

Eco-evolutionary dynamics of finite populations from first principles

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Ananda Shikhara Bhat



Indian Institute of Science Education and Research Pune

Dr. Homi Bhabha Road,

Pashan, Pune 411008, INDIA.

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Supervisor: Vishwesha Guttal

Co-supervisor: Rohini Balakrishnan

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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.

Vishwesha Guttal

Rohini Balakrishnan

Committee:

Vishwesha Guttal

Rohini Balakrishnan

Sutirth Dey

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

Vishwesha Guttal

Rohini Balakrishnan

Acknowledgments

Not more than 250 words

Abstract

Population biology is built on a strong mathematical foundation developed during the Modern Synthesis through fields such as theoretical population genetics, evolutionary game theory, and quantitative genetics. Historically, these formalisms have often worked with infinite populations, ignoring the effects of demographic stochasticity. Finite population models in population genetics usually assume a fixed population size and are of limited applicability in the real world, where population sizes routinely fluctuate. In this thesis, I use ideas from statistical physics to analytically describe evolving populations from biological first principles. Starting from a density-dependent ‘birth-death process’ describing an arbitrary closed population of individuals with discrete traits, I derive a set of stochastic differential equations (SDEs) for how trait frequencies change over time. Along with recovering the effects of the standard evolutionary forces of selection, mutation, and drift, these SDEs also reveal a new directional evolutionary force, ‘noise-induced selection’, that is particular to finite populations and has been largely overlooked in standard formulations of evolution. Noise-induced selection can reverse the direction of evolution predicted by infinite-population frameworks, with implications for simulation studies and real world populations. Well-known results such as the replicator-mutator equation and Fisher’s fundamental theorem are recovered in the infinite population limit. Finally, I extend these ideas to one-dimensional quantitative traits through a ‘stochastic field theory’ that yields frameworks such as Kimura’s continuum-of-alleles and gradient dynamics in the infinite population limit. My work thus generalizes the formal structures of population biology to finite fluctuating populations and predicts a new evolutionary force unique to such populations.

Contents

Front Matter	i
Contents	xvi
List of Tables	1
List of Figures	4
I Background	5
1 Introduction	7
1.1 Idealization and generality in ecology	8
1.2 A (very, very) brief history of high-level modelling frameworks in population biology	9
1.3 Outline of the rest of this thesis	12

II Theory	15
2 Population dynamics from stochastic first principles	17
2.1 Mathematical Background	17
2.1.1 Birth-death processes	18
2.1.2 SDEs and the Fokker-Planck equation	18
2.1.3 Density-dependence and the intuition for system-size expansions in ecology	22
2.1.4 The intuition for the weak noise approximation in ecology	23
2.2 Warm up: One-dimensional processes for population size	24
2.2.1 Description of the process and the Master Equation	24
2.2.2 The system-size expansion	27
2.2.3 Stochastic fluctuations and the weak noise approximation	28
2.3 Multi-dimensional processes for discrete traits	32
2.3.1 Description of the process and the Master Equation	32
2.3.2 The system-size expansion	34
2.3.3 Functional forms of the birth and death rates	35
2.3.4 Statistical measures for population-level quantities	36
2.3.5 Stochastic Trait Frequency Dynamics	37
2.3.6 The infinite population limit	38
2.3.7 Stochastic fluctuations and the weak noise approximation	40
3 Stochastic field equations for the evolution of quantitative traits	45
3.1 Description of the process and the Master Equation	47
3.2 The functional system-size expansion	50

3.3	The infinite population limit	52
3.4	Stochastic trait frequency dynamics in the infinite-dimensional case	59
3.5	Stochastic fluctuations and the weak noise approximation	59
III	Major Takeaways & Discussion	63
4	A unified view of population dynamics	65
4.1	Fundamental theorems of evolution in finite population	67
4.1.1	The fundamental theorem for changes in type frequencies in the population	67
4.1.2	The fundamental theorem for the mean value of a type-level quantity in the population	68
4.1.3	The fundamental theorem for the variance of a type-level quantity in the population	72
4.2	A stochastic field theory for quantitative traits	75
4.3	Discussion & Outlook	79
Appendices		85
A	Deriving the Fokker-Planck equations for Itô SDEs	85
B	Deriving stochastic trait frequency dynamics using Itô’s formula	89
C	A Price-like equation for the variance of a type-level quantity	95
D	Some Examples	101
D.1	An example in one dimension: The stochastic logistic equation	101

D.2 An example for discrete traits: Lotka-Volterra and matrix games in finite populations	104
D.3 Interlude: Detecting modes in quantitative trait distribution through Fourier analysis	108
D.4 An example for quantitative traits: The quantitative logistic equation	113
References	138

List of Tables

4.1 Summary of the various birth-death processes studied in this thesis	66
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List of Figures

2.1	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.	26
2.2	Schematic description of a one-dimensional birth-death process. (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.	33
3.1	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.	48

D.1 Comparison of a single realization of the exact birth-death process (D.1), the deterministic trajectory (D.3), the non-linear Fokker-Planck equation (D.2), and the weak noise approximation (D.5) for (A) $K = 500$, (B) $K = 1000$, and (C) $K = 10000$. $\lambda = 2, \mu = 1$ for all thee cases.	103
D.2 Comparison of the steady-state densities given by (D.1), (D.2), and (D.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.	104
D.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) ϕ_k . In the Fourier dual space, we can look at the peaks of each of these Fourier modes: The magnitude of ϕ_k tells us how much it contributes to the actual function of interest ϕ	109
D.4 Effect of population size on evolutionary branching. Two different realizations of the system (3.2) with $n(x) = \exp((x^2)/\sigma_K^2)$. Simulation parameters are $\sigma_K = 1.9, \sigma_\alpha = 0.7, \sigma_m^2 = 0.05$ for top: $K = 1000$ and bottom: $K = 10000$. Each point represents an individual. Note that the model on top remains monomorphic whereas the model on the bottom exhibits evolutionary branching, where an initially monomorphic population evolves to become dimorphic.	114

Part I

Background

Chapter 1

Introduction

The theory of evolution by natural selection is an ecological theory—founded on ecological observation by perhaps the greatest of all ecologists. It has been adopted by and brought up by the science of genetics, and ecologists, being modest people, are apt to forget their distinguished parenthood

John Harper

More than 150 years have passed since Charles Darwin first published *Origin* (in 1859) and Ernst Haeckel first coined the term ‘ecology’ (in 1866). Today, both ecology and evolution are incredibly interdisciplinary fields, borrowing techniques and ideas from diverse areas such as computer science, statistics, economics, dynamical systems, physics, and information theory. With this development has come a cornucopia of models that try to understand biological phenomena in the language of these borrowed tools and techniques. Though many of these ideas are used to accurately describe and analyze specific systems, there is also value to formulating general models in abstract terms that only incorporate a small number of ‘fundamental’ processes and try to capture the ‘essence’ of a biological pattern (Frank, 2012; Vellend, 2016; Luque and Baravalle, 2021). Such general organizing models are vital

to theory-building (Luque and Baravalle, 2021) because they help clarify conceptual similarities and unifying factors between apparently disparate modelling frameworks, helping us seamlessly translate essential ideas from one theoretical language to another.

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) and evolution (Provine, 2001). 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. Some philosophers of science have recently argued that “the epistemic goal of science is not truth, but understanding” (Potochnik, 2018). 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 too general and may seem to ignore many biological details. 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, formulating such (blurry-eyed) general organizing frameworks can be greatly beneficial as an aid to thinking. In biology, arguably the greatest such general organizing framework was the idea of evolution by natural selection as synthesized from myriad detailed observations by Charles Darwin. Theoretical population genetics has also had a long-standing tradition in building general organizing frameworks that ‘abstract away’ some biological details but are ‘general’ in the sense of capturing broad features of biological systems (as opposed to the mathematician’s notion of ‘general’ in sense of always being true).

1.2 A (very, very) brief history of high-level modelling frameworks in population biology

In population genetics, the relevant high-level forces are the standard evolutionary forces of natural selection, genetic drift, dispersal, and mutation. The description of evolution in terms of these forces was first laid out in formal mathematical terms during the Modern Synthesis by authors such as Wright, Fisher, and Haldane, an extremely successful venture

that unified two major schools of thought — Mendelian genetics and Darwinian evolution — that were, at the time, thought to be incompatible (Provine, 2001).

Formal models in classical population genetics often regarded forces like selection and mutation as fundamental, and the success of this approach during the Modern Synthesis illustrates the value of formulating high-level, abstract models that only provide a ‘high-level’ description of the fundamental processes required to capture the essence of a biological pattern. However, this evolutionary play famously unfolds in the ecological theatre (Hutchinson, 1965). Thus, quantities like fitness are not truly fundamental but instead emerge as the net result of various ecological interactions, tradeoffs, and constraints (Metz et al., 1992), a fact that can have important consequences for evolution (Coulson et al., 2006; Kokko et al., 2017). Trying to understand such ‘eco-evolutionary dynamics’ has sprouted a rich body of theoretical literature under the broad heading of ‘evolutionary ecology’ and led to the development of theoretical frameworks like evolutionary game theory and adaptive dynamics, fields which have greatly enriched our understanding of biological populations (Brown, 2016). Eco-evolutionary population dynamics can (very) broadly be organized under a single unifying framework, the Price equation, that yields all the relevant formal structures (such as evolutionary game theory and classic population genetics) as special cases (Page and Nowak, 2002; Queller, 2017; Lion, 2018). The Price equation partitions changes in population composition into multiple terms, each of which lends itself to a straightforward interpretation in terms of the high-level evolutionary forces of selection, mutation, and drift, thus providing a useful conceptual framework for thinking about how populations change over time (Frank, 2012). The Price equation also leads to a small number of simple yet insightful ‘fundamental theorems’ of population biology (Queller, 2017; Lion, 2018; Lehtonen, 2018) and unifies several various seemingly disjoint formal structures under a single theoretical banner (Lehtonen, 2020; Luque and Baravalle, 2021)

One of the general guiding principles of much of this mathematization has been the assumption that incorporating the reality of finite population sizes into models leads to no major qualitative differences in behavior, only ‘adding noise’ or ‘blurring out’ the predictions of simpler infinite population models (Page and Nowak, 2002). Consequently, several major theoretical frameworks in the field, such as adaptive dynamics, are explicitly formulated in deterministic terms at the infinite population size limit. However, this assumption is largely unjustified, and since populations in the real world are finite and stochastic, checking whether stochastic models differ from their deterministic analogs is vital to furthering our

understanding of the fundamentals of population biology (Hastings, 2004; Coulson et al., 2004; Shoemaker et al., 2020). Today, we increasingly recognize that incorporating the finite and stochastic nature of the real world routinely has much stronger consequences than simply ‘adding noise’ to deterministic expectations (Boettiger, 2018), with important consequences for both ecological (Schreiber et al., 2022) and evolutionary (DeLong and Cressler, 2023) theory. In ecology and evolution, stochastic models often do not exhibit phenomena that occur in deterministic models (Proulx and Day, 2005; Johansson and Ripa, 2006; Claessen et al., 2007; Wakano and Iwasa, 2013; Débarre and Otto, 2016; B. Johnson et al., 2021), exhibit phenomena that do not occur in deterministic models (Rogers et al., 2012a; Rogers et al., 2012b; Rogers and McKane, 2015; Veller et al., 2017; DeLong and Cressler, 2023), and can even completely reverse the predictions of deterministic models (Houchmandzadeh and Vallade, 2012; Houchmandzadeh, 2015; Constable et al., 2016; McLeod and Day, 2019). Studies of neutral or near-neutral dynamics in population and quantitative genetics usually do take stochasticity seriously, explicitly modeling finite populations that follow stochastic dynamics. Unfortunately, the classic or standard stochastic models in both population genetics (Fisher, 1930; S. Wright, 1931; Moran, 1958; Kimura, 1964) and quantitative genetics (Crow and Kimura, 1970; Lande, 1976) typically assume a fixed total population size and their validity is therefore rather restrictive since population sizes routinely fluctuate in the real world. Importantly, the Price equation itself is usually formulated in a deterministic, dynamically-insufficient manner (but see Rice, 2008 for a stochastic formulation of the Price equation). Since real-life populations are stochastic, finite, and of non-constant population size, it is thus imperative that we develop a theoretical framework that can handle such systems directly, instead of only working with deterministic, infinite-population approximations.

Incorporating stochasticity into deterministic systems is a tricky business, and, if done in a phenomenological manner by adding noise to a ‘deterministic skeleton’ (Coulson et al., 2004) in an ad-hoc fashion, can lead to nonsensical predictions and inconsistencies (Strang et al., 2019). Stochastic individual-based models, in which (probabilistic) rules are specified at the level of the individual and population level dynamics are systematically derived from first principles, are self-consistent (Strang et al., 2019), much more natural (Black and McKane, 2012), and can fundamentally differ from the predictions made by simply adding noise terms to a deterministic model (Strang et al., 2019). Formulating the fundamental formal structures of evolutionary biology in terms of the mechanistic demographic processes of birth and death at the individual level is also greatly desirable for biological reasons (Met-

calf and Pavard, 2007a; Geritz and Kisdi, 2012) because ‘all paths to fitness lead through demography’ (Metcalf and Pavard, 2007b). In other words, since demographic processes such as birth and death rates explicitly account for the ecology of the system, they can more accurately reflect the complex interplay between ecological and evolutionary processes and provide a more fundamental mechanistic description of the relevant evolutionary forces and population dynamics (Doebeli et al., 2017).

1.3 Outline of the rest of this thesis

In this thesis, I present a formulation of population dynamics constructed from mechanistic first principles grounded in individual-level birth and death. Part II presents the mathematical formalism in a detailed, self-contained, pedagogical manner.

Chapter 2 deals with the evolution of discrete traits. In this case, the system is finite-dimensional, since we can completely specify the state of the system by simply listing out the number of individuals of each type in a vector. To facilitate readership by a broad audience, I only assume passing familiarity with calculus (derivatives, integrals, Taylor expansions) and probability. Familiarity with stochastic calculus is helpful for some sections but is not required. I present a brief introduction to the relevant mathematics in section 2.1 and present a toy example of tracking population size of a population of identical individuals in section 2.2. 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, thus illustrating all the major tools required. In section 2.3, I present a multivariate process to describe the evolution of discretely varying traits, and, as before, use the system size expansion to arrive at a continuous description of change in trait frequencies as an SDE under mild assumptions on the functional forms of the birth and death rates. Unlike many classic stochastic formulations in evolutionary theory (Fisher, 1930; S. Wright, 1931; Moran, 1958; Crow and Kimura, 1970; Lande, 1976), I do not assume a fixed (effective) population size and instead allow the total population size to fluctuate over time. I show that the deterministic limit of this process is the well-known replicator-mutator equation (or equivalently, the Price equation), thus establishing the microscopic basis of well-known equations from stochastic first principles. I also illustrate some general predictions that can be made using the weak noise approximation for the sake of

completeness. While the mathematics of section 2.3 is standard and well-understood, it has, to the best of my knowledge, not been used in this context in the generality we use here. Several specific models of specific systems do use these mathematical techniques, but these papers are often written assuming familiarity with notions in physics and/or mathematics and thus may not be very accessible to theoretical ecologists who do not have formal training in these subjects (but see Czuppon and Traulsen, 2021 for a recent pedagogical review on the general approach as applied to Wright-Fisher and Moran processes, where total population size is constant). As such, chapter 2 also serves as a tutorial and technical introduction to the major ideas - For ecologists, the chapter introduces ‘system size expansions’ and illustrates their use in a general setting, and can be seen as a tutorial on modelling finite populations analytically with minimal assumptions; For population geneticists, the chapter illustrates how system-size approximations (‘diffusion approximations’ in the population genetics literature) can be carried out without assuming a constant (effective) population size and how this generalization has important consequences for the evolutionary forces at play; For physicists and applied mathematicians, the chapter presents a study of the consequences of applying the system-size expansion to the kind of density-dependent birth-death processes that are widely applicable in ecology and evolution.

Chapter 3 introduces a function-valued process¹ to model the evolution of quantitative traits such as body size, which can take on uncountably many values. This function-valued process can then also be analyzed via an analog of the system-size approximation to arrive at a ‘functional’ Fokker-Planck equation in which derivatives are replaced by functional derivatives. I show that classic equations from quantitative genetics such as Kimura’s infinite alleles model and Lande’s gradient dynamics can be derived as the infinite population limit of this stochastic process. I also conduct a weak noise approximation to arrive at a linear functional Fokker-Planck equation that can be analyzed for specific systems as required. Unlike the systems studied in Chapter 2, formalizing the study of the kind of processes we study in Chapter 3 is an active area of mathematical research (Carmona and Rozovskii, 1999; Da Prato and Zabczyk, 2014; Prévôt and Röckner, 2007; Liu and Röckner, 2015; Bogachev et al., 2015; Balan, 2018) and the mathematics itself is far from settled. Chapter 3 generalizes the work of Tim Rogers and colleagues (Rogers et al., 2012a; Rogers et al., 2012b; Rogers and McKane, 2015), and to the best of my knowledge, has never been presented in full generality before. Mathematically, chapter 3 presents heuristic, accessible alternatives

¹This is really a measure-valued process but we will pretend we don’t know this in the interest of accessibility

to the rigorous tools of martingale theory and measure-valued branching processes that are usually employed to describe the evolution of quantitative traits (Champagnat et al., 2006; Etheridge, 2011; Week et al., 2021) by generalizing the idea of a system size expansion of density-dependent (finite-dimensional) birth-death processes to the infinite-dimensional case using the notion of functional differentiation. Biologically, Chapter 3 provides ‘stochastic field equations’ that describe the dynamics of one-dimensional quantitative traits in finite populations and illustrates that these equations are consistent with well-known formalisms in quantitative genetics at the infinite population limit. Some concrete models are presented as examples in Appendix D for clarity regarding the major ideas.

Part III summarizes the major results of our formalism and presents some simple equations that can be argued to be ‘fundamental theorems’ of population biology in the sense of Queller, 2017 or ‘unifying factors’ in the sense of Lion, 2018. These equations reduce to well-known results such as the Price equation, the replicator-mutator equation from evolutionary game theory, and Fisher’s fundamental theorem from population genetics in the infinite population limit. For finite populations, these same equations predict a new evolutionary force, ‘noise-induced selection’, that has still not found its way into the standard formal canon of evolutionary biology and whose significance is only recently being recognized (Constable et al., 2016; McLeod and Day, 2019; Mazzolini and Grilli, 2022; Kuosmanen et al., 2022). Implications of noise-induced selection are also discussed in part III. Readers who are averse to or do not care for mathematical details can safely skip part II entirely and directly read part III for the major takeaways of this thesis, though I strongly recommend working through the formalism properly if possible.

Part II

Theory

Chapter 2

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

Kenneth Boulding

2.1 Mathematical Background

Here, I provide a brief, informal introduction to basic notions in stochastic processes that will be helpful for some technical portions of this thesis. Interested readers looking for a more comprehensive source can refer to standard mathematics texts such as Øksendal, 1998 or Karatzas and Shreve, 1998 for a more rigorous treatment of the mathematical foundations, or physics-style texts such as Gardiner, 2009 or Van Kampen, 1981 for useful tools and techniques to study real systems.

2.1.1 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.

2.1.2 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

$$X_t = \int_0^t F(s, X_s) ds + \int_0^t G(s, X_s) dB_s \quad (2.1)$$

where $F(t, x)$ and $G(t, x)$ are ‘nice’ functions¹ 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:

- 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

¹For 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.

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 (2.1) is Itô's 'stochastic integral', and is to be interpreted in the following sense: Fix a time $T > 0$. For any $n \geq 2$, let $\Pi_n = \{t_1, t_2, \dots, t_n\}$ be a partition of the interval $[0, T]$. In other words, Π_n divides $[0, T]$ into n slices 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:

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

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 (2.1) is often represented in the compact form:

$$dX_t = F(t, X_t)dt + G(t, X_t)dB_t \quad (2.2)$$

. The physics literature also often uses the 'Langevin form':

$$\frac{dx}{dt} = F(t, x) + G(t, x)\eta(t) \quad (2.3)$$

where $\eta(t)$ is supposed to be 'Gaussian white noise', defined indirectly such that $\int_0^t G(s, x)\eta(s)ds$ behaves identically to $\int_0^t G(s, X_s)dB_s$. However, it is important to remember that these are both purely formal expressions - Equation (2.2) is meaningless on its own and is really just shorthand for equation (2.1), which is well-defined as explained above; Equation (2.3) 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 (2.1), 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 shown² that the stochastic integral also

²We 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

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 (2.2):

	dt	dB_t
dt	0	0
dB_t	0	dt

which becomes very useful for formal manipulation. One important consequence is that we can no longer rely on the normal rules of calculus when dealing with stochastic integrals. In regular calculus, if we had a quantity $x(t)$ satisfying $\dot{x} = f(x, t) + g(x, t)$ for two ‘nice’³ real functions f and g , then, given any function $h(x)$, we have the chain rule of differentiation, which says that

$$\frac{dh}{dt} = \frac{dh}{dx} \frac{dx}{dt} = h'(x)f(x) + h'(x)g(x)$$

i.e.

$$dh = h'(x)f(x)dt + h'(x)g(x)dt$$

Naively, we may expect the same logic to still hold true for one-dimensional Itô processes of the form (2.2) with gdt simply being replaced by GdB_t on the RHS. However, this does not work. The correct relation is instead given by *Itô’s formula*⁴:

$$dh(X_t) = h'(X_t)F(X_t)dt + h'(X_t)G(X_t)dB_t + \frac{h''(X_t)}{2}G^2(X_t)dt$$

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.

