_{i=1}^n \frac{\partial}{\partial x_i} (\mu_i(\mathbf{x}, t)P(\mathbf{x}, t)) + \frac{1}{2} \sum_{i=1}^n \sum_{j=1}^n \frac{\partial^2}{\partial x_i \partial x_j} (D_{ij}P(\mathbf{x}, t)) \quad (\text{A.6})$$

where  $\mathbf{D} = \sigma\sigma^T$ .



## Appendix B

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# Deriving stochastic trait frequency dynamics using Itô's formula

We first recall the version of the multi-dimensional Itô's formula that will be relevant to us. Consider an  $m$ -dimensional real Itô process  $\mathbf{X}_t$  given by the solution to

$$d\mathbf{X}_t = \boldsymbol{\mu}(\mathbf{X}_t)dt + \boldsymbol{\sigma}(\mathbf{X}_t)d\mathbf{B}_t$$

where  $\boldsymbol{\mu} : \mathbb{R}^m \rightarrow \mathbb{R}^m$  is the ‘drift vector’ and  $\boldsymbol{\sigma} : \mathbb{R}^m \rightarrow \mathbb{R}^{m \times m}$  is the ‘diffusion matrix’. Let  $f : \mathbb{R}^m \rightarrow \mathbb{R}$  be an arbitrary  $C^2(\mathbb{R}^m)$  function. Then, Itô’s formula (Øksendal, 1998, Section 4.2) states that the stochastic process  $f(\mathbf{X}_t)$  must satisfy:

$$df(\mathbf{X}_t) = \left[ (\nabla_{\mathbf{X}}f)^T \boldsymbol{\mu} + \frac{1}{2} \text{Tr}[\boldsymbol{\sigma}^T (H_{\mathbf{X}}f) \boldsymbol{\sigma}] \right] dt + (\nabla_{\mathbf{X}}f)^T \boldsymbol{\sigma} d\mathbf{B}_t \quad (\text{B.1})$$

where  $\text{Tr}[\cdot]$  denotes the trace of a matrix,  $(\cdot)^T$  denotes the transpose, and we have suppressed the  $\mathbf{X}_t$  dependence of  $\boldsymbol{\mu}$  and  $\boldsymbol{\sigma}$  to reduce clutter. Here,  $\nabla_{\mathbf{X}}f$  is the  $m$  dimensional *gradient vector* of  $f$  and  $H_{\mathbf{X}}f$  is the  $m \times m$  *Hessian matrix* of  $f$ , respectively defined for  $f(x_1, \dots, x_m)$  as:

$$\begin{aligned} (\nabla_{\mathbf{x}}f)_j &= \frac{\partial f}{\partial x_j} \\ (H_{\mathbf{x}}f)_{jk} &= \frac{\partial^2 f}{\partial x_j \partial x_k} \end{aligned}$$

In our case, we have the Itô process given by (3.31), which defines how the density of each type of individual changes over time. We thus have  $\boldsymbol{\mu}(\mathbf{X}_t) = \mathbf{A}^-(\mathbf{X}_t)$  and  $\boldsymbol{\sigma}(\mathbf{X}_t) = \mathbf{D}(\mathbf{X}_t)/\sqrt{K}$ . For each fixed  $i \in \{1, 2, \dots, m\}$ , let us define a scalar function  $f_i : \mathbb{R}^m \rightarrow \mathbb{R}$  as

$$f_i(\mathbf{x}) = \frac{x_i}{\sum_{j=1}^m x_j}$$

Thus,  $f_i(\mathbf{X}_t)$  gives us the frequency of type  $i$  individuals when the population is described by the vector  $\mathbf{X}_t$ . This function is obviously  $C^2(\mathbb{R}^m)$ , and we can thus use Itô's formula (B.1) to describe how it changes over time. The  $j^{\text{th}}$  element of the gradient of  $f_i$  is given by:

