Meta–Stability of Interacting Adaptive Agents

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Abstract

The adaptive process can be considered as being driven by two fundamental forces: exploitation and exploration. While the explorative process may be deterministic, the resultant effect may be stochastic. Stochastic effects may also exist in the expoitative process. This thesis considers the effects of stochastic fluctuations inherent in the adaptive process on the behavioural dynamics of a population of interacting agents. It is hypothesied that in such systems, one or more attractors in the population space exist; and that transitions between these attractors can occur; either as a result of internal shocks (sampling fluctuations) or external shocks (environmental changes). It is further postulated that such transitions in the (microscopic) population space may be observable as phase transitions in the behaviour of macroscopic observables.

A simple model of a stock market, driven by asexual reproduction (selection plus mutation) is put forward as a testbed. A statistical dynamics analysis of the behaviour of this market is then developed. Fixed points in the space of agent behaviours are located, and market dynamics are compared to the analytic predictions. Additionally, an analysis of the relative importance of internal shocks(sampling fluctuations) and external shocks(the stock dividend sequence) across varying population size is presented.

Keywords: adaptation, interaction, self-organisation, market dynamics

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Publications

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Chapter 1

Background: The Evolution of Populations of Interacting Agents

> 'There is no such thing as society. There are only individuals.' *Margaret Thatcher*

The above quote sums up a popular political ideology of the late twentieth century. It appears to reject notions of co-operative actions amongst groups in favour of action motivated only by individual gain. This thesis considers issues concerning individual vs. group actions in situations where individual agents adapt to the changing environment they find themselves in. There may be no consideration by agents of the effects of their actions on other agents or the environment, but such effects do occur in the systems studied. Such a system is described as interactive, because the actions of agents affect other agents, and adaptive, because agents can change their response to adapt to the environment.

The focus of this thesis is upon the *behavioural dynamics* of such systems: how the collective behaviour of the population changes as a result of adaptation driven by the results of interaction. In particular, questions of the stability of collective behaviours are explored. Do collective behaviours remain constant, or are there sudden changes, where the whole population seemingly 'changes its mind' about how it will behave? This thesis explores the conditions under which collective behaviours change, and the roles played by the internal dynamics of the population, and by external, environmental forces acting on the population.

1.0.1 Motivation and Justification

The motivation for this work is the observation that many systems of adaptive interactive agents appear have a number of seemingly stable modes of collective operation. Such systems exhibit intermittent transitions between their modes. Systems that exhibit this behaviour are described as *meta-stable*.

The thesis proceeds from the underlying hypothesis that this common phenomenology results from a common ontology. Examples of the phenomenon of meta-stability from a number of differing fields are presented and drawn together to give a coherent picture of the phenomenon of meta-stability.

The purpose of this work is to explore this hypothesised common ontology of meta-stability in adaptive interacting agent populations. A mathematical model of meta-stability is put forwards, drawing heavily upon work on adaptation in various fields. This model posits that the cause of metastability is stochastic, and explains why the stochasticities remain important even in relatively large populations.

This work also explores the relationship between the internal fluctuations of the system, due to the interactions between agents, and the adaptation of individuals within the population, and the external forces such as environmental fluctuations.

Existing models of interacting adaptive populations tend to have been heavily grounded in the social or biological sciences, concentrated mainly around economics, game theory and population biology. Due to the complexity of interactions which take place between agents in these problem domains, these models have tended to be explanatory in nature, and they do not directly address meta-stability as such.

The growth in computing power and connectivity in the past ten years has resulted in a vast increase in the number of systems organised in a bottom-up manner, where the control of the collective behaviour of the system is distributed between the elements of the system. Most notable in this field is the internet. However, other systems, such as air-traffic control systems can also be cast as collective or group behaviour problems.

Not only have problems of group behaviour escaped from the social and biological spheres, but they have also begun to incorporate computational intelligence techniques. The manner in which 'intelligent systems' respond to what they perceive as fluctuations in their environment can have far-reaching consequences across wide areas. To follow the internet and air-traffic examples given above, the adaptations made in individual locations can affect the frequency and severity of network brownouts, or the speed and robustness of recovery of the USA's air-travel network after the closure of a major hub airport due to bad weather.

Meta-stability is an important phenomenon to understand. Firstly, it is a valid field of academic enquiry in its own right. But beyond that, an understanding of the causes of this phenomenon may allow the better design of systems of distributed adaptive agents, or distributed control systems. Given an understanding of the causes of meta-stability, it may be possible to predict and control the distribution of waiting times in particular modes, or the probable direction of transition between modes.

This chapter provides an introduction to the field of adaptive systems of interacting agents. The evidence for meta-stability as a common phenomenology is reviewed here. The significance of the problem to evolutionary theorists and modellers is explained, and recent research and theories are discussed. This chapter does not seek to describe or explain mathematical models of evolutionary dynamics; these matters are covered in chapters 2 and 3.

1.1 Fundamentals of Adaptation

Adaptation is the fundamental force that has driven life on Earth since its inception 4500 million years ago. An adaptive drive underlies not only evolution, but also many forms of neural activity. At a higher level it would not be inappropriate to describe the dynamics of many forms of group or group activities, such as corporations, market traders and other social or economic agents as being driven by adaptation. In Artificial Intelligence (AI) and Artificial Life (ALife) adaptation is recognised as central to the quest for more useful and intelligent agents.

In broad terms, this thesis is concerned with the dynamics of populations of adaptive agents. In particular it is concerned with populations whose adaptation is driven by interactive behaviours or social goals. The utility of an agent's behaviour is defined either internally by that agent, or externally as the utility of the entire agent. Utility maximisation is the driving force behind adaptation at the individual or population level. A positive feedback process exists: adaptation informs behaviour, but the collective consequences of behaviours across the population in turn direct the adaptive process.

1.1.1 A Definition of Adaptation

The term 'adaptation' has appeared in many contexts. In dictionary terms, it has been defined as 'adjustment to environmental conditions'[1]. Here we consider adaptation as an active, rather than a passive process. Underlying the various definitions and contexts

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[1] Merriam-Webster (hhtp://www.m-w.com/dictionary.html).

are a number of important common themes:

1. The agent must be situated within its environment. Agents cannot retreat from their world whilst the adaptive process takes place, but must continue to exist within it. Adaptation therefore involves compromises globally optimal solutions may not have been discovered by an agent, therefore sub-optimal solutions must be used. Adaptive agents use the best solutions that they have to hand, whilst continuing to search for even better responses.
2. Adaptation must in some way involve search. If an agent is to improve its responses to an environmental stimulus, it must be free to explore novel responses to the stimulus, as well as to exploit existing solutions to the problem.
3. Consequently, this search process must take place within the agent's environment. An agent is faced with the dilemma that on the one hand, its utility depends on correct responses to its environment, yet failure to risk trying novel responses may lead to ignorance of the best responses to the environment. This problem, referred to as the *two armed bandit problem* underlies all adaptive behaviours, and will be discussed further in Section 1.1.2.

Henceforth, adaptation will be defined in terms of two fundamental forces, *exploration* and *exploitation*. A process will be considered to be adaptive if it can be shown that both these elements are present within in.

1.1.2 The Statistics of Adaptive Behaviour

Here the recognition of exploitative and exploratory tendencies will be considered, and a rationale for simplifying assumptions that will underlie the mathematical models of adaptation (chapters 2, 3 and 4) will be presented.

Choice and Uncertainty: The n-armed Bandit

Whether the agents exist in a noisy environment or not, they will all face a fundamental problem of adaptation, namely the problem of minimising their potential losses due to making poor decisions. Such a problem is known as an *n-armed bandit.* In a fruit machine (the 1-armed bandit), the player faces a long term source of loss because the bandit is biased towards the operator. The n-armed bandit problem posits a machine with n arms. Each arm has its own bias, so there is a long term source of loss associated with each arm. The problem is to provide a decision method to minimise one's losses, given only the history of your plays on the bandit. Note that each play one makes on the bandit gives further information about the bias of a particular arm or set of arms.

This is a fundamental problem in adaptation, because with a limited number of historical precedents, associations between stimuli/responses and rewards may not be easily discernible, let alone correct. So the ability to minimise one's potential losses given an unknown situation, whilst gathering information, is important.

The relationship between the forces of exploration and exploitation, has long been recognised as a two-armed-bandit problem, and underlies early theories of evolutionary search [42]. The usual presentation of the problem is in terms of a player betting on a coin-tossing game with a coin with an unknown weighting. The player can use the history of plays to inform his or her choice of play, but risks two possible sources of loss. On the one hand, by basing a decision on the game history (exploitation), there is a source of loss by assuming that the game history gives a fair representation of the coin's weighting. On the other hand, by ignoring the game's history (exploration), the player may lose because the game history does actually reflect the coin weighting. Both are possible sources of loss to the agent, although the sizes of the loss may vary. Any adaptive agent faces the problem of arranging its responses to the environment to minimise its expected losses from these two forces. In practice, the adaptive techniques that are used by an agent may not make it easy to separate the exploitative and exploratory modes, indeed both may be happening simultaneously. However it is still possible to meaningfully discuss the kinds of behaviour that may be observed

Exploitation

The key to exploitation is the re-use of previously successfully responses to environmental stimuli. Depending on individual circumstances of the agent or system of agents, there may not be a necessity for an agent to re-use their own prior response; agents may instead chose to imitate successful strategies for dealing with particular situations that they have observed other agents using. This tends particularly to be the case when dealing with economic, social and ALife agents, and also underlies aspects of evolution. In evolutionary systems, agents with successful responses to their environment will pass on these responses, or the potential for these responses to their offspring.

A distinction lies between *global* and *local* adaptation. Global adaptation is the response of an entire population to a changing environment. Individual agents do not adapt, but the composition of the entire population changes, so the response of members of the population to particular stimuli may change over time. Evolution systems are the prime exemplars of this category. In contrast, local adaptation is the adaptation of individual members of the population. Agents change their responses over their lifetime; the same agents may respond differently to the same environmental stimulus at different times. A population of learning agents exemplifies this type of adaptation.

Exploration

Exploration is the search for new, better, responses to environmental stimuli. As such it has often been cast as a random, non-deterministic process. This is not necessarily the case. Alchian [1] points out that statistically, it is quite possible that the set of actions of a community of exploring economic agents may appear to have been generated by a stochastic process, even if this is not the case. He writes:

> "Where there is uncertainty, people's judgments and opinions, even when based upon the best available evidence, will differ; no one of them may be making his choice by tossing coins; yet the aggregate *set* of actions of the entire group of participants may be indistinguishable from a set of individual actions; each selected at random."

This point is particularly important. On the one hand, the fact that there appears to be a stochastically driven exploration within a set of agents does not preclude agents from performing some form of intelligent or directed search. On the other hand, even if agents are carrying out some form of intelligent or directed search, statistically it may still be possible to model the exploration as a stochastic process. In the quest for mathematically tractable models of adaptation, this simplifying assumption is often made.

Noise in the adaptive process

Further to this point, there is also the question of information available to adaptive agents (for example, see Witt [84]). For instance, classical equilibrium economics makes strong assumptions about the information available to agents within the system; the usual assumption is that agents have access to perfect information immediately. In practice, information is not always instantly available, and even when it is, it is not always correct[2]. An assumption of a small amount of noise in the information that

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[2] The importance of immediate access to correct, relevant information is empirically confirmed by Reuters balance sheet.

agents are basing decisions upon, supports the notion of exploration as a stochastic process. Not only can agents with purely exploratory goals perform exploration, but agents attempting to exploit good situation-response pairs found by other agents may, as a result of imperfect information (either about the way that other agents have acted, or about the present state of the environment, or about the assumption of the environment in which a copied behaviour is favourable) perform exploration by mistake.

1.2 Natural and Artificial Evolution

In this section, the motivation behind using evolutionary models to describe the group dynamics of systems of interacting adaptive agents is considered. The basics of current evolutionary theory, especially in terms of artificial evolution, and the relationship between current evolutionary theories and the computational models that they have engendered are also described.

1.2.1 The Advantages of Evolutionary Models

Evolution and evolutionary models are of particular interest in the study of the dynamics of groups of interacting adaptive agents for three reasons. First, the study of the dynamics of evolutionary processes has a long and fruitful history, and has been backed up by a number of well-tested and useful mathematical models. There has been a continual interplay between the biological and mathematical sciences, which means that the best mathematical models are well grounded in experimental fact. Mathematical models of evolution and evolutionary operators are reviewed in Chapter 2.

Second, there is the more recent use of artificial evolution (genetic algorithms, genetic programming, etc.) as an AI and Alife technique. Techniques such as genetic algorithms, genetic programming, morphogenic codings, and co-evolving populations are regularly used in many domains. AI and ALife are not restricted to following strictly biological pathways, so the research that has been done on evolution and evolutionary operators has allowed many useful simplifications to be made whilst retaining the essence of the evolutionary algorithm.

Third, evolution is necessarily a group technique. Technically, asexual reproduction (including mutation) from a single parent, producing a single offspring which replaces the parent, is possible. However, this is identical to a random walk over the search space. The power of evolution comes from its parallelism. Different types of adaptive search place alternate emphases on the explorative and exploitative processes, and exploit the parallelism is differing ways. This point is discussed in detail by Holland [42], although there has been recent criticism of Holland's analysis of the working of a particular evolutionary algorithm, the canonical genetic algorithm [79, 29, 35, 36].

If the evolutionary algorithm is set up correctly, it can be used as a model of the dynamics of a group of adaptive agents (for instance, the Santa Fe Artificial Stock Market, discussed in Section 1.3.1). In particular, it may be possible to use an evolutionary algorithm as a link between a given adaptive group and a mathematical model. If an evolutionary algorithm can be found that successfully models the characteristic features of the system of interest, it may be possible to write down the operator that governs the evolution of that system. Mathematical approaches, particularly diffusion equation, stochastic system, and thermodynamic approaches (as discussed in Chapter 2) may then be used to model the trajectory of such a system under a given evolutionary operator, and a given utility or fitness measure. In this manner, it is possible to consider the *group* dynamics without reference to the particular circumstances of individual adaptive agents within the system.

1.2.2 Basics of Evolutionary Theory

Broadly speaking, modern evolutionary theory may be summed up as a neo-Darwinian synthesis; that is to say that it is a synthesis of ideas derived from and inspired by the ideas of Darwin and Wallace [20, 82], and filtered through the theory of molecular biology [67]. The bare bones of the theory are sketched out below. However it should be stressed that the devil is in the detail; a broad approach can only fail to do justice to the intricacies of evolution.

Darwinian evolution starts from the distinction between an individual's genotype and phenotype. Every individual contains a blueprint detailing its own construction, coded within the DNA in the nucleus of every cell. From this blueprint the phenotype, or physical form of the individual, is produced in a morphogenic process. The *central dogma* of molecular biology is that information can only pass in one direction, from genotype to phenotype. It is this central dogma that distinguishes neo-Darwinian evolution from earlier proposals such as those made by Lamarck [53].

Onto a population of individuals a *selection pressure* is postulated. This is a differential mechanism, which discriminates between members of the population, and results in differences in the probability, frequency or success of mating between members of the population. Such a pressure may be very simple and overt, for example predation removing weaker and older members of the population; alternatively, it may be more subtle. For example, females may discriminate between potential mates on account of differences in plumage or display [3]. Theorists (e.g. Hamilton & Zuk [40]) explain such discriminations in terms of their demonstrating the strength of such individuals. This

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[3] A great deal of effort has been expended by evolutionary biologists in explaining how seemingly extravagant plumage (for example, a male peacock's fan) either directly improve an individual's probability of survival, or serve to demonstrate to a potential mate the strength of that individual.

selection pressure can be summed up with the clichéd phrase 'the survival of the fittest'. This means no more, and no less than that those individuals which are best able to survive in the environment in which they find themselves are most likely to breed.

Those individuals that do survive and find mates will breed, and pass on parts of their genetic material to their offspring, who will inherit physical characteristics from their parents[4].

1.2.3 Foundations of Genetic Algorithms

The field of genetic algorithms (GA's) stems from the work of John Holland from the 1960s onwards (summed up in [42]). Whilst the mathematical explanations offered by Holland for the workings of the GA (and in general to the processes of Darwinian evolution) have been subject to much recent criticism and re-examination [79, 29, 35, 36], the basic model (known now as the canonical-GA) has become the basis of an expanding field of study.

The description of the GA that is offered at this point is purposefully a simple sketch, sufficient only to enable the discussion in following sections. It is not a precise description of any particular algorithm. The theory and mathematics of genetic algorithms and other evolutionary models will be discussed in much greater detail in Chapter 2. Algorithmically, the genetic algorithm is based upon a gross simplification of the processes described by modern evolutionary theory. The process begins with a fixed population of randomly chosen strings, each of which is a coding of a potential solution to the problem under consideration. This string may be considered as an individual's genotype. Each of these strings undergoes an evaluation process which assigns

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[4] A variety of other processes, collectively described as *mutation* may introduce variations into the genetic material of offspring, which are not traceable back to the genotypes of their parents.

a numerical measure (the *fitness*) of the success of the string as a solution. This evaluation process can range from the naively simplistic (e.g. the number of blocks of bits all taking a given value in the case of the Royal Road Genetic Algorithm [60, 79]) to the computationally complex (e.g. many engineering design problems [68]). The evaluation process is commonly referred to as the *fitness function*. In a biological context, the fitness of an individual is usually expressed in terms of the number of offspring it has; here the process is reversed. What is usually described as the 'fitness function' in GA theory is a conflation of two distinct mappings: a genotype to phenotype mapping, and a phenotype to utility mapping. This conflated mapping determines both the individual's chances of survival through to the next epoch, and the number of offspring that the individual is likely to have. These differences are usually glossed over in GA theory.

Once the members of the population of potential solutions have been evaluated via the fitness function, the population is ranked, and a certain portion of the weaker members of the population is discarded. The population is brought back up strength by creating new members via a process analogous to sexual reproduction. A pair of individuals are chosen as 'parents', and the 'child' is formed by creating a string which incorporates elements of the genotypes of both parents. The following two processes are usually (but not always involved):

Mutation

This is an analogue of the set of processes mentioned in the preceding section and referred to collectively as mutation. In the theory of natural systems, there may be valid explanations for sections of DNA not conforming to the DNA of either parent, which do not invoke any non-deterministic explanation such as damage to the DNA from cosmic rays. In GA theory such explanations are usually discarded, and the mutation operator is considered as a stochastic process, which acts with a fixed probability on each site in the genome, changing the allele at that site to a random state (where there are more than two possible states of the allele), or to the opposite value of the one it presently holds (in the case that the allele can only take two possible values). Mutation is a purely exploratory operator; it uses no information about the possible location of optima in the search space, but picks a random point in the space according to some distribution, and places an individual at that point.

As will be demonstrated in the following chapter, the mutation of a population of individuals away from a given state can be considered as a diffusion process, capable of being modelled via partial differential operators. In the absence of any selective pressure or fitness function, mutation will cause a population to spread across the available space to a macroscopic entropy maximising state.

Mutation can be considered to be the most fundamental genetic operator, and in natural terms it is certainly the most ancient, having a role in the reproduction of all organisms in the history of life on earth.

Crossover

This is the process which combines the genomes of two parents to form a child. In the simplest version, *1-point crossover*, a single cut point is picked at random; the child's genome consists of a copy of the first portion of one parent's genome, concatenated with the second portion of the other parent's genome. In more complex versions, *n-point crossover*, the genome string is considered to be a loop, and a total of n cut points are chosen. The child's genome consists of alternate portions of the parents' genomes.

Crossover operators have also been produced to fit specific types of genome used in particular problems. The best known examples are the *re-ordering* crossover operators, used in evolutionary approaches to travelling salesman type problems. These alternate operators are tailored for problems where constraints on phenotypic structure have been resolved by imposing the constraints at a genotypic level. In the travelling salesman problem, the constraint of not visiting any city more than once is imposed at a genotypic level, by restricting each allele to appear once and once only.

The theory of the canonical crossover operator is very controversial, and is generally held to be not fully understood at this time. Rival theories as to the operation of the crossover operator are discussed briefly in Section 6.3.3. Early theories [42] held crossover to build up larger areas of (potentially) favourable genes on the genome from smaller, favourable 'building blocks'. More recent work [79] indicates that crossover may act to spread the genes of the best individuals through the population quicker than would be possible than by a policy of replacement with mutation.

Crossover is a combination operator, it implements both exploration and exploitation. The offspring of a pair of agents has a genome which lies between its parents. Whilst it is assumed that both parents implement good solutions that have been found, there is no absolute guarantee that the offspring will, although it can be shown [42] that if the landscape has sufficient exploitable regularities, the offspring will probably contain beneficial aspects of its parents genetic makeup. Thus, there is both an exploitative and an exploratory aspect to crossover.

Asexual Reproduction

Asexual reproduction is the simplest possible reproductive scheme. Here there is only one parent, and its offspring inherit all the genetic material of that parent. Whilst this operator is only used in the simplest organisms in nature (the so called 'ancient asexuals' group), it has an important place in GA theory, particularly in the analysis of evolutionary search. This is because asexual reproduction implements pure exploitation: there is no opportunity to explore the genome space when this operator is used.

By using a combination of asexual reproduction plus mutation, and replacing the entire population at each generation, a simple evolutionary search is implemented, in which the exploratory and exploitative operators are separated. Whilst this is not the most efficient evolutionary search algorithm, it is the one which most easily submits to a mathematical treatment. The exploitative and exploratory operators can be considered separately, and written down. The resulting evolutionary operator is the result of an exploitative operator applied to the existing population, then modified by an exploratory operator.

1.2.4 Selection Pressures from Within a Population

Classical evolutionary theory conceives of abstract selection pressures. In the study of individual organisms, or of specific webs of organisms, some of these pressures may be identified and/or quantified. In cases where mating or breeding success appears dependent upon some interaction between members of the population (e.g. some form of courtship ritual), the purpose of the interaction is explained as a demonstration of that individuals fitness to face some external pressure.