³We just need the solution $x(t)$ to be a continuous function

⁴Itô’s formula also additionally requires $h \in C^2(\mathbb{R})$, meaning that h is continuous and the first and second derivatives of h exist and are also continuous

Note that there is now an extra $h''(X_t)G^2(X_t)/2$ term that does not exist in the deterministic setting. In some sense, this term is present because the random fluctuations of Brownian motion are ‘too erratic’ and do not follow our deterministic intuitions. Using Itô’s formula and some simple algebra, one can then show that given any process X_t taking values in \mathbb{R} satisfying the SDE (2.2), the associated probability density $P(x, t)$ of finding the process in a state $x \in \mathbb{R}$ satisfies the PDE

$$\frac{\partial P}{\partial t}(x, t) = -\frac{\partial}{\partial x}\{F(t, x)P(x, t)\} + \frac{1}{2}\frac{\partial^2}{\partial x^2}\{(G(t, x))^2P(x, t)\} \quad (2.4)$$

I present a simple informal derivation in Appendix A for the sake of completeness. Equation (2.4) 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. As I explain in Appendix A, the Fokker-Planck equation can be viewed as a ‘conservation law’ for probability that mathematically expresses the common-sense observation that the sum (or integral) of probabilities over the entire state space cannot change over time (since it must always equal 1). If the function G is independent of x , it comes out of the derivatives in equation (2.4), 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 (2.4) corresponds to the solution of an SDE of the form (2.2), 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 (2.2) or as the solution to a Fokker-Planck equation of the form (2.4). System-size expansions facilitate such a description for birth-death processes.

2.1.3 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, where it goes by the name of the ‘diffusion approximation’ (Ewens, 2004) or ‘continuum limit’ (Czuppon and Traulsen, 2021), and has been heavily used by Kimura (Crow and Kimura, 1970) in his stochastic models. However, the population genetics version of the approximation usually either relies on total population size being fixed (Crow and Kimura, 1970; Lande, 1976; Ewens, 2004) or is conducted in an ad-hoc manner without specifying an explicit system size parameter (*i.e.* is closer to a Kramers-Moyal expansion than a Van Kampen expansion).

2.1.4 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.

2.2 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. I will use this toy system as an illustration of the techniques that will be used for the actual problems we intend to tackle in the next sections. The mathematics below are adapted from sections 6.3 and 7.2 of (Gardiner, 2009).

2.2.1 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 2.1). 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

$$b(n) := \lim_{\epsilon \rightarrow 0} \frac{1}{\epsilon} \mathbb{P}(N_{t+\epsilon} = n + 1 | N_t = n) \quad (2.5)$$

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

$$d(n) := \lim_{\epsilon \rightarrow 0} \frac{1}{\epsilon} \mathbb{P}(N_{t+\epsilon} = n - 1 | N_t = n) \quad (2.6)$$

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 μ 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.

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 $n - 1$

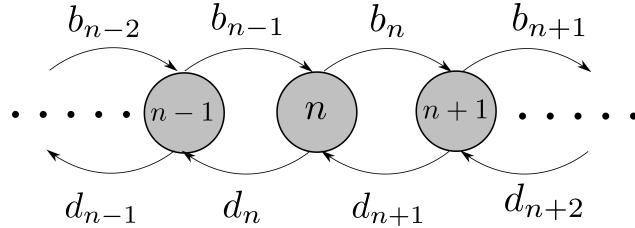


Figure 2.1: Schematic description of a one-dimensional birth-death process. Consider a population of identical individuals. The state of the system can be described by a single number, in this case, the population size. Births and deaths result in changes in the total population size, and the birth and death rates are dependent on the current population size.

individuals, with a birth rate of $b(n - 1)$. Thus, the rate of ‘inflow’ to the state n is given by

$$R_{\text{in}}(n, t) = b(n - 1)P(n - 1, t) + d(n + 1)P(n + 1, t) \quad (2.7)$$

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

$$R_{\text{out}}(n, t) = b(n)P(n, t) + d(n)P(n, t) \quad (2.8)$$

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

$$\begin{aligned} \frac{\partial P}{\partial t}(n, t) &= R_{\text{in}}(n, t) - R_{\text{out}}(n, t) \\ &= b(n - 1)P(n - 1, t) + d(n + 1)P(n + 1, t) - b(n)P(n, t) - d(n)P(n, t) \end{aligned} \quad (2.9)$$

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

$$\frac{\partial P}{\partial t}(n, t) = (\mathcal{E}^- - 1)b(n)P(n, t) + (\mathcal{E}^+ - 1)d(n)P(n, t) \quad (2.10)$$

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 (2.10) directly.

2.2.2 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 (2.10) becomes

$$\frac{\partial P}{\partial t}(x, t) = (\Delta^- - 1)Kb_K(x)P(x, t) + (\Delta^+ - 1)Kd_K(x)P(x, t) \quad (2.11)$$

where we now have the new step operators

$$\Delta^\pm f(x, t) = f\left(x \pm \frac{1}{K}, t\right) \quad (2.12)$$

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 (2.11) and neglecting terms of $\mathcal{O}(K^{-3})$ and higher, we obtain

$$\frac{\partial P}{\partial t}(x, t) = -\frac{\partial}{\partial x}\{A^-(x)P(x, t)\} + \frac{1}{2K}\frac{\partial^2}{\partial x^2}\{A^+(x)P(x, t)\} \quad (2.13)$$

where

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

Equation (2.13) has the form of a so-called ‘Fokker-Planck equation’, and corresponds to the SDE:

$$dX_t = A^-(X_t)dt + \sqrt{\frac{A^+(X_t)}{K}}dB_t \quad (2.14)$$

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} .

2.2.3 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 (2.14) describes a deterministic process, obtained as the solution to

$$\frac{dx}{dt} = A^-(x) = b_K(x) - d_K(x) \quad (2.15)$$

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 α 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:

$$y = \sqrt{K}(x - \alpha(t))$$

$$s = t$$

$$\tilde{P}(y, s) = \frac{1}{\sqrt{K}} P(x, t)$$

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

$$\begin{aligned} \frac{\partial \tilde{P}}{\partial t} &= \frac{\partial \tilde{P}}{\partial y} \frac{\partial y}{\partial t} + \frac{\partial \tilde{P}}{\partial s} \frac{\partial s}{\partial t} \\ &= \frac{\partial \tilde{P}}{\partial y} \left(-\sqrt{K} \frac{d\alpha}{dt} \right) + \frac{\partial \tilde{P}}{\partial s} \\ &= -\sqrt{K} A^-(\alpha(s)) \frac{\partial \tilde{P}}{\partial y} + \frac{\partial \tilde{P}}{\partial s} \end{aligned} \quad (2.16)$$

and

$$\frac{\partial}{\partial y} = \frac{1}{\sqrt{K}} \frac{\partial}{\partial x} \quad (2.17)$$

Reformulating (2.13) in terms of y, s and \tilde{P} and substituting (2.16) and (2.17) yields:

$$\begin{aligned} -A^-(\alpha) \frac{\partial \tilde{P}}{\partial x} + \frac{\partial \tilde{P}}{\partial s} &= -\sqrt{K} \frac{\partial}{\partial y} \left(A^-(\alpha + \frac{y}{\sqrt{K}}) \tilde{P} \right) + \frac{1}{2} \frac{\partial^2}{\partial y^2} \left(A^+(\alpha + \frac{y}{\sqrt{K}}) \tilde{P} \right) \\ \Rightarrow \frac{\partial \tilde{P}}{\partial s} &= -\frac{\partial}{\partial y} \left[\sqrt{K} \left(A^-(\alpha + \frac{y}{\sqrt{K}}) - A^-(\alpha) \right) \tilde{P} \right] + \frac{1}{2} \frac{\partial^2}{\partial y^2} \left(A^+(\alpha + \frac{y}{\sqrt{K}}) \tilde{P} \right) \end{aligned} \quad (2.18)$$

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 (2.18) to obtain:

$$\begin{aligned} \sum_{n=0}^{\infty} \left(\frac{1}{\sqrt{K}} \right)^n \frac{\partial \tilde{P}_n}{\partial s} &= -\frac{\partial}{\partial y} \left[\sqrt{K} \left(\sum_{n=1}^{\infty} A_n^-(s) \left(\frac{y}{\sqrt{K}} \right)^n \right) \left(\sum_{m=0}^{\infty} \tilde{P}_m \left(\frac{1}{\sqrt{K}} \right)^m \right) \right] \\ &\quad + \frac{1}{2} \frac{\partial^2}{\partial y^2} \left[\left(\sum_{n=0}^{\infty} A_n^+(s) \left(\frac{y}{\sqrt{K}} \right)^n \right) \left(\sum_{m=0}^{\infty} \tilde{P}_m \left(\frac{1}{\sqrt{K}} \right)^m \right) \right] \end{aligned} \quad (2.19)$$

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 (2.19) 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:

$$\frac{\partial \tilde{P}_r}{\partial s} = -\frac{\partial}{\partial y} \left(\sum_{m=0}^r \tilde{P}_m A_{r-m+1}^- y^{r-m+1} \right) + \frac{1}{2} \frac{\partial^2}{\partial y^2} \left(\sum_{m=0}^r \tilde{P}_m A_{r-m}^+ y^{r-m} \right) \quad (2.20)$$

If we assume we can obtain a reasonable approximation by retaining only the first term of the expansion and neglecting all higher-order terms⁵, we are left with the expression:

$$\frac{\partial \tilde{P}_0}{\partial s} = -A_1^-(s) \frac{\partial}{\partial y} (y \tilde{P}_0) + \frac{A_0^+(s)}{2} \frac{\partial^2 \tilde{P}_0}{\partial y^2} \quad (2.21)$$

⁵For example, if the deterministic trajectory is at a stable fixed point and subject to weak fluctuations

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

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

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

$$Y_t = Y_0 \exp\left(\int_0^t A_1^-(s)ds\right) + \int_0^t \exp\left(-\int_s^t A_1^-(v)dv\right) \sqrt{A^+(\alpha(s))} dB_s \quad (2.22)$$

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 (2.22) and using results presented in 2.1.2 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 (2.22) 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.

2.3 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.

2.3.1 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 2.2A). 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 2.2B). 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

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

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 $[v_1, \dots, v_i -$

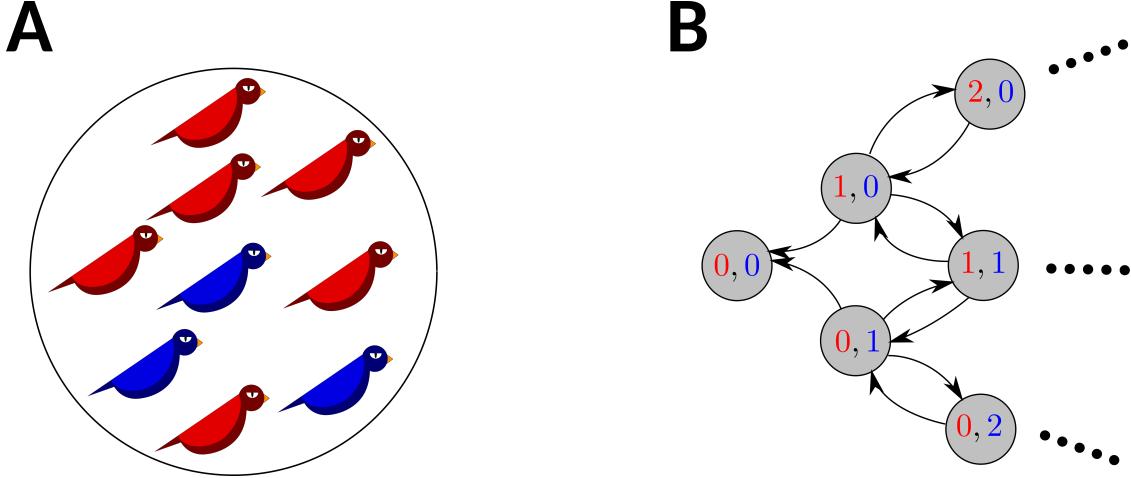


Figure 2.2: Schematic description of a one-dimensional birth-death process. (A) Consider a population of birds in which individuals are either red or blue. In this case, we have $m = 2$, since there are two types of individuals in the population. (B) The state of the system can be described by a vector 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.

$1, \dots, v_m]$ 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

$$\begin{aligned} R_{\text{in}}(\mathbf{v}, t) &= \sum_{j=1}^m b_j([v_1, \dots, v_j - 1, \dots, v_m]) P([v_1, \dots, v_j - 1, \dots, v_m], t) \\ &\quad + \sum_{j=1}^m d_j([v_1, \dots, v_j + 1, \dots, v_m]) P([v_1, \dots, v_j + 1, \dots, v_m], t) \end{aligned} \quad (2.23)$$

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

$$R_{\text{out}}(\mathbf{v}, t) = \sum_{j=1}^m b_j(\mathbf{v}) P(\mathbf{v}, t) + \sum_{j=1}^m d_j(\mathbf{v}) P(\mathbf{v}, t) \quad (2.24)$$

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:

$$\mathcal{E}_i^\pm f([v_1, \dots, v_m], t) = f([v_1, \dots, v_i \pm 1, \dots, v_m], t) \quad (2.25)$$

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

$$\frac{\partial P}{\partial t}(\mathbf{v}, t) = R_{\text{in}}(\mathbf{v}, t) - R_{\text{out}}(\mathbf{v}, t) \quad (2.26)$$

Substituting (2.23), (2.24), and (2.25), we obtain:

$$\frac{\partial P}{\partial t}(\mathbf{v}, t) = \sum_{j=1}^m [(\mathcal{E}_j^- - 1)b_j(\mathbf{v})P(\mathbf{v}, t) + (\mathcal{E}_j^+ - 1)d_j(\mathbf{v})P(\mathbf{v}, t)] \quad (2.27)$$

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

2.3.2 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 Δ_i^\pm by their action on any real-valued function $f(\mathbf{x}, t)$ as

$$\Delta_i^\pm f([x_1, \dots, x_m], t) = f([x_1, \dots, x_i \pm \frac{1}{K}, \dots, x_m], t) \quad (2.28)$$

In terms of these new variables, (2.27) becomes

$$\frac{\partial P}{\partial t}(\mathbf{x}, t) = K \sum_{j=1}^m [(\Delta_j^- - 1)b_j^{(K)}(\mathbf{x})P(\mathbf{x}, t) + (\Delta_j^+ - 1)d_j^{(K)}(\mathbf{x})P(\mathbf{x}, t)] \quad (2.29)$$

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 (2.29), yields the equation

$$\boxed{\frac{\partial P}{\partial t}(\mathbf{x}, t) = \sum_{j=1}^m \left[-\frac{\partial}{\partial x_j} \{A_j^-(\mathbf{x})P(\mathbf{x}, t)\} + \frac{1}{2K} \frac{\partial^2}{\partial x_j^2} \{A_j^+(\mathbf{x})P(\mathbf{x}, t)\} \right]} \quad (2.30)$$

where

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

Equation (2.30) is an m -dimensional Fokker-Planck equation, and corresponds to the m -dimensional Itô process

$$d\mathbf{X}_t = \mathbf{A}^-(\mathbf{X}_t)dt + \frac{1}{\sqrt{K}}\mathbf{D}(\mathbf{X}_t)d\mathbf{B}_t \quad (2.31)$$

where $\mathbf{A}^-(\mathbf{X}_t)$ is the m dimensional ‘drift vector’ with i^{th} element $= A_i^-(\mathbf{X}_t)$. $\mathbf{D}(\mathbf{X}_t)$ is the $m \times m$ ‘diffusion matrix’ with ij^{th} element $(\mathbf{D}(\mathbf{X}_t))_{ij} = \delta_{ij} (A_i^+ A_j^+)^{\frac{1}{4}}$, where δ_{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 2.1.2). This is the ‘mesoscopic’ description of our process.

2.3.3 Functional forms of the birth and death rates

We assume that the birth and death rate functions have the functional form

$$\begin{aligned} b_i^{(K)}(\mathbf{x}) &= x_i b_i^{(\text{ind})}(\mathbf{x}) + \mu Q_i(\mathbf{x}) \\ d_i^{(K)}(\mathbf{x}) &= x_i d_i^{(\text{ind})}(\mathbf{x}) \end{aligned} \quad (2.32)$$

where $b_i^{(\text{ind})}(\mathbf{x})$ and $d_i^{(\text{ind})}(\mathbf{x})$ are non-negative functions that respectively describe the per-capita birth and death rate of type i individuals, $\mu \geq 0$ is a constant describing the mutation rate in the population, and $Q_i(\mathbf{x})$ is a non-negative function that describes the additional birth rate of type i individuals due to mutations in the population \mathbf{x} that cannot be captured

in the per-capita birth rate⁶. Our assumptions of the functional forms (2.32) 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 for each type. We define the *Malthusian fitness* of the i^{th} type as $w_i(\mathbf{x}) := b_i^{(\text{ind})}(\mathbf{x}) - d_i^{(\text{ind})}(\mathbf{x})$, and the *per-capita turnover rate* of the i^{th} type as $\tau_i(\mathbf{x}) = b_i^{(\text{ind})}(\mathbf{x}) + d_i^{(\text{ind})}(\mathbf{x})$. The quantity $w_i(\mathbf{x})$ describes the per-capita growth rate of type i individuals in a population \mathbf{x} discounting mutation. 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 both w_i and τ_i depend on the state of the population as a whole (*i.e.* \mathbf{x}) and not just on the density of the focal type. Thus, in general, both the fitness and the turnover rate in our model are frequency-dependent.

2.3.4 Statistical measures for population-level quantities

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

$$\begin{aligned} N_K(t) &:= \sum_{i=1}^m x_i(t) = \frac{1}{K} \sum_{i=1}^m v_i(t) \\ p_i(t) &:= \frac{x_i(t)}{N_K(t)} \end{aligned} \tag{2.33}$$

These definitions are important because evolution is often measured as changes in type frequency (and *not* necessarily changes in type density). Note that type frequency is a population level. Indeed, even though the causes of evolution are generally at the individual level, we are very often interested in quantities *described* at a population level, such as the mean fitness or mean phenotype in the population (Bourrat, 2019). Furthermore, the relevant quantities at the individual level, such as individual fitness or phenotype, are typically equal for all individuals of the same type (in some sense this is our basis for defining different types in the first place), and we, therefore, call them ‘type-level’ quantities below. Let f be any type-level quantity with (possibly time-dependent) value f_i for the i^{th} type. For example, if

⁶When $x_i = 0$, *i.e.* there are no type i individuals in the population, individuals of type i may still be born through mutations during births of the other types. This cannot be captured in $b_i^{(\text{ind})}(\mathbf{x})$ because the term $x_i b_i^{(\text{ind})}(\mathbf{x})$ vanishes when $x_i = 0$. Note that no analogous problem exists for the death rate, since the death rate of type i individuals must be 0 when x_i is 0 to ensure that we never have negative population densities.

each type is a phenotype for a trait such 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. To facilitate the description of such quantities, we define the statistical mean value of any quantity f in the population as

$$\bar{f}(t) := \sum_{i=1}^m f_i p_i \quad (2.34)$$

the statistical covariance of two such quantities f and g as

$$\text{Cov}(f, g) := \overline{fg} - \bar{f}\bar{g} \quad (2.35)$$

and the statistical variance of a quantity f as $\sigma_f^2 := \text{Cov}(f, f)$. It is important to recognize that these quantities are distinct from and independent of the *probabilistic* expectation, variance, and covariance obtained by integrating over realizations in the underlying probability space. Indeed, for finite populations, the statistical mean, statistical variance, and statistical covariance are all themselves stochastic processes: For each instant of time, these population-level quantities are a random variable (*i.e.* a *function* and not just a number) depending on \mathbf{p} , the (random) vector of type frequencies in the population. For infinite populations, the statistical mean, variance, and covariance are entirely deterministic time-dependent quantities that simply describe how f is distributed across the population. Failure to clearly make this distinction between statistical operations and probabilistic operations has led to much confusion with regard to the infinite population Price equation (Van Veelen, 2005), which is entirely deterministic.