$$\begin{aligned} (\nabla_{\mathbf{x}} f_i)_j &= \frac{\partial}{\partial x_j} \left( \frac{x_i}{\sum_{k=1}^m x_k} \right) \\ &= \left( \frac{1}{N} \frac{\partial x_i}{\partial x_j} - \frac{x_i}{N^2} \sum_{k=1}^m \frac{\partial x_k}{\partial x_j} \right) \\ &= \frac{1}{N} (\delta_{ij} - p_i) \end{aligned} \tag{B.2}$$

where we have defined the total (scaled) population size<sup>1</sup>  $N = \sum_i x_i$  and the frequency of the  $i^{\text{th}}$  type  $p_i = f_i(x)$  and used the fact that  $\frac{\partial x_j}{\partial x_k} = \delta_{jk}$ . The  $jk^{\text{th}}$  element of the Hessian is given by:

$$\begin{aligned} (H_{\mathbf{x}} f_i)_{jk} &= \frac{\partial^2}{\partial x_j \partial x_k} \left( \frac{x_i}{\sum_{l=1}^m x_l} \right) \\ &= \frac{\partial}{\partial x_j} \left( \frac{\delta_{ik}}{N} - \frac{x_i}{N^2} \right) \\ &= \frac{1}{N^2} (2p_i - \delta_{ij} - \delta_{ik}) \end{aligned} \tag{B.3}$$

Thus, for the first term of (B.1), we have:

$$(\nabla_{\mathbf{x}} f_i)^T \mathbf{A}^- = \sum_{j=1}^m ((\nabla_{\mathbf{x}} f_i)_j) A_j^-$$

---

<sup>1</sup>This is  $N_K(t)$  in the main text, but we omit the subscript here to reduce notational clutter

$$\begin{aligned}
&= \frac{1}{N} \sum_{j=1}^m (\delta_{ij} - p_i) A_j^- \\
&= \frac{1}{N} \left( A_i^- - p_i \sum_{j=1}^m A_j^- \right)
\end{aligned} \tag{B.4}$$

If the birth and death rates take the form of (3.33), then it is easy to see using (3.34) that equation (B.4) is exactly the RHS of (3.37). Thus, when the birth and death rates take the form of (3.33), then (B.4) describes the deterministic component of the dynamics as described by the replicator-mutator equation, Price equation, etc. in the infinite population limit. These are the effects of selection and mutation at the infinite population limit. However, the finiteness of the population adds a second term to these dynamics, described by the second term that multiplies  $dt$  in (B.1). To calculate it, we first calculate:

$$\frac{1}{\sqrt{K}} (H_{\mathbf{x}} f_i \mathbf{D})_{jk} = \frac{1}{\sqrt{K}} \sum_{l=1}^m (H_{\mathbf{x}} f_i)_{jl} (\mathbf{D})_{lk}$$

$$= \frac{1}{\sqrt{K} N^2} \sum_{l=1}^m (2p_i - \delta_{ij} - \delta_{il}) \delta_{lk} (A_l^+ A_k^+)^{\frac{1}{4}} \tag{B.5}$$

$$= \frac{1}{\sqrt{K} N^2} \left( (2p_i - \delta_{ij}) (A_k^+)^{\frac{1}{2}} - \delta_{ik} (A_i^+ A_k^+)^{\frac{1}{4}} \right) \tag{B.6}$$

$$= \frac{1}{\sqrt{K} N^2} (2p_i - \delta_{ij} - \delta_{ik}) (A_k^+)^{\frac{1}{2}} \tag{B.7}$$

and thus:

$$\begin{aligned}
\frac{1}{K} (\mathbf{D}^T H_{\mathbf{x}} f_i \mathbf{D})_{lk} &= \frac{1}{K} \sum_{j=1}^m (\mathbf{D}^T)_{lj} (H_{\mathbf{x}} f_i \mathbf{D})_{jk} \\
&= \frac{1}{KN^2} \sum_{j=1}^m \delta_{lj} (A_l^+ A_j^+)^{\frac{1}{4}} (A_k^+)^{\frac{1}{2}} (2p_i - \delta_{ij} - \delta_{ik})
\end{aligned} \tag{B.8}$$

$$= \frac{1}{KN^2} (A_k^+)^{\frac{1}{2}} \left( 2p_i (A_l^+)^{\frac{1}{2}} - (A_i^+)^{\frac{1}{2}} \delta_{il} - (A_l^+)^{\frac{1}{2}} \delta_{ik} \right) \tag{B.9}$$