It is not the case that all pressures may be directly externalised. Organisms that lie at the top of food chains tend not to have any predators, and their population is limited by their food sources; they are unable to sustain a population beyond the limits of their prey's sustainability. In many cases this can lead to unstable populations following Lotka-Volterra dynamics [62]. In many cases the selection pressure is now not imposed externally by the predations of other species, but internally by members of the population choosing mates[5].

Recent work with artificial evolution (GA theory) has also involved selection pressures within a population. There exist a number of papers describing work in which populations of agents play various economic games (especially the Iterated Prisoner's Dilemma (IPD) game [10, 65, 11, 56, 77] and artificial stock markets [5]).

The common feature of all these models is that the fitness of an individual is no longer solely a function of that individual's phenotype (and therefore genotype), but is rather determined by one or more interactions with another member or members of the population. If members of the population cannot choose which other members of the population they interact with, and the behaviour of an agent during an interaction is under genetic control in some way, then the fitness of an individual is determined not only by its own genotype, but also by the distribution of the genotypes of the whole population. The result is that (in terms of GA theory) the fitness function is dependent upon the population distribution, and yet serves as the selection pressure which dictates the evolution of this same population. It is by no means clear that the dynamics of the population will follow those in GA models without interactions.

1.2.5 Co-evolution vs. Interaction Within a Population

As stated previously, this thesis concerns populations of agents whose adaptation is determined by their utility in achieving interactive or social goals. Contrast this study with the field of *co-evolutionary* theory, which seeks to describe how species evolve under selection pressures imposed by each other. The difference lies in the adaptative scheme. In an interacting population, mating takes place in the entire population, whereas in

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[5] In natural evolution, it is usual that all the females breed, but only the strongest males get to breed.

co-evolutionary models, the subpopulations represent different species, unable to mate across species boundaries.

The simplest model of co-evolution is of two species, for example a predator and a prey. The species interact in a simple manner: the predators attempt to kill and eat the prey. It is this interaction that drives the selection of individuals within both species. Fitter members of the prey are more likely to avoid the predators, and thus pass on their genes to the next generation. In a similar manner, fitter predators are more likely to catch the prey, and thus survive to pass on their genes, whereas the weaker predators die of starvation.

The dynamics of such a co-evolutionary system are commonly described as the 'Red Queen effect' [80] or as an 'evolutionary arms–race'. Both species are constantly seeking improvements to counteract the new improvements in their opponent; they are constantly running to stand still.

Co-evolutionary phenomena are an expanding and fast moving field of study at present. Much of the work is based around the Bak–Sneppen model (original paper [8], review paper [66]). This is a simple mathematical model of co-evolution which displays self-organised criticality. A co-evolutionary system appears to evolve towards a critical state in which 'avalanches' of changes caused by changes at individual sites ripple across the entire system. These avalanches are of all scales. This model demonstrates the phenomena of *punctuated evolution* observed in the historical record [73, 74, 75]. Extinction events on all scales take place, the frequency of extinction events scaling with event size by a power law. The Bak–Sneppen model, and other work (e.g. Newman [63]) detail models of extinction which duplicate the historical record, and which do not need to invoke external environmental shocks (e.g. meteor strike) in order to explain the fossil record.

Borgine & Snyers [14] produce a formulation of what they describe as a co-evolutionary model, based on Lokta-Volterra dynamics [62], using an Eigen-Fisher model. This model reduces to a Schrödinger wave equation. Whilst this model claims to be co-evolutionary, the experimental results presented (based on Kaneko & Suzuki's bird model [44]) are based on a population of interacting agents; there being a single population under an asexual reproduction plus mutation operator. Bourgine & Snyers claim that their study indicates that the co-evolutionary dynamics (hill climbing on a sinking landscape), which gives rise to punctuated equilibria is a general feature of exploitation plus exploration processes, rather than a consequence of the discreteness of mutations. Their analysis appears to conflate two separate effects. First, evolution on plateaued landscapes is punctuated due to entropic effects analogous to a first passage time in a random walk. This is discussed further in Section 2.2.4. Second, there is the Fisher Law, which posits species undertaking a hill-climbing evolution on a sinking landscape caused by co-evolution. They appear to rule out the possibility that a meta-stable symbiotic relationship between species occupying various niches can ensue: This has been observed in discrete phenotypic spaces (Section 1.3.2). It is not clear that such a symbiotic relationship cannot occur in a continuous phenotypic space.

In the following section, a number of models are reviewed which demonstrate meta-stability. These are examples of interactive systems which would appear stable in the infinite population limit, but which display meta-stability only in finite populations. The main difference between co-evolution of a number of species and interaction within a population is one of stability. Co-evolutionary systems tend to follow Lokta-Volterra dynamics, that is to say that the evolution of each species is regulated by the other. Whilst, as is discussed above, this can lead to interesting dynamics including punctuated equilibria, it differs from an interactive system in that a co-evolutionary system generally only has a one-way dependence (e.g. predator eats prey), whereas in an interactive population the dependencies run in both directions. Here the utility of each agent can be dependent on the actions of all agents[6].

A fundamental question, whose answer lies beyond the scope of this thesis, is whether co-evolutionary systems and interacting adaptive populations share the same dynamics, or belong to different classes of dynamical systems. On the one hand, an interacting adaptive system might be pictured as a co-evolutionary system with a large number of co-evolving species (mapping each individual in the interacting adaptive system to a species in the co-evolutionary system). This can be countered by an argument that there is still an essential difference in that co-evolutionary systems are not stable in the infinite population limit, but continue to evolve in a deterministic manner, based on the relative fitnesses of members of the mutational cloud of each separate species. In contrast, members of an interacting adaptive system may make mutational as well as selective moves across the landscape; the mutational moves are stochastic as opposed to deterministic. However; the dynamics of both types of system can be captured using statistical dynamics formulations, the Bak–Sneppen model [8, 66] in co-evolutionary systems, and various approaches in the case of interacting adaptive systems (see Section 2.2). It is an open question as to whether both types of system can be described by the same statistical dynamics formulation.

1.3 Models of Interacting Populations

There are a number of well established lines of research into the evolution of interacting populations. Whilst the directions and aims of these models are varied, they all

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[6] This will vary with the system. In the system considered by this thesis, this is the case. In other systems reviewed in this thesis, the dependency is stochastic.

use evolutionary computing methods to optimise a population of agents whose utility depends on their effectiveness at performing some form of social interaction. Their purpose is either to draw conclusions about the optimal ways in which the population self-organises under the given fitness function, or to test theories about the nature of the interactive regimes. In short, these lines of research seek to use evolutionary methods on populations of interacting agents as a means of exploring the nature of the interactions, or to find the types of populations that are engendered by using success at these particular interactions, not to investigate the more general issues of how populations of interacting agents evolve.

1.3.1 Artificial Stock Markets

The theory of stock markets is one of the primary examples of the adaptation of a population of interacting agents. Arthur [4] explains the problem succinctly: An agent's optimal strategy is dependent upon its expectation of the strategies of other agents. To quote Keynes [48], the problem of valuing stocks depends upon "what average opinion expects the average opinion to be". Clearly the payoff (or fitness) received by any particular agent is dependent not only on that agent, but upon the rest of the population.

One very interesting strand of work that has been pursued over the past few years is the use of Alife techniques to produce an artificial stock market (ASM). The rationale for this work is that by creating an ASM, researchers have a laboratory in which they can test theories concerning the interaction of economic agents. The advantages of this approach over on using real stock market data to test economic theories are that:

1. The rationality of the agents is known, that is to say the computational power of the agents is known.

2. The trading strategy of the agents is known.
3. In a real stock market the markets in different stocks are not independent; the effect of one stock on other stocks (in unrelated industries) is well known. An artificial market can be created in a single stock.
4. An artificial stock market is insulated from external factors that influence real markets and which add 'noise' to the market. The *efficient market hypothesis* asserts that there is no such thing as noise in a stock market, all changes in asset prices are due to new information entering the market, and being discounted by traders into the asset prices. Whilst the timing and effects of individual items of information entering the market may not be predictable, the resultant effects may have a well defined distribution.

Not all ASM's use evolutionary techniques to modify the populations of agents, most of the recent ALife models are adaptive in that they allow agents to modify their strategies to improve their performance. Various adaptive processes have been used, including reinforcement learning and imitation of the strategies of more successful agents, as well as evolution under a GA. For example, Bak et al. [7] have allowed agents to modify their trading strategies to reflect current market conditions, and have also allowed agents to change their strategies to imitations of the strategies of more successful agents. Whilst this latter method is not strictly evolutionary, it is still adaptive; the composition of the population is under a pressure to mutate towards more successful areas of the space of traders.

From the standpoint of investigating the dynamics of evolution in populations of interacting agents, perhaps the most interesting model is the one that has been developed by Arthur and colleagues based at the Santa Fe Institute [4, 5]. In this model, a population of agents trade in a single asset. Whilst the details of asset pricing theory are of limited interest here, the nature of the agent interactions requires some explanation. All the agents have a choice between investing their assets in a stock which pays a randomly chosen dividend from a given distribution at each time period, or placing their assets in a risk free investment. Based upon price and dividend information, the agents each predict the next price of the stock. Classical economic theory predicts each agent's optimal distribution of their assets between the stock and the investments, given a knowledge of each agent's degree of risk aversion and prediction of the next price. These demands are then passed to an independent market supervisor, or *specialist* who determines the price of the stock, given that the stock must all be taken up at each time period. The new price and the next dividend are then passed to all the agents, who can then update their demands.

In the model used by Arthur et al. [4, 5], the market consists of a fixed number of agents, all of whom have a bank of possible strategies, each of which is a *classifier* (a decision rule coded as a binary string[7]). At regular intervals, each agent uses a GA to eliminate its weaker strategies and replace them with new, exploratory strategies based on its most successful current strategies. Whilst the thrust of this work is directed at explaining particular aspects of markets, there is a point which is particularly noteworthy in the present context. There appear to be two regimes available within the market, dependent upon the initial conditions of the model:

A fundamental trading regime. The model is set up so that all investors start with a common set of expectations (i.e. strategies), and these expectations are that the stock will have its *fundamental* value, the value that classical economic theory predicts that the stock should have.

> "If a large majority of investors believe the fundamentalist model,

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[7] see Holland [42] and Goldberg [37] for details of classifier systems.

> the resulting prices will validate it, and deviant predictions that arise by mutation in the population of expectational models will be rendered inaccurate. Thus in our market, the homogeneous rational expectations equilibrium of the standard literature is evolutionarily stable: it cannot be invaded by small numbers of deviating expectations."[8]

Thus, if the population of available strategies is clustered closely enough around a particular stationary point (predicted by the standard theory), then that point will lie in a deep attractor basin, i.e. members of the population will be unable to escape from the environs of that point.

A technical trading regime. In an identical model, if there is a wider distribution of initial strategies, then the fundamental regime will no longer be stable. It is now possible that non-fundamental strategies can be successful. These strategies will spread through the market, forming a *bubble*, where the stock value deviates systematically from its fundamental value. Other strategies may now arise to exploit the bubble, and a *crash* will result, as the fundamental stock value is reasserted. This regime is known as a *technical* trading regime, and is characterised by agents making predictions of future prices based on the recent price history.

The existence of these two regimes demonstrates that stationary points in the population space do actually exist when adaptive agents interact, and that these stationary points are not limited to fixed points, but include limit cycles, and possibly strange attractors as well. Arthur et al. have noted informally that once the technical regime (which they also describe as a complex regime) has been entered, then the market appears to be trapped in it.

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[8] Arthur [5].

Payoff		*p1*	
p1/p2		C	D
p2	C	R/R	T/S
	D	S/T	P/P

Table 1.1: Payoffs in the Prisoner's Dilemma Game. A Prisoner's Dilemma is any game in which $T > R > P > S$ and $2R > T + S$. The plays C, D stand for Co-operate and Defect respectively.

1.3.2 The Iterated Prisoner's Dilemma Game

The Prisoner's Dilemma (PD) game is a well established game that has been used to model interactions between individuals within a number of fields. It is a single shot non-zero sum game with payoff table given by Table 1.3.2.

It is well established that in the single shot game, the strategy of mutual defection DD is evolutionarily stable [77]. However, when the game is repeated indefinitely[9] the dynamics become more complex. Axelrod [6] has shown that there is no optimal strategy independent of an opponent's strategy. In an adaptive population, the adaptation will be directed by the results of the games recently played, and hence by the composition of that population

Evolutionary techniques have been widely used in studies of the iterated (IPD) game to establish which strategies are viable in evolutionary terms, and to investigate the way that various strategies interact with each other. A number of these studies are of particular interest, either because they demonstrate the meta-stability of populations, or because they demonstrate other features of interest. These studies have used a variety of means of enumerating strategies in such a way that they may be encoded in a binary

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[9] Either played ad infinitum, or with a fixed (small) probability of halting after each play.

genome. The most common are to encode various forms of finite state automata [2, 28] and game tree hierarchies or histories [54, 55, 56]. There have also been studies of both spatial and non-spatial IPD games. Here attention will be restricted to non-spatial versions of the game.

Lindgren [54] and Lindgren & Nordahl [55] coded the genome based on responses to possible recent game histories. The experimental set-up was designed to allow mutations which lengthened the genome, thus allowing for the evolution of memory by players. They note that the results of their simulations show the evolutionary dynamics of the system to consist of "a succession of stable periods separated by periods of rapid evolution ... reminiscent of punctuated equilibria" [55]. Moreover, their experiments show that it is not just individual strategies that can dominate the population. There is evidence of 'species' of agent rising to prominence together, displaying apparently correlated evolutionary dynamics, and becoming extinct together[10]. This indicates that the population is shifting between areas of the space of population distributions, first favouring one distribution of populations for a while, then moving to another area of this space where another distribution of agents between possible genotypes is favoured.

The work of Lomborg [56, 57] is significant in this context. He demonstrates the results of a large evolutionary simulation, where the genome uses a similar technique (but different implementational details) to that of Lindgren [54] and Lindgren & Nordahl [55] discussed above. In these experiments the history length is fixed, and Markov techniques are used to calculate the limit scores of agents within the population playing each other. In this way, he has managed to produce results for infinite game lengths without a major computational load. The results are very interesting: rather than any

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[10] This can unfortunately only be inferred from the diagrams accompanying their text. There is no mention of this feature in the text, but examination of the diagrams shows these dynamics quite clearly.

one 'species' dominating the population, the system settles down in a meta-stable state comprising of a mixture of possible strategies in constant proportions. Lomborg's analysis indicates that the populations consists of two elements, a *nucleus* of co-operative strategies which are easily exploitable, and a *shield* of unforgiving strategies (e.g. similar to TIT-FOR-TAT) which will respond to defection with mutual defection. The shield and nucleus remain in approximately fixed proportions, because the shield exploits the nucleus slightly, but not enough to become dominant. Lomborg discusses the evolutionary stability of such a population: The population can initially easily be invaded by any strategy that defects against co-operators. The proportion of co-operators in the population declines, and is replaced by the invading strategy and shield strategies. The invader will however trigger the defection of the shield strategies, which in turn leads to its own downfall, and the re-emergence of the exploitable nucleus strategies.

> "the answer to Axelrod's question, of what is the most robust strategy in the IPD game, has never been a single strategy, but is instead a set of strategies internally partitioned between a highly co-operative nucleus and a diverse and cautious shield."[11]

Lomborg too notices the meta-stability of the population: an evolutionary stable mix of strategies will persist for a large number of generations. However, it will not persist forever: catastrophic changes in the population occur occasionally, and one evolutionary stable mix is replaced by another one. His analysis of this is that in the period during which a meta-stable population is fighting off one intruder, another intruder may then exploit the combination if it arrives at the right moment. Lomborg points out that the most destabilising strategies are in fact the 'too nice' strategies which co-operate willingly. A population that is invaded by this form of mutant is far

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[11] Lomborg [57].

more vulnerable than a population that is 'too harsh'. The gentle exploitation of the nucleus by the shield has the effect of keeping the 'too nice' mutants at bay, but it is occasionally exploitable, and it is here that the systemic meta-stable nature of the population becomes apparent.

Batali & Kitcher [11] also note the meta-stability of populations of IPD playing agents in their simulations involving optional[12] and compulsory versions of the IPD. They note the long periods where the population appears trapped, with various strategies maintaining approximately fixed percentages, and the sudden shifts between population compositions. As they point out, in any situation where no phenotypic differences are observable, there is a possibility of genetic drift (see Section 1.4.1); neutral sites on the genome can mutate causing the genotype to vary massively without any effect on the phenotype, and therefore the performance of individuals. In this case the phenotypic similarities are that agents play the same when (for example) faced with co-operating opponents. Here their potential responses to non co-operators may face extensive genetic drift over a period of time, so an exploitative mutant in fact faces a genetically diverse population which may seek a different meta-stable configuration to its original one. They point out that,

> "The only way that a population playing the compulsory game can escape from a state of high defection is for several favorable mutations to occur at once ...
>
> In thinking about the evolution of social behaviour it is important to recognise that such behaviour occurs against a changing environment consisting of the behaviours of other members of the populations. Thus such an

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[12] In the optional version of the IPD game, there is a third possible play, 'N' which indicates that the player refuses to take part in that round.

> evolutionary process is a feedback system, and the global properties should be expected to fluctuate, perhaps chaotically ...
>
> ... In the long run, the evolutionary dynamical properties of strategies and their genetic representations may have the most significant effect on the careers of populations using those strategies."[13]

Similarly, in simulations using the n-player version of the IPD game (otherwise known as the public goods problem), both Bankes [10] and Glance & Hubermann [34] observed populations with high levels of co-operation, and with high levels of defection, with sudden intermittent shifts between these two types of population. They also note that a number of differing levels of co-operation in the multi-player game are stable, which leads to what they describe as a 'terraced' mean score/play trajectory. This trajectory has a number of similarities to that observed in studies of the Royal Road GA [79]. Again, the notion of genetic drift is invoked to explain these results.

Hubermann & Glance [43] explored conditional co-operation in a public goods problem, where individual agents decide whether to co-operate or not stochastically, based on the percieved fraction of agents co-operating in a previous epoch, and their perception of the effect of their decisions on other agents future decisions. A mathematical formulation has been devised, based on earlier work by Ceccatto & Huberman [17]. They show that in such a system there may be more than one optima (corresponding to alternate Nash equilibria), although only one is global. They then consider transitions between optima caused by agents misperceptions of the environment (the number of agents co-operating). This system is not truly adaptive, agents update their probability of co-operation to the optimal ratio based on the information they have. However, because this information may be erroneous, a degree of stochasticity is added to the

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[13] Batali & Kitcher [11].

system, because agents' perceptions of the optimal strategy may now differ.

Based on the formulation from Ceccatto & Huberman [17], Huberman & Glance [43] show that meta-stability may be present. Furthermore, they consider the transition times between the local optima. They note that the utility barrier separating local optima may have differing heights on each side. This means that the transition probability between optima is asymmetric. In the system they consider, there are only two optima. The system finds it fairly easy to jump from the local to the global optimum, and this is observed regularly. However, the transition time from the global to the local optima is a number of orders of magnitude larger, and this event is rarely observed.

1.3.3 The El Farol Problem and Other Co-ordination Problems

The El Farol problem, put forwards by Arthur [3] is a co-ordination problem under the constraint of bounded rationality. This means that it is a problem where agents must co-ordinate their responses, in a situation where they cannot make perfect predictions. Consider the original problem:

There is a bar in downtown Santa Fe called the El Farol. They have a fine salsa band playing on a Thursday night, and people go there to dance. Now obviously, it is a better night out when it is busy, but when it gets too busy it becomes less enjoyable. This is formalised as follows. There are a population of N agents, each of whom can make a choice A (go out), or B (stay in). There is a fixed small utility to staying in, and a greater utility to going out – if there are k or fewer other agents at the bar. If there are more than k agents at the bar, then there is zero utility to going out. The only information that all agents have, is the historical record of numbers at the bar on previous occasions. There is no direct communication between agents.

This problem, and other similar problems such as the spatial minority game [19, 88, 18] have profound consequences. The bounded rationality of agents limits their predictive powers; yet co-ordination emerges. Arthur [3] points out that whilst the number of agents in the bar (choice A) varies around k, the set of agent strategies is continually altering: if agents can find pattern in the collective behaviour, then they can exploit that pattern, causing it disappear:

> "If several people expect many to go because many went three weeks ago, they will stay at home"[14]

This underlies the efficient market hypothesis mentioned in Section 1.3.1. All pertinent information about stock prices in a market is discounted immediately. If agents can find a pattern in market prices which they can exploit, then that exploitation will tend to destroy the pattern. Markets are thus seen as moving under Gaussian noise, hypothesised (from experimental evidence) to approximate the distribution of changes in market prices due to new information being discounted.

Despite the apparent near stasis that emerges, approximately k agents going to the bar on each occasion, there is a rich dynamical structure underlying the system:

> "After some initial learning time, the hypotheses or mental models are mutually co-adapted. Thus we can think of a *consistent* set of mental models as a set of hypotheses that work well with each other under some criterion – that they have a high degree of mutual adaptedness. Sometimes there is a unique such set ... More often there is a high, possibly very high, multiplicity of such sets. In this case we might expect ... [such systems] to cycle through or temporarily lock into psychological patterns that may be non-recurrent,

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[14] Arthur [3].

path dependent and increasingly complicated."[15]

In this type of system, the collective dynamics remain stable, whilst the population may undergo shifts between various distributions of agent hypotheses. This will not always be the case. In the IPD, changes in agent hypothesis set can change the collective response of the system, affecting not just the utility of individual agents or hypotheses, but the collective behaviour of the entire population.

1.4 The Instability of Interacting Populations

In the above section, it has been established that the phenomenon of meta-stability in populations of interacting agents exists, and that it has been noted across a variety of simulations on a number of differing games. In the ASM's that have been discussed, differing initial conditions can result in either technical or fundamental trading regimes becoming prevalent. In the case of the technical regime there appears to be a quasi-cyclic behaviour consisting of bubbles and crashes. Whether this is a true cyclic behaviour, or is the result of systemic properties of the ASM simulation is an open question. That is to say that it is not known whether the quasi-cycle of bubbles and crashes should be considered as a cyclic behaviour with some stochasticity in the period, or whether they are two different regimes, with a stochastic process determining the transition between them. This question will be further discussed in section 6.1, in the light of experimental evidence. In the case of the IPD simulations the instabilities have been noted by a number of researchers, and take the form of sudden catastrophic shifts in the way that members of the population play against each other.