2.3.5 Stochastic Trait Frequency Dynamics

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 $\bar{w} = \sum w_i p_i$ and $\bar{\tau} = \sum \tau_i p_i$ be the average population fitness and turnover respectively, we show in appendix B that the frequency of the i^{th} type in the population $\mathbf{x}(t)$ changes

according to the equation:

$$\begin{aligned} dp_i(t) = & \left[(w_i(\mathbf{x}) - \bar{w})p_i + \mu \left\{ Q_i(\mathbf{p}) - p_i \left(\sum_{j=1}^m Q_j(\mathbf{p}) \right) \right\} \right] dt \\ & - \frac{1}{K} \frac{1}{N_K(t)} \left[(\tau_i(\mathbf{x}) - \bar{\tau})p_i + \mu \left\{ Q_i(\mathbf{p}) - p_i \left(\sum_{j=1}^m Q_j(\mathbf{p}) \right) \right\} \right] dt \\ & + \frac{1}{\sqrt{K}} \frac{1}{N_K(t)} \left[(A_i^+)^{1/2} dB_t^{(i)} - p_i \sum_{j=1}^m (A_j^+)^{1/2} dB_t^{(j)} \right] \end{aligned} \quad (2.36)$$

where $B_t^{(1)}, B_t^{(2)}, \dots, B_t^{(m)}$ are m independent one-dimensional standard Brownian motion processes and we have used the notation $Q_i(\mathbf{p}) = Q_i(\mathbf{x})/N_K(t)$ for notational clarity. We will show below that the first term in this expression describes directional changes in the population composition due to ‘classical’ evolutionary forces such as selection and mutation that occur in deterministic infinite population models. 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, as well as connections with previous studies, are discussed in detail in Chapter 4. Finally, the last term of equation (2.36) describes non-directional stochastic effects due to fluctuations and has a ‘spreading effect’.

2.3.6 The infinite population limit

Like in 2.2, we can once again take $K \rightarrow \infty$ in (2.31) to obtain a deterministic expression. Here, the expression reads

$$\frac{d\mathbf{x}}{dt} = \mathbf{A}^-(\mathbf{x}) = \mathbf{b}^{(K)}(\mathbf{x}) - \mathbf{d}^{(K)}(\mathbf{x}) \quad (2.37)$$

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^{th} element $b_i^{(K)}(\mathbf{x})$ and $d_i^{(K)}(\mathbf{x})$ respectively. For the trait frequencies, by taking $K \rightarrow \infty$ in (2.36), we obtain a deterministic equation that reads:

$$\frac{dp_i}{dt} = (w_i(\mathbf{x}) - \bar{w})p_i + \mu \left[Q_i(\mathbf{p}) - p_i \left(\sum_{j=1}^m Q_j(\mathbf{p}) \right) \right] \quad (2.38)$$

The first term of (2.38) describes changes due to faithful (non-mutational) replication, and the second describes changes due to mutation. For this reason, equation (2.38) 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 (2.38) 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 function⁷ (Page and Nowak, 2002). We can now calculate how the mean of any ‘type level’ quantity f , defined as f_i for the i^{th} type, changes in the population (For example, if each type is a phenotype for a trait such 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). The product rule of calculus tells us that we have the relation

$$\frac{d}{dt} \left(\sum_{i=1}^m f_i p_i \right) = \sum_{i=1}^m \left(f_i \frac{\partial p_i}{\partial t} + p_i \frac{\partial f_i}{\partial t} \right) = \sum_{i=1}^m f_i \frac{\partial p_i}{\partial t} + \overline{\left(\frac{\partial f}{\partial t} \right)} \quad (2.39)$$

Multiplying both sides of equation (2.38) by f_i and summing over all i , we obtain

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

Using the definition of statistical covariance from (2.35), we obtain

$$\sum_{i=1}^m f_i \frac{\partial p_i}{\partial t} = \text{Cov}(w, f) + \mu \left[\sum_{i=1}^m Q_i(\mathbf{p}) f_i - \left(\sum_{j=1}^m Q_j(\mathbf{p}) \right) \bar{f} \right] \quad (2.40)$$

⁷Mutational effects are often additionally assumed to act through direct ‘transmission probabilities’ of mutating from one type to another. This means that we can write $Q_i(\mathbf{p}) = \sum_j Q_{ij}p_j$, where $Q_{ii} = 0$, and for each $j \neq i$, $Q_{ij} \geq 0$ is a constant describing the probability of a $j \rightarrow i$ mutation (conditioned on the occurrence of a mutation). Substituting this into (2.38) yields an equation in terms of ‘ Q -matrices’ or ‘mutation matrices’ that may be more familiar to some.

Thus, substituting this into (2.39), we get

$$\boxed{\frac{d\bar{f}}{dt} = \text{Cov}(w, f) + \mu \left[\sum_{i=1}^m Q_i(\mathbf{p}) f_i - \left(\sum_{j=1}^m Q_j(\mathbf{p}) \right) \bar{f} \right] + \overline{\left(\frac{\partial f}{\partial t} \right)}} \quad (2.41)$$

This is a Price equation for quantities f_i which can vary over time. To obtain the more familiar Price equation seen in textbooks, we can consider time-independent f_i , *i.e.* situations in which each f_i is constant over time, and thus changes in \bar{f} are purely due to changes in the composition of the population. For such quantities, we have $\frac{\partial f_i}{\partial t} = 0 \forall i$ and thus obtain

$$\boxed{\frac{d\bar{f}}{dt} = \text{Cov}(w, f) + \mu \left[\sum_{i=1}^m Q_i(\mathbf{p}) f_i - \left(\sum_{j=1}^m Q_j(\mathbf{p}) \right) \bar{f} \right]} \quad (2.42)$$

, the famous Price equation in continuous time. 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’.

2.3.7 Stochastic fluctuations and the weak noise approximation

As in the one-dimensional case, we can go a little further if the noise is sufficiently weak. Let the deterministic trajectory obtained by solving (2.37) be given by $\boldsymbol{\alpha}(t)$. We can once again track stochastic fluctuations from the deterministic trajectory by introducing the new variables

$$\begin{aligned} \mathbf{y} &= \sqrt{K}(\mathbf{x} - \boldsymbol{\alpha}(t)) \\ s &= t \\ \tilde{P}(\mathbf{y}, s) &= \frac{1}{\sqrt{K}} P(\mathbf{x}, t) \end{aligned} \quad (2.43)$$

Then, after some algebra that follows the exact same steps as in section 2.2.3 and retaining only the highest order terms in \sqrt{K} , we obtain the equation:

$$\frac{\partial \tilde{P}_0}{\partial s}(\mathbf{y}, s) = \sum_{j=1}^m \left(-\frac{\partial}{\partial y_j} \left\{ (A_j^-)_1(s) \tilde{P}_0(\mathbf{y}, s) \right\} + \frac{1}{2} A_j^+(\boldsymbol{\alpha}(s)) \frac{\partial^2}{\partial y_j^2} \{ \tilde{P}_0(\mathbf{y}, s) \} \right) \quad (2.44)$$

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

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

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

$$(A_j^-)_1(s) = \sum_{i=1}^m y_i \left(\frac{\partial A_j^-(\mathbf{x})}{\partial x_i} \Big|_{\mathbf{x}=\boldsymbol{\alpha}(s)} \right) \quad (2.45)$$

In multi-variable calculus, the directional derivative⁸ $D_{\mathbf{v}}(f(\mathbf{x}))$ of a multidimensional function $f : \mathbb{R}^n \rightarrow \mathbb{R}$ along a vector \mathbf{v} is the function defined by:

$$D_{\mathbf{v}}(f(\mathbf{x})) := \sum_{i=1}^n \left(\frac{\partial f(\mathbf{x})}{\partial x_i} \right) v_i = \lim_{h \rightarrow 0} \frac{f(\mathbf{x} + h\mathbf{v}) - f(\mathbf{x})}{h} \quad (2.46)$$

Comparing with (2.45), we see that the weak-noise approximation of our process is:

$$\frac{\partial P}{\partial t}(\mathbf{y}, t) = \sum_{j=1}^m \left(-\frac{\partial}{\partial y_j} \{ D_{\mathbf{y}}(A_j^-(\boldsymbol{\alpha}))(t)P(\mathbf{y}, t) \} + \frac{1}{2} {A_j^+}(\boldsymbol{\alpha}(t)) \frac{\partial^2}{\partial y_j^2} \{ P(\mathbf{y}, t) \} \right) \quad (2.47)$$

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 $\boldsymbol{\alpha}(s)$ here is the multidimensional analogue of the derivative we had in (2.21). The meaning of equation (2.47) 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:

$$\frac{d}{dt} \mathbb{E}[y_i^n] = \frac{d}{dt} \int_{\mathbb{R}^m} y_i^n P(\mathbf{y}, t) d\mathbf{y} \quad (2.48)$$

$$= \int_{\mathbb{R}^m} y_i^n \frac{\partial P}{\partial t}(\mathbf{y}, t) d\mathbf{y} \quad (2.49)$$

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 $\int_{\mathbb{R}^m} f(\mathbf{y}) d\mathbf{y} =$

⁸Physicists sometimes use the notation $\partial_{\mathbf{v}} f(\mathbf{x})$ or $\mathbf{v} \cdot \nabla f(\mathbf{x})$ for this object.

$\int_{\mathbb{R}} \int_{\mathbb{R}} \dots \int_{\mathbb{R}} f(\mathbf{y}) dy_1 dy_2 \dots dy_m$. The one-dimensional integrals are over the entire real line and not just over $[0, \infty)$ because fluctuations can be either positive (greater than $\boldsymbol{\alpha}(t)$) or negative (lesser than $\boldsymbol{\alpha}(t)$). For notational brevity, let us use the shorthand $D_j = D_{\mathbf{y}}(A_j^-(\boldsymbol{\alpha}))(t)$. We can now substitute (2.47) into (2.49) to obtain

$$\frac{d}{dt} \mathbb{E}[y_i^n] = \int_{\mathbb{R}^m} y_i^n \left(\sum_{j=1}^m \left(-\frac{\partial}{\partial y_j} \{D_j P(\mathbf{y}, t)\} + \frac{1}{2} A_j^+(\boldsymbol{\alpha}(t)) \frac{\partial^2}{\partial y_j^2} \{P(\mathbf{y}, t)\} \right) \right) d\mathbf{y} \quad (2.50)$$

$$= \sum_{j=1}^m \left[- \int_{\mathbb{R}^m} y_i^n \frac{\partial}{\partial y_j} \{D_j P(\mathbf{y}, t)\} d\mathbf{y} + \frac{A_j^+(\boldsymbol{\alpha}(t))}{2} \int_{\mathbb{R}^m} y_i^n \frac{\partial^2}{\partial y_j^2} \{P(\mathbf{y}, t)\} d\mathbf{y} \right] \quad (2.51)$$

We will evaluate the integrals on the RHS of (2.51) using integration by parts. Recall that for any two functions u and v defined on a domain Ω , the general formula for integration by parts is given by:

$$\int_{\Omega} \frac{\partial u}{\partial x_i} v d\mathbf{x} = - \int_{\Omega} u \frac{\partial v}{\partial x_i} d\mathbf{x} + \int_{\partial\Omega} u v \gamma_i dS(\mathbf{x}) \quad (2.52)$$

where $\partial\Omega$ is the boundary of Ω , dS is the surface element of this boundary, and γ_i is the i^{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 (2.51) by using integration by parts and discarding the boundary term (The second term on the RHS of (2.52)). 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 (2.51) (once for the first term and twice for the second term), we obtain the considerably simpler expression

$$\frac{d}{dt} \mathbb{E}[y_i^n] = n \int_{\mathbb{R}^m} y_i^{n-1} D_i P(\mathbf{y}, t) d\mathbf{y} + \frac{n(n-1)}{2} A_i^+(\boldsymbol{\alpha}(t)) \int_{\mathbb{R}^m} y_i^{n-2} P(\mathbf{y}, t) d\mathbf{y} \quad (2.53)$$

$$\Rightarrow \frac{d}{dt} \mathbb{E}[y_i^n] = n \mathbb{E}[y_i^{n-1} D_i] + \frac{n(n-1)}{2} A_i^+(\boldsymbol{\alpha}(t)) \mathbb{E}[y_i^{n-2}] \quad (2.54)$$

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:

$$\frac{d}{dt} \mathbb{E}[y_i] = \mathbb{E}[D_i] \quad (2.55)$$

$$\frac{d}{dt} \mathbb{E}[y_i^2] = 2\mathbb{E}[y_i D_i] + A_i^+(\boldsymbol{\alpha}(t)) = 2\text{Cov}(y_i, D_i) + 2\mathbb{E}[y_i]\mathbb{E}[D_i] + A_i^+(\boldsymbol{\alpha}(t)) \quad (2.56)$$

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 (2.42), 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 (2.32), we have:

$$A_i^-(\mathbf{x}) = w_i(\mathbf{x})x_i + \mu Q_i(\mathbf{x}) \quad (2.57)$$

and thus, from (2.45), we can calculate the directional derivative D_i as

$$D_i = \sum_{k=1}^m y_k \left(\frac{\partial A_i^-(\mathbf{x})}{\partial x_k} \Big|_{\mathbf{x}=\boldsymbol{\alpha}(t)} \right) \quad (2.58)$$

$$= \sum_{k=1}^m y_k \left(\frac{\partial}{\partial x_k} (w_i(\mathbf{x})x_i + \mu Q_i(\mathbf{x})) \Big|_{\mathbf{x}=\boldsymbol{\alpha}(t)} \right) \quad (2.59)$$

$$= \sum_{k=1}^m y_k \left(a_i \frac{\partial w_i}{\partial x_k} \Big|_{\mathbf{x}=\boldsymbol{\alpha}(t)} \right) + y_i w_i(\boldsymbol{\alpha}) + \mu \sum_{k=1}^m y_k \left(\frac{\partial Q_i}{\partial x_k}(\mathbf{x}) \Big|_{\mathbf{x}=\boldsymbol{\alpha}(t)} \right) \quad (2.60)$$

$$= y_i w_i(\boldsymbol{\alpha}) + a_i D_{\mathbf{y}}(w_i(\boldsymbol{\alpha})) + \mu D_{\mathbf{y}}(Q_i(\boldsymbol{\alpha})) \quad (2.61)$$

Using this in (2.55), we see that the expected change of a fluctuation in the density of type i individuals evolves as:

$$\frac{d}{dt} \mathbb{E}[y_i] = \underbrace{w_i(\boldsymbol{\alpha}) \mathbb{E}[y_i]}_{\begin{array}{l} \text{Current fitness of type } i \\ \text{at deterministic trajectory } \boldsymbol{\alpha} \\ (\text{scaled by expected density } \mathbb{E}[y_i]) \end{array}} + \underbrace{a_i \mathbb{E}[D_{\mathbf{y}}(w_i(\boldsymbol{\alpha}))]}_{\begin{array}{l} \text{Expected change in fitness} \\ \text{of type } i \text{ in going from } \boldsymbol{\alpha} \text{ to } \mathbf{y} \\ (\text{scaled by deterministic density } a_i) \end{array}} + \underbrace{\mu \mathbb{E}[D_{\mathbf{y}}(Q_i(\boldsymbol{\alpha}))]}_{\text{Expected effect of mutations}} \quad (2.62)$$

Chapter 3

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

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 space¹. 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 (but see Week et al., 2021 for a very friendly introduction to the major ideas through heuristics). 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 adopt this attitude below and hope that all 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

¹The 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.

collective motion (Ó Laighléis et al., 2018). In the following sections, I will rely 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 ρ

$$\int \frac{\delta F}{\delta\phi(x)} \rho(x) dx = \lim_{h \rightarrow 0} \frac{F[\phi + h\rho] - F[\phi]}{h} \quad (3.1)$$

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 (2.46) yields (3.1).

3.1 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 $A \subset \mathcal{T}$. The Dirac mass is often written $\delta_{x_i} = \delta(y - x_i)$ as a ‘function’ of a dummy variable y which will be integrated over, since in this view the Dirac mass is a ‘function’ that can only occur inside an integral. I will stick to the notation δ_{x_i} because it emphasizes that δ_{x_i} is supposed 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 3.1) 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

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

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 $\int_{\mathcal{T}} f(y) \nu^{(t)} dy = \sum_{i=1}^{N(t)} f(x_i)$. Now that we have described the population, we must define the rules for how



Figure 3.1: 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.

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 ν . 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 ν , 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:

$$\begin{aligned} b(x|\nu) &= r \int_{\mathcal{T}} m(x,y)\nu(y) dy; \quad m(x,y) = \exp\left(\frac{-(x-y)^2}{\sigma_m^2}\right) \\ d(x|\nu) &= \frac{\nu(x)}{Kn(x)} \int_{\mathcal{T}} \alpha(x,y)\nu(y) dy; \quad \alpha(x,y) = \exp\left(\frac{-(x-y)^2}{\sigma_\alpha^2}\right) \end{aligned} \tag{3.2}$$

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 in chapter 2 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 $\nu \in \mathcal{M}(\mathcal{T})$, the transition rate from $\nu - \delta_x$ to ν is simply $\mathcal{E}_x^- b(x|\nu)$, and similarly, the transition rate from $\nu + \delta_x$ to ν is $\mathcal{E}_x^+ d(x|\nu)$. The transition rate out of ν 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 ν , we see that $P(\nu, t)$ must satisfy:

$$\frac{\partial P}{\partial t}(\nu, t) = \int_{\mathcal{T}} [(\mathcal{E}_x^- - 1)b(x|\nu)P(\nu, t) + (\mathcal{E}_x^+ - 1)d(x|\nu)P(\nu, t)] dx \quad (3.3)$$

This is the ‘Master equation’ of our process.

3.2 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

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

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

$$\frac{\partial P}{\partial t}(\phi, t) = K \int_{\mathcal{T}} [(\Delta_x^- - 1)b_K(x|\phi)P(\phi, t) + (\Delta_x^+ - 1)d_K(x|\phi)P(\phi, t)] dx \quad (3.4)$$

where we have introduced new step operators Δ_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 ρ_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

$$\begin{aligned} \Delta_x^\pm[F[\phi]] &= F[\phi] \pm \frac{1}{K} \int_{\mathcal{T}} \frac{\delta F}{\delta \phi(y)} \delta_x dy + \frac{1}{2K^2} \int_{\mathcal{T}} \int_{\mathcal{T}} \frac{\delta^2 F}{\delta \phi(y) \delta \phi(z)} \delta_x dy \delta_x dz + \mathcal{O}(K^{-3}) \\ &= F[\phi] \pm \frac{1}{K} \frac{\delta F}{\delta \phi(x)} + \frac{1}{2K^2} \frac{\delta^2 F}{\delta \phi(x)^2} + \mathcal{O}(K^{-3}) \end{aligned} \quad (3.5)$$

Neglecting terms of $\mathcal{O}(K^{-3})$, we can now substitute (3.5) into (3.4) 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’:

$$\frac{\partial P}{\partial t}(\phi, t) = \int_{\mathcal{T}} \left[-\frac{\delta}{\delta \phi(x)} \{\mathcal{A}^-(x|\phi)P(\phi, t)\} + \frac{1}{2K} \frac{\delta^2}{\delta \phi(x)^2} \{\mathcal{A}^+(x|\phi)P(\phi, t)\} \right] dx \quad (3.6)$$

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 of our process. We can once again appeal to the link between Fokker-Planck equations and Langevins (Lafuerza and McKane, 2016) to say that (3.6) corresponds to the Langevin equation:

$$\frac{\partial \phi}{\partial t}(x, t) = \mathcal{A}^-(x|\phi) + \frac{1}{\sqrt{K}}\eta(x, t) \quad (3.7)$$

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

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

If one wishes to be mathematically careful, the connection between (3.6) and (3.7) 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 for general measure spaces - We may need $\mathcal{M}_K(\mathcal{T})$ to have a considerable amount of structure (Ex: Separable Hilbert space) for things to work out (Da Prato and Zabczyk, 2014; Balan, 2018), and I do not know whether our domain is nice enough. For example, it is not immediately clear what conditions on $\mathcal{A}^\pm(x|\phi)$ are needed for (3.7) to even admit a solution. Nevertheless, we can recover some well-known deterministic equations from equation (3.8), and under certain assumptions, equations like (2.36) have been proved to exist.