Using this, we see that the trace of this matrix is given by:

$$\frac{1}{K} \text{Tr}[\mathbf{D}^T H_{\mathbf{x}} f_i \mathbf{D}] = \frac{1}{K} \sum_{k=1}^m (\mathbf{D}^T H_{\mathbf{x}} f_i \mathbf{D})_{kk}$$

$$= \frac{1}{KN^2} \sum_{k=1}^m \left( 2p_i (A_k^+ A_k^+)^{\frac{1}{2}} - (A_i^+ A_k^+)^{\frac{1}{2}} \delta_{ik} - (A_k^+ A_k^+)^{\frac{1}{2}} \delta_{ik} \right) \quad (\text{B.10})$$

$$= \frac{1}{KN^2} \left( 2p_i \left( \sum_{k=1}^m A_k^+ \right) - 2A_i^+ \right) \quad (\text{B.11})$$

and thus, the second term multiplying  $dt$  in (B.1) is given by:

$$\frac{1}{2K} \text{Tr}[\mathbf{D}^T H_{\mathbf{x}} f_i \mathbf{D}] = \frac{-1}{KN^2} \left( A_i^+ - p_i \left( \sum_{k=1}^m A_k^+ \right) \right) \quad (\text{B.12})$$

Finally, denoting  $d\mathbf{B}_t = [dB_t^{(1)}, dB_t^{(2)}, \dots, dB_t^{(m)}]^T$  where each  $dB_t^{(j)}$  is an independent one dimensional Wiener process, we have:

$$\begin{aligned} (\mathbf{D} d\mathbf{B}_t)_j &= \sum_{k=1}^m \mathbf{D}_{jk} dB_t^{(k)} \\ &= \sum_{k=1}^m \delta_{jk} (A_j^+ A_k^+)^{\frac{1}{4}} dB_t^{(k)} \end{aligned} \quad (\text{B.13})$$

$$= (A_j^+)^{1/2} dB_t^{(j)} \quad (\text{B.14})$$

Thus, using (B.2), we see that the last term on the RHS of (B.1) is given by

$$\begin{aligned} \frac{1}{\sqrt{K}} (\nabla_{\mathbf{x}} f)^T \mathbf{D} d\mathbf{B}_t &= \frac{1}{\sqrt{K}} \sum_{j=1}^m (\nabla_{\mathbf{x}} f_i)_j (\mathbf{D} d\mathbf{B}_t)_j \\ &= \frac{1}{N\sqrt{K}} \sum_{j=1}^m (\delta_{ij} - p_i) (A_j^+)^{1/2} dB_t^{(j)} \end{aligned} \quad (\text{B.15})$$

$$= \frac{1}{N\sqrt{K}} (A_i^+)^{1/2} dB_t^{(i)} - p_i \sum_{j=1}^m (A_j^+)^{1/2} dB_t^{(j)} \quad (\text{B.16})$$

Putting equations (B.4), (B.12) and (B.16) into (B.1), we see that  $p_i = f_i(\mathbf{X})_t$ , the frequency of the  $i^{\text{th}}$  type in the population  $\mathbf{X}_t$ , changes according to the equation:

$$\begin{aligned} N(t) dp_i &= \left( A_i^- - p_i \sum_{j=1}^m A_j^- \right) dt - \frac{1}{K} \frac{1}{N(t)} \left( A_i^+ - p_i \left( \sum_{k=1}^m A_k^+ \right) \right) dt \\ &\quad + \frac{1}{\sqrt{K}} \left[ (A_i^+)^{1/2} dB_t^{(i)} - p_i \sum_{j=1}^m (A_j^+)^{1/2} dB_t^{(j)} \right] \end{aligned} \quad (\text{B.17})$$

Substituting the functional forms given by (3.33) and repeating calculations for the  $A_i^+$  terms exactly analogous to those done in going from (3.37) to (3.38) now yields equation (3.40) in the main text.



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