This section explores the idea of stochasticity within populations from a non technical angle. The first notion considered is genetic drift, which has been held by many

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[15] Arthur [3].

(e.g. [11, 10, 34, 43]) to be responsible for the instability in populations of IPD playing agents. This is followed by an exploration of the basics of statistical dynamics, which has been used very successfully in thermodynamics, and a consideration of how its techniques might be of practical use in explaining evolutionary dynamics.

1.4.1 Genetic Drift: Mutation as a Diffusive Operator

Consider a population of individuals all sharing the same genotype. The mutation operator will, over time, alter various sites on the genomes of particular individuals, so the population now forms a cloud around the original genotype in the genome space. It will be shown in Section 2.1.1 that this is a Fokker-Planck process, i.e. the simple diffusion of the population around its original position. Obviously, whilst the genotypic cloud maintains the same phenotype, diffusion will continue unabated. However, if the phenotype alters at some point then there may be a drift towards the new phenotype (if it is favourable). A mathematical treatment of the probability of a favourable mutant becoming fixed within the population is given in Section 2.1.6.

Let us now further suppose that it is not possible to mutate from the original phenotype to a more favourable phenotype without first mutating to a less favourable phenotype. There is no path from the present genotype to one corresponding to a more favourable phenotype that does not first cross an area of lowered fitness. Now the diffusive mutation will spread the population until (in the limit) the population tends towards an entropy maximising distribution across this area. Clearly then, if the original genotype was not in the centre of the iso-phenotypic area, then the diffusion of the population across that area can lead to a population with a high variance and a mean at some distance from the original genotype.

This phenomenon is further discussed in Section 2.1.3. There are cases where rather than gaining a maximal entropy distribution, fixation of neutral alleles may occur within such a population. A *neutral* allele is one which confers neither an evolutionary advantage or disadvantage on its possessor. Biologists still argue about whether neutral alleles actually exist, but in GA theory the existence of neutral sites on the genome is accepted. In this case, a neutral site on the genome will lead to a plateau, or neutral area, in the fitness landscape; the favourability of the phenotype is unaffected by the contents of this particular site. There is no constraint on the point in the neutral area around which the population becomes fixed.

It is this phenomenon that accounts for the so-called genetic drift. When there is a change in the environment, which leads to different aspects of the phenotype becoming selected for, the population can respond in unexpected ways, because the continued phenotypic invariance is not reflected at a genotypic level. The sites that are neutral in the original environment may not remain neutral in a changed environment. Over a period of time, a population can forget its optimal response to an environment, because the genes that code for that response are no longer selected for. If the environment then returns to the original environment, the population may no longer respond in the original manner, and this can lead to events as extreme as extinctions. Even if the new environment mirrors the environment out of which the original genotype emerged, there is no guarantee that the population will still be viable in this new environment, as the genome cloud is centred about a different point in the space, which may now have differing characteristics. In the case of an interacting population this effect may be more pronounced as the variance of the population cloud can have a profound effect on the performance of individuals within that cloud.

Diffusive mutation can not only take place across neutral landscapes (i.e. areas of the genome space which are equi-fitness under currently obtaining environmental conditions), but also takes place where there is a fitness gradient. The drift can occur either in parallel or normal to the direction of the gradient. Whilst the population may be moving in a specific direction, the diffusion around the centre of that population will still occur, and can still be modelled using a Fokker-Planck process. The most interesting case detailed by Kauffman [46], is where the population is initially centred about a local fitness-maxima. The rate at which the population spreads is determined by the local gradient of the fitness landscape and the mutation rate.

Assume that the centre of the cloud remains static. The cloud now surrounds a peak within the fitness landscape. The population is attempting to diffuse across the landscape by a process of point mutations on individual sites on the genomes of each member of the population; each site on every genome having a small, finite chance of mutation. Against this pressure outwards away from the peak is the selection pressure, forcing the population to stay on the peak. Assume [16] that the selection is deterministically based upon the fitness, which is in turn deterministic. Then only the k individuals closest to the fitness peak will survive each generation. There will be some turnover and movement within this population, caused by mutation of the population. This fairly static population will occupy the area closest to the fitness peak, and its area will be determined by the relative strengths of the selection and mutation pressures. Around this area is a second zone which also contains members of the population, which are the mutated offspring of the surviving population. Individuals within this population are very unlikely to survive to reproduce. In the case that none of the individuals within this zone survive to reproduce, the distribution of the portion of the population within this zone is dependent only upon the mutation rate. The stochastic process used to model mutation is capable of producing jumps across the landscape of arbitrary length[17]. It is

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[16] Although this may not be true in every case.

[17] When measured using some appropriate metric, such as the Hamming metric.

thus possible for the population to become established on peaks in distant parts of the landscape, given a sufficient waiting time. This principal will be of prime importance in Chapter 3.

1.4.2 Statistical and Thermodynamic Formulations

In Section 1.3 a number of systems have been discussed as systems of interacting agents. In some of these systems, a discrepancy can be observed between the collective behaviour of the system, and the behaviour of individuals. Most striking in this respect are the co-ordination problems, where a stable collective behaviour emerges despite the rich dynamics of the underlying population. This is analogous to thermodynamics and statistical physics, where order at a macroscopic or collective level can hide stochasticity or disorder at a lower, microscopic level. In this section, the approaches of statistical physics and thermodynamics are discussed at a non-technical level. The relationship between events at the micro- and macroscopic levels will be discussed, especially the influence of microscopic events on macroscopic behaviours.

Statistical dynamics is based upon the premise that when dealing with a system containing a very large number of identical parts, it is possible to describe some aspects of the system (usually some functions of the lower order cumulants or moments of some property of individuals) without knowing the state of the entire system. For example, in thermodynamics, six real parameters (a six dimensional vector) are required to describe the state of an individual molecule (3 for position and 3 for momentum) at any point in time. In a gas with the order of 10^{23} or so molecules it would require a massive state space to describe the state of the gas fully, and this would be far beyond conceptual or computational resources. The alternative is to try and describe the gas using, for example, statistical measures of the energy of the particles, to provide information on temperature and pressure. The mathematics of this is rather involved (using the calculus of variations), but leads to models of the behaviour of gases which account very well for the observed behaviour of gases.

The statistical techniques applied usually involve a reduction in the dimensionality of the problem by binning the elements of the system. The statistics of the ensemble can be considered by taking the statistics of the set of bins. Stochastic approaches can be used to model the transition probabilities of individual elements between bins (the so-called *master-equation* approach, which will be used in Chapter 2), even when these elements behave deterministically. In very large populations, the accuracy of the approximations is usually good, because the affects of individual transitions wash each other out. Macroscopic stability can thus emerge, despite the rich dynamical behaviour at a microscopic level.

There are two ways in which this separation between levels can break down, allowing microscopic events to determine macroscopic structure:

Reduction in Population Size If the number of elements in the system is not sufficiency large, the dynamics of groups of individual elements are no longer well approximated by a stochastic approach. The stochastic fluctuations in macroscopic structure are usually considered to be of order $1/\sqrt{n}$, in a system of n elements. As n becomes small, the magnitude of these fluctuations can become significant; discrepancies between observed and predicted behaviour are observed within finite waiting times. This can lead to bifurcations in finite systems. This point will be returned to in Section 3.3.

Breakdown of the Strong Law of Large Numbers There are many systems for which the stochastic approach fails to accurately model the dynamics of the system. This is because, even with increasing numbers of elements, the variance of the approximating distribution fails to converge to zero. In this case, the microscopic dynamics play a significant role in determining macroscopic behaviours, even in effectively infinite populations. This can lead to global co-ordination in systems without global transport or information mechanisms, for example many physio-chemical systems such as the Beloutov–Zhabotinski reaction. Such systems are discussed in depth by Nicolis & Prigogine [64].

Similar techniques may be used with evolutionary dynamics. The idea here is that within a large population it is not necessary (or even feasible) to know the exact state of the genotype of every individual within that population. By defining suitable order parameters which characterise the infinite limit behaviour of the system, the description of the full system can be reduced to a description of the dynamics of the order parameters. In order for this to be possible, these order parameters must be closed in the infinite limit. This means that in this limit, the dynamics of the order parameters must be dependent upon those order parameters, and not upon the underlying population distribution. The dynamics of the Royal Road GA have been analysed using this technique [79], and this work will be reviewed in Section 2.2.3.

This technique is particularly applicable to an evolutionary model of a population of adaptive interactive agents. In general, interactions within the population take place between groups of randomly chosen individuals (ranging from a minimum of two, up to the whole population), that is to say that each individual has no control over which other individuals it may interact with. The evolution of the population is thus dependent on the expected composition of such interacting groups. In Chapter 4 this approach will be developed for a particular model by a reduction of the system to a set of behavioural groups. Stochastic approximations based upon a master equation approach are then used to model the transition probabilities between such groups under particular evolutionary operators.

1.5 Aims and Methods of this Thesis

The aim of this thesis is to investigate the stability of populations of interacting agents. In this chapter a number of empirical studies of populations of interacting agents have been discussed. In all of these works, transitions between behavioural regimes have occurred, and in some cases the efficient or material causes of these transitions have been explored. This thesis will attempt a discussion of the formal causality of such transitions: it attempts to answer the question 'why do such behavioural transitions occur?' with an explanation in terms of the underlying commonalties in the structure of all such systems.

In the following chapters the problem of the stability of a population of interacting agents is explored further. In Chapter 2, the mathematical preliminaries will be dealt with. Various approaches to mathematical population genetics will be discussed, together with their limitations. Specifically, the two main approaches to this field will be discussed, the diffusion equation approach, and the statistical dynamics or thermodynamic approach. These will be placed in the context of the theory of genetic algorithms, and of evolutionary search. Chapter 2 also contains a discussion of the behaviour of dynamical systems under the influence of noise. This will be shown to induce meta-stability in otherwise stable systems.

In Chapter 3, an approach to the dynamics and stability of populations of interacting agents will be developed, based upon the ideas discussed in Chapter 2. First, the evolution of a population of interacting agents under asexual reproduction and mutation is discussed from a diffusion equation approach. The additional non-linearities that are introduced are pointed out. At this point, the discussion will focus on the transition from the infinite limit to an extremely large finite population, and thence downwards towards smaller finite populations. The stochastic deviations from the infinite limit dynamics will be discussed in detail; the dynamics of a finite system of interacting agents will be shown to correspond to the infinite limit dynamics with an additive noise term. Finally, Chapter 3 discusses how a statistical formulation of such a system might overcome some of the analytical problems discussed.

Chapter 4 develops a simple model of a population of interacting adaptive agents. This is a highly simplified artificial stock market. The rationale and design criteria for this model are discussed, along with the detail of the model itself. Order parameters for the model, based on behavioural classes are put forward, and a mathematical treatment of the dynamics of these behavioural classes in the infinite limit is put forward. The approach is from a statistical dynamics standpoint, heavily dependent upon the backdrop of Chapter 2.

In Chapter 5, the empirical behaviour of the model is put forward. An information theoretic approach to the validation of the statistical formulation in the infinite limit is put forward; the predicted behaviour and the observed behaviour are shown to converge as population size increases. Fixed points of the statistical formulation are calculated by numerical methods, and the trajectory of various order parameters around their fixed point values are exhibited for various population sizes. Certain aspects of system dynamics are examined in detail; the dynamics of 'boom and bust' events are analysed and shown to have a strong deterministic component, even in small populations. Finally, Chapter 5 considers the relative dependence of the system dynamics upon statistical and environment fluctuations.

Chapter 6 attempts to integrate the underlying stochasticity of interacting adaptive systems presented in Chapter 3, with the details of the model in Chapter 4 and the empirical observations in Chapter 5. An explanation is put forwards for the behaviour of the model; the observed behaviour is consistent with the system having at least two attracting regimes. One is a fixed point corresponding to the fundamental regime noted by Arthur et al. [5]. The other attractors correspond to risinig and falling returns; when the system enters the basin of such an attractor 'boom and bust' dynamics are observed.

The effects of population size on the dynamics of the system are also considered in Chapter 6. Three dynamical regimes are suggested for systems of interacting adaptive agents, although no sharp bifurcations in system behaviour are noted. This Chapter also contains a critique of the work presented in Chapters 3,4, and 5, and particularly of both the model chosen and the mathematical approach to that model. The thesis closes with a discussion of possible directions for future work.

1.5.1 Contribution

Meta-stability is an established phenomenon in the literature. This thesis demonstrates that a range of models and simulations of interacting groups of agents share a common phenomenology; periods of stability punctuated by sudden shifts in the make up of the group. This common phenomenology is characterised as meta-stability. The thesis postulates that the shared phenomenology is due to a shared ontology; the meta-stability is due to a common formal cause. This cause is identified as a dependency of the fundamental forces of exploration and exploitation (which underlie adaptation) on a social measure of utility. This acerbates the stochastic fluctuations inherent in the explorative and exploitative forces; these fluctuations remain a significant factor in determining a system's trajectory even in quite large populations. In particular, the thesis makes four contributions to the understanding of the dynamics of adaptation in interacting populations.

1. The thesis draws together mathematical models from various disciplines, all of which are in some way concerned with the dynamics of adaptation. Based upon these models, a mathematical approach to the dynamics of adaptive populations of interacting agents is formed. It is hypothesised that metastability is caused by the fluctuations inherent in the adaptive process, magnified by the non-linearities in the system due to the interactions between agents.

2. The thesis identifies the requirements of a computational model of metastability.

    (a) It must be simple enough to allow a degree of mathematical analysis of the model.

    (b) It must retain enough complexity to display meta-stable behaviour.

3. The analysis of the computational model relies on its characterisation in terms of behavioural order parameters. Others, for example, Glance [33], have described systems in terms of behaviour. However, this is a novel characterisation, recognising behaviours as order parameters of an underlying and more complex microscopic system. Such systems have previously been described using aspects of agent fitness as order parameters.

4. The model demonstrates important features of adaptive interacting systems, in particular the relationship between stochastic and deterministic components of the system. This effect of population size on this relationship is examined.

It is believed that the cross-entropic methods used to validate the correspondence between the computational model and its analytic formalisation may also be novel.

Chapter 2

Mathematical Preliminaries

In the previous chapter, the general field of the evolution of interacting agents has been reviewed. In this chapter, various mathematical approaches to the analysis of the evolution of a population will be considered. These basically fall into two categories. First there are what might be termed the *classical* approaches to population genetics. These tend to be based on differential equations, and produce limiting results for $\lim_{t\to\infty}$. There are also more recent approaches to the problem, which are based heavily on GA theory, and use statistical dynamics formulations borrowed from thermodynamics. These will be described as *thermodynamic* approaches to population genetics. This chapter also considers the evolution of continuous dynamical systems when they are subjected to additive or multiplicative noise terms.

The comparative review conducted in this chapter will be used to inform the development of both the mathematical models in Chapter 3, and the experimental model considered in Chapter 4.

2.0.2 Notation

This chapter, and the chapters that follow it, contain much mathematical analysis. Whilst the notation is all standard, a number of common abbreviations used are noted below:

p.d.e.	partial differential equation
l.h.s.	left hand side
r.h.s.	right hand side
p.d.f.	probability density function

2.1 Classical Approaches

Here the term 'classical' is taken to imply that the approaches are based on differential and partial differential equation formalisations of the problems of population genetics. Historically, these originate with the work of Wright [86, 87], extended by Kimura [50, 51]. These were further extended by Moran [61], Watterson [83] and Ewens [22, 23], who examined waiting time problems in population genetics and an assessment of the accuracy of diffusion equation approximations, although this work is not reviewed here.

The following is based on the review article by Kimura [51], which is also summarised by van Nimwegen [78]. The original use of these approaches has been in the analysis of single genes, their probabilities of fixation, the evolution of the population under various conditions. However, there is no fundamental reason why such an approach might not be used in a multidimensional case, with a number of independent genes.

2.1.1 The Diffusion Model

This is a treatment similar to a p.d.e. approach to the motion of particles in a potential field, where there is a significant diffusion. It is an approximation, a discrete time stochastic process (mutation) is modelled as a continuous time diffusion process. However, where the analysis remains tractable, and the system falls within limitations discussed in Section 2.1.7, it yields precise predictions of system evolution.

There are a number of differing ways of gaining the diffusion model. This one is based upon the expansion of the Taylor Series around a point in the distribution of gene frequencies. Another approach (which is considered in Section 3.2) is based upon the idea of the flow of gene frequency across a point. Both approaches lead to the same equation, although the former is more rigorous, and the latter more intuitive.

Consider a population of N diploid individuals (that is to say, each individual has two chromosomes at each locus on its genome). Each chromosome may take the form of one of two alleles A_1, A_2. At time t the frequency of allele A_1 is x, and of A_2 is $1-x$. The original frequency of allele A_1 at $t = 0$ is p. Assume that the population is large, so that the gene frequency distribution will effectively behave as a continuous variable. The process of gene frequency change will be modelled as a continuous stochastic process. A continuous stochastic process is one in which, given any positive value ϵ, the probability that a change δx in x will be greater than ϵ in time period $t, t+\delta t$ is $o(\delta t)$, an infinitesimal of higher order than δt. Less formally, this means that as the time periods considered are reduced towards zero, the amount of change in gene frequency, x also becomes zero. This process is also considered to be *Markovian*: there is a one-step dependence of the present state on the immediate past state, but no further historical dependencies.

Let $\phi(p, x; t)$ be the conditional probability density that at time t the gene frequency is x given that it was p at time $t = 0$. Then the probability that x lies within any range dx will be $\phi(p, x; t)dx$. Given a population of a total of $2N$ genes at the locus, the gene frequency will be

$$f(x,t) = \phi(p, x; t)\tfrac{1}{2N} \quad (0 < x < 1) \tag{2.1}$$

Note the limits for which this equation is valid. At the boundary points $x = 0$ and $x = 1$ this is no longer valid.

Let $g(\delta x, x, \delta t, t)$ be the probability that x changes from x to $x + \delta x$ in the time period $(t, t + \delta t)$. Then

$$\phi(p, x; t + \delta t) = \int_{\delta x} g(\delta x, x, \delta t, t)\phi(p, x; t) d(\delta x) \tag{2.2}$$

Using the Taylor Series expansion

$$f(a + h) = f(a) + hf'(a) + \frac{h^2}{2!}f''(a) + \ldots \tag{2.3}$$

and writing $\phi(p, x; t)$ as ϕ and $g(\delta x, x, \delta t, t)$ as g then the r.h.s. of 2.2 may be expanded as

$$\phi g - \delta x \frac{\delta}{\delta x}(\phi g) + \frac{(\delta x)^2}{2!}\frac{\delta^2}{\delta x^2}(\phi g) + \ldots \tag{2.4}$$

hence

$$\begin{aligned} \phi(p, x; t + \delta t) &= \phi \int g d(\delta x) \\ &\quad - \frac{\delta}{\delta x}\left[\phi \int \delta x g d(\delta x)\right] \\ &\quad + \frac{1}{2}\frac{\delta^2}{\delta x^2}\left[\phi \int (\delta x)^2 g d(\delta x)\right] \\ &\quad - \ldots \end{aligned} \tag{2.5}$$

Now $\int g d(\delta x) = 1$, so the first term on the r.h.s. evaluates to ϕ. Subtracting ϕ from both sides and dividing through by δt gives

$$\frac{\phi(p, x; t + \delta t) - \phi((p, x; t)}{\delta t} = -\frac{\delta}{\delta x}\left[\frac{\phi}{\delta t}\int \delta x g d(\delta x)\right]$$

$$+\frac{1}{2}\frac{\delta^2}{\delta x^2}\left[\frac{\phi}{\delta t}\int(\delta x)^2 g d(\delta x)\right]$$

$$-\ldots \tag{2.6}$$

Recall that $\int(\delta x)gd(\delta x) = \int(\delta x)g(\delta x, x, \delta t, t)d(\delta x)$, it becomes clear that as $\lim \delta t \to 0$ is approached, the r.h.s. becomes the sum of the moments of g w.r.t. δx: Let

$$\lim_{\delta t \to 0}\frac{1}{\delta t}\int(\delta x)g(\delta x, x, \delta t, t)d(\delta x) = M(x,t) \tag{2.7}$$

$$\lim_{\delta t \to 0}\frac{1}{\delta t}\int(\delta x)^2 g(\delta x, x, \delta t, t)d(\delta x) = V(x,t) \tag{2.8}$$

Here M and V are respectively the first and second order moments, the mean and variance of the distribution X of the allele A_1

Then, assuming that all higher order terms in δx tend to zero as $\lim \delta t \to 0$ is approached, 2.6 reduces to

$$\frac{\delta\phi(p,x;t)}{\delta t} = \frac{1}{2}\frac{\delta^2}{\delta x^2}\left(V(x,t)\phi(p,x;t)\right) - \frac{\delta}{\delta x}\left(M(x,t)\phi(p,x;t)\right) \tag{2.9}$$

This is the basic diffusion equation, known as the *Fokker-Planck* or *Kolmagorov forward* equation. On the assumption that $M(x,t)$ and $V(x,t)$ are time independent, and writing them as $M_{\delta x}$ and $V_{\delta x}$ respectively gives

$$\frac{\delta\phi}{\delta t} = \frac{1}{2}\frac{\delta^2}{\delta x^2}\left(V_{\delta x}\phi\right) - \frac{\delta}{\delta x}\left(M_{\delta x}\phi\right) \tag{2.10}$$

This simplified version of the Fokker-Planck equation suffices for the particular cases that Kimura [51] considers.