3.3 The infinite population limit

Taking $K \rightarrow \infty$ in equation (3.7) then yields a PDE:

$$\frac{\partial \psi}{\partial t}(x, t) = \mathcal{A}^-(x|\psi) = b_K(x|\psi) - d_K(x|\psi) \quad (3.8)$$

where we have used a different symbol ψ simply to highlight that $\psi(x, t)$ as the solution to equation (3.8) is a deterministic function, whereas $\phi(x, t)$ as defined in equation (3.7) is really a stochastic process $\{\phi^{(t)}\}_{t \geq 0}$. Equation (3.8) 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 studies of Adaptive Diversification (Doebeli, 2011). Equation (3.8) is also the basic equation of ‘oligomorphic dynamics’ (Sasaki and Dieckmann, 2011; Lion et al., 2022) 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. Models of the form (3.8) are also used to study intraspecific trait variation in community ecology (Nordbotten et al., 2020). A prominent recent example is the ‘trait space equations’ of (Wickman et al., 2022) in their framework for eco-evolutionary community dynamics. As before, I assume that the birth and death functions take the form:

$$\begin{aligned} b_K(x|\psi) &= \psi(x, t)b^{(\text{ind})}(x|\psi) + \mu Q(x|\psi) \\ d_K(x|\psi) &= \psi(x, t)d^{(\text{ind})}(x|\psi) \end{aligned} \tag{3.9}$$

As in chapter 2, $Q(x|\psi)$ describes birth due to mutations and $\mu \geq 0$ is a constant 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 individuals in a population ψ . These functions could in principle model several ecological factors. For example, $b^{(\text{ind})}(x|\psi)$ may incorporate the effects of mate choice in the sexual case or intrinsic duplication rates in the asexual case, and $d^{(\text{ind})}(x|\psi)$ may model death due to intraspecific competition for resources. Note that the definition of the mean value (2.34) of a type level quantity $f(x)$ now becomes

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

Substituting equation (3.9) into (3.8), we obtain

$$\frac{\partial \psi}{\partial t}(x, t) = w(x|\psi)\psi(x, t) + \mu Q(x|\psi) \tag{3.10}$$

where we have defined $w(x|\psi) := b^{(\text{ind})}(x|\psi) - d^{(\text{ind})}(x|\psi)$, 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

$$\begin{aligned} N_K(t) &:= \int_{\mathcal{T}} \psi(x, t) dx \\ p(x, t) &:= \frac{\psi(x, t)}{N_K(t)} \end{aligned} \quad (3.11)$$

The population mean fitness is:

$$\bar{w}(t) = \int_{\mathcal{T}} w(x|\psi)p(x, t) dx \quad (3.12)$$

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 (3.10), we now obtain

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

where we have used the definition of $p(x, t)$ in the second line. Using (3.12) and rearranging the terms gives us:

$$\frac{\partial p}{\partial t}(x, t) = [w(x|\psi) - \bar{w}(t)] p(x, t) + \frac{\mu}{N_K(t)} \left[Q(x|\psi) - p(x, t) \int_{\mathcal{T}} Q(y|\psi) dy \right] \quad (3.13)$$

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, $Q(x|\psi)$ 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 $Q(y|\psi) = \int_{\mathbb{R}} m(y-z)\psi(z,t)dz$, where $m : \mathbb{R} \rightarrow [0, \infty)$ 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, for any fixed $t > 0$, we have $m(y-z)\psi(z,t) \in \mathcal{L}^1(\mathbb{R} \times \mathbb{R})$ and we can use the Fubini-Tonnelli theorem to interchange the order of integration of iterated integrals of $m(y-z)\psi(y)$. We are now ready to evaluate the rightmost integral of (3.13).

We have:

$$\begin{aligned}
\int_{\mathbb{R}} Q(y|\psi)dy &= \int_{\mathbb{R}} \int_{\mathbb{R}} m(y-z)\psi(z,t)dzdy \\
&= \int_{\mathbb{R}} \int_{\mathbb{R}} m(y-z)\psi(z,t)dydz \\
&= \int_{\mathbb{R}} \psi(z,t) \left(\int_{\mathbb{R}} m(y-z)dy \right) dz \\
&= \int_{\mathbb{R}} \psi(z,t) \int_{\mathbb{R}} m(u)dudz \\
&= \int_{\mathbb{R}} \psi(z,t)dz \int_{\mathbb{R}} m(u)du \\
&= N_K(t) \int_{\mathbb{R}} m(u)du
\end{aligned} \tag{3.14}$$

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 (3.14) therefore becomes

$\int_{\mathbb{R}} Q(y|\psi) dy = N_K(t)$. Substituting this in (3.13), 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

$$\frac{\partial p}{\partial t}(x, t) = [w(x|\psi) - \bar{w}(t)] p(x, t) + \mu \left[\int_{\mathbb{R}} m(x-z)p(z, t) dz - p(x, t) \right] \quad (3.15)$$

which is Kimura's continuum of alleles model.

We can now use the same trick we used in deriving (2.41) from (2.38). By multiplying both sides of equation (3.13) by a type level quantity² $f(x, t)$ and integrating over the trait space, we obtain

$$\begin{aligned} \frac{d\bar{f}}{dt} &= \int_{\mathcal{T}} f(x, t) w(x|\psi) p(x, t) dx - \bar{w}(t) \int_{\mathcal{T}} f(x, t) p(x, t) dx \\ &\quad + \frac{\mu}{N_K(t)} \int_{\mathcal{T}} f(x, t) \left[Q(x|\psi) - p(x, t) \int_{\mathcal{T}} Q(y|\psi) dy \right] dx \\ &= \bar{f}\bar{w} - \bar{w} \cdot \bar{f} + \frac{\mu}{N_K(t)} \int_{\mathcal{T}} f(x, t) \left[Q(x|\psi) - p(x, t) \int_{\mathcal{T}} Q(y|\psi) dy \right] dx \end{aligned} \quad (3.16)$$

We now observe that

$$\text{Cov}(f, w(x|\psi)) = \bar{f}\bar{w} - \bar{f} \cdot \bar{w} \quad (3.17)$$

is the statistical covariance of the quantity f 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

$$M_{\bar{f}}(x|\psi) := \frac{\mu}{N_K(t)} \left[\int_{\mathcal{T}} f(x, t) Q(x|\psi) dx - \left(\bar{f} \int_{\mathcal{T}} Q(x|\psi) dx \right) \right] \quad (3.18)$$

²This is now a function $f(x, t)$ of two variables, the trait value and time. We assume this function is nice enough for all the below operations to make sense

reflects the transmission bias of mutations. Thus, we see that equation (3.16) reads

$$\boxed{\frac{d\bar{f}}{dt} = \text{Cov}(f, w(x|\psi)) + M_{\bar{f}}(x|\psi) + \overline{\left(\frac{\partial f}{\partial t}\right)}} \quad (3.19)$$

from which it is clear that we have obtained a version of the Price equation (2.41) for quantitative traits (Note that (3.19) is precisely the equation obtained by informally taking $m \rightarrow \infty$ in (2.41)). For the special case $f(x) = x$, we have $\partial f / \partial t = 0$ and thus:

$$\frac{d\bar{x}}{dt} = \text{Cov}(x, w(x|\psi)) + M_{\bar{x}}(x|\psi) \quad (3.20)$$

We can also recover some more familiar dynamics under the following additional assumptions:

- Rare mutations, *i.e.* $\mu \rightarrow 0$.
- Small mutational effects with ‘almost faithful’ reproduction, meaning $Q(x|\psi) \rightarrow 0$, 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 $w(y|\delta_{y(t)}) = 0$.

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 (3.20), we have

$$\begin{aligned} \frac{d\bar{x}}{dt} &= \int_{\mathcal{T}} (x - \bar{x}(t))(w(x|\psi) - \bar{w}(t))p(x, t)dx \\ \Rightarrow \frac{dy}{dt} &= \int_{\mathcal{T}} (x - \bar{x}(t))w(x|N_K\delta_{y(t)})\delta_{y(t)}dx \end{aligned} \quad (3.21)$$

Our assumptions on mutation rate and mutational effects 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 (3.21), 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:

$$\frac{dy}{dt} = B(y) \left(\frac{d}{dz} w(z|N_K\delta_{y(t)}) \Big|_{z=y} \right) \quad (3.22)$$

Note that by definition, $B(y(t))$ is the statistical 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. Equation (3.22) is the canonical form of a broad class of systems called ‘gradient equations’ or ‘gradient dynamics’ in quantitative genetics (Lande, 1976; Abrams et al., 1993; Lehtonen, 2018; Lion, 2018), and captures the approximate evolutionary dynamics of quantitative traits under certain mutation limits. It is also deeply related (Lehtonen, 2018; Lion, 2018) to the canonical equation of adaptive dynamics (Dieckmann and Law, 1996; Doebeli, 2011). The major difference is that in the ‘proper’ canonical equation of adaptive dynamics (as formulated in Dieckmann and Law, 1996), the function $B(y)$ explicitly relies on mutations as a continual source of variation, whereas in gradient dynamics and our equation (3.22), $B(y)$ captures the standing genetic variation in the population but does not specify the source of this variation. 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 vanishingly

rare and mutants 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 rigorously using much more sophisticated mathematical tools grounded in martingale theory (Champagnat et al., 2006). A heuristic derivation of the canonical equation of adaptive dynamics is provided in the classic article by Dieckmann and Law, 1996.

3.4 Stochastic trait frequency dynamics in the infinite-dimensional case

In chapter 2, we also derived SDEs for the trait frequency dynamics of the complete stochastic case using Itô’s formula. Doing the same for quantitative traits in our framework is tricky because it requires us to find a version of Itô’s formula that holds for SPDEs of the form (3.7). The formulation of Itô formulas and/or an infinite-dimensional stochastic calculus for general function (measure) valued stochastic processes is an active area of research in pure mathematics (Da Prato and Zabczyk, 2014), and without further information on the nature of the domain $\mathcal{M}_K(\mathcal{T})$, it is not clear (to me at least) whether an Itô’s formula exists for our case in general. If $\mathcal{A}^\pm(x|\phi)$ in (3.6) are Gaussian functions, then it has been proven (Week et al., 2021) that the SDEs ‘work as expected’ if we take $m \rightarrow \infty$ in (2.36) (see 4.1.2 and 4.1.3 in chapter 4). However, carrying out a general derivation is beyond the scope of this thesis.

3.5 Stochastic fluctuations and the weak noise approximation

We can also formally carry out a functional analogue of the weak noise expansion as we did in chapter 2. Assume that $\psi(x, t)$ is the deterministic trajectory obtained as the solution to (3.8). 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:

$$\begin{aligned}\zeta^{(s)}(x) &= \sqrt{K}(\phi^{(t)}(x) - \psi(x, t)) \\ s &= t \\ \tilde{P}(\zeta, s) &= \frac{1}{\sqrt{K}}P(\phi, t)\end{aligned}\tag{3.23}$$

Note that the following relations hold:

$$\frac{\delta F[\zeta]}{\delta \phi(x)} = \int_{\mathcal{T}} \frac{\delta F[\zeta]}{\delta \zeta(y)} \frac{\delta \zeta(y)}{\delta \phi(x)} dy = \sqrt{K} \frac{\delta F[\zeta]}{\delta \zeta(x)} \quad (3.24)$$

$$\frac{\partial}{\partial s} = \frac{\partial}{\partial t} \quad (3.25)$$

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

$$\begin{aligned} \frac{\partial \tilde{P}}{\partial t}(\zeta, s) &= \frac{\delta \tilde{P}}{\delta \zeta} \frac{\partial \zeta}{\partial t} + \frac{\partial \tilde{P}}{\partial s} \frac{\partial s}{\partial t} \\ &= \frac{\delta \tilde{P}}{\delta \zeta} \left(-\sqrt{K} \frac{\partial \psi}{\partial t} \right) + \frac{\partial \tilde{P}}{\partial s} \\ &= -\sqrt{K} \frac{\delta}{\delta \zeta} \{ \mathcal{A}^-(x|\psi) \tilde{P}(\zeta, s) \} + \frac{\partial \tilde{P}}{\partial s} \end{aligned} \quad (3.26)$$

Reformulating equation (3.6) in terms of the new variables (3.23) and using the relations (3.24), (3.25) and (3.26), 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:

$$\begin{aligned} \frac{\partial \tilde{P}}{\partial s} &= -\sqrt{K} \int_{\mathcal{T}} \frac{\delta}{\delta \zeta(x)} \left\{ \left(\mathcal{A}^- \left(x \middle| \psi + \frac{\zeta}{\sqrt{K}} \right) - \mathcal{A}^-(x|\psi) \right) \tilde{P}(\zeta, s) \right\} dx \\ &\quad + \frac{1}{2} \int_{\mathcal{T}} \frac{\delta^2}{\delta \zeta(x)^2} \{ \mathcal{A}^+ \left(x \middle| \psi + \frac{\zeta}{\sqrt{K}} \right) \tilde{P}(\zeta, s) \} dx \end{aligned} \quad (3.27)$$

We will now Taylor expand our functionals about ψ (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 (3.27) 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:

$$\frac{\partial \tilde{P}_0}{\partial s}(\zeta, s) = \int_{\mathcal{T}} \left(-\frac{\delta}{\delta \zeta(x)} \left\{ \mathcal{D}_{\zeta}[\mathcal{A}^-](x) \tilde{P}_0(\zeta, s) \right\} + \frac{1}{2} \mathcal{A}^+(x|\psi) \frac{\delta^2}{\delta \zeta(x)^2} \{ \tilde{P}_0(\zeta, s) \} \right) dx \quad (3.28)$$

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 ζ .

Part III

Major Takeaways & Discussion

Chapter 4

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. In the finite-dimensional case, the infinite population limit corresponds to the equations of population genetics and evolutionary game theory. In the infinite-dimensional case, we instead obtain the equations of quantitative genetics, and, in some further limits, gradient dynamics. In both cases, the mean value of the trait in the population changes according to an equation resembling the Price equation. My derivation highlights the natural connections between the various equations of population dynamics - 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 and extending known similarities to the finite population case. The major formulations are summarized in Table 4.1.

Number of possible distinct types/trait variants (m)	State Space	Model parameters	Mesoscopic description	Infinite population limit
$m = 1$ (Identical individuals)	$[0, 1, 2, 3, \dots]$ (Population size)	Two non-negative 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)	Dynamics of populations of identical individuals
$1 < m < \infty$ (Discrete traits)	$[0, 1, 2, 3, \dots]^m$ (Number of individuals of each trait variant)	$2m$ non-negative 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)	$\left\{ \sum_{i=1}^n \delta_{x_i} \mid n \in \mathbb{N}, x_i \in \mathcal{T} \subseteq \mathbb{R} \right\}$	(Each Dirac mass δ_{x_i} is an individual with trait value x_i in the trait space \mathcal{T})	Functional Fokker-Planck equation/Field theory (SPDEs)	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 Gradient Dynamics Price equation (quantitative traits)

Table 4.1: Summary of the various birth-death processes studied in this thesis

4.1 Fundamental theorems of evolution in finite population

4.1.1 The fundamental theorem for changes in type frequencies in the population

Equation (2.36), which we derived in chapter 2, is a very general equation for how frequencies change over time in stochastic populations. To recap, we started with a population which can contain up to m different types of individuals, and used ecological arguments to posit the existence of a ‘system-size’ parameter K that leads to density-dependent growth and prevents the population from growing infinitely large. The population as a whole is characterized by a vector $\mathbf{x} = [x_1, \dots, x_m]$ indexing the density (*i.e.* number divided by K) of each type of individual. Changes of the population are through either birth or death of individuals. Each type has a per-capita birth rate $b^{(\text{ind})}(\mathbf{x})$, a per-capita death rate $d^{(\text{ind})}(\mathbf{x})$, and an additional term $\mu Q_i(\mathbf{x})$ representing mutational effects. All three of these functions depend on the density (and *not* just the total number) of individuals of each type in the population, and may in general also be frequency-dependent. In the regime where K is not too small (corresponding to ‘medium sized’ populations), we identified two quantities, $w_i(\mathbf{x}) = b_i^{(\text{ind})}(\mathbf{x}) - d_i^{(\text{ind})}(\mathbf{x})$ and $\tau_i(\mathbf{x}) = b_i^{(\text{ind})}(\mathbf{x}) + d_i^{(\text{ind})}(\mathbf{x})$, the Malthusian fitness and per-capita turnover rate of the i^{th} type respectively, that emerge as being important for trait frequency dynamics. In particular, we saw that p_i , the frequency of the i^{th} type in the population, changes according to the equation:

$$\begin{aligned}
dp_i(t) = & \underbrace{\left[(w_i(\mathbf{x}) - \bar{w})p_i + \mu \left\{ Q_i(\mathbf{p}) - p_i \left(\sum_{j=1}^m Q_j(\mathbf{p}) \right) \right\} \right]}_{\text{Infinite population predictions: selection-mutation balance for higher fitness}} dt \\
& - \underbrace{\frac{1}{K} \frac{1}{N_K(t)} \left[(\tau_i(\mathbf{x}) - \bar{\tau})p_i + \mu \left\{ Q_i(\mathbf{p}) - p_i \left(\sum_{j=1}^m Q_j(\mathbf{p}) \right) \right\} \right]}_{\text{Directional noise-induced effects: selection-mutation balance for lower turnover rates}} dt \\
& + \underbrace{\frac{1}{\sqrt{K} N_K(t)} \left[(A_i^+)^{1/2} dB_t^{(i)} - p_i \sum_{j=1}^m (A_j^+)^{1/2} dB_t^{(j)} \right]}_{\text{Non-directional noise-induced effects due to stochastic fluctuations}}
\end{aligned} \tag{4.1}$$

where $N_K = \sum x_i$ is the total population size scaled by K (and thus KN_K is the total population size), $A_i^+ = x_i\tau_i(\mathbf{x}) + \mu Q_i(\mathbf{x})$, and each $B_t^{(i)}$ is an independent one-dimensional standard Brownian motion. Equation (4.1) is in ‘replicator-mutator’ form, and letting $K \rightarrow \infty$ recovers the standard replicator-mutator equation in the infinite population limit. The first term represents the direct effects of forces captured in classic deterministic models, and reflects a selection-mutation balance. However, finite populations experience a new directional force dependent on $\tau_i(\mathbf{x})$, the per-capita turnover rate of type i , that cannot be captured in infinite population models (Kuosmanen et al., 2022). Remarkably, this term acts in a way that is mathematically identical to the classical action of selection and mutation in infinite population models as captured by the first term in (4.1), but in the opposite direction - A higher relative τ_i leads to a decrease in frequency (Notice the minus sign before the second term in (4.1)).

4.1.2 The fundamental theorem for the mean value of a type-level quantity in the population

We can now calculate how the statistical mean value of a type-level quantity changes over time. Let f be any type level quantity, with value $f_i(t)$ for the i^{th} type. We allow for the possibility of f_i to vary over time. By multiplying both sides of equation (4.1) by f_i and summing over all i (The same steps as going from (2.38) to (2.41)), we see that the statistical mean \bar{f} of the quantity in the population varies as:

$$\begin{aligned}
 d\bar{f} = & \underbrace{\text{Cov}(w, f)dt}_{\text{Classical selection}} - \underbrace{\frac{1}{KN_K(t)} \text{Cov}(\tau, f)dt}_{\text{Noise-induced selection}} + \underbrace{\overline{\left(\frac{\partial f}{\partial t}\right)} dt}_{\text{Ecological timescale feedbacks due to time-dependence of } f_i} \\
 & + \underbrace{\mu \left(1 - \frac{1}{KN_K(t)}\right) \left(\sum_{i=1}^m f_i Q_i(\mathbf{p}) - \bar{f} \sum_{i=1}^m Q_i(\mathbf{p})\right) dt}_{\text{Transmission bias/mutational effects}} \\
 & + \underbrace{\frac{1}{\sqrt{KN_K(t)}} \left(\sum_{i=1}^m (f_i - \bar{f}) \sqrt{A_i^+} dB_t^{(i)}\right)}_{\text{Stochastic fluctuations}}
 \end{aligned} \tag{4.2}$$

where all covariances are understood in the statistical sense (Note that since w_i , τ_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 (4.2) recovers the standard Price equation as the infinite population limit (either (2.41) or (2.42) based on whether f_i varies with time). We saw in chapter 3 using field equations that very similar methods of attack to those used outlined in chapter (2) also hold for quantitative traits. For example, equation (3.13) and (3.20) are respectively exactly the infinite dimensional analogs of the deterministic replicator-mutator equation (2.38) and the deterministic Price equation (2.42) when f is the trait value. We may therefore expect to find equations similar to (4.1) and (4.2) for quantitative traits. Indeed, measure-theoretic tools have recently been used to rigorously show that an infinite-dimensional version of (4.2) holds for one-dimensional quantitative traits when f is the trait value and $b(x|\phi) \pm d(x|\phi)$ are Gaussian (see equation (21b) in Week et al., 2021). Equations (4.1) and (4.2) are thus fundamental theorems for the evolution of finite populations, with the replicator-mutator and Price equations as their respective infinite population limits (also see (Rice, 2020) for a stochastic Price equation in a discrete-time setting).