2.1.2 The Kolmagorov Backwards Equation in Population Genetics

The derivation given above considers the evolution of a population where the initial gene frequency across the population is known and derives a differential equation that gives the probability that the gene frequency takes any particular value after a fixed period t. It is also possible to reverse the derivation, and obtain the probability distribution across initial gene frequencies at time $t = 0$ given that at time t, the frequency x takes a given value. This reverse form of the equation is known as the *Kolmagorov Backward equation.* Based upon the principle of the derivation of the Fokker-Planck equation, the Kolmagorov backward equation will be derived [51].

The derivation is very similar to that of the forward equation; the only additional assumption being one of time homogeneity. That is to say that it is assumed that the underlying processes are independent of the time at which they occur. The transformation from a distribution x_1 at time t_1 to x_2 at time t_2 (given $t_1 < t_2$) is independent of t_1 and t_2, and is dependent only upon the intervening period $t_2 - t_1$.

$$\phi(p, x; t) = \int g(\delta p, p; \delta t)\phi(p + \delta p, x; t)d(\delta p) \tag{2.11}$$

Note that the time homogeneity condition now makes g independent of t. A similar derivation to that of 2.9 gains

$$\frac{\delta\phi(p, x; t)}{\delta t} = \frac{V(x)}{2}\frac{\delta^2}{\delta p^2}\phi(p, x; t) - M(x)\frac{\delta}{\delta p}\phi(p, x; t) \tag{2.12}$$

which can be written as

$$\frac{\delta\phi}{\delta t} = \frac{V_{\delta p}}{2}\frac{\delta^2\phi}{\delta p^2} + M_{\delta p}\frac{\delta\phi}{\delta p} \tag{2.13}$$

The Kolmagorov backward equation can be used to derive two interesting results. $x = 1$ implies that a gene is *fixed* within the population, i.e. all members of the population carry that gene. Denote the probability that the gene is fixed within the population at time t by $u(p,t)$. Then

$$\frac{\delta u(p,t)}{\delta t} = \frac{V_{\delta p}}{2}\frac{\delta^2 u(p,t)}{\delta p^2} + M_{\delta p}\frac{\delta u(p,t)}{\delta p} \tag{2.14}$$

which can be solved given $V_{\delta p}$ and $M_{\delta p}$, under the boundary conditions $u(0,t) = 0$ and $u(1,t) = 1$. One might also be interested in

$$u(p) = \lim_{t\to\infty} u(p,t) \tag{2.15}$$

the limit probability of a gene being fixed. Here $\delta u/\delta t = 0$, and the equation reduces to

$$\frac{V_{\delta p}}{2}\frac{\delta^2 u(p,t)}{\delta p^2} - M_{\delta p}\frac{\delta u(p,t)}{\delta p} = 0 \tag{2.16}$$

under the boundary condition $u(0) = 0, u(1) = 1$.

2.1.3 Random Drift in the Narrow Sense

Suppose there exists an isolated population of N diploid individuals, who all possess either allele A_1 or A_2 which have frequencies $x, 1-x$ within the population respectively. Mating between individuals is random between pairs of individuals taken from the population, taking 1 allele from each parent [1]. Hence there are a total of $2N$ alleles in the population. There is no mutation, so once either allele has become fixed (either

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[1] Kimura's derivation is under the (biological) assumption that the population contains equal numbers of males and females, and that in each mating, one allele is taken from a male, and one from a female. Whilst this assumption is stated, it does not affect the form of the equations, which are equally valid in GA theory.

$x = 0$ or $x = 1$) it cannot become unfixed. Assume that there is no selection pressure towards either allele, and that the variance term can be approximated by the variance in a binomial population of $2N$ alleles, i.e.

$$\begin{aligned} M_{\delta p} &= 0 \qquad (2.17) \\ V_{\delta p} &= \frac{x(1-x)}{2N} \qquad (2.18) \end{aligned}$$

Substituting into 2.10

$$\frac{\delta \phi}{\delta t} = \frac{1}{4N} \frac{\delta^2}{\delta x^2} \left(x(1-x)\phi\right) \quad 0 < x < 1 \qquad (2.19)$$

At time $t = 0$ the frequency of the gene within the population is p. The conditional probability density at this time takes the form of a Dirac delta function

$$\phi(p, x; 0) = \delta(x - p) \qquad (2.20)$$

The solution method proceeds from assuming that the solution takes the form $\phi = TX$ where T is a function of t alone, and X is a function of x alone. Substituting this into 2.19, and dividing through by TX gives

$$\frac{1}{T} \frac{\delta T}{\delta t} = \frac{1}{4NX} \frac{\delta^2}{\delta x^2} \left(x(1-x)X\right) \qquad (2.21)$$

Note the form of this equation. The l.h.s. is a function of t alone, and the r.h.s is a function of x alone. For these two to be equal, they must both be equal to some constant, $-\lambda$, say. Both sides may be solved independently to gain T and X. Separating gives

$$\frac{1}{T} \frac{\delta T}{\delta t} = -\lambda \qquad (2.22)$$

$$\frac{1}{4NX} \frac{\delta^2}{\delta x^2} \left(x(1-x)X\right) = -\lambda \qquad (2.23)$$

2.22 has a solution of the form

$$T \propto e^{-\lambda t} \tag{2.24}$$

while 2.23 can be expanded to

$$x(1-x)\frac{\delta^2 X}{\delta x^2} + 2(1-2x)\frac{\delta X}{\delta x} - (2-4N)\lambda X = 0 \tag{2.25}$$

which is of the form of the hypergeometric equation

$$x(1-x)X'' + [\gamma - (\alpha+\beta+1)x]X' - \alpha\beta X = 0 \tag{2.26}$$

where

$$\begin{aligned} \alpha &= \frac{3+\sqrt{1+16N\lambda}}{2} \\ \beta &= \frac{3-\sqrt{1+16N\lambda}}{2} \\ \gamma &= 2 \end{aligned}$$

subject to the boundary condition that the solution must be finite at $x = 0$ and $x = 1$.

The solution to 2.19 is complicated by the fact that there are an infinite number of possible values that λ can take. The values of α, β, γ imply that the set of values that λ can take, known as the *eigenvalues*, λ_i is given by

$$\lambda_i = \tfrac{i(i+1)}{4N} \quad i = 1, 2, 3, \ldots \tag{2.27}$$

The solution to 2.25 can be expressed as the infinite weighted sum of a set of orthogonal functions. In this case we chose to use the *Gegenbauer polynomials*,

$$T^1_{i-1}(z) = \frac{i(i+1)}{2} F(i+2, 1-i, 2; \frac{1-z}{2}) \tag{2.28}$$

where F is the hypergeometric function and $z = 1 - 2x$. The solution to 2.25 now becomes

$$\phi(p, x; t) = \sum_{i=1}^{i=\infty} C_i T_{i-1}^{1}(z) e^{-\frac{i(i+1)t}{4N}} \tag{2.29}$$

The initial condition given in 2.20 can now be used to determine the weights C_i. The resulting weighted infinite sum of hypergeometric functions may be expressed as

$$\begin{aligned} \phi(p, x; t) &= 6p(1-p)e^{-t/(2N)} \\ &\quad +30p(1-p)(1-2x)e^{-3t/(2N)} \\ &\quad +\ldots \end{aligned} \tag{2.30}$$

For $t > 0$ this series is uniformly convergent in both x and p, and the higher order terms are negligent. Asymptotically the first term becomes dominant, and is a fairly good approximation to the solution. Now clearly

$$\Phi(t) = \int_{0+}^{1-} \phi(p, x; t) dx \tag{2.31}$$

gives the probability that alleles A_1 and A_2 still co-exist in the population. Note the limits of the integral; the derivation is not valid at the absorbing boundaries. The exponential decay terms in 2.30 indicate that the probability $\Phi(t)$, 2.31, is constantly decreasing; as time goes on, the probability becomes greater and greater that either one of the alleles has become fixed within the population. In this case, the system could be thought of as having two attractors $x = 0$ and $x = 1$, either of which may be approached as $t \to \infty$. It is possible to show that if the original frequency of a_1 is p, then the asymptotic probability that A_1 will become fixed is also p [78].

2.1.4 Random Fluctuation of Selection Intensities

Another interesting case which illustrates the power of the diffusion equation approach, and which shows an interesting behaviour, is the case of random fluctuations in the selection intensity.

Assume that the population is infinite (so the effects of random sampling may be ignored), and that the allele A_1 is selectively neutral in the long run. That is to say that given a long enough time period, A_1 will neither be selected for, nor against. Introduce fluctuations in the selective advantage of A_1 over A_2. Let the rate of change of frequency of A_1 be $sx(1-x)$, where s is the (varying) selection rate. Let the variance in the selection rate be a constant, V_s. Then

$$\begin{aligned} M_{\delta x} &= 0 \\ V_{\delta x} &= V_s x^2(1-x)^2 \end{aligned}$$

Substituting into 2.10 gives

$$\frac{\delta\phi}{\delta t} = \frac{V_s}{2}\frac{\delta^2}{\delta x^2}\left[x^2(1-x)^2\phi\right] \tag{2.32}$$

This equation may be solved by the substitution [51]

$$\begin{aligned} u &= \frac{1}{2}e^{V_s\frac{t}{8}}x^{\frac{3}{2}}(1-x)^{\frac{3}{2}} \\ \xi &= \log\frac{x}{1-x} \end{aligned}$$

which reduces 2.32 to the heat diffusion equation over the range $-\infty < \xi < \infty$.

$$\frac{\delta u}{\delta t} = \frac{V_s}{2}\frac{\delta^2 u}{\delta \xi^2} \tag{2.33}$$

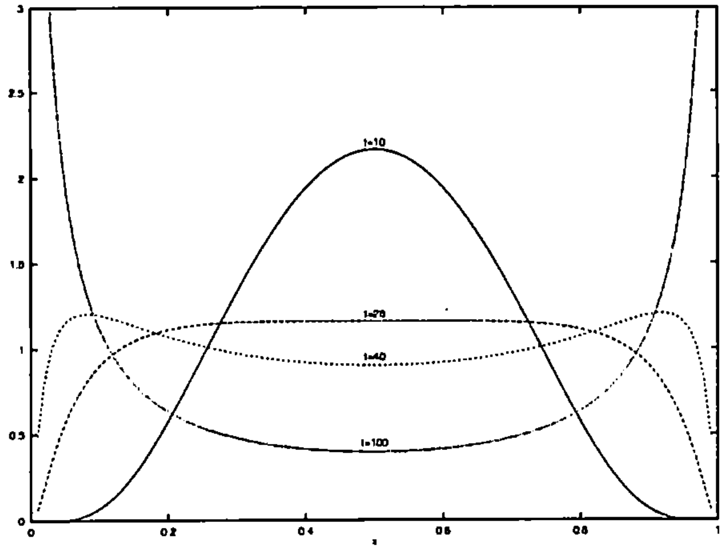

Figure 2.1: The process of change in the gene frequency distribution under a random fluctuation of selection intensities. There is no long term selection pressure towards either allele, there is no dominance, and initially $p = 0.5$ and $V_s = 0.0483$. Based on a figure in Kimura [51]

The solution to the heat diffusion equation is well known, and takes the form

$$u(\xi, t) = \frac{1}{\sqrt{2\pi V_s t}} \int_{-\infty}^{\infty} \exp\left\{-\frac{(\xi - \eta)^2}{2V_s t}\right\} u(\eta, 0)\, d\eta \tag{2.34}$$

Substituting back for u and ξ gives a solution from any initial frequency distribution. Given a known initial frequency p the solution can be further reduced to become

$$\phi(p, x; t) = \frac{1}{\sqrt{2\pi V_s t}} \exp\left\{-\frac{V_s}{8}t - \frac{\left[\log \frac{x(1-p)}{(1-x)p}\right]^2}{2V_s t}\right\} \frac{\sqrt{p(1-p)}}{(\sqrt{x(1-x)})^3} \tag{2.35}$$

A set of solutions to this equation, over a range of values or t with an initial fixed distribution is shown in Figure 2.1. The important point to note is that despite the initial fixed frequency, and in the absence of any long term selection pressure, one of the two alleles can become (almost) fixed. In fact, ϕ takes on a value of 0 at both terminals, so this phenomenon is referred to as *quasi-fixation* [49].

2.1.5 Gene Frequency Distribution at Equilibrium

If $\frac{\delta\phi}{\delta t} = 0$ in 2.10 one may explicitly solve for the equilibrium gene frequency distribution. Simple manipulation reveals that

$$\phi(x) \propto \exp\left[2\int \frac{M_{dx}(x)}{V_{dx}(x)}dx\right] \tag{2.36}$$

Suppose the forwards and backwards mutation rates are q and v respectively. Then $M_{dx}(x) = qx + v(1-x)$ and $V_{dx}(x) = \frac{x(1-x)}{M}$. 2.36 becomes

$$\phi(x) \propto x^{2Mv-1}(1-x)^{2Mq-1} \tag{2.37}$$

This is an important equation. It states that the equilibrium gene frequency distribution depends on the interplay between the population size M and the forward and backward mutation rates q and v. Assume (as is usually the case) that $q = v$. For large populations relative to the mutation rate ($2Mq \gg 1$) we find a binomial distribution about $x = 0.5$, which is what one might intuitively expect for a large or infinite population. As the population drops we find that the population distribution changes. For $2Mq = 1$ we have a uniform distribution, and for $2Mq \ll 1$ the population distribution is essentially U-shaped. Here the sampling fluctuations within a small population effectively overwhelm the diffusive effects, and the population is likely to become quasi-fixed about one allele or the other.

2.1.6 Fixation of Mutant Genes within a Population

An important question to be considered is the probability that a favourable mutant gene will become fixed within a population. It is not the case that every time a favourable mutant is introduced into a population it will survive. If the frequency of the favourable mutant is p at $t = 0$, then by using the Kolmagorov Backward equation, the limiting probability

$$\phi(p) = \lim_{t\to\infty} \phi(p,t) \tag{2.38}$$

can be obtained. Since $\delta\phi(p)/\delta t = 0$ at this limit, 2.13 reduces to the ordinary differential equation

$$\frac{V_{\delta p}}{2}\frac{d^2\phi(p)}{dp^2} + M_{\delta p}\frac{d\phi(p)}{dp} = 0 \tag{2.39}$$

under the boundary conditions $\phi(0) = 0, \phi(1) = 1$. The general solution of this is

$$\phi(p) = \frac{\int_0^p G(x)dx}{\int_0^1 G(x)dx} \tag{2.40}$$

where

$$G(x) = \exp\left(-\int \frac{2M_{\delta x}}{V_{\delta x}}\right) \tag{2.41}$$

$M_{\delta x}$ and $V_{\delta x}$ are respectively the mean and variance of the expected change in gene frequency per generation.

The simplest case, which is of most interest here, is that of genic selection, where a mutant gene with selective advantage s in a haploid population of size N, i.e. a population which has only one chromosome per locus on the genome[2]. The initial frequency of the mutant gene is simply $1/N$. Then $M_{\delta x} = sx(1-x)$ and $V_{\delta x} = x(1-x)/N$. Hence 2.40 reduces to

$$\phi(p) = \frac{1-e^{-4Nsp}}{1-e^{-4Ns}} \tag{2.42}$$

which, for $\mid s \mid$ small, can be approximated by

$$\phi = \frac{2s}{1-e^{-2Ns}} \tag{2.43}$$

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[2] This condition occurs in many lower organisms, and at certain stages of the life-cycle of higher organisms.

2.1.7 Limitations to the Diffusion Equation Approach

Gillespie [32] discusses limitations of the diffusion equation approach in population genetics. There are two areas that these limitations fall into, problems involving unequal parameters, and problems involving fluctuating parameters. In general terms, these problems result in alternative differential equation formulations being more appropriate to particular problems than a diffusion equation.

Unequal parameters

Classical approaches to the population genetics approximate a discrete time stochastic process, selection under mutation, with continuous time processes that yield differential equations. This approach relies on various assumptions. Karlin & McGregor [45] point out that such a model relies on an implicit limiting argument concerning a rescaling of time, and the rates at which various parameters tend to zero. The resulting differential equation is dependent upon the relative rates at which these parameters approach zero. The following example (from [32]) is instructive.

Consider a population of size n with a choice of two possible alleles, with forwards and backwards mutation rates u. The mean and variance of the change of frequency of one of the alleles is

$$\begin{aligned} \overline{\Delta x} &= 2u(\frac{1}{2} - x) \\ \sigma^2(\Delta x) &\approx \frac{x(1-x)}{n} \end{aligned} \tag{2.44}$$

The standard approach assumes that u and $1/n$ are small and of the same magnitude, and that time is measured in units of n generations. The limit $n \to \infty$ yields the diffusion

$$E(dx) = 2u(\frac{1}{2} - x)dt \tag{2.45}$$

$$E(dx^2) \approx x(1-x)dt$$

The terms $E(dx)$ and $E(dx^2)$ are the first and second order moments of the resulting distribution, corresponding to the terms M and V respectively, in Section 2.1.1. Mathematically, 2.45 requires $u = O(1/n)$. If this is not the case, then the resulting differential approximation may not be a diffusion, or if it is, may lead to a different diffusion. For example, if $u = O(1/\sqrt{n})$, then the resulting diffusion corresponds to the Ornstein-Uhlenbeck process. The physical interpretation of this is a diffusion process corresponding to a set of particles under Brownian motion with an elastic force [25]. Given a constant mutation rate, the appropriate classical model of the system may vary as the population size changes, even when the population size is large enough that the stochastic fluctuations are negligible. Feller [24] derives a full equation showing the interdependence of gene frequency and population size.

Similar arguments hold concerning the relationship between selection and mutation strengths, and selection and population size, which can yield quite different approximations to the standard diffusion approach. However, Gillespie points out that mathematical tractability to a large extent determines the choice of models:

> "The pre-eminent position of the neutral allele theory as an explanation for molecular evolution may be due more to the simplicity of its mathematics than to its biological underpinnings."[3]

Fluctuating parameters

Recall the discussion of adaptation in Section 1.1.1. It was noted that adaptive processes are situated in their environment. Here the effect of the environment in changing the relative values that parameters take is considered. For example, the binomial sampling

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[3] Gillespie [32].

of selectively neutral alleles is held to account for genetic drift. In binomial sampling, the moments of order greater than two of the resulting distribution converge at a greater rate than the lower order moments. In an infinite limit this implies convergence to a Gaussian distribution. However, there is no *a-priori* justification of such an assumption of the relative convergence rates of moments. Environmental fluctuations may have a bearing on sampling distributions; and thus alter population dynamics. In particular, Gillespie [32] considers that the power law distribution may be far more relevant in a variety of natural processes. Certainly the Bak-Sneppan [8, 66] model of co-evolution leads to phenomena distributed according to a power law (see Section 1.2.5 for discussion of the Bak-Sneppan model).

2.2 Statistical Dynamics Approaches

In this section, we will review approaches to the dynamics of populations of adaptive agents via an approach borrowed from statistical physics. In particular, approaches will be considered to the population dynamics of infinite and finite populations of agents under a genetic algorithm. In this approach a statistical view of the mutation, selection (and possibly also crossover) operators that are commonly used is taken. The actual genotypic state of any member of the population becomes a microscopic parameter, and the above operators act at a microscopic level. Statistical methods can be used to gauge the effects of these operators on macroscopic parameters, such as the low order cumulants of the fitness distribution. For certain problems, these methods have proved remarkably effective in explaining the evolutionary dynamics of the population.

2.2.1 Microscopic Dynamics of a Genetic Algorithm

Vose and Liepens [81] put forwards a macroscopic description of the workings of a genetic algorithm, in terms of a pair of operators, a mixing operator $\mathcal{M}$ and a fitness operator $\mathcal{F}$. Whilst the detail of this paper lies beyond the mathematical competence of the author, an outline of the basic results will be given.

The general approach of this paper is to model a genetic search process as a Markov process, in order to find the infinite population limit population distribution. The most interesting point raised by this paper is the reduction of the evolutionary operator to the combination of mixing and fitness operators: this allows the separation of the exploratory and exploitative aspects of evolutionary search. Moreover, the paper presents theorems which allow the selection of evolutionary operators in which these components are separable. These theorems rely on properties of the mixing matrix, when transformed into a basis of Walsh functions, which have been shown [12, 35, 36] to have important applications in GA theory. They then go on to show that in the case where the fitness operator is linear, there is a single attracting fixed point to the system.

Whilst this paper has a very interesting, and highly mathematical approach to the problem of genetic search, it is not unproblematic in various respects:

1. The approach taken is to consider a system with n possible genotypes as an n-dimensional dynamical system under a combination of matrix operators, $\mathcal{F}$ and $\mathcal{M}$. In any realistic genetic search problem, this is analytically impractical, as the size of the problem scales as $O(2^n)$, where n is the genome length.

2. The Walsh-basis approach is very much founded upon the schemata-theory approach of Holland [42]. This has come in for recent criticism from Nimwegen et al. [78], who claim that rather than combine useful building blocks, crossover acts as a non-linear mixing operator on sites not fixed in the best member of the

population. This effectively increases the mutation rate. In short, doubt has been cast on the usefulness of the schemata approach.

3. Whilst this paper does further the understanding of genetic search, it is limited to cases where the fitness operator is linear. Where fitness is dependent upon agent interactions, the fitness operator is highly non-linear, thus limiting the applicability of this work in the present context.

4. The Markov approach predicts the infinite limit population. It is conjectured (see Section 3.2.6) that the finite population dynamics may show marked deviations from the dynamics in the infinite limit, especially in populations of interacting agents, where there is a highly non-linear selective operator).

2.2.2 Statistical Dynamics of Fitness Distributions

Prügel-Bennett & Shapiro [69, 70] have produced an analysis of the dynamics of a genetic algorithm from a statistical mechanics viewpoint. The problem they chose as a testbed for their analysis of genetic search, is the distribution of spin-states in a simple Ising spin model. This is an interesting choice of problem as it allows them to directly look at the role of crossover in making and breaking links between different parts of the genome. This leads (more generally) towards the study of representation within genetic algorithms. However, this paper is not discussed here primarily for those reasons; rather it is the statistical mechanics approach to GA theory which is of interest within the present context. In their formulation, mutation plays a very small effect as an exploratory operator; their discussion is couched in terms of selection as an exploitative operator, and crossover as a mixing or explorative operator.