Each term in equation (4.2) lends itself to a simple biological interpretation. The first term, $\text{Cov}(w, f)$, is well-understood in the classical Price equation and represents the effect of natural selection in the infinite population setting. In the stochastic Price equation (4.2), the effects of the second term of (4.1) decompose into a selection term $\text{Cov}(\tau, f)$ for reduced turnover rates and a transmission bias term that vanishes in the weak mutation ($\mu \rightarrow 0$) limit. Following Constable et al., 2016 and Week et al., 2021, we refer to the effect of the covariance term (the second term of equation (4.2)) as *noise-induced selection* since it occurs exactly analogously to classical natural selection (but for lower τ) and is induced purely by the finiteness of the population. Since this evolutionary force is unique to finite populations and has therefore been overlooked in classical population genetics, it warrants some more detailed discussion. Biologically, the $\text{Cov}(\tau, f)$ term (with a negative sign) describes a biasing effect due to differential turnover rates and can intuitively be understood as being similar to gambler's ruin in probability theory through the following reasoning: If a type i has a higher τ_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 τ_i . More events mean greater demographic stochasticity, and types with a higher τ_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 (4.1), 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 et al., 2016; McLeod and Day, 2019). Note that types that tend to increase the *total* population size $KN_K(t)$ (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. Further, if altruists/mutualists act by reducing the death rate (rather than increasing the birth rate) of other individuals, their presence causes higher w and lower τ in the beneficiary individuals, both of which are favored by selection (but note that if they act by increasing the birth rate, they increase the magnitude of negative noise-induced selection disfavoring the beneficiary individual), which explains why this effect preferentially favors mutualists in reversing the direction of deterministic selection in finite population models with fluctuating population sizes if interaction effects are on the death rate (McLeod and Day, 2019). Thus, selection for reduced turnover rate could help explain why cooperation often persists in finite population IbMs of social evolution (Houchmandzadeh and Vallade, 2012; Houchmandzadeh, 2015; Chotibut and Nelson, 2015; Behar et al., 2016; McLeod and Day, 2019) despite infinite population models predicting their extinction. The fact that total population size controls the strength of noise-induced selection also explains why cooperation is favored 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 favoring cooperation. The fact that the entire term scales inversely with the total population size $KN_K(t)$ suggests that the effect of this force is weak for large populations, which explains why the persistence of cooperators is often only observed in restrictive sounding conditions such as quasi-neutrality, timescale separation, or a weak selection + weak mutation limit (McLeod and Day, 2019). In all three of these cases, the first term on the RHS of (2.36) becomes identically 0. It therefore no longer contributes to the trait frequency dynamics, thus allowing us to see the (otherwise weak) contributions of the second term.

The third term of (4.2) is relevant in both finite and infinite populations whenever f_i can vary over time and represents feedback effects on the quantity f_i of the i^{th} species over short (‘ecological’) time-scales. Such feedback is often through a changing environment or phenotypic/behavioral plasticity, but other biological phenomena may also be at play. The

fourth term of (4.2) is a transmission bias term, with a correction factor due to noise-induced selection. Finally, the last term of (4.2) describes the role of stochastic fluctuations. The contributions of this last term are ‘directionless’ due to the dB_t factors, and this term vanishes when we take a conditional expectation value over the underlying probability space. I will denote this probabilistic expectation value operation by $\mathbb{E}[\cdot]$ to distinguish it from the statistical mean \bar{f} of a type-level quantity in the population (see section 2.3.4 for a brief discussion on the difference between statistical averages and probabilistic expectations in this context). Note that this expectation is conditioned on the initial state of the population, and thus $\mathbb{E}[\cdot]$ is really shorthand for $\mathbb{E}[\cdot \mid \mathbf{X}_0 = \mathbf{x}_0]$.

Two particularly interesting implications of (4.2) are realized upon ignoring mutations by setting $\mu = 0$ and then substituting $f = w$ and $f = \tau$. We first note that:

$$\text{Cov}(w, \tau) = \text{Cov}(b^{(\text{ind})}(\mathbf{x}) - d^{(\text{ind})}(\mathbf{x}), b^{(\text{ind})}(\mathbf{x}) + d^{(\text{ind})}(\mathbf{x})) \quad (4.3)$$

$$= \sigma_{b^{(\text{ind})}(\mathbf{x})}^2 - \sigma_{d^{(\text{ind})}(\mathbf{x})}^2 \quad (4.4)$$

It is important to remember once again that just like the statistical mean, the statistical variance $\sigma_f^2(t)$ of a type-level quantity f is a random variable obtained by calculating the variance of the quantity *in the population* at time t , and is not to be confused with the probabilistic/ensemble variance obtained by calculating the variance of a quantity *over different realizations* of the stochastic process (see section 2.3.4). Upon substituting $f = w$ in (4.2) and taking expectations over the underlying probability space, we obtain:

$$\mathbb{E}\left[\frac{d\bar{w}}{dt}\right] = \underbrace{\mathbb{E}\left[\sigma_w^2\right]}_{\substack{\text{Fisher's} \\ \text{Fundamental} \\ \text{theorem}}} - \underbrace{\mathbb{E}\left[\frac{\sigma_{b^{(\text{ind})}}^2 - \sigma_{d^{(\text{ind})}}^2}{KN_K(t)}\right]}_{\substack{\text{Noise-induced} \\ \text{selection}}} + \underbrace{\mathbb{E}\left[\overline{\frac{\partial w}{\partial t}}\right]}_{\substack{\text{Short-term (ecological)} \\ \text{feedbacks to fitness}}} \quad (4.5)$$

Taking $K \rightarrow \infty$ in (4.5) recovers a well-known equation in population genetics upon noting that the process tends to a deterministic process as $K \rightarrow \infty$, as noted in section 2.3.6, and thus the expectation value in the infinite population case is superfluous. The first term, σ_w^2 , is the subject of Fisher’s fundamental theorem (Fisher, 1930; Price, 1972; Frank and Slatkin, 1992; Kokko, 2021). The second term of equation (4.5) is a manifestation of noise-induced selection and vanishes in the infinite population limit, and is thus particular to finite populations. Finally, the last term arises in both finite and infinite populations whenever w_i can vary over time (Frank and Slatkin, 1992; Kokko, 2021; Baez, 2021), be-

it through frequency-dependent selection, phenotypic plasticity, varying environments, or other ecological mechanisms, and represents feedback effects on the fitness w_i of the i^{th} species over short ('ecological') time-scales. The fact that Fisher appears to have been rather vague and dismissive of this feedback (Fisher, 1930) has led to much discussion, debate, and confusion about the interpretation, importance, and implications of his 'fundamental theorem' (see Kokko, 2021 and sources cited therein).

Carrying out the same steps with $f = \tau$ in (4.2) yields a new equation/theorem due to Kuosmanen et al., 2022 that has only recently been recognized as important. This theorem is an analog of Fisher's fundamental theorem for the turnover rates, and reads:

$$\mathbb{E} \left[\frac{d\bar{\tau}}{dt} \right] = \underbrace{\mathbb{E} [\sigma_{b^{(\text{ind})}}^2 - \sigma_{d^{(\text{ind})}}^2]}_{\text{Classical selection effects}} - \underbrace{\mathbb{E} \left[\frac{\sigma_\tau^2}{KN_K(t)} \right]}_{\text{Noise-induced selection effects}} + \underbrace{\mathbb{E} \left[\overline{\frac{\partial \tau}{\partial t}} \right]}_{\text{Short-term (ecological) feedbacks to } \tau_i} \quad (4.6)$$

The implications of this theorem have been extensively discussed in (Kuosmanen et al., 2022), which is where we refer the interested reader.

4.1.3 The fundamental theorem for the variance of a type-level quantity in the population

Equation (4.2) is a general equation for the mean value of an arbitrary type level quantity f in the population. In many real-life situations, especially those pertaining to finite populations, we are interested in not just the mean, but also the variance of a type-level quantity. In Appendix C, I show that the statistical variance of any type level quantity f obeys

$$\begin{aligned} d\sigma_f^2 &= \text{Cov}(w, (f - \bar{f})^2) dt - \frac{1}{KN_K} [\bar{\tau}\sigma_f^2 + 2\text{Cov}(\tau, (f - \bar{f})^2)] dt \\ &\quad + 2\text{Cov}\left(\frac{\partial f}{\partial t}, f\right) dt + M_{\sigma_f^2}(\mathbf{p}, N_K) dt + \frac{1}{\sqrt{KN_K(t)}} dB_{\sigma_f^2} \end{aligned} \quad (4.7)$$

where

$$M_{\sigma_f^2}(\mathbf{p}, N_K) = \mu \left[\left(1 - \frac{2}{KN_K}\right) \left(\sum_{i=1}^m (f_i - \bar{f})^2 Q_i(\mathbf{p})\right) + \sigma_f^2 \left(1 - \frac{1}{KN_K}\right) \sum_{i=1}^m Q_i(\mathbf{p}) \right] \quad (4.8)$$

is a mutational term that vanishes in the $\mu \rightarrow 0$ limit and

$$dB_{\sigma_f^2} = \sum_{i=1}^m (f_i - \bar{f})^2 \sqrt{A_i^+} dB_t^{(i)} \quad (4.9)$$

is a stochastic integral term measuring the (non-directional) effect of stochastic fluctuations that vanishes upon taking an expectation over the probability space. In the case of one-dimensional quantitative traits, an infinite-dimensional version of (4.7) has recently been rigorously derived (Week et al., 2021) using measure-theoretic tools under certain additional assumptions (See equation (21c) in Week et al., 2021). Taking expectations over the probability space in (4.7) and substituting mutation as acting via a Gaussian kernel also recovers equations previously derived (Débarre and Otto, 2016) in the context of evolutionary branching in finite populations as a special case (Equation A.23 in Débarre and Otto, 2016 is equivalent to equation (4.7) for their choice of functional forms upon converting their change in variance to an infinitesimal rate of change *i.e.* a derivative). An infinite population ($K \rightarrow \infty$) version of equation (4.7) also appears in Lion, 2018.

Once again, terms of equation (4.7) lend themselves to straightforward biological interpretation. The quantity $(f_i - \bar{f})^2$ is a measure of the distance of f_i from the population mean value \bar{f} , and thus covariance with $(f - \bar{f})^2$ quantifies the type of selection operating in the system: A negative correlation is indicative of stabilizing selection, and a positive correlation is indicative of disruptive (*i.e.* diversifying) selection. An extreme case of diversifying selection for fitness occurs if the mean fitness is at a local minimum for fitness but $f_i \not\equiv \bar{f}$ (*i.e.* the population still exhibits some variation in f). In this case, if the variation in f is associated with a variation in fitness, then $\text{Cov}(w, (f - \bar{f})^2)$ is strongly positive and the population experiences a sudden explosion in variance, causing the emergence of polymorphism in the population. If $\text{Cov}(w, (f - \bar{f})^2)$ is still positive after the initial emergence of multiple morphs, evolution eventually leads to the emergence of stable coexisting polymorphisms in the population - This phenomenon is a slight generalization of the idea of evolutionary branching that occurs in frameworks such as adaptive dynamics (Geritz et al., 1998).

The $\text{Cov}(\partial f / \partial t, f)$ term once again represents the effect of eco-evolutionary feedback loops due to rapid change in f that is not solely due to changes in \mathbf{p} . The $M_{\sigma_f^2}(\mathbf{p}, N_K)$ term quantifies the effect of mutations on the variance of f . Note that each $Q_i(\mathbf{p}) \geq 0$ by its definition in (2.32) and thus $\sum_i Q_i(\mathbf{p}) > 0$ if there are any mutational effects (and = 0 otherwise). Furthermore, the total population size $KN_K > 2$ for most interesting

evolutionary questions. Thus, from (4.8), it is clear that when $\mu > 0$ (*i.e.* there is mutation in the system), we have $M_{\sigma_f^2}(\mathbf{p}, N_K) > 0$, meaning that mutations always increase the variance of f in the population.

The $\bar{\tau}\sigma_f^2$ term represents a loss of diversity due to stochastic extinctions (*i.e.* demographic stochasticity). To see this, it is instructive to consider the case in which this is the only force at play. Let us imagine a population of asexual organisms in which each f_i is simply a label or mark arbitrarily assigned to individuals in the population at the start of an experiment/observational study and subsequently passed on to offspring - For example, a neutral genetic tag in a part of the genome that experiences a negligible mutation rate. Let us set $\mu = 0$ so that the labels cannot change between parents to offspring. This means that we have $M_{\sigma_f^2}(\mathbf{p}, N_K) \equiv 0$. Further, since the labels are arbitrary and have no effect whatsoever on the biology of the organisms, we have $\text{Cov}(w, (f - \bar{f})^2) \equiv \text{Cov}(\tau, (f - \bar{f})^2) \equiv 0$. Since the labels do not change over time, we also have $\text{Cov}(\partial f / \partial t, f) = 0$. From (4.7), we see that in this case, the variance changes as

$$d\sigma_f^2 = -\frac{\bar{\tau}\sigma_f^2}{KN_K}dt + \frac{1}{\sqrt{KN_K(t)}}dB_{\sigma_f^2} \quad (4.10)$$

On taking expectations, the second term on the RHS vanishes and we see that the expected variance in the population obeys

$$\frac{d\mathbb{E}[\sigma_f^2]}{dt} = -\left(\mathbb{E}\left[\frac{\bar{\tau}}{KN_K}\right]\right)\mathbb{E}[\sigma_f^2] \quad (4.11)$$

where we have decomposed the expectation of the product on the RHS into a product of expectations, which is admissible since the label f is completely arbitrary and thus independent of both $\bar{\tau}$ and $N_K(t)$. Equation (4.11) is a simple linear ODE and has the solution

$$\mathbb{E}[\sigma_f^2](t) = \sigma_f^2(0)e^{-\mathbb{E}\left[\frac{\bar{\tau}}{KN_K}\right]t} \quad (4.12)$$

which tells us that the expected diversity (variance) of labels in the population decreases exponentially over time. The rate of loss is $\mathbb{E}[\bar{\tau}(KN_K)^{-1}]$, and thus, populations with higher mean turnover $\bar{\tau}$ and/or lower population size KN_K lose diversity faster. This is because populations with higher $\bar{\tau}$ experience more stochastic events per unit time (a gambler's ruin type scenario), while extinction is 'easier' in smaller populations because a smaller number of deaths is required to eliminate a label from the population completely. Note

that *which* labels/individuals are lost is entirely random (since all labels are arbitrary), but nevertheless, labels tend to be stochastically lost until only a small number of labels remain in the population.

4.2 A stochastic field theory for quantitative traits

In chapter 3, we formulated a ‘field equation’ for the evolution of one-dimensional quantitative traits in populations. To recap, given a one-dimensional quantitative trait that takes values in a trait space $\mathcal{T} \subseteq \mathbb{R}$, we defined the set $\mathcal{M}(\mathcal{T}) = \{\sum_{i=1}^n \delta_{x_i} \mid n \in \mathbb{N}, x_i \in \mathcal{T}\}$, where each δ_{x_i} is a Dirac mass centered at x_i . We then formulated a model in which the population at time t is characterized as a whole by a randomly varying density distribution (‘stochastic field’) $\nu^{(t)} : \mathcal{M}(\mathcal{T}) \rightarrow [0, \infty)$ such that for any subset $A \subseteq \mathcal{T}$, the number of individuals that have trait value in A is given by integrating $\nu^{(t)}$ over A . The change of this field is determined entirely by two functionals, $b(x|\nu)$ and $d(x|\nu)$ from \mathcal{T} to $[0, \infty)$, that respectively describe the birth rate and death rate of individuals of type x in a population ν . Under the assumption that there exists a suitable system size parameter $K > 0$, we moved from the space of ‘number’ distribution functions $\mathcal{M}(\mathcal{T})$ to the space of ‘density’ distribution functions $\mathcal{M}_K(\mathcal{T}) = \{\sum_{i=1}^n \delta_{x_i}/K \mid n \in \mathbb{N}, x_i \in \mathcal{T}\}$ via a functional analog of the system size expansion. By appropriately rescaling the birth and death rate functionals, we then determined that $P(\phi, t)$, the probability that the population is described by the distribution $\phi \in \mathcal{M}_K(\mathcal{T})$ at time t , (approximately) satisfies the ‘stochastic field equation’:

$$\frac{\partial P}{\partial t}(\phi, t) = \int_{\mathcal{T}} \left[-\frac{\delta}{\delta \phi(x)} \{ [\phi(x)w(x|\phi) + \mu Q(x|\phi)] P(\phi, t) \} + \frac{1}{2K} \frac{\delta^2}{\delta \phi(x)^2} \{ [\phi(x)\tau(x|\phi) + \mu Q(x|\phi)] P(\phi, t) \} \right] dx \quad (4.13)$$

where $w(x|\phi)$, $\tau(x|\phi)$, and $Q(x|\phi)$ are functionals that respectively describe the Malthusian fitness, per-capita turnover rate, and birth rate due to mutations (with mutation rate μ) of type $x \in \mathcal{T}$ individuals (now a continuous variable) in a population ϕ . We then saw that this equation yields some well-known frameworks of quantitative genetics in the infinite population ($K \rightarrow \infty$) limit, thus illustrating consistency with known theories. If the ‘intuitive’ version of Itô’s formula for $\mathcal{M}_K(\mathcal{T})$ valued stochastic processes obtained by ‘taking the limit’ $m \rightarrow \infty$ in the Itô’s formula for m -dimensional stochastic processes holds, then the exact same steps carried out in Appendices B and C will ‘go through’ essentially unchanged for quantitative traits and yield the equations obtained by simply taking $m \rightarrow \infty$ in (4.1), (4.2) and (4.7) (with sums replaced by integrals and derivatives replaced by functional derivatives

as appropriate) as the ‘fundamental theorems’ for the evolution of quantitative traits. Indeed, Week et al., 2021 have recently proposed exactly the Itô formula we would need via a heuristic Itô multiplication table for $L^2(\mathbb{R}, m)$ valued processes with a.s. finite Hilbert-Schmidt norm and have shown that their heuristics are equivalent to the rigorous infinite-dimensional stochastic calculus proposed by Da Prato and Zabczyk, 2014 for more general Hilbert space valued processes¹. Furthermore, using these ‘spacetime white noise heuristics’ together with a particular functional form for (weak) solutions to certain SPDEs, Week et al., 2021 have arrived at precisely the infinite-dimensional version of equations (4.2) and (4.7) obtained by ‘taking the limit’ $m \rightarrow \infty$ in (4.2) and (4.7) from the ‘SPDE side’ under certain additional assumptions required to ensure existence/uniqueness of solutions to the relevant SPDEs. Equation (4.13) can thus be argued to be the (functional) Fokker-Planck view of the stochastic processes for the evolutionary ecology of quantitative traits recently studied in Week et al., 2021. Like Week et al., 2021, I believe that rigorously establishing the precise criteria needed for general existence and uniqueness of solutions to equations of the form (4.13) (or the SPDE versions presented in Week et al., 2021, which resemble our equation (3.7)) presents an important mathematical direction for future work that may yield new insights into both the biology of quantitative traits and the mathematics of measure-valued stochastic processes.

More generally, the well-known intimate relation between Itô SDEs and Fokker-Planck equations (see section 2.1) is extremely useful, and indeed has been extensively exploited (Van Kampen, 1981; Øksendal, 1998; Gardiner, 2009), because many problems are much more easily attacked using probabilistic tools that operate on Itô process, whereas others are more amenable to study using tools from PDE theory that operate on the Fokker-Planck equations. In the infinite-dimensional case, working with the ‘physics’ side through functional Fokker-Planck equations such as (4.13) allows us to use tools with an essentially ‘differential equation’ flavor such as spectral methods (Rogers et al., 2012a; Rogers and McKane, 2015; See also Appendix D for a general model-independent pedagogical example for studying phenotypic clustering and evolutionary branching), slow manifold (‘adiabatic’) approximations (Parsons and Rogers, 2017), and WKB style expansions (Rogers et al., 2012a; Assaf and Meerson, 2017; though it bears noting that WKB theory is closely related to large deviation

¹If this sentence sounds like technical gibberish to you, don’t worry too much about the details - The essence is that Week et al., 2021 have proven the ‘correct’ formula we need holds whenever $b(x|\nu)$, $d(x|\nu)$ and $\mathcal{M}_K(\mathcal{T})$ together fulfill certain technical requirements. My heuristics here are only a ‘first step’ and have focused on accessibility over mathematical propriety, and thus make no attempt to verify whether and when these technical requirements are satisfied.

principles that occur in the study of Markov processes and come in a distinctly ‘probabilistic’ flavor, see for example Dembo and Zeitouni, 1998). On the other hand, many biologically interesting questions are much easier to approach from the ‘mathematics’² side by working with branching processes/SPDEs and using tools that have an essentially ‘probabilistic’ flavor such as duality (Dawson, 1975; Greenman, 2020), infinitesimal generators (semigroup theory), weak/mild solutions, and the martingale problem (See for example Etheridge, 2011 or Week et al., 2021). Rigorously establishing a relation between functional Fokker-Planck equations of the form (4.13) and SPDEs of the form (3.7) (or those studied in Week et al., 2021) for measure-valued branching processes could thus prove very fruitful for developing more integrative eco-evolutionary theory since it allows us to seamlessly transition between complementary views of the same object.

To the best of my knowledge, a general formulation of stochastic field equations for the population dynamics of quantitative traits from the functional Fokker-Planck side in the manner I have carried out here has not been done before. Similar equations have been formulated for some specific stochastic models of quantitative trait evolution (Rogers et al., 2012a; Rogers and McKane, 2015) and population ecology of size-structured communities (O’Dwyer et al., 2009). Stochastic field equations are also known in mathematical neurobiology (Buice and Cowan, 2007; Bressloff, 2010; Coombes et al., 2014), and have recently been proposed in a model of collective motion (Ó Laighléis et al., 2018). Broadly similar deterministic field theoretic approaches have also been proposed to study bio-geography and spatial biodiversity patterns such as the species-area relationship (O’Dwyer and Green, 2010; But see Grilli et al., 2012 for an explanation of why the calculations presented in O’Dwyer and Green, 2010 are not exactly correct³). The ubiquity of such approaches in diverse areas of theoretical biology suggests that the formal systematic study and analysis of such equations could have wide-spread applications. Currently, (stochastic) field equations are primarily used by physicists working in areas such as statistical field theory and quantum field theory, and are largely attacked using ingenious and often somewhat system-specific tools that may not necessarily be mathematically well understood (Carmona and Rozovskii, 1999; but see Bogachev et al., 2015 for a rigorous treatment of some infinite-dimensional Fokker-Planck equations). Equation (4.13) opens up the study of quantitative trait dynamics in finite fluctuating popu-

²The ‘mathematics’ vs ‘physics’ distinction is just a caricature and is not intended to be read into or thought about too deeply :)

³The essential problem is that an assumption about time reversibility (‘detailed balance’ in more accurate physics lingo), usually made for equilibrium systems, is not satisfied. Nevertheless, the general *approach* is still interesting and seems reasonable

lations to analysis using some of these tools - For example, a careful reading of the literature provides many hints and recent attempts illustrating how the major ideas behind the Fock space representation (Del Razo et al., 2022), perturbative ‘loop diagrams/expansions’ (Dodd and Ferguson, 2009), and the path integral formalism (Doi, 1976; Peliti, 1985; Chow and Buice, 2015; Weber and Frey, 2017) can all be co-opted to coax biological insights from the sort of stochastic processes modeled by (4.13).

Equation (4.13) thus provides a (relatively) more accessible alternative formulation that does not (explicitly) rely on tools from relatively ‘advanced’ mathematical fields such as martingale theory and stochastic analysis that are typically used to study the evolution of quantitative traits in finite, fluctuating populations (Dawson, 1975; Fleming and Viot, 1979; Ethier and Kurtz, 1986; Champagnat et al., 2006; Etheridge, 2011; Week et al., 2021). This is intended to make the models and ideas more accessible to theorists without formal training in mathematical areas such as measure theory and functional analysis and encourage the use of techniques from physics and related domains, as outlined in the paragraphs above. Importantly, the formalism I develop here in terms of functional Fokker–Planck equations likely does *not* carry over to the study of higher dimensional quantitative traits (or populations which vary in two or more one-dimensional quantitative traits) because these processes are routinely badly behaved in higher dimensions: In particular, a probability density $P(\phi, t)$ with respect to the reals frequently does not even exist in higher dimensions if one has any biologically non-trivial features such as interactions between types (Fleming and Viot, 1979; Walsh, 1986; Also see for example Evans and Perkins, 1994), rendering equation (4.13) entirely meaningless. My (admittedly limited) understanding is that such processes are also rather difficult to study in two or more dimensions from the SPDE side for similar reasons since one is forced to work with distribution valued (rather than function valued) solutions and thus needs to use a considerable amount of advanced functional analysis to establish even basic existence-uniqueness results (Walsh, 1986; Carmona and Rozovskii, 1999; Prévôt and Röckner, 2007; Liu and Röckner, 2015; Balan, 2018). It may well be the case that concrete biologically useful progress in this direction requires new mathematics altogether, a situation increasingly also encountered in other areas of mathematical biology (Vittadello and Stumpf, 2022). Just as theoretical physics has done in the past, the pursuit of general mathematical descriptions of biological theory may therefore also inspire new ideas that are of independent interest to ‘pure’ mathematicians (Cohen, 2004).

4.3 Discussion & Outlook

Stochastic finite population models often exhibit behaviors that are markedly different from their deterministic limits. 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 trying to work with stochastic models, several theorists have called for a reformulation of eco-evolutionary dynamics of finite populations starting from stochastic birth-death processes on the grounds that such a formulation is more fundamental and mechanistic (Metcalf and Pavard, 2007a; Geritz and Kisdi, 2012; Doebeli et al., 2017). Part II of this thesis develops such a mechanistic theory for both populations of individuals that vary in some discrete character (chapter 2) as well as populations of individuals that vary in a single one-dimensional quantitative character (chapter 3). The central result of this reformulation is an equation for change in type frequencies in the population (equation (4.1)) that generalizes the replicator-mutator equation to finite, fluctuating, closed populations evolving in continuous time. From this, we can derive an equation for changes in the population mean of a type-level quantity (equation (4.2)) that is a generalization of the Price equation to finite populations, as well as an equation for changes in population variance of a type-level quantity (equation (4.7)) in such populations. My work thus generalizes some fundamental formal structures of eco-evolutionary population dynamics to finite, fluctuating populations. In particular, my equations generalize the unifying formalism described in Lion, 2018⁴ to finite, fluctuating populations - Taking $K \rightarrow \infty$ in equations (4.1), (4.2), and (4.7) recover equations (6), (11), and (14) in Lion, 2018 respectively as their infinite population limits. Several theorists have called for a reformulation of eco-evolutionary dynamics starting from stochastic birth-death processes on the grounds that such a formulation is more fundamental and mechanistic (Metcalf and Pavard, 2007a; Geritz and Kisdi, 2012; Doebeli et al., 2017). My work provides some fundamental relations that any such reformulation must satisfy. These relations deal with biologically important quantities, lend themselves to simple biological interpretation, and are very general. They thus fulfill the criteria to be called ‘fundamental theorems’ (in the sense of Queller, 2017), or ‘unifying principles’ (in the sense of Lion, 2018) for the dynamics of finite populations. While my equations recover standard results such as

⁴which itself is a reformulation of the relatively well-known unification of eco-evolutionary dynamics via the Price equation (Frank, 2012; Queller, 2017; Luque and Baravalle, 2021) in a dynamically sufficient continuous time framework

the Price equation and the replicator-mutator equation in the infinite population limit, they also predict that these results do not completely capture the behavior of finite populations.

More precisely, the formalism studied in this thesis predicts a directional evolutionary force acting on variation in per-capita turnover rate τ that I call ‘noise-induced selection’. Noise-induced selection is only seen in finite populations and arises due to different types of individuals in the population experiencing a different number of stochastic events (birth and death) in a given time interval. Several specific finite population models illustrate that evolution in finite population can proceed in the direction opposite to that predicted by the infinite population limit, a phenomenon sometimes referred to as ‘reversing the direction of deterministic selection’ (Parsons et al., 2010; Houchmandzadeh, 2015; Behar et al., 2016; Constable et al., 2016; McLeod and Day, 2019). Most recently, a study showed that in a very broad class of competition models, noise-induced selection in finite populations can act in opposition to the direction of natural selection predicted in the infinite population limit (Mazzolini and Grilli, 2022). My thesis generalizes this particular result of Mazzolini and Grilli, 2022 to models with arbitrary interaction types and presents the relevant equations in a formalism that is more in accordance with standard biological models such as the Price equation. It is worth noting that the existence of noise-induced selection directly implies (from equation (4.1) or (4.2)) that evolution is not expected to maximize fitness in finite populations even if fitness is entirely frequency independent as long as there is some (heritable) variation in the turnover rates τ_i , further underscoring the now well-appreciated point that the view of evolution as ‘climbing a hill’ on a fitness landscape and thereby maximizing fitness is rather limited (Grodwohl, 2017).

The equations of section 4.1 also imply that for the evolution of a trait to be *truly* neutral in finite populations (in the sense of all m types in a system having equal fixation/extinction probability if we start with an initial state in which every type has frequency $1/m$), it is not sufficient for the trait in question to be neutral with respect to fitness w . Instead, we also require the trait to be neutral with respect to turnover rate τ . Indeed, in ecological models, previous work has numerically shown that in finite, fluctuating populations, the equal growth rate of types is not sufficient to ensure equal fixation probabilities and that there is a slight biasing for types with lower turnover rates, sometimes interpreted as a selection ‘for longevity’ (Lin et al., 2012; Oliveira and Dickman, 2017; Balasekaran et al., 2022). In models of evolutionary game theory in fluctuating finite populations, individuals with lower death rates have higher fixation probability even when growth rates are equalized (Huang

et al., 2015; Czuppon and Traulsen, 2018). Similarly, models of cell cycle dynamics find that selection favors cell types that periodically arrest their cell cycle relative to non-arresting cells even when their growth rates are equal (Wodarz et al., 2017). In the language of our birth-death formalism, all of these studies equalize the growth rates w of competing types but allow the turnover to vary (by reducing the birth rate through arresting the cell cycle, for example), thus allowing noise-induced selection for reduced turnover to operate in the system. My derivations show analytically that such deviations from neutrality in finite populations are a generic phenomenon explained by noise-induced selection and should be expected whenever there is variation in turnover rates. Selection on turnover rates also leads to insights on life-history evolution, and these insights have been extensively reported in a recent paper that uses certain discrete time stochastic processes and their approximation via techniques reminiscent of numerical stochastic integration to arrive at a formalism mathematically equivalent to our equations (Kuosmanen et al., 2022). The equivalent of my stochastic equations has also recently been derived for quantitative traits from a very different starting point⁵ using the theory of measure-valued branching processes (Week et al., 2021) - Equations (21b) and (21c) in Week et al., 2021 are exactly the $m \rightarrow \infty$ version of our equations for changes in the mean value of a type-level quantity and changes in the variance of a type-level quantity respectively for the special case in which the type-level quantity is the value of the quantitative trait being studied.

On the practical side, the existence of noise-induced selection implies that simulation studies working with evolutionary individual-based or agent-based models should be careful about whether interaction effects are incorporated into birth rates or death rates since this seemingly arbitrary choice can have unintended consequences due to noise-induced selection, thus potentially biasing results (McLeod and Day, 2019; Kuosmanen et al., 2022). Being mindful of noise-induced selection is also important for applied fields like conservation and population management which regularly deal with small populations. For example, when trying to increase the population of a hypothetical desired species in a multispecies community, increasing the birth rate is *not* equivalent to reducing the death rate even though both result in an increase in the Malthusian fitness (growth rate) w_i . Decreasing the death rate leads to a decrease in τ_i , which leads to positive noise-induced selection, whereas increasing the birth rate leads to an increase in τ_i , which leads to noise-induced selection acting to reduce the abundance of the focal species from the community. If the total community

⁵See Section 4.2 above for a detailed discussion on how the field equation approach I used in 3 for quantitative traits is related to Week et al., 2021's SPDE approach

size is small, increasing the birth rate of a species can thus lead to noise-induced selection completely eliminating the focal species from the community despite the fact that we *increased* the growth rate of this species. Raatz and Traulsen, 2023 have recently used a similar birth-death framework to study cancer treatment and thus provide a concrete example of the consequences of this asymmetry between changing birth rates and death rates: Due to the presence of noise-induced selection, the potential of a tumorous growth to adapt to treatments and experience evolutionary rescue depends inversely on the per-capita turnover τ_i of the constituent cancer cells in their model, with obvious implications for optimal treatment strategies. My results also indicate that measuring the growth rate of populations is not, in general, sufficient for accurate prediction/inference of future trajectories of the relative abundance of a species (or phenotype, allele, etc.) from empirical data even in completely controlled environments. The growth rate $w_i = b_i^{(\text{ind})} - d_i^{(\text{ind})}$ of a species i only specifies the difference between its per-capita birth and death rates. In contrast, the complete stochastic dynamics also depend on the total turnover $\tau_i = b_i^{(\text{ind})} + d_i^{(\text{ind})}$ (*i.e.* the sum of the per-capita birth and death rates).

At first glance, the idea of an evolutionary force that selects individuals with lower birth and death rates over individuals with higher birth and death rates may be reminiscent of notions in life-history evolution like r vs K selection or selection on the pace of life in stochastic models (Stearns, 1977). However, it is unclear whether this similarity reflects some deep principle or whether it is just superficial. Models in life-history theory are often primarily concerned with spatio-temporally fluctuating (external) environments, and thus the stochasticity in those models is extrinsic to the population. Ecological frameworks such as modern coexistence theory, which deal with similar questions about population dynamics as our model and would benefit from a first principles stochastic birth-death formulation, also typically work with fluctuating external environments (Chesson, 1982; Chesson, 1994). We have entirely neglected such extrinsic factors in our formalism. In principle, it is possible to make the birth and death rates (2.32) in our model also depend on a temporally varying external environment $E(t)$ (whose variation may possibly depend on the population $\mathbf{v}(t)$). Incorporating such a term would ensure that the ‘ecological feedback’ terms in equations (4.2) and (4.7) are non-zero, but may also lead to much more complex dynamics. If the variation of the environment $E(t)$ has some associated stochasticity, the complete dynamics of the system would be the result of interactions between two qualitatively different forms of noise — *extrinsic* noise from the environment, and *intrinsic* noise from the finiteness of the population — and thus will be rather complicated and likely difficult to handle

analytically. Indeed, experimental studies indicate that (fluctuating) finite population size and fluctuating environments can interact in complex and sometimes counter-intuitive ways, with implications for evolvability and adaptation in spatio-temporally fluctuating environments (Chavhan et al., 2020; Chavhan et al., 2021). Thus, while integrating the birth-death framework I outline here with ecological ideas such as the pace-of-life syndrome (Mathot and Frankenhuis, 2018; J. Wright et al., 2019) or modern coexistence theory (Chesson, 1994; E. Johnson and Hastings, 2022) is biologically appealing, it is likely far from trivial and may present a promising avenue for future work.

Lion, 2018 has pointed out that in the dynamic setting (for infinite populations), the replicator-mutator equation (2.38) is in some sense the ‘most fundamental’ of the lot, and equations like the Price equation are best viewed as a hierarchy of moment equations for the population mean, population variance, etc. of a type-level quantity. This is also true in my framework - Equation (4.1) is the most fundamental equation for population dynamics, and equations like (4.2) and (4.7) can then be derived from (4.1) through repeated application of Itô’s formula, in principle for any moment of the distribution of the quantity f in the population (though this quickly becomes too tedious to actually carry out in practice). If we additionally assume that the quantity f follows a Gaussian distribution in the population, then the mean and variance completely characterize the distribution of f , and equations (4.1), (4.2), and (4.7) together specify the complete stochastic dynamics of the system. Note that even in this case, actually solving these equations analytically for equilibrium/stationary state distributions of \mathbf{p} , \bar{f} , and σ_f^2 will quickly become impossibly difficult if the birth and death rate functions are complicated. Indeed, previous studies indicate that in high dimensions, evolutionary birth-death models can exhibit a dizzying array of complicated phenomena, including limit cycles and evolutionary chaos (Doebeli and Ispolatov, 2017). My framework also works with unstructured populations, neglecting any population structure due to age, class, developmental stage, or space, all of which can lead to complex dynamics and greatly reduce analytical tractability. Lastly, I have also neglected any potential complications introduced by genotype-phenotype maps and genetic processes such as dominance, epistasis, and pleiotropy since they can (in principle) be incorporated while defining the per-capita birth and death rates and our equations hold for arbitrarily complicated birth and death rates as long as they are of the functional form (2.32).

The points outlined above present practical impediments to actually solving the equations I present for particular models. However, I argue that trying to solve these equations

‘misses the point’ of formulating our model. The equations of section 4.1 are very general, since part II makes essentially no assumptions other than density dependence, the impossibility of infinite growth starting from finite population size, and the ability to define per-capita birth and death rates. Further, as we saw in section 4.1, the terms of the equations lend themselves to simple biological interpretation. Like the classical Price equation, the utility of the equations of section 4.1 lies not (necessarily) in their solutions for specific models, but instead in their generality and the fact that their terms help us clearly understand the various forces operating in biological populations (Frank, 2012; Luque, 2017; Luque and Baravalle, 2021). The general spirit of this thesis is thus in line with the idea of building a ‘model-independent’ eco-evolutionary theory that has recently been gaining popularity in the literature (Grafen, 2014; Queller, 2017; Lion, 2018; Allen and McAvoy, 2019; Rice, 2020; Week et al., 2021; Wickman et al., 2022; Kuosmanen et al., 2022; Mazzolini and Grilli, 2022; Lion et al., 2023; Allen et al., 2023). Descriptions such as the classical Price equation and the equations I present in this thesis ‘abstract away’ system-specific details and almost inevitably come at the cost of precision (Levins, 1966; Potochnik, 2018). These approaches are thus intended to complement empirical studies and modelling approaches that carefully study specific systems. To quote Robert Millikan’s 1924 Nobel lecture, “Science walks forward on two feet, namely theory and experiment [...] Sometimes it is one foot which is put forward first, sometimes the other, but continuous progress is only made by the use of both - by theorizing and then testing, or by finding new relations in the process of experimenting and then bringing the theoretical foot up and pushing it on beyond, and so on in unending alterations.”

Appendix A

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 $\Omega \subseteq \mathbb{R}$ that admits a probability density function $P(x, t)$ on $\Omega \times [0, \infty)$. Let $f : \mathbb{R} \rightarrow \mathbb{R}$ be an arbitrary $C^2(\mathbb{R})$ function. By Itô's formula, we have:

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

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’, 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 γ 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

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

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 $f(x)$, we are thus led to conclude that the density function $P(x, t)$ must satisfy:

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

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

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

where $\mathbf{D} = \sigma\sigma^T$. Some authors like to define the ‘probability current’ $\mathbf{J}(\mathbf{x}, t)$, an m -dimensional function with i^{th} element

$$J_i(\mathbf{x}, t) := \mu_i(\mathbf{x}, t)P(\mathbf{x}, t) - \frac{1}{2} \sum_{j=1}^m \frac{\partial}{\partial x_j}(D_{ij}P(\mathbf{x}, t))$$

In this notation, equation (A.6) can be written in the more compact form:

$$\frac{\partial P}{\partial t} + \nabla \cdot \mathbf{J} = 0 \quad (\text{A.7})$$

where $\nabla \cdot$ is the divergence operator (also denoted div in some texts). Those familiar with physics should immediately recognize that equation (A.7) is in the form of a so-called ‘continuity equation’ for a conserved quantity. Continuity equations turn up in various areas of applied mathematics, most famously in electromagnetism (conservation of charge from Maxwell’s equations), fluid dynamics (continuity equations for mass of a flowing fluid from the Euler equations), and molecular diffusion (Fick’s law). This explains the name ‘probability current’ as an analogy to currents in physics such as electrical current or fluid current. The continuity equation representation also makes it clear that the Fokker-Planck equation describes the ‘flow of probability’ in the system. In particular, equation (A.7) says that the total probability in the system is ‘conserved’, and is thus simply a mathematical formalization of the common-sense idea that whenever the probability of the system of being in a given state decreases, the probability of it being in some other state must increase (and vice versa).

Appendix B

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 $f([x_1, \dots, x_m]^T)$ 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 (2.31), 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^{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 size¹ $N = \sum_i x_i$ and the frequency of the i^{th} type $p_i = f_i(x)$ and used the fact that $\frac{\partial x_j}{\partial x_k} = \delta_{jk}$. The jk^{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:

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

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

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

This term describes the effects of selection and mutation at the infinite population limit. However, the finiteness of the population adds a second directional term to these dynamics, described by the second term that multiplies dt in (B.1). To calculate it, we first calculate:

$$\begin{aligned}
\frac{1}{\sqrt{K}} (H_{\mathbf{x}} f_i \mathbf{D})_{jk} &= \frac{1}{\sqrt{K}} \sum_{l=1}^m (H_{\mathbf{x}} f_i)_{jl} (\mathbf{D})_{lk} \\
&= \frac{1}{\sqrt{K} N^2} \sum_{l=1}^m (2p_i - \delta_{ij} - \delta_{il}) \delta_{lk} (A_l^+ A_k^+)^{\frac{1}{4}}
\end{aligned} \tag{B.5}$$

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

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

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:

$$\begin{aligned}
\frac{1}{K} \text{Tr}[\mathbf{D}^T H_{\mathbf{x}} f_i \mathbf{D}] &= \frac{1}{K} \sum_{k=1}^m (\mathbf{D}^T H_{\mathbf{x}} f_i \mathbf{D})_{kk} \\
&= \frac{1}{KN^2} \sum_{k=1}^m \left(2p_i (A_k^+ A_k^+)^{\frac{1}{2}} - (A_i^+ A_k^+)^{\frac{1}{2}} \delta_{ik} - (A_k^+ A_k^+)^{\frac{1}{2}} \delta_{ik} \right)
\end{aligned} \tag{B.10}$$

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

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

$$\begin{aligned} dp_i &= \underbrace{\frac{1}{N(t)} \left(A_i^- - p_i \sum_{j=1}^m A_j^- \right) dt}_{K \rightarrow \infty \text{ prediction}} - \underbrace{\frac{1}{K} \frac{1}{N^2(t)} \left(A_i^+ - p_i \left(\sum_{k=1}^m A_k^+ \right) \right) dt}_{\substack{\text{Directional finite size effects} \\ \text{due to differential turnover rates}}} \\ &\quad + \underbrace{\frac{1}{\sqrt{K}N(t)} \left[(A_i^+)^{1/2} dB_t^{(i)} - p_i \sum_{j=1}^m (A_j^+)^{1/2} dB_t^{(j)} \right]}_{\substack{\text{Non-directional finite size effects} \\ \text{due to stochastic fluctuations}}} \end{aligned} \quad (\text{B.17})$$

Plugging the functional forms of (2.32) and the definitions of w_i and τ_i into the definitions of A_i^- and A_i^+ , we obtain the relations

$$\begin{aligned} A_i^- &= x_i w_i(\mathbf{x}) + \mu Q_i(\mathbf{x}) \\ A_i^+ &= x_i \tau_i(\mathbf{x}) + \mu Q_i(\mathbf{x}) \end{aligned} \quad (\text{B.18})$$

Thus, for the first term of (B.17), we have

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

Where we have used the definition of p_i from (2.33). Now using the definition of mean fitness from (2.34) and rearranging terms gives us

$$\frac{1}{N(t)} \left(A_i^- - p_i \sum_{j=1}^m A_j^- \right) = (w_i(\mathbf{x}) - \bar{w})p_i + \mu \left[Q_i(\mathbf{p}) - p_i \left(\sum_{j=1}^m Q_j(\mathbf{p}) \right) \right] \quad (\text{B.19})$$

where we have defined $Q_j(\mathbf{p}) = Q_j(\mathbf{x})/N(t)$. Repeating the exact same calculations for the A_i^+ terms in the second term of (B.17) now yields equation (2.36) in the main text.