Prügel-Bennett & Shapiro demonstrate a formulation of the dynamics of the genetic algorithm in terms of the lower order cumulants of the fitness distribution. They are able to formulate the dynamics of these cumulants in statistical mechanics terms. Alternately, the approach may be described as follows. The population distribution is transformed to a cumulant basis. Higher order terms are then discarded, and the system is modelled as a low-order dynamical system within this new basis. This approach aids the analysis of the GA in two directions.

First, as mentioned above, it allows an analysis of the role of crossover in making and breaking links between interconnected parts of the genome. This analysis is based on the exact problem domain; the location of minimum energy states in an Ising spin glass system. However, the results of this analysis should be more generally applicable to a much wider domain.

Second, this approach allows a comparison of the relative effects of selection and recombination. Prügel-Bennett & Shapiro consider the relative effects of selection and recombination. Where the 'interface energy' (the energy bound in the interface between the parental genomic elements combined to form a child)[4] is high, then strong selection is beneficial, as it involves fewer crossovers. On the other hand, where the interface energy is low, then the mixing effects of crossover can be utilised in a stronger fashion to speed the search.

One important aspect of this work is the adoption of a maximum-entropy approach (also discussed in [76]); where the order parameter does not give specific information about some aspect of the system needed for analysis, that aspect of the system is assumed to be in a state that maximises its entropy. The close match between theoretical predictions and experimental results on the problem they chose seems to indicate that this maximum-entropy assumption is justified in this case.

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[4] In the general case, this term appears to be the difference between the fitness of the child and a linear estimation of the child's fitness in terms of the fitnesses of its parents.

> "That this [maximum entropy] assumption works, suggests that there is 'microscopic disorder', that is that the GA is sufficiently mixing so that all strings with the same fitness are equally likely. Whether it is a property of the simple system we looked at, or of classes of problems is an important question."[5]

Later work by Rattray & Shapiro [72] and by Rattray [71] using this approach with alternate GA problems (perceptron weight allocation and subset sum, respectively) also produces good theoretical predictions of experimental results. This indicates that the maximum entropy assumption may be well founded in general within GA theory.

This paper also considers differences between infinite limit and finite population dynamics, concentrating on systematic errors in the cumulants that arise when a finite population is modelled using the infinite limit cumulants. In particular, Prügel-Bennett & Shapiro [70] note that the third cumulant (related to distribution skewness) scales inversely with population size, so whilst it is zero in an infinite population, it is non-zero in a finite population, and in small populations has a significant effect on the evolution of that population. Thus, there are qualitative differences between finite and infinite population behaviours.

The effect of the third cumulant is to produce an under-populated high fitness tail to the population distribution. There is a long tail of low-fitness individuals, yet relatively few with greater than average fitness; the maximum fitness becomes closer to the average fitness. This reduces the effectiveness of the GA, because selection is picking average rather than above average individuals as parents of the next generation.

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[5] Prügel-Bennett & Shapiro [70].

2.2.3 Statistical Dynamics of the Royal Road GA: Infinite Populations

The Royal Road GA is a 'toy' problem that has been used extensively in the analysis of the behaviour of genetic algorithms [58, 59, 29]. The binary genotype consists of N blocks, each consisting of K sites, and has a length of $L = NK$. The fitness function is simply the number of filled, or aligned, blocks: that is to say the number of blocks which have all sites containing a '1'. This GA therefore has a single peaked fitness function, and a plateau landscape.

The analysis that is presented here is due to Erik van Nimwegen and colleagues at the Santa Fe Institute [78], and builds upon the work reviewed in Sections 2.2.1 and 2.2.2.

Consider a population of M agents under the Royal Road GA, with an initially random state. The population may be partitioned into $N + 1$ fitness classes, as the fitness of any member of the population may be in the integer range $(0, N)$. The analysis develops by considering the fitness distribution between these $N + 1$ classes as a macroscopic parameter, and developing terms for the evolutionary operator G on the population.

Informally, the evolutionary operator G performs the following actions. First it evaluates the fitness of each string, then it creates a new population of strings by picking strings in the old population with a probability proportional to the fitness of the string. Finally, it mutates every site in each string in the population with a fixed low probability q. More formally, the evolutionary operator G can be represented as the product of two operators, the selection operator S, and the mutation operator, M.

Rather than consider the evolution of the population state vector $\vec{p}(t)$, consider instead the transitions between strings of different fitnesses. Initially this will be done in the infinite population limit $M \to \infty$, where the fundamental theorem of probability applies; later the dynamics of finite populations will be considered from the foundation of the infinite population model.

The mutation operator M

The dynamics[6] of block alignment, A, and disalignment, D, will be discussed separately; the mutation operator will then be constructed out of their combination. First consider the dynamics of block alignment. The probability that a block in state j will be transformed to state i can be found using a Markov chain analysis under the assumption that bits in the block have random alignments: the entries in the Markov transition table will be given by

$$T_{ij} = \sum_{k=0}^{K-j} \sum_{l=0}^{j} \delta_{j+k-l,i} \begin{pmatrix} K-j \\ k \end{pmatrix} \begin{pmatrix} j \\ l \end{pmatrix} q^{k+l}(1-q)^{K-k-l} \tag{2.46}$$

where δ is the Kronecker delta. We shall consider state K to be an absorbing state (when the block is completely filled). The Markov chain analysis allows us to calculate the expected time for an initially randomly seeded block to become filled. This can be expressed as a weighted sum of eigenvalues of the non-absorbing sub-matrix, and it can be shown that the largest eigenvalue dominates this expression.

The entries F_{ij} of fundamental matrix of the Markov Chain, $F = (I - T')^{-}1$ give the expected number of times that that system, starting from state j will visit state i before reaching the absorbing state K. From this we can derive

$$T(q,K) = \sum_{i,j=0}^{K-1} F_{ij} S_j \tag{2.47}$$

the expected time until block alignment starting from an initial configuration $\vec{S}$. For short block lengths, this can be done in closed form. From $T(q,K)$, we may go on to

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[6] The derivations of these operators are rather involved, so we shall not derive them fully, rather point out the general method. The full derivations can be found in the appendices to [79].

estimate the probability of aligning a block as $A = 1/T(q, K)$. For small q, it is possible to derive an analytic first order approximation

$$A(K) = \frac{2^K q}{c_K} \tag{2.48}$$

where

$$c_K = \sum_{i=1}^{K} i^{-1} \left(\begin{array}{c} K \\ i \end{array} \right) \left(\sum_{j=0}^{i-1} \left(\begin{array}{c} K \\ j \end{array} \right) \right)^2 \tag{2.49}$$

At this point, the problem is that the unaligned blocks fall into two types, those that have never been aligned before (for which the expected alignment time has just been stated), and those blocks which have previously been aligned, and have become unaligned due to mutation. The ratio of these two types of blocks is unknown, and there is no expression for the realignment time for a previously aligned block. Upper and lower bounds can be placed on the alignment probability of any block; the lower bound will be by assuming the block has not previously been aligned, and uses the term given in 2.48. The upper bound is given by assuming that any blocks has previously been aligned, and is now unaligned in only one bit; i.e. that a suitable one bit mutation will restore the alignment in any block. This gives an upper bound on the alignment probability of

$$A_r = q(1-q)^{K-1} \tag{2.50}$$

The alignment probability of any block will therefore lie in the range $A(K) \leq A \leq A_r$. In fact, it will turn out that the results are largely insensitive to block alignment times; so they will be assumed to lie at the lower bound.

The destruction operator D is much simpler, the probability that an aligned block will be destroyed by mutation is $D = 1 - (1-q)^K$.

A and D may now be used to generate an overall term M_{ij}, the probability that a block containing j aligned sites will, after mutation with a constant mutation rate

q across sites, end up with i aligned sites. This can be written as the sum over all probabilities that k unaligned blocks will be aligned, and $k+j-i$ blocks will be unaligned. This is

$$\sum_{k=0}^{N-j}\sum_{l=0}^{k}\delta_{k+j-i,l}\begin{pmatrix} N-j \\ k \end{pmatrix}\begin{pmatrix} j \\ l \end{pmatrix} A^k(1-A)^{N-j-k}D^l(1-D)^{j-l} \tag{2.51}$$

This operator is valid in the limit of an infinite population; that is to say where sampling fluctuations play no role in the model. Here the operator M will act upon a vector $\vec{P}$ of probabilities that the string has j blocks aligned, to form a new vector $\vec{P}^m$, the probabilities that the string has i blocks aligned after mutation.

The Selection Operator S

The selection operator is somewhat simpler than the mutation operator. Recall that the GA is a combination of mutation and fitness proportional selection. Therefore the expected probability of an individual with i blocks already aligned being selected is proportional to the number of individuals who have that number of blocks aligned, and the relative fitness of those individuals within the population. This matrix is a diagonal matrix, and takes the form

$$S_{ij} = \delta ij \frac{i}{\langle f \rangle} \tag{2.52}$$

Note that this operator is non-linear, as it depends on the mean fitness of the population that it acts upon.

The Generation Operator G

By combining the mutation and selection operators the generation operator G is gained.

$$G_{ij} = \sum_{k=0}^{k=N} M_{ij} S_{kj} \tag{2.53}$$

In order to analyse the dynamics of this operator, a linearised version of it is constructed. Noting that the only non-linearity is the normalisation factor $\frac{1}{\langle f\rangle}$, the normalisation factor is taken out of the matrix

$$\begin{aligned} S &= \frac{1}{\langle f\rangle}\tilde{S} && (2.54) \\ \tilde{G} &= M.\tilde{S} && (2.55) \end{aligned}$$

Here $\langle f\rangle$ is the mean value of f. The operator $\tilde{G}$ is an ordinary $N+1$ dimensional matrix operator. The time evolution of the population is governed by

$$\vec{P}(t+1) = G^t\vec{P}(0) \tag{2.56}$$

which can be expanded to

$$\vec{P}_i(t) = \sum_j C(t,\vec{P}(0))G^t_{ij}P_j(0) \tag{2.57}$$

The constant C, may be easily solved for, since $\vec{P}(t)$ must be normalised

$$C(t,\vec{P}(0)) = \left[G^t\vec{P}(0)\right]^{-1} \tag{2.58}$$

Now G may be explicitly solved to find the fixed points of the system. Diagonalising $\tilde{G}$ gives its eigenvalues, g_i and from here the eigenvectors $\vec{R}_0 \ldots \vec{R}_N$ can be obtained. Define R to be the matrix of the eigenvectors of G. Note that as the eigenvectors are normalised, the columns of R all add to 1. The operator $\tilde{G}^t$, the application of $\tilde{G}$ t times, may be written as

$$\tilde{G}^t_{ij} = \sum_{k=0}^{N} R_{ik}g^t_k R^{-1}_{kj} \tag{2.59}$$

Substitute this expression into 2.57 to gain an explicit expression for the evolution of the system

$$\vec{P}_i(t) = C(t,\vec{P}(0))\sum_{j,k} R_{ik}g^t_k R^{-1}_{kj}P_j(0) \tag{2.60}$$

At this point, transfer to the eigenbasis of G. One may write both the fitness distributions in the eigenbasis

$$\alpha(i) = \sum_{k=0^N} R^{-1}_{ik} P_k(t) \tag{2.61}$$

and the constant C in the eigenbasis

$$C(t, \vec{P}(0)) = \left[\sum_{i,j,k=0}^{N} R_{ik} g_k^t R^{-1}_{kj} P_j(0) \right]^{-1} = \left[\sum_{k=0}^{N} g_k^t \alpha_k(0) \right]^{-1} \tag{2.62}$$

Hence one may express 2.57 as

$$\alpha_i(t) = \frac{g_i^t \alpha_i(0)}{\sum_{j=0}^{N} g_j^t \alpha_j(0)} \tag{2.63}$$

Now it can quite easily be shown that all the eigenvalues of $\tilde{G}$ are the mean fitnesses of their respective eigenvectors, i.e. $g_k = \langle f \rangle$ at the eigenvector R_k. Hence

$$\langle f \rangle = \sum_i i P_i = \sum_i g_i \alpha_i \tag{2.64}$$

This gives a direct expression for the mean fitness of an infinite population at time t in terms of the initial distribution of fitnesses, and the linearised generation operator $\tilde{G}$

$$\langle f(t) \rangle = \frac{\sum_i g_i^{t+1} \alpha_i(0)}{\sum_{j=0}^{N} g_j^t \alpha_j(0)} \tag{2.65}$$

It may appear from the above equation that there are up to $N+1$ stable distributions that the infinite population may take on. This is not the case; in order to be a probability distribution, a vector must be positive definite (i.e. all its entries must be greater than or equal to zero). Van Nimwegen et al. show that only the eigenvector corresponding to the largest eigenvalue is positive definite; all the other eigenvectors have at least one negative entry. This is quite intuitive really: the only stable state for the system is the one with maximal fitness. Given that the Royal Road GA has a plateaued Fujiama[7] landscape, we should expect that the only stable population is one centred

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[7] A Fujiama landscape rises smoothly to a single peak, much in the manner of classical Japanese water-colours of Mount Fuji.

about the single peak in the landscape. Henceforth order the eigenvalues (and their corresponding eigenvectors) in a monotonically increasing order $g_0 < g_1 < \ldots < g_N$.

The above derivation gives results which correspond very closely with the observed behaviour of the Royal Road GA for large populations relative to the mutation rate $(2Mq \gg 1)$[8].

2.2.4 Statistical Dynamics of the Royal Road GA: Finite Populations

Van Nimwegen et al.[79] not only demonstrate the dynamics of the Royal Road GA in the infinite case, but also in the case of finite dynamics where epochal phenomena and meta-stability are commonly observed. Onto the system at the thermodynamic limit, a noise term is added, corresponding to the stochastic fluctuations of a finite population. The distribution of the noise is obtained by an analysis of the moments of the fluctuations, and leads to a Fokker-Planck formulation of the noise term: the noise is thus assumed to be Gaussian, with components inversely proportional to fitness of the dimensions.

Van Nimwegen et al. assume that since the actual population is a multinomial sampling from the generation operator applied to the previous population, mapping $\vec{P}_n = M^{-1}(n_0, \ldots, n_N)$ to $\vec{P}_m = M^{-1}(m_0, \ldots, m_N)$:

$$p[\vec{P}_n \to \vec{P}_m] = M! \prod_{i=0}^{N} \frac{\left[G_i(\vec{P}_n)\right]^{m_i}}{m_i!} \tag{2.66}$$

which has mean $G(\vec{P}_n)$, then the form of the noise will be a multinomial.

Recall Section 2.1.7. The effect of both convergence rates of parameters in the infinite limit, and of fluctuating parameters was discussed in relation to classical approaches. In van Nimwegen et al.'s formulation

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[8] See 2.1.5 for the derivation of this result.

1. Selection intensity is a non-linear function of the population distribution, being based upon mean population fitness.
2. Their formulation is an attempt to explain the observed behaviour of the Royal Road GA over a range of population sizes. It is not clear that the assumption that the mutation rate is of the same order of magnitude as $1/M$, (the reciprocal of the population size) is valid over the range of population sizes that they wish to consider.

To summarise, van Nimwegen et al. use multinomial sampling from an infinite population distribution to justify an assumption that sampling fluctuations are Gaussian. They derive the sampling fluctuations by a classical approach, deriving the magnitude of the first two moments of the distribution from the properties of the generation operator G. However, the arguments given by Gillespie [32] cast doubt on whether these assumptions are justified. It is not clear that the sampling fluctuations can be modelled as a diffusion, and even if they can, it is not clear that the Fokker-Planck formulation is justified. Feller [24] derives a diffusion equation in two variables, gene frequency and population size, which may be more appropriate.

From this approximation, various properties of the Royal Road GA are examined. First the observed intermittency in cases where there are many fixed points is explained, and related to the error threshold in the theory of molecular evolution. The better adapted to the environment a phenotype is, the more it is dependent on all the sites in its genotype. Although the mutational pressure remains constant; the probability of a single mutation having a deleterious effect on an individual's fitness increases as its fitness becomes more dependant upon all sites in the genome. A point described as the *error threshold* is reached, where selection is no longer able to maintain the genome close to the optimum due to the increasingly deleterious effects of single mutations. This is observed in the Royal Road GA, and is successfully explained by van Nimwegen et al. In systems with large numbers of local optima, they claim that the error-threshold causes the system to lose the higher fitness optima, and successfully predict the timescales over which this occurs.

Second, the approximation of sampling fluctuations is used to predict the length of time that the system spends in each epoch. This is less successful. The system spends longer in each of the epochs than is predicted by the model, although the model does predict the position of the epochs, and the fluctuation widths correctly. The reason given is that there is a spontaneous symmetry breaking when the system moves from one epoch to another. A new epoch is almost always founded by a single individual discovering a new aligned block, which is then spread rapidly through the population. Therefore the assumption that the sites in the block are randomly distributed between alleles (equation 2.46) no longer holds. Van Nimwegen (personal correspondence) claims that an alternative formulation of the mutation operator, assuming that the population diverges from an initially converged population by a random walk process, improves prediction accuracy. He also notes that the population never fully diverges, because the sampling of the population tends to keep the population somewhat converged [21]. No successful analytic formulation of this latter effect has yet been found.

Finally, van Nimwegen et al. contrast the mechanism behind meta-stability in the Royal Road GA with the view that they are transits between local optima induced by stochastic fluctuations. They note that there are no fitness barriers between local optima within the Royal Road GA, yet meta-stable behaviour still occurs. They posit an entropic cause to meta-stable behaviour: the time taken to find a better local optima is the time to explore the plateau of the present optima, to find an edge which is contiguous with a higher-fitness plateau.

2.3 Noise in Non-Linear Dynamical Systems

In this section, the effect of both additive and multiplicative noise on a discrete dynamical system is considered. Such noise will allow the system to escape from attractors, thus rendering all attractors meta-stable,

> "The long time behaviour of a noisy dissipative system is thus intermittent, consisting of motion near the various attractors of the system alternating with transitions between the attractors. In the limit of small noise the time spent on the attractors becomes longer, and the transitions rarer"[9]

The approach of Knobloch & Weiss [52] is to consider the trajectory of a continuous non-linear system perturbed by a small noise term. This is then related to an iterative map under noise. The effect of the noise on this map is then considered. Whether the noise is additive or multiplicative depends on the formulation of the problem that is adopted. Additive noise in a time-T map (a map of the positions of a T-periodic system at intervals of T) becomes multaplicative noise in a return map. This is because the return time to any point depends on noisy parameters.

Whilst the thrust of the Knobloch & Weiss [52] paper is to consider the effect of noise in iterative maps containing phase-locking phenomena, and in a simple map with multiple attracts (the cubic map), there are important general points made concerning noise in maps with multiple attractors. First, Knobloch & Weiss consider the effect of additive noise in directions with differing stability. They point out that in stable directions (negative eigenvalues) the effect of noise is oppose the contraction of a dissipative system onto the attractors, forcing meta-stability. In the case of neutrally stable directions (zero eigenvalues) the resulting effects are similar to an unbiased random walk, and result in diffusion processes. In unstable directions (positive eigenvalues) the

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[9] Knobloch & Weiss [52].

noise may slow the escape of the system. They point out that in the case of a small noise term, escapes usually take place across saddle nodes. Here the energetic barrier that has to be overcome is lowest, so the system can most easily escape. Recalling van Nimwegen et al.'s [79] discussion of transitions between states in the Royal Road GA, (Section 2.2.4) where there is no energetic barrier to be overcome, there still exists an entropic barrier. Whilst the system can easily escape from what is effectively a saddle node; it has first to find the appropriate boundary to escape over. This search time constrains the evolution of the system. Generalising from this, it is clear that in the case of a transition across a saddle node between attractors, there may be an entropic as well as an energetic barrier to overcome. This will be returned to later in this section.

Second, Knobloch & Weiss discuss the nature of transitions between attractors under the influence of noise. Their analysis of a system containing a period N map concludes that if the phase basins (i.e. the basins of attraction of each point in the cycle) have unequal size, then most escapes occur from the narrowest phase basin, regardless of the initial point of the system.

Third, there is a discussion of the manner in which escapes from an attractor basin are conducted. For a cubic map, Knobloch & Weiss construct a conditional probability distribution based upon an escape in the future, which they then compare to the assumed meta-stable distribution. This shows that most escape processes have a relatively short timescale. Escape events do not occur as a result of diffusion processes; there is a sharp transition between motion inside the meta-stable attractor, and motion outside the basin of attraction. This indicates that the escape comes about from individual stochastic events, not the combination of events. This suggests that the entropic barrier to finding the saddle node to escape over may be more significant than the energetic barrier.

Fourth, there is the question of motion outside the attractor basin. For the cubic map, motion outside the immediate basin of attraction takes the form of a chaotic transient [38, 39]. It is hard to predict the basin that the system will fall into, because the area immediately outside the local basins of attraction consists of finely interwoven attractors. However, the mean time in the transient between attractors is insensitive to the magnitude of the noise term.

2.4 Conclusions

In this chapter a number of approaches to the problem of modelling the trajectory of an evolutionary system have been considered. Four basic approaches have been considered. First there is the classical approach, based on the use of continuous time models of discrete time processes. As has been discussed, this involves assumptions on relative convergence rates of processes as the limit of an infinite population approaches. Second, there is the statistical dynamics approach of van Nimwegen et al., who model the system in terms of a few order parameters. This approach is successful for large populations. They then model the sampling fluctuations inherent in the evolutionary operator for finite populations using a classical approach, based on calculating the lower order moments of the distribution of fluctuations from the form of the evolutionary operator. Assuming that the higher order cumulants are negligible, this gives a Fokker-Planck diffusion for the fluctuation distribution. Third, there is the microscopic approach adopted by Vose, which proves unwieldy in practice. Fourth, there is the approach of Prügel-Bennet, Rattray and Shapiro. They calculate the average distribution of the first few cumulants of the fitness distribution. This approach does not allow examination of the detailed structure of the trajectory of the system, which is of prime interest here. However, this approach does consider the problems of moving from infinite limit approximations to the dynamics of finite populations.