Appendix C

A Price-like equation for the variance of a type-level quantity

Let σ_f^2 denote the statistical variance of a type-level quantity, defined as:

$$\sigma_f^2 := \overline{(f^2)} - (\overline{f})^2 \quad (\text{C.1})$$

where \overline{X} is the statistical mean value defined by (2.34). By the product rule, we have

$$\frac{d\sigma_f^2}{dt} = 2\overline{f}\frac{\partial f}{\partial t} + \sum_{i=1}^m f_i^2 \frac{dp_i}{dt} - \frac{d}{dt}(\overline{f}^2) \quad (\text{C.2})$$

We will evaluate the RHS term by term. The first term is as simplified as can be without more information about f . For the second term, we can substitute dp_i from (4.1) and use the same steps used in going from (2.38) to (2.42) to write

$$\begin{aligned} \sum_{i=1}^m f_i^2 dp_i &= \text{Cov}(w, f^2)dt - \frac{1}{KN_K} \text{Cov}(\tau, f^2)dt \\ &\quad + \mu \left(1 - \frac{1}{KN_K(t)} \right) \left(\sum_{i=1}^m f_i^2 Q_i(\mathbf{p}) - \overline{f^2} \sum_{i=1}^m Q_i(\mathbf{p}) \right) dt \\ &\quad + \frac{1}{\sqrt{KN_K(t)}} \left(\sum_{i=1}^m (f_i^2 - \overline{f^2}) \sqrt{A_i^+} dB_t^{(i)} \right) \end{aligned} \quad (\text{C.3})$$

For the third term, we need to use Itô's formula. Here, the relevant version of Itô's formula is the one-dimensional version of (B.1). Given a one-dimensional process $dX_t = S(X_t)dt + \sum D_j(X_t)dB_t^{(j)}$ with S, D_j being suitable real functions and each $B_t^{(j)}$ being an independent Wiener process, Itô's formula says that given any $C^2(\mathbb{R})$ function $g(x)$, we have the relation:

$$dg(X_t) = \left(S(X_t)g'(X_t) + \frac{g''(X_t)}{2} \sum_j D_j^2(X_t) \right) dt + \sum_j D_j(X_t)g'(X_t)dB_t^{(j)} \quad (\text{C.4})$$

In our case, we have a one-dimensional process for the mean value \bar{f} of the type level quantity, and the $C^2(\mathbb{R})$ function $g(x) = x^2$. Itô's formula thus says that the third term of (C.2) is given by:

$$d(\bar{f}^2) = \left(2\bar{f}S(X_t) + \sum_j D_j^2(X_t) \right) dt + \sum_j 2\bar{f}D_j(X_t)dB_t^{(j)} \quad (\text{C.5})$$

where the relevant functions S and D_j can be read off from (4.2). Since the dB terms are unwieldy, we will denote the contribution of all the dB_t terms collectively by $dB_{\sigma_f^2}$ to reduce notational clutter and only explicitly calculate these terms at the end. We also note that the covariance operator is a bilinear form, *i.e.* given any three quantities X, Y and Z and any constant $a \neq 0$, we have the relations:

$$\begin{aligned} \text{Cov}(aX, Y) &= a\text{Cov}(X, Y) = \text{Cov}(X, aY) \\ \text{Cov}(X, Y + Z) &= \text{Cov}(X, Y) + \text{Cov}(X, Z) \end{aligned}$$

Substituting equations (C.3) and (C.5) into equation (C.2) and using this property of covariances, we obtain:

$$\begin{aligned} d\sigma_f^2 &= \text{Cov}(w, f^2 - 2\bar{f}f)dt - \frac{1}{KN_K} (\text{Cov}(\tau, f^2 - 2\bar{f}f)) dt + 2 \left(\bar{f} \overline{\frac{\partial f}{\partial t}} - \bar{f} \overline{\left(\frac{\partial f}{\partial t} \right)} \right) dt \\ &\quad + \mu \left(1 - \frac{1}{KN_K(t)} \right) \left(\sum_{i=1}^m (f_i^2 - 2\bar{f}f_i)Q_i(\mathbf{p}) - (\bar{f}^2 - 2\bar{f}^2) \sum_{i=1}^m Q_i(\mathbf{p}) \right) dt \\ &\quad - \frac{1}{KN_K^2(t)} \left(\sum_{i=1}^m (f_i - \bar{f})^2 A_i^+ \right) dt \\ &\quad + dB_{\sigma_f^2} \end{aligned} \quad (\text{C.6})$$

Now, we note that

$$\frac{1}{N_K} A_i^+ = \frac{1}{N_K} (\tau_i x_i + \mu Q_i(\mathbf{x})) \quad (\text{C.7})$$

$$= \tau_i p_i + \mu Q_i(\mathbf{p}) \quad (\text{C.8})$$

and thus the third line of (C.6) is

$$\frac{1}{KN_K^2(t)} \left(\sum_{i=1}^m (f_i - \bar{f})^2 A_i^+ \right) dt = \frac{1}{KN_K} \sum_{i=1}^m (f_i - \bar{f})^2 (\tau_i p_i + \mu Q_i(\mathbf{p})) \quad (\text{C.9})$$

$$= \frac{1}{KN_K} \sum_{i=1}^m (f_i - \bar{f})^2 (\tau_i p_i + \mu Q_i(\mathbf{p})) \quad (\text{C.10})$$

$$= \frac{1}{KN_K} \left(\overline{\tau (f - \bar{f})^2} + \mu \sum_{i=1}^m (f_i - \bar{f})^2 Q_i(\mathbf{p}) \right) \quad (\text{C.11})$$

$$= \frac{1}{KN_K} \left(\text{Cov}(\tau, (f - \bar{f})^2) + \bar{\tau} \overline{(f - \bar{f})^2} + \mu \sum_{i=1}^m (f_i - \bar{f})^2 Q_i(\mathbf{p}) \right) \quad (\text{C.12})$$

$$= \frac{1}{KN_K} \left(\text{Cov}(\tau, (f - \bar{f})^2) + \bar{\tau} \sigma_f^2 + \mu \sum_{i=1}^m (f_i - \bar{f})^2 Q_i(\mathbf{p}) \right) \quad (\text{C.13})$$

where we have used the definition of statistical covariance in the second to last line and used the definition of statistical variance in the last line. Substituting (C.13) into (C.6) and using $M_{\sigma_f^2}(\mathbf{p}, N_K)$ to denote the contributions of all the mutational terms (*i.e.* all terms with a μ factor) for notational brevity, we obtain

$$\begin{aligned} d\sigma_f^2 &= \text{Cov}(w, f^2 - 2\bar{f}f)dt - \frac{1}{KN_K} \left(\text{Cov}(\tau, f^2 - 2\bar{f}f) + \text{Cov}(\tau, (f - \bar{f})^2) + \bar{\tau} \sigma_f^2 \right) dt \\ &\quad + 2\text{Cov}\left(\frac{\partial f}{\partial t}, f\right) dt + M_{\sigma_f^2}(\mathbf{p}, N_K)dt + dB_{\sigma_f^2} \end{aligned} \quad (\text{C.14})$$

We can now complete the square inside the covariance terms of the first line of the RHS by writing $f^2 - 2\bar{f}f = (f - \bar{f})^2 - \bar{f}^2$ to obtain

$$\begin{aligned} d\sigma_f^2 &= \left[\text{Cov}(w, (f - \bar{f})^2) - \text{Cov}\left(w, (\bar{f})^2\right) \right] dt \\ &\quad - \frac{1}{KN_K} \left[\text{Cov}(\tau, (f - \bar{f})^2) - \text{Cov}\left(\tau, (\bar{f})^2\right) + \text{Cov}(\tau, (f - \bar{f})^2) + \bar{\tau}\sigma_f^2 \right] dt \quad (\text{C.15}) \\ &\quad + 2\text{Cov}\left(\frac{\partial f}{\partial t}, f\right) dt + M_{\sigma_f^2}(\mathbf{p}, N_K)dt + dB_{\sigma_f^2} \end{aligned}$$

To simplify the covariance terms of the first line of the RHS, we observe that

$$\begin{aligned} \text{Cov}\left(w, (\bar{f})^2\right) &= \overline{(w(\bar{f})^2)} - \bar{w}\overline{(\bar{f})^2} \\ &= (\bar{f})^2 \sum_{i=1}^m w_i p_i - \bar{w}(\bar{f})^2 \sum_{i=1}^m p_i \\ &= (\bar{f})^2 \bar{w} - \bar{w}(\bar{f})^2 = 0 \end{aligned}$$

and similarly,

$$\text{Cov}\left(\tau, (\bar{f})^2\right) = 0$$

and thus, using this in (C.15), we see that the rate of change of the variance of any type-level quantity f in the population satisfies:

$$\begin{aligned} d\sigma_f^2 &= \text{Cov}(w, (f - \bar{f})^2) dt - \frac{1}{KN_K} [\bar{\tau}\sigma_f^2 + 2\text{Cov}(\tau, (f - \bar{f})^2)] dt \\ &\quad + 2\text{Cov}\left(\frac{\partial f}{\partial t}, f\right) dt + M_{\sigma_f^2}(\mathbf{p}, N_K)dt + dB_{\sigma_f^2} \quad (\text{C.16}) \end{aligned}$$

This is precisely equation (4.7) in the main text. To calculate the mutation term, we substitute (C.13) into (C.6) to find

$$\begin{aligned} M_{\sigma_f^2}(\mathbf{p}, N_K) &= \mu \left(\sum_{i=1}^m \left(f_i^2 - 2\bar{f}f_i - \bar{f}^2 + 2\bar{f}^2 \right) Q_i(\mathbf{p}) \right) \\ &\quad - \frac{\mu}{KN_K} \sum_{i=1}^m \left(f_i^2 - 2\bar{f}f_i - \bar{f}^2 + 2\bar{f}^2 + (f_i - \bar{f})^2 \right) Q_i(\mathbf{p}) \quad (\text{C.17}) \end{aligned}$$

We can further simplify the first term of the RHS as

$$\begin{aligned} f_i^2 - 2\bar{f}f_i - \bar{f}^2 + 2\bar{f}^2 &= (f_i^2 + \bar{f}^2 - 2\bar{f}f_i) - (\bar{f}^2 - \bar{f}^2) \\ &= (f_i - \bar{f})^2 + \sigma_f^2 \end{aligned}$$

and similarly, the second term as

$$f_i^2 - 2\bar{f}f_i - \bar{f}^2 + 2\bar{f}^2 + (f_i - \bar{f})^2 = 2(f_i - \bar{f})^2 + \sigma_f^2$$

thus, the contributions of mutations to the change in the variance of f are given by

$$\begin{aligned} M_{\sigma_f^2}(\mathbf{p}, N_K) &= \mu \left(\sum_{i=1}^m ((f_i - \bar{f})^2 + \sigma_f^2) Q_i(\mathbf{p}) \right) \\ &\quad - \frac{\mu}{KN_K} \sum_{i=1}^m (2(f_i - \bar{f})^2 + \sigma_f^2) Q_i(\mathbf{p}) \end{aligned} \tag{C.18}$$

which after slight rearrangement becomes

$$M_{\sigma_f^2}(\mathbf{p}, N_K) = \mu \left(\sum_{i=1}^m \left[\left(1 - \frac{2}{KN_K} \right) (f_i - \bar{f})^2 Q_i(\mathbf{p}) \right] + \sigma_f^2 \left(1 - \frac{1}{KN_K} \right) \sum_{i=1}^m Q_i(\mathbf{p}) \right) \tag{C.19}$$

which is equation (4.8) in the main text. For the dB terms, we can use equations (C.3) and (C.5) to calculate:

$$dB_{\sigma_f^2} = \frac{1}{\sqrt{KN_K(t)}} \left(\sum_{i=1}^m (f_i^2 - \bar{f}^2 - 2\bar{f}(f_i - \bar{f})) \sqrt{A_i^+} dB_t^{(i)} \right) \tag{C.20}$$

$$= \frac{1}{\sqrt{KN_K(t)}} \left(\sum_{i=1}^m (f_i^2 - \bar{f}^2 - 2\bar{f}f_i - 2\bar{f}^2) \sqrt{A_i^+} dB_t^{(i)} \right) \tag{C.21}$$

$$= \frac{1}{\sqrt{KN_K(t)}} \left(\sum_{i=1}^m (f_i - \bar{f})^2 \sqrt{A_i^+} dB_t^{(i)} \right) \tag{C.22}$$

which is equation (4.9) in the main text.

Appendix D

Some Examples

D.1 An example in one dimension: The stochastic logistic equation

Here, we analyze example 1. To recap, we had a population of individuals that exhibit a constant per-capita birth rate $\lambda > 0$, and a per-capita death rate that had the linear density-dependence $d(n) = (\mu + (\lambda - \mu)\frac{n}{K})n$, where μ and K are positive constants. Thus, we have the equations

$$\begin{aligned} b(n) &= \lambda n \\ d(n) &= \left(\mu + (\lambda - \mu)\frac{n}{K}\right)n \end{aligned} \tag{D.1}$$

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 (2.14), we see that the ‘mesoscopic view’ of the system is given by the solution of the SDE

$$dX_t = rX_t(1 - X_t)dt + \sqrt{\frac{X_t(v + rX_t)}{K}}dB_t \quad (\text{D.2})$$

From equation (2.15), we see that the deterministic dynamics are

$$\frac{dx}{dt} = A^-(x) = rx(1 - x) \quad (\text{D.3})$$

showing that in the infinite population limit, we obtain the logistic equation. Letting $\alpha(t)$ be the solution of the logistic equation (D.3), We can Taylor expand $A^\pm(x)$ for the weak noise approximation, and we find:

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

Thus, the weak noise approximation of D.1 is given by

$$X_t = \alpha(t) + \frac{1}{\sqrt{K}}Y_t \quad (\text{D.4})$$

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

$$\begin{aligned} dY_t &= A_1^-(t)Y_tdt + \sqrt{A_0^+(t)}dB_t \\ \Rightarrow dY_t &= r(1 - 2\alpha(t))Y_tdt + \sqrt{\alpha(t)(v + r\alpha(t))}dB_t \end{aligned} \quad (\text{D.5})$$

The time series predicted by these three processes look qualitatively similar and all seem to fluctuate about the deterministic steady state (Figure D.1).

The deterministic trajectory (D.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 (D.2) and (D.5) depend not only on r , but also on v , the sum of the birth and death rates. It has been proven that

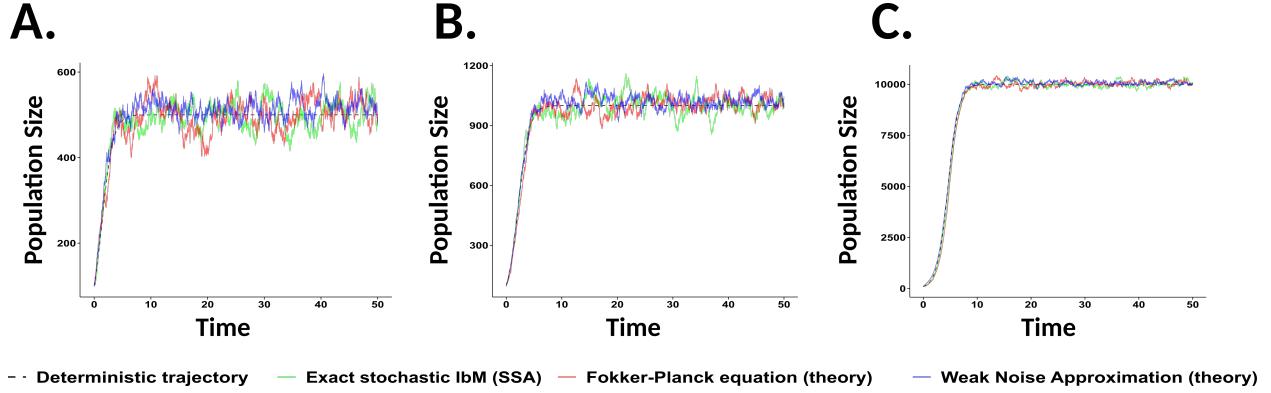


Figure D.1: Comparison of a single realization of the exact birth-death process (D.1), the deterministic trajectory (D.3), the non-linear Fokker-Planck equation (D.2), and the weak noise approximation (D.5) for (A) $K = 500$, (B) $K = 1000$, and (C) $K = 10000$. $\lambda = 2, \mu = 1$ for all thee cases.

$X_t = 0$ is the only recurrent state for the full stochastic dynamics (D.2), meaning that every population is guaranteed to go extinct¹ 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 (D.2) has a ‘quasistationary’ distribution about the deterministic attractor $X_t = 1$, with some variance reflecting the effect of noise-induced fluctuations in population size (Nåsell, 2001) due to the finite size of the population. The weak-noise approximation (D.5) implicitly assumes non-extinction by only measuring small fluctuations from the deterministic solution to (D.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 (D.1) is compared with that predicted by (D.2) and (D.5) for various values of K in figure D.2.

¹This 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.

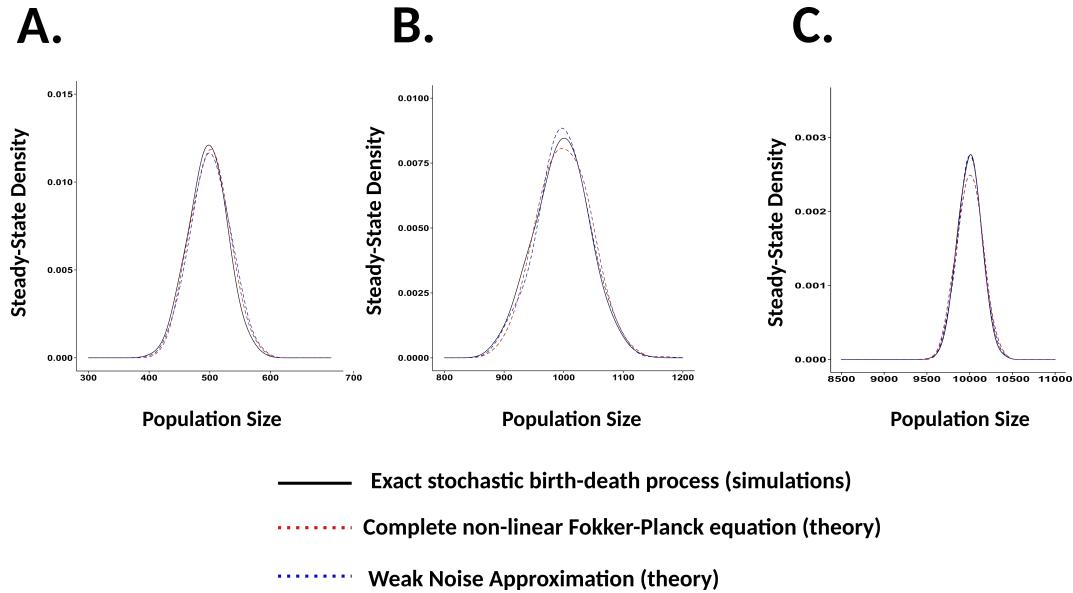


Figure D.2: Comparison of the steady-state densities given by (D.1), (D.2), and (D.5) for (A) $K = 500$, (B) $K = 1000$, and (C) $K = 10000$. $\lambda = 2, \mu = 1$ for all thee cases. Each curve was obtained using 1000 independent realizations.