The underlying difficulty that must be faced is that the sampling fluctuations add noise to the system at each time step, which can have a major effect on system trajectory, especially in relatively small populations. It is apparent from the review conducted above, that the modelling of such fluctuations in a non-linear system is not well understood at present. There are many relevant parameters in an evolutionary system: changing any of these parameters can alter the distribution of the noise induced by sampling fluctuations.

There are two aspects to this problem: a formal, theoretical one, and a practical one. Formally, questions about the distribution of noise induced by sampling fluctuations in an evolutionary system are of great interest. But they are also not well understood at all. In more practical terms, the question is what distribution of noise seems to fit the observed facts well, and gives models of evolutionary systems predictive power. Van Nimwegen (personal correspondence) observes:

> "So generally, there is not a good mathematical justification for applying a diffusion equation method. Note that this is also the case for the models that Kimura introduced. It turns out though that the results predict simulation results very well. This is why I decided to use the diffusion equation method; it allows you to actually calculate something, and the results seem to hold up well against the simulation data. So although one can make all kinds of formal arguments for why it should work, in the end the comparison with the simulations is what mainly justifies the approach."

The relevance of this chapter is twofold. First, it prepares then way for an analytic exploration of populations of interacting adaptive agents that is put forward in the next chapter. Second, the discussion of the dependence of both the analytic model, and the system's behaviour on the interdependence of a number of factors, especially population size, informs the experimentation presented in Chapters 4 and 5. Small, toy systems may not serve as adequate models of full size systems of interacting adaptive agents because their behaviour is not consistent over changes of scale. This is an important practical point. Planning of large systems of (adaptive) agents, such as large computing and telecommunications networks, may be difficult, because such systems may not maintain consistent behaviours across scale. The planning of such systems may face twin problems: Firstly, the systems are at the limit of analytic tractability, if they succumb to analysis at all, Secondly, small scale models may be limited as a planning tool because there is no guarantee of consistent behavioural patterns across changing system size.

Chapter 3

Sampling Fluctuations in Finite Populations of Interacting Agents

In the previous chapter the dynamics of a simple population of adaptive agents has been considered from a variety of standpoints. In this chapter, attention will be turned to the analytic formulation of an interacting population of adaptive agents. In particular, the effects of sampling fluctuations within the adaptive process on the evolutionary dynamics of the entire system will be examined. It is required that any derived formulation be informative not only in the case of an infinite, or very large population, but also through a range of finite population sizes, so that the effects of the sampling fluctuations may be examined.

3.1 Formalisation of an Interacting Adaptive Agent Population

The immediate problem that must be considered is how the population should be represented within such an analytic formulation. In the previous chapter, three possible approaches have been examined.

First, there is the approach of Vose et al. [81], in which every possible population distribution is considered. The dynamics of the system are considered as the dynamics of a probability density function over the space of all possible populations, via a Markov system approach. This has been ruled out as computationally impractical, because the space of all possible populations is huge.

Second, there is the classical population biology approaches, exemplified by Kimura [51], in which the frequency of an allele at a given site on the genome is considered. This approach is also problematic, for two reasons. First, there are likely to be a large number of sites on the genome, which may or may not be independent, and second, the fitness contributions cannot be independently assessed. This combination means that the resulting formulation will have a large number of variables, with many probably unknown interdependencies.

Third, there are the fitness based approaches adopted by Shapiro and co-workers [69, 70, 76, 72, 71], and by van Nimwegen et al. [79]. Such measures are generally unsatisfactory in a population of interacting adaptive agents. The fitness of an agent is dependent upon its interaction with other agents. It is hard to see how macroscopic measures of the fitness of agents could be used to predict the values of those macroscopic parameters. This formalisation loses the essential detail of the system; the system dynamics are determined by the interactions that take place.

None of the formalisations of an adaptive agent population that have been considered so far appear suitable in the case of a population of interacting adaptive agents. It should be noted, however, that all these approaches are based around probability density functions. In the case of Vose, the probability that the population is in a particular state, in the case of Kimura, the probability that an agent possesses a given allele, and in the case of Shapiro and co-workers, and van Nimwegen, the probability that an agent has a given fitness. The fundamental question is whether there is another parameter that can be used to characterise the dynamics of a population of interacting adaptive agents?

3.1.1 Order Parameters for Interacting Adaptive Systems

Essentially, we seek an order parameter for an interacting adaptive agent population. This is a macroscopic parameter that may be used to describe the behaviour of the system, without the need for knowledge of the microscopic states of the elements that make up the system. This type of measure originates in statistical physics, where macroscopic order parameters such as the energy of a system can be used instead of the states of every particle in the system to make predictions about system behaviour. In a similar fashion, statistical models of genetic systems have used measures of agent fitness as order parameters. It is not necessary to know the precise genotype of every individual in the population, merely the distribution of fitnesses, and the transition probabilities between fitnesses.

The proposal at the centre of this thesis, is that agent behaviour may form an appropriate order parameter for an interacting adaptive agent system. In such a system, an agent's utility is determined by the behaviour it exhibits; agents that successfully interact with other agents have higher utility than those that do not. The essence of interaction lies in the behaviours exhibited by the interactees.

Agent behaviour lies at an intermediate level in possible characterisations of such a system. It is certainly at a higher level than the detail of the precise state of the agent. Whether the adaptive schema is at an individual or a population level is immaterial; it is sufficient to be able to calculate the transition probabilities between possible behaviours based on the implementational details of the adaptive schema. Behaviour might be seen to lie at a lower level than agent fitness; the behaviours that an agent exhibits will determine its fitness within the population. However, it must be noted that the fitness of an agent is based upon its interactions with other agents, and which will therefore be dependent upon the distribution of agent behaviours within the population. In some sense then, the distribution of agent behaviours is the highest level parameter that it is possible to find within a system of interacting adaptive agents: it is abstracted from the implementational details, and also determines the shape of the landscape upon which adaptation takes place.

3.1.2 Properties of the Mapping from Microscopic Population to Behavioural Order Parameters

The characterisation of a system in terms of a set of macroscopic order parameters entails a reduction in the dimensionality of the system space; therefore a many-one relationship between points in the microscopic space and points in the macroscopic order parameter space will ensue. In this case, we are considering an adaptive system where the set of order parameters (behaviours) directly feeds the fitness function. This is noteworthy: all individuals with the same behaviour will be selected for or against at the same rate. Therefore, all such points are selectively neutral with respect to one another. A sub-population of agents sharing any given behaviour will be free to spread across the set of states that give rise to any particular behaviour without any selective advantage or disadvantage.

Now clearly the discussions of selective neutrality and genetic drift (Sections 2.1.3, 2.1.4 and 2.2.4) still apply. The spread across microstates giving the same behaviour may be limited by selection (random genetic drift), fluctuation of selection intensities (probably important in an interacting population where the speed of environmental changes is high compared to the evolution rate), and the existence of entropic barriers to the spread of a population through selectively neutral mutations. On the other hand, under certain environmental conditions, the spread of a population through a selectively neutral set of microstates whilst maintaining a given behaviour may prove to be important in keeping the system poised to be able to exploit changing environmental conditions.

Recall Section 2.2.4. Van Nimwegen et al. [78] characterise the noise term introduced by the reduction from an infinite population to a finite population as being multinomial in form; this noise is caused by taking a finite number of samples from an infinite distribution. This formulation of the noise will be followed here. In Section 3.2.4 the evolutionary operator, $\mathcal{E}$, was considered as a conflation of the exploratory and exploitative operators, $\mathcal{M}$ and $\mathcal{S}$, respectively. In the finite case, we shall consider $\mathcal{E}$ to consist of the sum two components, $\mathcal{E}_D$, a deterministic component corresponding to the conflation of $\mathcal{M}$ and $\mathcal{S}$, as discussed in Section 3.2.4 (although the formulation will not be in terms of differential equations, but in terms of difference equations), and a stochastic component $\mathcal{E}_S$, an additive noise term following a multinomial distribution.

In large populations, the effect of $\mathcal{E}_S$ will be negligible; the evolution of the system will tend towards the deterministic formulation $\mathcal{E}_D$. As the population size is reduced, the stochastic component, $\mathcal{E}_S$, will have a relatively greater and greater effect, until a point is reached with a small population where the effect of the deterministic operators $\mathcal{M}$ and $\mathcal{S}$, acting in concert as $\mathcal{E}_D$, cannot be discerned.

3.1.3 Observables: a Further Level of Description

At this point, the dynamics of the system have been discussed on two levels. First, there is the microscopic dynamics of the system. A formulation of the microscopic dynamics of the system will give a complete description of the trajectory of the system. In practice, such a formalisation lies far beyond the realms of analytic tractability. To overcome this problem, an abstraction of the system is used. In Sections 2.1 and 2.2 various possible abstractions have been discussed. Such an abstraction must preserve the essential features of the microscopic dynamics.

A third level of description of the system will now be introduced, the *observable* dynamics of the system. The aim of this thesis is to examine the dynamics of systems of interacting adaptive systems. Whilst a behavioural analysis of the system is postulated to successfully capture the dynamics of a model system, a behavioural analysis may not be possible in a real world system. In many real-world systems (e.g. economic systems) the behaviours exhibited by individual agents may not be observable, either by agents within the system, or by an outside observer. Define the collective properties of the system that are open to view, either by agents within the system, or by outside observers, as the *observables* of the system. In some cases, where there are no individual interactions in the system, only collective interactions, the observables will guide the actions of individual agents. In other cases, agents may respond to the individual behaviours of other agents, but these will be hidden from other agents and outside observers. It is important to consider the *observable dynamics* of the system in order to relate observed phenomena to the underlying behavioural and microscopic dynamics, which may be hidden from view.

3.1.4 Approaches to Behavioural Dynamics

If the agent behaviours exhibited within a population of interacting adaptive agents are to form the basis of a formalisation of such a system, the next consideration must be the approach used. In the previous chapter, we have observed three differing approaches, based on whether the system has a discrete set of possible parametric states, or a continuous range of states. Before considering these possible approaches, let us first consider whether behaviour should lie within a discrete or continuous range.

Certainly, there are instances where the range of agent behaviours has been considered to be continuous (or, at least lying within a high precision floating point range in a computational model). For example, within simple economic games such as the IPD, the behaviour of an agent might be characterised as the probability of defection on any given play. However, there is a powerful case that such a real domain is not realistic. The set of agent behaviours does not in fact have an infinite cardinality, for any real world set of agents. Animal or human behaviours follow a small number of patterns; computer agents are limited by the precision of their arithmetic. This may be due to a limitation in the responses of the agents, or alternatively from a limitation in the sensory abilities of agents. Agents are constrained to behave in a limited number of ways, because they are incapable of sensing more than a limited number of differing states in their environment. Hence we will consider, in the abstract, both continuous and discrete behavioural sets, and decide upon the appropriate approach in each case.

In the discrete case, there is only one approach: the Markov system approach, as used by Vose [81], and by van Nimwegen et al. [79]. In the continuous case, two formulations are possible, the diffusion equation type approach as used by Kimura [51] and the cumulant approach used by Shapiro and co-workers [69, 70, 76, 72, 71].

In the continuous case, there are two possible approaches, both of which have limitations. The approach of Shapiro and co-workers [69, 70, 76, 72, 71] (detailed in Section 2.2.2) characterises the system by the lower order cumulants of the behavioural distribution. However, there may be problems inherent in such an approach. The dynamics of the system can be successfully reduced to the dynamics of the lower order cumulants only if it can be shown that the higher order cumulants have a negligible effect on the dynamics of the lower order cumulants. In the type of non-interacting system studied so far with this approach, the population distributions have always been, if not Gaussian or binomial, then at least unimodal. In a population of interacting adaptive agents there is no guarantee that a continuously parameterised population may have a unimodal probability density function in such a parameter space. If this is not the case, then the higher order cumulants may have strong effects on the dynamics of the lower order cumulants, breaking the premise on which the model is founded.

There is also the diffusion equation approach of Kimura, which may be characterised as an expansion of a Taylor series about a small increment in time, on the probability density function of agent behaviours (detailed in Section 2.1.1). This appears initially to be an attractive approach, but it is in fact very problematic, so it will be considered in further detail. Here an alternative derivation (also presented by Kimura [51]) is used, which leads to the same result (Equation 2.10) in the context of population biology. Unfortunately, it would appear that the Taylor series approach, whilst attractive, presents difficulties in the context of an interacting agent population. The problem will be further discussed in the following section.

3.2 The Diffusion Equation for a Population of Interacting Agents

3.2.1 Notation

In this section, a number of mathematical concepts are discussed. To aid the understanding of these concepts, the following typeface notations are adopted.

Real variable e.g. time	x	lower-case roman
Real space e.g $(0, 1)$	X	upper case roman
Real function	f	lower-case roman
Density function	ϕ	lower-case greek
Space of density functions	Φ	upper-case greek
Adaptive Operator	$\mathcal{M}$	upper-case calligraphic
Random variable	$\mathbf{R}$	bold upper-case roman
Other variable	y	lower-case san-serif
Other space	Y	upper-case san-serif

The convention adopted is that the space corresponding to a lower case variable, will, if possible, be notated by the upper-case version of the same symbol.

Other important conventions that are adopted within this chapter are the use of angled brackets, $\langle\rangle$, to denote an expectation, and the use of the symbol p to denote a probability.

Consider an infinite population of interacting adaptive agents, An infinite population may be thought of as an infinite set; in this discussion the biological terminology will be followed. The term 'interacting adaptive agent' will be defined more closely below. At this point, the intuitive definition that this term refers to an agent whose adaptation is somehow driven by upon its interaction with other members of the population, will suffice. This infinite population has a pair of operators acting upon it, an exploratory operator $\mathcal{M}$ and an exploitative operator $\mathcal{S}$. These correspond (in genetic terms) to simple mutation applied to the entire population, and fitness proportional selection respectively. This pair of operators will be composed to form the evolutionary operator, $\mathcal{E}$.

The operator $\mathcal{E}$ that will be derived below corresponds to mutation and selective asexual reproduction acting independently and simultaneously. In the discrete case, selective asexual reproduction followed by mutation forms a first order approximation to the diffusion approach. The derivation of a set of diffusion equations for the case of an interacting adaptive population is, of course, dependent upon the relative values that certain parameters take, as discussed in Section 2.1.7.

The notion of agenthood is not necessarily within the proper scope of a mathematical definition. However, a mathematical treatment of the evolution of a population of adaptive interactive agents requires some well defined definition of agenthood. Without any closer definition, consider an agent a which lies within a space of possible agents A. These terms are deliberately vague, and will be replaced by much more closely defined terms at the earliest opportunity.

Definition 3.2.1 *An* agent, a *will be characterised by its quantifiable properties. In particular, abstract the behaviour of an agent in the presence of other agents to a single real parameter,* $x \in X$*, where* X *is the continuous range* (a, b). X *will be described as the* space of possible agents *or* agent space. *There exists a mapping* $g : \mathsf{A} \to \mathrm{X}$.

It is assumed that the timescale over which the interaction between agents takes place is sufficiently small with respect to the timescale over which the evolution takes place that the behaviour, x, of an agent can be considered constant during any interaction.

For example, consider a population of agents playing the 'matching pennies' game[1]. Whatever the internal structure or decision making process which an agent goes through, we choose to characterise an agent by the probability with which it plays H(eads). In this case an agent would be described by a single real variable x ($= p(H)$).

The definition given above (Definition 3.2.1) is in a single dimension. Of course, there may be more than one dimension to agent behaviour. However, care should be exercised to ensure that if more than one dimension of agent behaviour exists, that all dimensions are orthogonal. This may be difficult to prove analytically, but it is possible that techniques such as principle components or curves analysis may be able to extract orthogonal behavioural dimensions. This would lead to a multidimensional analogue of the case presented here.

This derivation is in many ways analogous to one presented by Kimura [51]. Indeed, a similar derivation is presented by Kimura as an alternative to the derivation presented in Section 2.1.1. The difference is that Kimura is examining the time evolution of the probability that an individual will possess a particular gene at a given site; here we wish to examine the probability that an agent has a property, expressible as a single real parameter. By contrast, Kimura's derivation would lead to a set of n equations, for a population of agents with an n-bit binary genome. However, even if there are no direct dependencies between sites on the genome, the interactive nature of the population will cause dependencies between site on the genome, and hence lead to a set of n simultaneous partial differential equations. Whilst this may have an analytic solution in a case where n is very small, in general it is assumed that analytic solutions to this problem may be hard to find. Numerical methods may be employed, but they may only find fixed points, rather than cyclic or more complex solutions.

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[1] Players simultaneously reveal a coin that they placed with one side or the other upwards. One player (pre-chosen) wins if they match, the other if they do not.

Definition 3.2.2 *The* population density function *of an infinite population of agents, with respect to a single real agent-defining parameter x is defined as*

$$\phi(x) = \lim_{\Delta x \to 0} \lim_{n \to \infty} \frac{no\,(\mathsf{a} \in \mathsf{A_n} : \mathrm{g}(\mathsf{a}) \in (\mathrm{x}, \mathrm{x} + \Delta\mathrm{x}))}{n \Delta x} \tag{3.1}$$

where n is the population size, and the subspaces A_n are chosen to ensure that $\lim_{n\to\infty}$ *exists*

The notion of a population density function is analogous to that of a probability density function found in probability theory. Indeed, in Section 3.2.6, the notion of a probability density function will be introduced (see Definition 3.13). As regards the interactive behaviour of agents, the population density function, ϕ is a complete description of the population.

Definition 3.2.3 *A* fitness function, *f, is a mapping from an agent* a *to a real value, usually in the range (0,1). The range of values of f will be defined as F. Distinguish between $f^\dagger$ and f, by their domain*

$$f^\dagger : \mathsf{A} \to \mathrm{F}$$

$$f : x \to F$$

In the derivation that follows, the selective operator, S, will be shown to have a dependency upon the derivative $\frac{\partial f}{\partial x}$. Therefore constrain f to be *smooth*, i.e. that $\frac{\partial f}{\partial x}$ is finite across the entire range X.

In biology, the fitness of an individual with a given genotype is usually defined as its expected number of offspring. The biological definition gives a measure of fitness relative to other members of the population; it is usual (but not universal) in GA theory to construct f as an absolute measure of agent fitness. The latter convention will be adopted here.

At this point, Definition 3.2.1 may be revisited. x may be redefined more closely as a single real parameter that encapsulates those aspects of an agent that are relevant to determining its fitness.

At this point a mathematical definition of interaction may be given.

Definition 3.2.4 *An* interacting *agent is one whose fitness is dependent no only upon its own characteristics, but also upon the characteristics of the other agents it interacts with. The* payoff *to an agent* a *from its interaction with another agent* b *will be notated* $f_p^\dagger(\mathsf{a}, \mathsf{b})$*, or alternatively* $f_p(x, y)$*, where* $x = g(\mathsf{a})$ *and* $y = g(\mathsf{b})$*.*

Generally, individual agents may not be able to choose which other agents they interact with; indeed no definition has been offered of the number of agents involved in each interaction, or the nature of the interaction. The expected payoff will be used as a measure of agent fitness in the absence of specific knowledge concerning the precise interactions that take place within the population.

Definition 3.2.5 *Redefine the* fitness *of an interacting agent,* a *as its expected payoff* $\langle f_p^\dagger(\mathsf{a}, \mathsf{b})\rangle$ *from an interaction with some other member of the population* b*. The fitness of a particular agent is now no longer* $f(x)$*, but* $f(x, \phi)$*; the fitness of any member of the population is dependent upon the composition of the entire population.*

$$f(x, \phi) = \int_{y \in X} f_p(x, y)\phi(y)\,dy \tag{3.2}$$

The controlling equation for the evolution of the population density function over an evolutionary time scale may now be derived. At time t, the population density function $\phi(x)$ will be written as $\phi(x, t)$ as necessary to avoid any danger of ambiguity. In a similar fashion, $f(x, \phi)$ will be written as $f(x, \phi, t)$. The derivation leads to a Fokker-Planck type equation, similar to that presented in Section 2.1.1.

Parameter size effects on the form of diffusion equations have already been noted in Section 2.1.7. Following that discussion, the exploration rate m will be assumed to be of the order $O(1/n)$, where n is the population size. The resulting operator will be valid when m is of this order.

Consider now the change in ϕ over a small discrete time period δt, due to the action of $\mathcal{E}$, i.e. $\phi(x, t + \delta t) = \mathcal{E}\phi(x, t)$. Over this small period there will be two sources of change to $\phi(x)$, one due to $\mathcal{M}$, the other due to $\mathcal{S}$. At this point in time, consider both these operators to act simultaneously and independently on ϕ. This is the simplest combination of the exploration and exploitation operators possible; it corresponds to asexual reproduction with mutation. The effects of genetic operators have already been discussed in Section 1.2.3.

The derivation provided below is not valid at the endpoints of the range. Consider, therefore, a situation where the endpoints of the domain (a, b) are periodic from the perspective of agent behaviour.

$f(x, \phi)$ may be thought of as imposing an energy surface which controls the trajectory of the population. Exploitative processes will tend to shift the population towards areas of higher fitness (analogous to some form of hill climbing), whereas exploitative processes will tend to spread the population across the domain. The evolution of the system will be modelled as a diffusive process across this energy surface. The behaviour of the population over time will be derived from the following constraints:

1. The population will flow towards areas of higher fitness at a rate proportional to the rate of change of fitness with respect to behaviour. Define the constant of proportionality as k.

2. The rate at which the population flows away from any point will be proportional to the exploration (or mutation) rate, m.

3. The rate at which the population flows away from any point is proportional the population density function at that point.

Between them, these constraints describe the actions of the explorative and exploitative operators discussed in Section 1.1.2. Constraints 1 and 3 above, when expressed formally (see below) control the exploration operator, whilst constraints 2 and 3 control the exploitation operator.

3.2.2 The Effect of the Exploitative Operator S

Consider the time evolution of the probability of an individual lying in the range $[x - \Delta x, x + \Delta x]$. Constraint 1 is taken to imply a dependence upon k and $\frac{\partial f}{\partial x}$. Constraint 3 is expressed by considering the flow of population density at two points $x - \Delta x, x + \Delta x$, a small distance $2\Delta x$ apart. This provides an expression for the net flow into a rhomboid of width $2\Delta x$ in time Δt

$$\begin{aligned} & 2\Delta x \phi(x, t + \Delta t) - \Delta x \phi(x, t) \\ & = \tfrac{k}{2}\Delta t \quad \left[\frac{\partial f(x - \Delta x, \phi, t)}{\partial x} \phi(x - \Delta x, t) \right. \\ & \qquad \left. - \frac{\partial f(x + \Delta x, \phi, t)}{\partial x} \phi(x + \Delta x, t) \right] \end{aligned} \tag{3.3}$$

where $k/2$ is a rate constant. Dividing through by $\Delta t \Delta x$, and taking the limit $\Delta t \rightarrow 0$ gives

$$\begin{aligned} \frac{\partial \phi}{\partial t}(x, t) &= \frac{k}{2\Delta x} \left[\frac{\partial f(x - \Delta x, \phi, t)}{\partial x} \phi(x - \Delta x, t) \right. \\ & \qquad \left. - \frac{\partial f(x + \Delta x, t)}{\partial x} \phi(x + \Delta x, \phi, t) \right] \end{aligned} \tag{3.4}$$

Adding and subtracting a term on the r.h.s gives

$$\begin{aligned}\frac{\partial\phi}{\partial t}(x,t) &= -\frac{k}{2\Delta x}\left(\frac{\partial f(x-\Delta x,\phi,t)}{\partial x}\phi(x-\Delta x,t)-\frac{\partial f(x+\Delta x,\phi,t)}{\partial x}\phi(x-\Delta x,t)\right)- \\ &\quad \frac{k}{2\Delta x}\left(\frac{\partial f(x+\Delta x,\phi,t)}{\partial x}\phi(x-\Delta x,t)-\frac{\partial f(x+\Delta x,\phi,t)}{\partial x}\phi(x+\Delta x,t)\right)\end{aligned} \tag{3.5}$$

which may be rearranged as

$$\begin{aligned}\frac{\partial\phi}{\partial t}(x,t) &= -k\phi(x-\Delta x,t)\frac{\frac{\partial f(x-\Delta x,\phi,t)}{\partial x}-\frac{\partial f(x+\Delta x,\phi,t)}{\partial x}}{2\Delta x} \\ &\quad -k\frac{\partial f(x+\Delta x,\phi,t)}{\partial x}\frac{\phi(x+\Delta x,t)-\phi(x-\Delta x,t)}{2\Delta x}\end{aligned} \tag{3.6}$$

Taking the limit $\Delta x \to 0$, and simplifying the notation (since the point in time and space is now unambiguous) gives the differential equation

$$\frac{\partial\phi}{\partial t} = -k\left(\phi\frac{\partial^2 f}{\partial x^2}+\frac{\partial f}{\partial x}\frac{\partial\phi}{\partial x}\right) \tag{3.7}$$

This may be simplified to

$$\frac{\partial\phi}{\partial t} = -k\frac{\partial}{\partial x}\left(\frac{\partial f}{\partial x}.\phi\right) \tag{3.8}$$

This is the simplest possible equation that might govern the time evolution of a population across a fitness landscape, and is the controlling equation of the operator $\mathcal{S}$. The population will migrate towards local maxima via a gradient ascent algorithm, as required by the given constraints.

3.2.3 The Effect of the Exploratory Operator $\mathcal{M}$

In the same way as the above discussion has considered the action of the exploitative operator $\mathcal{S}$, consider now the action of the exploratory operator $\mathcal{M}$. This operator has a very simple action: it will act to increase the entropy of the population by dispersing the population across the space. This can be considered as occurring via a diffusive pressure in each cell of width Δx, proportional to the population in that cell. There will therefore be a flow across the left and right boundaries of each cell, proportional to the gradient of the population density function at that boundary. Note the difference from the derivation of the exploitative operator, $\mathcal{S}$; constraint 2 is now expressed as a partial derivative, and constraint 3 appears as a constant of proportionality, m. Over time Δt this will be

$$\Delta x\phi(x,t+\Delta t) = \Delta x\phi(x,t) + \frac{m}{2}\left(\phi(x,t)\frac{\partial\phi(x+\Delta x,t)}{\partial x} - \phi(x,t)\frac{\partial\phi(x,t)}{\partial x}\right)\Delta t \quad (3.9)$$

This states that the change in population within any cell is the sum of the gains across each boundary. This may rearranged by moving the first term on the r.h.s. to the l.h.s., and dividing through by $\Delta t\Delta x$ to give

$$\frac{\phi(x,t+\Delta t)-\phi(x,t)}{\Delta t} = \frac{m}{2}\left(\frac{\phi(x,t)\frac{\partial\phi(x+\Delta x,t)}{\partial x} - \phi(x,t)\frac{\partial\phi(x,t)}{\partial x}}{\Delta x}\right) \quad (3.10)$$

If one now lets $\Delta x \to 0$ and $\Delta t \to 0$ simultaneously (and simplifying the notation since points in time and space are now unambiguous) the action of $\mathcal{M}$ becomes

$$\frac{\partial\phi}{\partial t} = \frac{m}{2}\frac{\partial^2\phi}{\partial x^2} \quad (3.11)$$

This is the controlling equation of the exploratory operator $\mathcal{M}$. It corresponds to a Fokker-Planck diffusion in the absence of a potential field. This is unsurprising: one would not expect the dynamics of exploration to be altered by the interaction between population members.

3.2.4 The Evolutionary Operator $\mathcal{E}$

From a practical perspective, both the above derivations are idealistically simplistic. There are several important points that should be made here:

1. In the derivation of the exploitative operator $\mathcal{S}$, there is an assumption that the exploitative process is one of local hillclimbing. Agents with behaviour x will adopt behaviour $x + \Delta x$ if it leads to higher fitness. Agents with behaviour x will not adopt a behaviour y if x and y are not adjacent in the space. The local nature of the hillclimbing precludes the exploitation of non-adjacent points in the space. This is a serious limitation; globally optimal behaviours cannot be reached by all members of the population, even if they are present within that population.

   In Section 3.1.1 the divergence between the two alternate versions of the Fokker-Planck equation (Equation 2.10) derived in Section 2.1.1 is alluded to. In the interactive case, (Equation 3.12), the selective operator (see Section 3.2.2 is problematic. Recall the basis of Kimura's [51] use of a diffusion equation approach. From an initial condition of an allele with a given frequency within the population, Kimura used a diffusion equation approach to calculate the probability that the allele had a given frequency within the population at some later time. The underlying assumption is that the population remains in a unimodal distribution; the Taylor series approach associates terms in the Taylor series with moments of the distribution. In the interactive case under consideration here, no such assumption of unimodality exists. Of course, any distribution can be defined to arbitrary accuracy by means of an appropriate series of moments, so strictly a Taylor series approach will work. The problem lies in interpreting these moments in terms of the derivatives of the fitness function. In addition, a large number of terms may be required to obtain the required level of modelling accuracy, which tends to defeat the purpose of obtaining an analytically tractable model of the population dynamics[2].

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[2] If this sort of approach were to be considered, the moment based approach of Shapiro and co-

2. In both derivations there is an implicit assumption that it is possible for an agent to traverse the behavioural range (a, b) in a smooth fashion. This is not always the case. For example, in an evolutionary system, a genotype-phenotype distinction must be made. The behaviour of an agent is dependent upon its phenotype. This in turn is dependent upon the genotype. Adaptation (both the exploratory and exploitative operators) act on the genotype. There is no guarantee that a small smooth change in the population density function over the genotype space will lead to a continuous change in the population density function over phenotype space or behaviour space.

The evolution of the population is controlled by the evolutionary operator, $\mathcal{E}$, a combination of the exploratory operator, $\mathcal{M}$, and the exploitative operator, $\mathcal{S}$. In reality, these operators are not independent; exploration can occur during the exploitative process. Consider two common adaptive schemes: the canonical genetic algorithm (CGA) as described by Holland [42], and the backpropogation algorithm within a multilayer perceptron (MLP) network [41]. In the former, exploration and exploitation are provided separately by the mutation and crossover operators, working at the level of the entire population. Here the higher order terms are brought in because the crossover operator is not purely selective, it finds a point in the genotype space between two known good points. This is partially exploitative in that the fitness of the new point selected is not known *a priori*. In the MLP, the backpropogation algorithm performs an iterative gradient descent on an error surface in a weight space. However, to reduce computational expense, this descent takes place in finite steps across the weight space. Exploitation and exploration are inseparable because the finite steps sample

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workers might well provide an ideal starting point. This approach has been discussed already, in Sections 2.2.2 and 3.1.

points of unknown error, although on a smooth surface, the error at the next point in the iteration can be estimated with a high degree of accuracy.

Hence, in most practical adaptive schemae, a degree of interdependence between the explorative and exploitative operators may exist, which gives rise to higher order terms. These will not be considered here. The approximation adopted is to consider these two operators as acting independently and simultaneously upon the population. The controlling equation of the evolutionary operator $\mathcal{E}$ will thus be the sum of the effects of its two constituent parts

$$\frac{\partial \phi}{\partial t} = -k \frac{\partial}{\partial x}\left(\frac{\partial f}{\partial x}.\phi\right) + \frac{m}{2}\frac{\partial^2 \phi}{\partial x^2} \tag{3.12}$$

Note the correspondence with the Fokker-Planck equation (2.10). The first term on the r.h.s. corresponds to the first order moment term; only here the rate is dependent upon a local fitness field. The second term is identical to that in the Fokker-Planck equation. The constants k, m control the respective strengths of the exploratory and exploitative operators in the system. As has already been mentioned, this equation is only valid for a population size/ exploration rate ratio of $O(1/N)$. Other ratios will lead to different diffusion formulations. This equation governs the evolution of an infinite, continuous time, continuous space population of interacting agents.

3.2.5 Behavioural dynamics of an Infinite Population

Equation 3.12 describes the time evolution of an infinite population of interacting agents. There is already some indication of the expected behaviour of such a population: the conditions given in Section 3.2 will constrain the evolution of the system described by Equation 3.12. It is well known that in the infinite time limit the behaviour of a system described by Equation 3.12 will tend towards an attractor of that system, be it a simple fixed point, a limit cycle, or some more complex type of attractor such as a strange attractor. Such a system can be described by means of an 'energy' surface: the attractors are local minima on such a surface. Note that such an energy surface is different from the fitness landscape; fitness is a function of an agent's behaviour, and of the rest of the population (see Definition 3.2.5). In contrast, the energy surface lies over Φ, the space of all possible population distribution functions.

Ideally, one would hope that an analytic solution to Equation 3.12 could be found, or failing that numerical methods could be used to identify fixed points within the state space Φ. However, before embarking on such a computationally expensive exercise, dependent upon the exact circumstances (i.e. fitness function f), it would be wise to consider the likely topology of the underlying energy surface.

In this section, related work, principally that of Kauffman and co-workers, and of Friston and others will be used to try and more fully understand the likely characteristics of the energy surface corresponding to Equation 3.12.

Kauffman [46] and co-workers have studied a class of models known as NK models. An NK model consists of N binary sites, each linked to K other sites. Each site contributes to the fitness of the entire system, based on its own state, and the state of the K loci it is connected to. Therefore each locus can contribute one of 2^{K+1} possible fitnesses. As these are unknown, they are taken at random from a uniform distribution. The fitness of the whole system is the mean of the fitness of its constituent parts.

These systems have been extensively studied, and their properties are well known. Such a system is in many respects well defined by these two parameters N and K. In particular, as K, the number of other sites that the fitness of a particular site is dependent upon, increase, the resulting fitness landscape becomes more and more rugged and multipeaked. Moreover, by altering K for any given N, it is possible to tune the resulting fitness landscape.

Such systems have also been used as models of co-evolutionary systems. Kauffman and Miller (reported in [46]) have re-interpreted the *NK* model as a co-evolutionary model. In this case each of the N sites is considered as an agent playing some co-evolutionary game. At each time step, every agent re-assesses their current state, and chooses for its next play the state that will maximise its fitness under the (myopic) assumption that all other agents will not change their plays. In this way every agent simultaneously makes an adaptive step towards what they conceive of as a local optima. Describe this as a *NK Boolean game*. Equilibria in a NK network mirror pure strategy Nash equilibria in the *NK* Boolean game. At such a point every agent has a fitness maximising play, given that no other connected agent changes its play.

How does a *NK* Boolean game or a *NK* system relate to a population of interacting adaptive agents, be it finite or infinite? In a *NK* Boolean game, each agent plays against a given number of other agents, whereas in the systems under consideration in this thesis, the interaction may or may not be dependent upon a set of specific interactions, or it may be dependent upon a more generalised group interaction. However, it is noted that as K, the number of interactions that the fitness of a specific site is dependent upon, is increased, the resulting fitness landscape becomes less and less correlated.

Therefore, one should expect that the energy landscape underlying an infinite population of adaptive interacting agents may well contain a large number of local minima. From any particular initial population distribution, the population will flow across the landscape, until it asymptotically reaches a stable distribution, a minima of the energy surface.

Now consider also the views expressed by Friston [31]. His concern is the dynamics of a neural architecture made up of a number of groups of highly connected neurons, with sparse connections between groups. The system is not adaptive; the individual neuronal groups are set up to exhibit chaotic dynamics, and the connectivity between groups is under experimental control.

Alteration of a control parameter (the mean connection strength between neurons in different groups) has the effect of changing the dynamics of the system through a variety of behaviours, ranging from stable incoherence (when the inter-group connections are scant), through to stable coherence and behaviours such as phase locking when the connections are strong. Between these two lies a set of states that Friston (following Kelso [47]) characterises as dynamically stable or meta-stable. This is a completely different phenomenon to the meta-stability that is under discussion in this thesis. The phenomenon referred to by Friston and Kelso is the change in the dynamics of an attractor as some control parameter is altered, such as a Rayleigh-Bénard convection cell moving from a rest state to a macromotion convective rolling state as the temperature of the liquid (the control parameter) is varied. In this case, the changes in the attractor are revealed as transient neuronal dynamics.

Transients in dynamical systems are usually associated with the relaxation of a system from some initial state to an attractor. Friston suggests that whilst the system will remain at a single attractor, there being no adaptive or stochastic elements to the system; the attractor manifold has a complex form. The system can become trapped in a sub-manifold, in which it remains until it can escape via overcoming the entropic barrier that holds it there. Upon escape it will then enter another sub-manifold; the system will exhibit a transient associated with the entry into the new sub-manifold which dies off as the system relaxes into this area of the attractor.

How does this relate to other descriptions of the dynamics of an interacting adaptive population? If one considered the neuronal subpopulations as individual agents, then he is describing a system of weakly interacting non-adaptive agents. In this case, the collective behaviours that the system exhibits might well change over time in the absence of an adaptive force. The system would not leave an attractor, but the changes would be associated with various sub-manifolds of that attractor.

In the case of an adaptive population such entropic barriers may well also exist, but there will also be energetic barriers between attractors, that can only be surmounted by exploratory forces within the adaptive process. Behavioural changes may well be induced by transitions between sub-manifolds of one attractor, as well as via the adaptively or stochastically induced transitions between attracators. It is questionable as to whether collective behavioural changes of the system caused by transitions between sub-manifolds of an attractor can exist in such a way so as not to change the selective advantage of individual behaviours. If they can, then the complex attractor dynamics described by Friston are a possibility. If not, the attractor dynamics must necessarily be more simple; sub-manifolds of a complex attractor may become separate attractors in an adaptive system.

3.2.6 Reconciling Finite and Infinite Population Approaches

In this section a diffusion equation approach to the dynamics of a finite population of interacting agents will be considered. The exploratory and exploitative operators were discussed in Section 1.1. It was noted that both these operators could be considered as stochastic operators. In the limit of an infinite population, the frequency with which a given interactive behaviour, x, is observed within the population converges to the population density function, $\phi(x)$, of that behaviour. Not only that, but the frequency with which a particular adaptive change, be it caused by the explorative or exploitative operator, will also converge to a well defined value in the infinite limit. This allows the derivation of the time-evolution of a population of interacting adaptive agents, as discussed in the preceding section.

The approach taken will be based on the discussion in the preceding section. A finite population will be considered to adapt at discrete time intervals, Δt (here, $\Delta t = 1$). The discrete time dynamics of an infinite population will form a Poincarré section through the continuous time trajectory. The approach taken will be to consider the population at time t as a population density function, expressing the present state of the system. For a system of n agents this population density function will be written $\phi_n(t)$. The evolutionary operator, $\mathcal{E}$ will be applied to this population density function $\phi(t)$ to form a *probability* density function $\phi_\infty(t+1)$. This represents the population density function that would have resulted under $\mathcal{E}$, if an infinite population with an identical density function to $\phi_n(t)$. The actual population at time $t+1$, $\phi_n(t+1)$ is gained by taking n samples from a random variable $\mathbf{R}$ with probability density function $\phi_\infty(t+1)$.

By considering how the approach taken for an infinite population may be adapted to a finite population, problems with the infinite population approach will become apparent. First, consider how the population density of a finite population of agents may be defined, in such a way that its extension to an infinite population will correspond functionally to that given in Definition 3.2.2.

Definition 3.2.6 *For a population of n agents, the* population *density function* , ϕ_n *will be given by*

$$\frac{1}{n}\sum_{i=1}^{n}\delta\left(g(\mathsf{a_i})\right) \tag{3.13}$$

where $\delta(x)$ is a Dirac delta function centred about x.[3] It is here that the problems become apparent: In order that 3.13 should converge to 3.1 it is necessary that the population not only become infinite, but become uncountably infinite. X is a real

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[3] The Dirac delta function can be considered as $\lim_{\sigma^2 \to 0} N(x, \sigma^2)$, where N is a Gaussian mean x, variance σ^2. By this means one can ensure that $\frac{\partial \phi}{\partial x}$ remains finite at all points.

domain, hence it contains an uncountably infinite number of points.

Recall the constraints put forwards at the end of Section 3.2.1. The population is constrained to flow towards areas of increased fitness. The combination of this constraint, and the third constraint (population flow away from each point at a rate dependent upon the population size at that point) describe the action of the exploitative operator. This makes the assumption that the fitness of every point in the domain X is known a priori. This is simply not the case: the fitness of a point $x \in X$ can only be known if there is an agent with behaviour x at that time. If no such agent exists, then the fitness of that point is unknown, and so there is no knowledge to be exploited.

In the uncountably infinite case, there is no problem. The exploratory operator produces a diffusive pressure on the population, causing the population to flow from regions of X with high density towards regions of X with low density. This is checked by the exploitative operator which forces the population towards regions of high fitness. The presence of the explorative operator will force $\phi(x)$ to be strictly non zero (although quite possibly approaching zero) everywhere. In this sense the population will have knowledge of the fitness function f across the entire domain X.

In the case of a finite, or even countably infinite population, an inconsistency becomes apparent. Clearly the distribution ϕ_N will be zero almost everywhere. Either the assumption that keeps $\frac{\partial \phi}{\partial x}$ finite is retained (taking the Dirac delta function as the limit of a Gaussian curve as the variance tends to zero), or it is not. In the former case, the result is an assumption that ϕ must be strictly non zero everywhere along the range, which is known to be false, but allows the exploitation operator to transport the population towards local peaks in the fitness landscape. On the other hand, if this assumption is not made, then ϕ remains strictly zero for every behaviour in X which is not applied by an agent. This prevents the exploitative operator from exploiting points whose fitnesses are not known.

This is a serious problem. The diffusion approach appears tractable in the finite case only if an assumption is made that will give a finite case behaviour, breaking the premise on which the model was founded.

The second problem is how to formulate the population density of a finite population of interacting agents. It might appear odd to have a population density function that is zero almost everywhere. However, $\phi_N(t)$ is used only to calculate $\phi_\infty(t+1)$, which provides a probability density function to the random variable, which is then sampled from to give a population at the next time step, $t+1$.

There is also a third problem in producing an analytic formulation of the behaviour of a system of a finite number of interacting adaptive agents. Recall Section 2.1.7. In this section the underlying assumptions about convergence rates implicit in the derivation of the dynamics of an infinite population evolutionary system were considered. This section was briefly alluded to again in Section 3.2. To recap, it has been shown that the form of the diffusion obtained is not independent of the size of various parameters (e.g. the mutation rate) relative to the population size (although of course the resulting model is strictly an infinite population model applied to a very large finite population). In dealing with a finite population, one must be aware that as the population size changes, then the relative magnitude of the mutation rate and other significant parameters will also change. This means that the controlling diffusion equation will not remain constant as the population size alters. This is problematic: the aim of this thesis is to study meta-stability in populations of interacting adaptive agents. It is hypothesised that the cause of this meta-stability is stochasticities inherent in the adaptive process in a finite population. It is difficult to conceive how the effect of such stochasticities (which are assumed to be due to sampling fluctuations) can adequately be studied when the underlying infinite population baseline is itself shifting as the population size is varied.

For these three reasons it is necessary to abandon the diffusion equation approach as a tool for understanding the finite population behaviour of systems of interacting adaptive agents. Henceforth, we shall adopt a Markov approach, considering a population whose behaviours can be described as lying in a number of discrete categories or bins. Each agent will be characterised by the behaviour that it exhibits, and the set of possible behaviours will be small. The system can now be described as a frequency vector: each component of the vector giving the frequency of agents within the population that lie within the respective behavioural class. The exploratory and exploitative operators, $\mathcal{M}$ and $\mathcal{S}$, can now be described by matrix transformations. This approach has already been detailed in Section 2.2.3. Moreover, in this section the stochastic fluctuations within the adaptive operators in finite populations have been explored to some degree, and can provide a model of the fluctuations in an interacting population. The key differences are that first, the population is now split into behavioural classes, and second, the interactive nature of the fitness function will add further non-linearities to the exploratory operator.