D.2 An 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 interacting according to some ecological rules. 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:

$$\begin{aligned} b_i(\mathbf{v}) &= \left(\lambda + \frac{1}{K} \left(\sum_{j=1}^m \beta_{ij} v_j \right) \right) v_i \\ d_i(\mathbf{v}) &= \left(\mu + \frac{1}{K} \left(\sum_{j=1}^m \delta_{ij} v_j \right) \right) v_i \end{aligned} \quad (\text{D.6})$$

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 β_{ij} and δ_{ij} are constants describing the effect of type j individuals on the birth and death rate of type i individuals respectively. The sign of $M_{ij} := \beta_{ij} - \delta_{ij}$ determines whether type j has a net positive or negative effect on the growth of type i . In ecological communities, this is a per-capita ecological interaction effect. In game-theoretic terms, we can interpret M_{ij} as the payoff obtained by a type j individual playing against a type i individual. I assume that $|M_{ij}| \ll K$. The values M_{ij} are often collected in an $m \times m$ matrix \mathbf{M} called the ‘payoff matrix’ (in evolutionary game theory) or ‘interaction matrix’ (in Lotka-Volterra models). Lotka-Volterra models also frequently assume that the diagonal elements M_{ii} are all equal, though I 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:

$$\begin{aligned} b_i^{(K)}(\mathbf{x}) &= \left(\lambda + \sum_{j=1}^m \beta_{ij} x_j \right) x_i \\ d_i^{(K)}(\mathbf{x}) &= \left(\mu + \sum_{j=1}^m \delta_{ij} x_j \right) x_i \end{aligned} \quad (\text{D.7})$$

Thus, we have

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

Defining $r := \lambda - \mu$, $\nu := \lambda + \mu$, and $T_{ij} := \beta_{ij} + \delta_{ij}$, we see from equation (2.31) that the mesoscopic view is the m dimensional SDE given by

$$d\mathbf{X}_t = \mathbf{A}^-(\mathbf{X}_t) dt + \frac{1}{\sqrt{K}} \mathbf{D}(\mathbf{X}_t) d\mathbf{B}_t \quad (\text{D.8})$$

where

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

and

$$(\mathbf{DD}^T)_i = (\mathbf{X}_t)_i \left(\nu + \sum_{j=1}^m T_{ij} (\mathbf{X}_t)_j \right)$$

From (2.37), we see that the deterministic limit is a set of m coupled ODEs given by

$$\frac{dx_i}{dt} = x_i \left(r + \sum_{j=1}^m M_{ij} x_j \right) \quad (\text{D.9})$$

These are precisely the Lotka-Volterra equations for a system of m species. By matching the terms of (D.7) with those of (2.32), we can identify that we have $\mu = 0$ and

$$w_i(\mathbf{x}) = r + \sum_{j=1}^m M_{ij} x_j \quad (\text{D.10})$$

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

$$\bar{w}(t) = \sum_{i=1}^m w_i p_i \quad (\text{D.11})$$

$$= \sum_{i=1}^m \left(r + \sum_{j=1}^m M_{ij} x_j \right) p_i \quad (\text{D.12})$$

$$= r + \sum_{i=1}^m p_i \left(\sum_{j=1}^m M_{ij} x_j \right) \quad (\text{D.13})$$

where we have used the fact that $\sum_i p_i = 1$ in the last line. Using (2.38) to write down the equations for the frequencies p_i , we obtain

$$\frac{1}{N_K(t)} \frac{dp_i}{dt} = [(\mathbf{Mp})_i - \mathbf{p} \cdot \mathbf{Mp}] p_i \quad (\text{D.14})$$

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 M to obtain exactly the replicator equation as presented in most ecology/evolution textbooks. Both the stochastic dynamics (D.8) and the deterministic limit (D.9) can be simplified from an m dimensional system to an $m - 1$ dimensional system by a coordinate transformation that projects the dynamics onto an appropriate curve: If we go from the variables x_1, \dots, x_m to the variables p_1, \dots, p_{m-1}, N_K , 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, I will not explore such dimensional reduction techniques further in this manuscript, and refer the reader to (Constable et al., 2013) and (Parsons and Rogers, 2017) for a review of the ideas of (stochastic) dynamics on slow manifolds.

Let the solution to the equations (D.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 (2.61) to compute the directional derivative as:

$$D_i = y_i w_i(\mathbf{a}) + a_i \sum_{k=1}^m y_k \left(\frac{\partial w_i}{\partial x_k} \Big|_{\mathbf{x}=\mathbf{a}(t)} \right) \quad (\text{D.15})$$

$$= y_i w_i(\mathbf{a}) + a_i \sum_{k=1}^m y_k \left(\frac{\partial}{\partial x_k} \left(r + \sum_{j=1}^m M_{ij} x_j \right) \Big|_{\mathbf{x}=\mathbf{a}(t)} \right) \quad (\text{D.16})$$

$$= y_i w_i(\mathbf{a}) + a_i \sum_{k=1}^m y_k M_{ik} \quad (\text{D.17})$$

$$\Rightarrow D_i = y_i w_i(\mathbf{a}) + a_i w_i(\mathbf{y}) - r a_i \quad (\text{D.18})$$

where we have used the fact that $w_i(\mathbf{y}) = r + \sum_{k=1}^m y_k M_{ik}$ (from (D.10)) in the last step. Thus, in the weak noise approximation of our process, the dynamics are given by

$$\mathbf{x}(t) = \mathbf{a}(t) + \frac{1}{\sqrt{K}} \mathbf{y}(t) \quad (\text{D.19})$$

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

$$\frac{\partial P}{\partial t}(\mathbf{y}, t) = \sum_{i=1}^m \left(-\frac{\partial}{\partial y_i} \{(y_i w_i(\mathbf{a}) + a_i w_i(\mathbf{y}) - r a_i) P(\mathbf{y}, t)\} + \frac{1}{2} \left(a_i \left(\nu + \sum_{j=1}^m T_{ij} a_j \right) \right) \frac{\partial^2}{\partial y_i^2} P(\mathbf{y}, t) \right) \quad (\text{D.20})$$

Using (D.18) in (2.55), we see that the fluctuations are expected to evolve as:

$$\frac{d}{dt} \mathbb{E}[y_i] = w_i(\mathbf{a}) \mathbb{E}[y_i] + a_i \sum_{k=1}^m M_{ik} \mathbb{E}[y_k] \quad (\text{D.21})$$

or, in matrix form:

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

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). In the $m = 2$ case, Tao and Cressman, 2007 have shown that $\mathbb{E}[y_i] = 0 \forall i$ is a stable fixed point for this system iff the point \mathbf{y} is an ESS (in the usual game-theoretic sense) for the matrix game defined by the payoff matrix \mathbf{M} .

D.3 Interlude: Detecting modes in quantitative trait distribution through Fourier analysis

In Chapter 3, we used various approximations to arrive at the linear functional Fokker-Planck equation

$$\frac{\partial P}{\partial t}(\zeta, t) = \int_{\mathcal{T}} \left(-\frac{\delta}{\delta \zeta(x)} \{\mathcal{D}_\zeta[\mathcal{A}^-](x) P(\zeta, t)\} + \frac{1}{2} \mathcal{A}^+(x|\psi) \frac{\delta^2}{\delta \zeta(x)^2} \{P(\zeta, t)\} \right) dx \quad (\text{D.23})$$

for describing stochastic fluctuations ζ from the deterministic solution obtained by solving (3.8). 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. Following the methods used by Tim Rogers and colleagues for various special cases (Rogers et al., 2012a; Rogers et al., 2012b; Rogers and McKane, 2015), we will do this in a general manner by measuring the autocorrelation of the distribution of the population over trait space, a task made easier by moving to Fourier space. Specifically, a convenient theorem due to Weiner

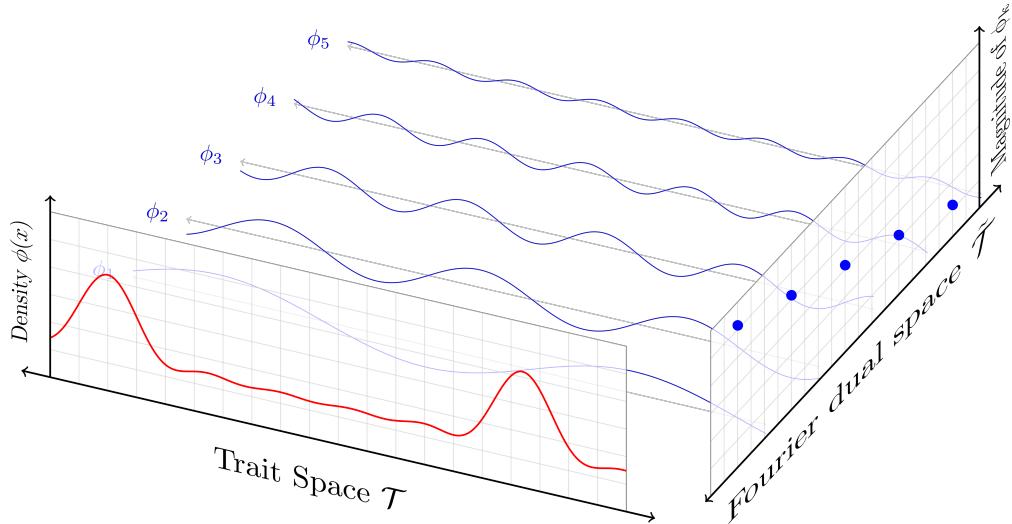


Figure D.3: Schematic description of Fourier analysis. A function $\phi(x)$ (shown in red) over the trait space can be decomposed as the sum of infinitely many Fourier modes (shown in blue) ϕ_k . In the Fourier dual space, we can look at the peaks of each of these Fourier modes: The magnitude of ϕ_k tells us how much it contributes to the actual function of interest ϕ .

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 by carrying 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-invariant² linear operator, then $\exp(ikx)$ acts as an eigenfunction, significantly simplifying the calculations. We therefore assume that

²This 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. $T_c[L[f]] = L[T_c[f]] \forall f \in \mathcal{F} \forall c \in \mathbb{R}$. This is not as restrictive as it initially sounds. For example, both the Laplacian operator and the convolution operator are linear and translation invariant

$\mathcal{D}_\zeta[\mathcal{A}^-]$ 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 ζ , and $\mathcal{A}^+(x|\psi)$ admit the Fourier basis representations:

$$\begin{aligned}\zeta(x, t) &= \sum_{k=-\infty}^{\infty} e^{ikx} \zeta_k(t) \quad ; \quad \zeta_k(t) = \int_{\mathcal{T}} \zeta(x, t) e^{-ikx} dx \\ \mathcal{A}^+(x|\psi) &= \sum_{k=-\infty}^{\infty} e^{ikx} A_k(t) \quad ; \quad A_k(t) = \int_{\mathcal{T}} \mathcal{A}^+(x|\psi) e^{-ikx} dx\end{aligned}\tag{D.24}$$

In this case, the functional derivative operator obeys:

$$\frac{\delta}{\delta \zeta(x)} = \sum_{k=-\infty}^{\infty} e^{-ikx} \frac{\partial}{\partial \zeta_k} \tag{D.25}$$

and since L is linear and translation-invariant, we also have the relation³:

$$L[\zeta] = \sum_{k=-\infty}^{\infty} L_k \zeta_k e^{ikx} \tag{D.26}$$

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 $t > 0$:

$$\frac{\partial}{\partial \zeta_j(t)} F(\zeta_i(t)) = \delta_{ij} F'(\zeta_j(t)) \tag{D.27}$$

where δ_{ij} is the Kronecker delta symbol. Using (D.24), (D.25), and (D.26) in (3.28), we get,

³This 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 $e_k = \exp(ikx)$.

for the first term of the RHS:

$$\begin{aligned}
& - \int_{\mathcal{T}} \frac{\delta}{\delta \zeta(x)} \{L[\zeta(x, t)]P(\zeta, t)\} dx \\
&= - \int_{\mathcal{T}} \sum_k e^{-ikx} \frac{\partial}{\partial \zeta_k} \left\{ \sum_n e^{inx} L_n \zeta_n P \right\} dx \\
&= - \int_{\mathcal{T}} \sum_k \sum_n e^{-i(k-n)x} \frac{\partial}{\partial \zeta_k} \{L_n \zeta_n P\} dx \\
&= -2\pi \sum_k L_k \frac{\partial}{\partial \zeta_k} \{\zeta_k P\}
\end{aligned} \tag{D.28}$$

and for the second:

$$\begin{aligned}
& \int_{\mathcal{T}} \sum_k e^{ikx} A_k \left(\sum_m \sum_n e^{-i(m+n)x} \frac{\partial}{\partial \zeta_m} \frac{\partial}{\partial \zeta_n} P \right) dx \\
&= \int_{\mathcal{T}} \sum_k \sum_m \sum_n e^{i(k-m-n)x} A_k \frac{\partial}{\partial \zeta_m} \frac{\partial}{\partial \zeta_n} \{P\} dx \\
&= 2\pi \sum_m \sum_n A_{m+n} \frac{\partial}{\partial \zeta_m} \frac{\partial}{\partial \zeta_n} \{P\}
\end{aligned} \tag{D.29}$$

Substituting (D.28) and (D.29) into (3.6), we see that the Fokker-Planck equation in Fourier space reads:

$$\frac{\partial P}{\partial t} = -2\pi \sum_k L_k \frac{\partial}{\partial \zeta_k} \{\zeta_k P\} + \pi \sum_m \sum_n A_{m+n} \frac{\partial}{\partial \zeta_m} \frac{\partial}{\partial \zeta_n} \{P\} \tag{D.30}$$

It is important to remember that since $\zeta(x, t)$ is a stochastic process, ζ_i is really a stochastic process and thus $\zeta_i(t)$ is actually shorthand for the random variable $(\zeta_i)_t(\omega)$, where ω is a sample path in the Fourier dual of our original probability space. Multiplying both sides of (D.30) by ζ_r and integrating over the probability space to obtain expectation values, we see that

$$\begin{aligned}
\frac{d}{dt} \mathbb{E}[\zeta_r] &= -2\pi \sum_k \int \zeta_r L_k \frac{\partial}{\partial \zeta_k} \{\zeta_k P\} d\omega + \pi \sum_m \sum_n A_{m+n} \int \zeta_r \frac{\partial}{\partial \zeta_m} \frac{\partial}{\partial \zeta_n} \{P\} d\omega \\
&= 2\pi \sum_k L_k \int \zeta_k \frac{\partial \zeta_r}{\partial \zeta_k} P d\omega + \pi \sum_m \sum_n A_{m+n} \int \frac{\partial^2 \zeta_r}{\partial \zeta_m \partial \zeta_n} P d\omega \\
&= 2\pi L_r \mathbb{E}[\zeta_r]
\end{aligned} \tag{D.31}$$

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 (D.27) to arrive at the final expression. Similarly, multiplying (D.30) by $\zeta_r \zeta_s$, integrating over the probability space and using integration by parts, we get:

$$\begin{aligned} \frac{d}{dt} \mathbb{E}[\zeta_r \zeta_s] &= 2\pi \sum_k L_k \int \zeta_k P \frac{\partial}{\partial \zeta_k} \{\zeta_r \zeta_s\} d\omega + \pi \sum_m \sum_n A_{m+n} \int_{-\infty}^{\infty} P \frac{\partial}{\partial \zeta_m} \frac{\partial}{\partial \zeta_n} \{\zeta_r \zeta_s\} d\omega \\ &= 2\pi(L_r + L_s)\mathbb{E}[\zeta_r \zeta_s] + \pi(A_{2r} + A_{2s}) \end{aligned} \quad (\text{D.32})$$

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

$$\mathbb{E}[\zeta_r \zeta_s] = -\frac{A_{2r} + A_{2s}}{2(L_r + L_s)} \quad (\text{D.33})$$

Recall that the Fourier modes of any real function φ must satisfy $\varphi_{-r} = \bar{\varphi}_r$. Since ζ , A and L are all real, we can substitute $s = -r$ in equation (D.33) to obtain the autocovariance relation:

$$\mathbb{E}[|\zeta_r|^2] = -\frac{\text{Re}(A_{2r})}{2\text{Re}(L_r)} \quad (\text{D.34})$$

The presence of phenotypic clustering can be detected using the ‘spatial covariance’ of our original process ϕ , defined as (Rogers et al., 2012a):

$$\Xi[x] = m(\mathcal{T}) \int_{\mathcal{T}} \mathbb{E}[\phi_{\infty}(x)\phi_{\infty}(y-x)] dy \quad (\text{D.35})$$

where ϕ_{∞} 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:

$$\Xi[x] = m(\mathcal{T}) \left[\int \psi_{\infty}(x)\psi_{\infty}(y-x) dy + \frac{1}{K} \sum_{r=-\infty}^{\infty} \mathbb{E}[|\zeta_r|^2] e^{irx} \right] \quad (\text{D.36})$$

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.

D.4 An example for quantitative traits: The quantitative logistic equation

Recall the birth and death functionals given by (3.2). That is, the functionals

$$\begin{aligned} b(x|\nu) &= r \int_{\mathcal{T}} m(x, y)\nu(y)dy; \quad m(x, y) = \exp\left(\frac{-(x-y)^2}{\sigma_m^2}\right) \\ d(x|\nu) &= \frac{\nu(x)}{Kn(x)} \int_{\mathcal{T}} \alpha(x, y)\nu(y)dy; \quad \alpha(x, y) = \exp\left(\frac{-(x-y)^2}{\sigma_\alpha^2}\right) \end{aligned} \quad (\text{D.37})$$

corresponding to an asexual population having a constant (per-capita) birth rate r and mutations 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 $\alpha(x, y)$). In terms of the scaled variable $\phi = K\nu$, these functions read:

$$\begin{aligned} b_K(x|\phi) &= \frac{1}{K}b(x|\nu) = \frac{1}{K} \left(r \int_{\mathcal{T}} m(x, y)K\phi(y)dy \right) \\ d_K(x|\phi) &= \frac{1}{K}d(x|\nu) = \frac{1}{K} \left(\frac{K\phi(x)}{Kn(x)} \int_{\mathcal{T}} \alpha(x, y)K\phi(y)dy \right) \end{aligned} \quad (\text{D.38})$$

Thus, using equation (3.8), the deterministic trajectory becomes:

$$\frac{\partial \psi}{\partial t}(x, t) = r \int_{\mathcal{T}} m(x, y)\psi(y, t)dy - \frac{1}{n(x)}\psi(x, t) \int_{\mathcal{T}} \alpha(x, y)\psi(y, t)dy \quad (\text{D.39})$$

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 quantitative logistic equation as the deterministic limit:

$$\frac{\partial \Psi}{\partial t}(x, t) = r \int_{\mathcal{T}} m(x, y)\Psi(y, t)dy - \frac{\Psi(x, t)}{Kn(x)} \int_{\mathcal{T}} \alpha(x, y)\Psi(y, t)dy$$

$$\approx r\Psi(x, t) - \frac{\Psi(x, t)}{K(x)} \int_{\mathcal{T}} \alpha(x, y)\Psi(y, t)dy + D_m \nabla_x^2 \Psi(x, t)$$

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.

We can also calculate $\mathcal{D}_\zeta[\mathcal{A}^-]$ as

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

Using this in equation (D.36), Rogers et al., 2012a (and later Rogers and McKane, 2015) have shown that the contribution of demographic stochasticity can lead to inhibition of branching, and thus, while the population undergoes infinitely many branching events in the infinite population prediction, this does not happen for finite populations. It is left

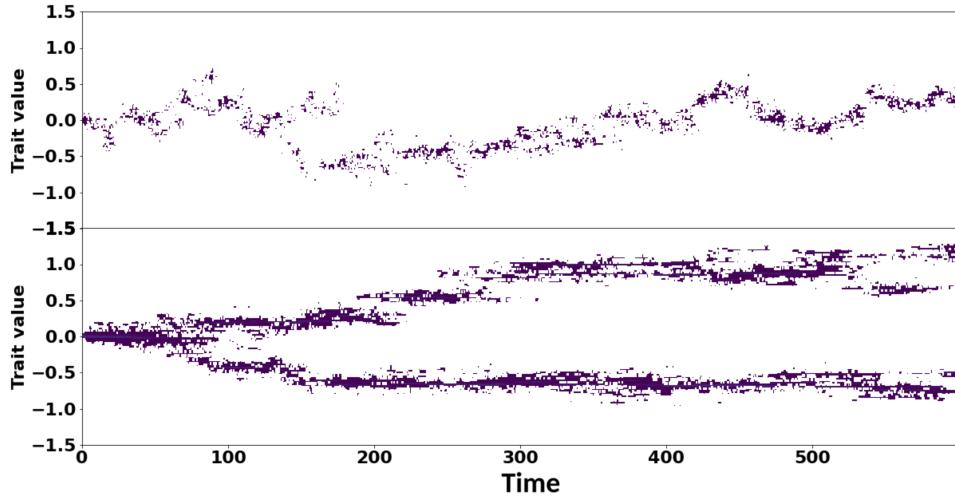


Figure D.4: Effect of population size on evolutionary branching. Two different realizations of the system (3.2) with $n(x) = \exp((x^2)/\sigma_K^2)$. Simulation parameters are $\sigma_K = 1.9$, $\sigma_\alpha = 0.7$, $\sigma_m^2 = 0.05$ for **top:** $K = 1000$ and **bottom:** $K = 10000$. Each point represents an individual. Note that the model on top remains monomorphic whereas the model on the bottom exhibits evolutionary branching, where an initially monomorphic population evolves to become dimorphic.

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 (3.2)) and the death rate functional $d(x|\phi) = \phi(x)(\mu + (\lambda - \mu)\phi(x)/K)$, the infinite-population limit yields the famous Fisher-KPP equation with growth rate $r = \lambda - \mu$ and diffusion constant $D = \lambda\sigma_m^2/2$.

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