In following chapters, the modelling of a particular population of adaptive interactive agents via a Markov system approach will be considered in detail. Further discussion of the approach will therefore be confined to these chapters.

In Section 3.1.2, the stochasticieties in the adaptive process caused by sampling fluctuations within a finite population were alluded to. Let us therefore consider how these fluctuations might affect the behaviour of an interacting adaptive population.

3.3 Meta-stability in Finite Populations

Consider a finite population of interacting adaptive agents. Two points have already been established regarding such a population.

1. In general, the evolution of an infinite population of interacting agents can be formulated as a highly non-linear differential operator. The general form of this operator is analogous to an equation for diffusion across a potential field.
2. In the case of a finite population, the evolution of the system can be thought of as having two components.
   (a) A deterministic component,$\mathcal{E}_{\mathcal{D}}$, corresponding to a Poincarré section through the differential operator. The image of a population distribution under this operator specifies the mean of the stochastic component.
   (b) A stochastic component, $\mathcal{E}_{\mathcal{S}}$, sampled from a random variable with well defined mean. The form of this distribution is unknown, but it may well be binomial in form. The variance of this distribution is bounded from above and below, and asymptotically converges to zero with increasing population size.

   Note the following two points:

      i. The form of the noise distribution has not been specified. As discussed in Sections 2.1.7 and 2.2.2, the relative size of system parameters and the reduction of the system to a finite population can both affect the expected distribution.
      ii. Additionally, the relationship between the deterministic and stochastic components has not been specified. Whilst it might well be convenient to assume an additive noise, this may not be the case.

This combination is an alternative formulation to the following (which is a more realistic physical description of the operation of the system). The deterministic operator maps a *population* density function to a *probability* density function, which is then sampled from an appropriate number of times to give a new population. The advantage of the formulation is that it explicitly separates the system into deterministic and stochastic elements, where there is only one sample taken. Moreover, this formulation explicitly demonstrates the reduced effect of the stochastic operator as population size increases.

Consider how this combination of deterministic and stochastic operators will affect the evolution of a finite population of adaptive interacting agents which has a number of attractors in the solution space, and consider the expected behaviour of the system.

Before considering the behavioural patterns that result, one point needs to be made absolutely clear: The behaviours that are observed are dependent upon the *timescale* that they are observed over. In the case of a finite population of n agents there is a finite probability that the stochastic operator could result in a population far removed from the expected population. Whilst this probability may be very small for large populations, given a sufficient observational window, the probability of it occurring becomes significant. Indeed, given a (longer) observational period, the probability of *not* observing such an event becomes insignificant. Three behavioural phases are postulated:

Stable Dynamics Where the population is large enough, relative to the observational timescale, a stable behaviour would be expected. The system will evolve from its initial population towards the attractor whose basin it is in. The trajectory of the system will be close to that expected of an infinite population.

Meta–Stable Dynamics In a finite population, with a long enough observational window, the probability that the stochastic operator will move the population from one basin of attraction to another basin of attraction, becomes significant.

In this case one would expect to see stable periods of behaviour, separated by sudden behavioural transitions as the population moves from one basin of attraction to another. These may be observable as phase transitions in the macroscopic system variables. If the observational period is short, stable dynamics may be observed instead, if no transition occurs. On the other hand, if the observational period is long, but the observations are infrequent (i.e. not every evolutionary epoch of the system is observed), then the population may appear to demonstrate unstable dynamics. Meta-stability is a phenomenon dependent upon the observation window and schedule.

Unstable Dynamics When the population is very small, the lattice size can become significant in comparison the attractor basin size. Here the probability that the system may move from one attractor basin to another becomes overwhelming. In conjunction with this, it becomes hard to distinguish the boundaries of attractor basins; there may be few lattice points in each basin. The dynamics of the system are mainly stochastic here. It may not be appropriate to talk of the population lying within an attractor basin, as the timescales it lies in any basin may be minimal, and observationally it may become hard, if not impossible, to discern which basin the system is lying in.

3.3.1 Finite Population Dynamics under Internal and External Shocks

The finite population dynamics that have been discussed above, are driven by the *internal* dynamics of the population, under the influence of the stochastic evolutionary operator, $\mathcal{E}_S$. In many cases there is also a second force that drives the trajectory of the population: namely the environmental dynamic. It is this *external* dynamic that is under consideration here, together with the interplay between internal and external forces, and the resultant effects on the evolution of the population.

Populations of agents do not exist in isolation. They exist within a context. A network of adaptive routers exists in the context of network loadings. A market of adaptive traders exists in the context of stock returns. A population of situated adaptive robots exists in the context of a physical environment, with changing lighting, humidity, friction, and even changing environmental layout. This context is described as the environment in which agents exist. Changes in this environment will be described as external shocks, in contrast to internal shocks due to $\mathcal{E}_S$.

External shocks will directly affect the ability of agents to perform their allotted tasks, and thus directly affect the fitness of agents. In some systems the external shocks may affect all agents equally, in other systems they may affect some agents but not others. Even seemingly well adapted agents may be removed from the population if they encounter large enough environmental changes.

External shocks will clearly have no effect on the exploratory operator, $\mathcal{M}$; this operator acts only on surviving members of the population. External shocks will act only upon the exploitative operator, $\mathcal{S}$. These external shocks may have one of two effects, depending upon whether they operate upon the entire population uniformly, or whether the effect of the environment affects members of the population in a non-uniform manner.

In the first case, the effect of external shocks is to directly modulate the exploitative operator, $\mathcal{E}$. The resultant effect will be to modulate the deterministic component, $\mathcal{E}_D$, of the evolutionary operator. This will have a global effect on the evolution at all population sizes. One might characterise this as not affecting the convergence of the population towards fit phenotypes, but altering the relative fitness of phenotypes within that population. This relates directly to the discussion of evolutionary dynamics under varying selection pressure discussed in Section 2.1.4. Classical theory predicts that in the case where individual genes are selectively neutral in the long run, but varying randomly in the short term, fixation will eventually almost certainly occur. This is referred to as quasi-fixation. However, this analysis does not include any linkage between gene fitness and gene expression within the population, let alone the highly non-linear linkage postulated to exist in populations of interacting adaptive agents. It will therefore be interesting to observe whether quasi-fixation does actually occur in experimentation.

On the other hand, if the external shocks do not affect the population in a uniform manner, identical members of the population may be affected differently by the environment. This means that identical individuals may end up with widely varying fitnesses. Again, this may affect the exploitative operator S, but in a very different manner to the above case. In this case, the exploitative operator might be thought of as being 'blurred': identical phenotypes may have widely varying fitnesses. This will result in the selection operator being weakened as it becomes harder to discriminate between strong and weak phenotypes, and thus to pick the strongest genetic material for the next generation. In this case, one would expect the population to be driven more by the mutation operator than might otherwise be the case: the population will find it hard to hold fitness peaks[4] against the mutational pressure towards a maximum-entropy formulation.

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[4] Obviously, in this case, a 'fitness peak' may be a heterogeneous population.

Chapter 4

A Simple Stock Market Model

In this chapter, a simple model of a population of interacting adaptive agents is described. A mathematical treatment of this model is developed, based upon the statistical behavioural dynamics approach put forward in Section 3.1.1. Differences between the expected behaviour of the Simple Stock Market Model (SSMM) and the behaviour of the Santa Fe Artificial Stock Market (SFASM), upon which it is based, are considered.

4.1 The Simple Stock Market Model (SSMM)

In this section, a simple model of an artificial stock market is presented. At the outset, let it be clear that the purpose of this model is to explore the dynamics of a population of interacting adaptive agents. Whilst it is grounded in an economic context, it is not designed as an economic model, and the results should not be taken as indicative of any real-life economic behaviour.

4.1.1 Design Issues

This design of this model is subject to a number of constraints, which serve to ground the model in a number of areas. The purpose of this model is to explore and analyse the stability of attractors in the population space of a system of interacting adaptive agents, and phase transitions associated with shifts between attractors, due to internal and external shocks to the system. To this end, various constraints are imposed upon the model to aid this analysis. The restrictions on the model are as follows:

Analytical Tractability For the purposes of this study, an analytically tractable model is necessary. As has been discussed in Chapter 3, a number of analytic approaches are possible. However, there are no simple solutions. As has been indicated, the preferred analysis is in terms of behavioural order parameters (see Section 3.1.1). For analytical ease, a system is sought with a finite number of easily distinguishable finite agent behaviours.

A Well Understood Problem It is important that the model should implement an example of a well studied problem. This ensures that it is possible to back-check the behaviour of the model against other simulations and models within the same field. One would expect that any model should exhibit the same basic behavioural characteristics as other models within the field. A new model is implemented rather than use an existing model for the reason of analytical tractability discussed above.

Simple Dynamics The purpose of the model is to explore and analyse the stability of populations of interacting agents, and various phenomena associated with transitions between attractor basins in the population space. To that end a model with the simplest possible dynamics that may exhibit meta-stability is sought. Two constraints may immediately be stated:

Adaptive Processes In Section 1.1.1 adaptation has been described as the combination of an exploratory and an exploitative force. It is desired that these two forces be analytically separable in a mathematical treatment of the model. For this reason, the adaptive process implemented will be a genetic algorithm implementing asexual reproduction with mutation. Many selective schemata are possible, a roulette wheel selection method will be used because it is analytically tractable.

Temporal dependencies For analytical ease it is important that the model is *stationary*, i.e. that the statistics of its behaviour are independent of any time shift. Beyond this, it is desirable that the model behaviour should be restricted to a one-step temporal dependency: the behaviour of the model in the immediate future is dependent only upon its present state, and not on any previous state. This combination of properties restricts the behavioural dynamics of the system to be a *Markov* process, which is well understood.

For the above reasons the model chosen is a simple stock market, based heavily upon the Santa Fe Stock Market Model (SFASM) [5], but with a number of simplifications incorporated to aid the analytical tractability, and to simplify the dynamics of the system. The dynamics of the SFASM, and their relation to the dynamics of the SSMM will be considered in Chapter 6.

4.1.2 The Nature of the Market

The market is based around the simple neo-classical two asset model, consisting of a single bond and a single stock. The bond is a money equivalent. Holding the bond will guarantee a fixed return r at the end of each given period. The stock is a holding with a variable return: at the end of each trading period the stock will deliver a return, d_t drawn from a random variable. In this case, the random variable has a normal form, with mean r, variance σ and first order linear persistence (i.e. the returns from the stock form an AR(1) stochastic process, described in Equation 4.1. ϵ is a Gaussian random variable with mean 0 and variance σ^2, the mean value of the AR1 process, $\overline{d} = r$, and ρ is the regression parameter, which controls the speed at which the series returns towards the mean, $\overline{d}$).

$$d_t = \overline{d} + \rho(d_{t-1} - \overline{d}) + \epsilon_t \tag{4.1}$$

Each agent has a fixed capital, which can be held either in the bond, the stock, or a combination of both. The price of the bonds is fixed, and there is assumed to be no limit on the supply available to the traders. On the other hand, the stock is in limited supply (N units available), and the exchange rate between the stock and the bond will depend on the demand for the bond. This exchange rate will be referred to as the price of the stock, p_t.

In general terms, the dividend sequence forms an environment in which the system of agents is situated. The modelling of the dividend sequence as an AR(1) process is well grounded within economic literature [15]. In other systems, the environmental fluctuation may be grounded on other distributions, in particular power law distributions, as discussed in Section 2.1.7.

The market operates as follows. At the beginning of each time period the dividend from the stock and the price of the stock are posted, so that all agents can view them. Each agent then calculates their desired holding of the stock relative to the bond[1] (The detail of this is explained in Sections 4.1.3 and 4.1.4). Agents then submit the difference between their actual holding and their desired holding (i.e. a buy/sell order) to a market authority, known as the *market maker*, who fixes a price that reconciles the demand with the supply. Each agent then trades an appropriate proportion of their bid,

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[1] Economic theory gives an equation for calculating the desired holding as a function of the expected value of price plus dividend in the next time period.

effectively determined by the market maker. The agent then receives a payoff consisting of the return on each bond the agent holds plus the new dividend on each unit of stock the agent holds.

While agents have access to the present dividend and price of the stock, an external observer (e.g. the market maker) also has access to the volume of the stock traded in any particular period. The system observables (as discussed in Section 3.1.3) are the stock price and trading volume; these are macroscopic parameters dependent upon the state of the population, which give some (incomplete) information about the state of the population.

4.1.3 Market Clearing

There are many ways that a market can operate. The most common model is described as a *double auction* market; agents can submit bids (offers to buy) and asks (offers to sell). The sequences of bids and asks are monotonically increasing and decreasing respectively, and a transaction takes place when the most recent bid and ask coincide. There are various forms of double auction market in the literature (see [30] for a review), in which the detail of how the bid and ask sequence are established and related, and the amount of information available to traders, vary.

This is not the only way that a market can operate. An alternate system requires that all trading is conducted through a specialised agent called a market maker. This agent has privileged information not available to other agents, and acts to establish a price at which demand matches supply. At this point, the market is described as *cleared*; the market maker holds no stock itself. This system has been adopted for two reasons: first it simplifies the implementation of the model, and second, it is analytically tractable.

It is well known that under conditions of constant absolute risk aversion (CARA) utility (that is to say that the risk utility function takes a negative exponential form with rate λ) and Gaussian distributions for forecasts, an agent's demand x_t for the stock is of the form

$$x_t = \frac{E(p_{t+1} + d_{t+1}) - p(1+r)}{\lambda\sigma^2_{t,p+d}} \tag{4.2}$$

Here $E(p+d)$ is the return that an agent expects the stock to produce (i.e. the price plus dividend forecast for the next time period), as σ^2_{p+d} if the variance in an agent's predictions of that expectation.

The market maker can calculate the clearing price of the market at each time step. In a market with n agents, write each agent's expectation of the next price plus dividend as $E_{i,t+1}$ (the expectation), and the denominator of 4.2 as R_i. The numerator in 4.2 gives the difference between the expected total capital value of the stock plus its dividend, and the equivalent value of the bond plus their returns. The denominator then effectively gives a risk term, placing this difference in the context of a normally distributed set of agent expectations, and the agent's own risk utility[2]. The agent's risk function is assumed to be constant through time in this model.

Clearing demands that

$$\sum_{i=1}^{n} x_i = N \tag{4.3}$$

into which we can substitute 4.2:

$$\sum_{i=1}^{n} \frac{E_{i,t} - p(1+r)}{R_i} = N \tag{4.4}$$

The mean expectation of the next price plus dividend, $\overline{E_t}$ is defined by

$$\overline{E_t} = \frac{\sum_{i=1}^{n} E_{i,t}}{N} \tag{4.5}$$

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[2] As with many similar situations, this is a 2-armed bandit problem: the sources of loss being holding too much stock, and holding too much bond. Here the penalty function is symmetric, and the risk function quantifies the agents perception of the relative utilities of loss from each source.

In the markets we are considering, all agents have identical risk functions, R_i; the uniform risk function will henceforth be written as R. Moreover, the total stock available will be set at 1 unit of stock per agent within the market. This means that the dynamics of the market will be independent of the availability of stock, across a range of population sizes, i.e. $N/n = 1$. Rearranging Equation 4.5 and substituting it into 4.4 gives

$$p_t = \left(\frac{\overline{E_t}}{R} - 1\right) \frac{R}{1+r} \tag{4.6}$$

The above equation is used by the market maker to calculate the price that will clear the market, given the individual agent's expectations $E_{i,t+1}$, and their risk functions R_i. From the price it is then possible for the trading volume to be calculated using Equation 4.2 to gain the individual demands for stock from each agent. Note the assumption that at the beginning of each trading period the stock is uniformly distributed amongst the agents. The nature of the agents, and of the adaptive process (discussed in Section 4.1.4) makes it impossible to assume any continuity of agenthood. However, it ensures that the market has a uniform weighting during its evolution: the dynamics of the market cannot become biased towards a dependency on the actions of particular agents, because they control most of the stock. Whilst this gives the market a degree of unreality, the trading volume observable used proves very useful in separating different regimes existing in the market dynamics. Arthur et al. [5] relate periods of high trading volume to over- and under-pricing regimes, and periods of low trading volume to the fundamental pricing regime. The volume observable takes the form

$$v_t = \sum_{i=1}^{n} \left| \frac{N}{n} - x_{i,t} \right| \tag{4.7}$$

Now, by definition (see Equation 4.3) $\frac{N}{n}$ is the mean of the demand distribution. v_t can be rewritten as

$$v_t = \sum_{i=1}^{n} \sqrt{\left(\frac{N}{n} - x_{i,t}\right)^2} \tag{4.8}$$

This is bounded from below by the standard deviation of the demand for stock

$$\sigma^2(x) = \sqrt{\sum_{i=1}^{n} \left(\frac{N}{n} - x_{i,t}\right)^2} \tag{4.9}$$

Thus, one might expect to observe the trading volume in the market being correlated with the standard deviation of the demand for stock.

It is also interesting to consider the *residual*, the difference between the expected return predicted by a rational agent, and the return that agents actually receive. The magnitude of the residual has been used by Arthur et al. [5] to gives an indication of how much the market is deviating from a rational expectations regime. When the market deviates from a rational expectations regime, it is being driven by the collective will of the traders towards a position which is theoretically untenable. The *homogeneous rational endogenous expectations*, or h.r.e.e. price is the price that one would expect to be paid for the stock by a market of identical rational traders. This may be easily calculated.

In such a regime, all traders are identical, and their rationality implies that they will all have the same demand for stock. Therefore the stock will be split equally between all agents. The expectation can be easily calculated from Equation 4.2, and is given by

$$E_{hree} = p(1 + r) + R \tag{4.10}$$

The residual is simply the difference between this estimate and the actual return $p + d$.

4.1.4 The Nature of the Traders

The system consists of a number of identical agents; each trader is a simple rule based agent, which can respond to aspects of its environment to produce an action. Here the environment that the agents are responding to is the collective behaviour of the market, and the response is a prediction of the next expected return from the stock, $E_{i,t}$. This in turn motivates each agents demand for stock, which is met by the market maker imposing a clearing condition as described in the previous section (Section 4.1.3).

Each trader has a set of sensors, represented by a Boolean string. These sensors indicate whether certain conditions have been fulfilled. In this simplified case we restrict the sensors to giving information about the present state of the market (i.e. no historical information, or averaging information). This greatly restricts the dynamics, and (in a stable population) will prevent technical or noise trading from taking place[5]. In this model a set of four sensor bits are used, each of which has the form

$$S_j = \begin{cases} 0 & \text{if } \frac{p_t r}{d_t} \leq L_j \\ 1 & \text{otherwise} \end{cases} \tag{4.11}$$

for levels L_j associated with each of the n traders. Each sensor is switched on ($S_j = 1$) only when the price-earnings ratio of the stock, expressed relative to that of the bond, exceeds a certain value. The implementational detail of the model is discussed in Section 5.2.1.

Each trader then has a set of k rules which act on the sensors. Each rule acts as a predictive mechanism for a trader; upon certain environmental conditions being met (the market being in a particular state), the rule will make a prediction about the future state of the market, which is then used in calculating an agent's demand for the stock. Each rule takes the form of a trinary string, composed from the alphabet $\{0, 1, \#\}$. The symbol # is a wild card, interpreted as 'don't care'. A rule is activated if it corresponds to the sensor string, so a rule '10##' would be activated by sensor strings '1010' and '1011' but not by '0011'.

Each rule also has an extra pair of bits (the response bits), which determine the response of the agent when the rule is activated. This response takes the form of a prediction of the return that the agent expects from the stock in the next trading period. The two response bits mediate the values of the relative and absolute change in the expected price plus dividend, i.e.

$$E(p_{t+1} + d_{t+1}) = c_0(p_t + d_t) + c_1 \tag{4.12}$$

The two response bits modify the relative and absolute predictor parameters, c_0 and c_1, respectively, according to the mapping shown in Table 4.1.

Bit Value	c_0	c_1
0	$1 - C_0$	$-C_1$
#	1	0
1	$1 + C_0$	C_1

Table 4.1: Mapping from response bit values to predictor parameter values. For example, a response bit pair 01 would give rise to a prediction $E(p_{t+1} + d_{t+1}) = (1 - C_0)(p_t + d_t) + C_1$, as per Equation 4.12.

In the case where no rule is triggered, i.e. the sensor string does not match the sensory bits of any rule that a given trader possesses, that a trader will predict an unchanged return at the next time step, $E(p_{t+1} + d_{t+1}) = p_t + d_t$.

In the simulations presented a minimal rule set is implemented; each trader consists of precisely $k = 1$ rule. Furthermore, in this market, a condition of heterogeneity is placed upon the traders; each trader has identical parameters L_j and C_i. This implies that in every trader c_i can take one of three values; there are a total of nine possible predictions (which will be described as behaviours) available to traders in the market.

The parameters c_0, c_1 are dependent upon the rules activated, which in turn are dependent upon the current state of the market. In this way the agents interact, because their present behaviour is always dependent upon the prior collective behaviour of the entire population, as well as external environmental shocks.

Each agent can therefore be represented as a trinary bit string, consisting of a list of the rules that it contains. Suppose this list has l bits. As all the traders are identical in design, they are interchangeable. Describe the state of the system ϕ as a 3^l dimensional normal vector. Each element in the vector is the proportion of the population that has a particular set of rules. Such a formalisation rapidly becomes unwieldy as l increases. In Section 4.3 a low dimension approximation to this formalisation will be described.

4.1.5 Comparison with the Implementation of Santa Fe Artificial Stock Market

The Santa Fe Artificial Stock Market (SFASM) has already been introduced in Section 1.3.1, as an example of meta-stable behaviour. The Simple Stock Market Model (SSMM) developed in this chapter is derived from the SFASM. Here, the quantitive and qualitive differences between these two models will be discussed.

In most respects the SFASM and the SSMM are identical, certainly they both rely on identical market clearing and pricing mechanisms. The differences lie in the construction of the agents and the evolutionary algorithm: the SFASM agents are far more complex, and the evolution is carried out in a slightly different fashion.

SFASM agents are classifier systems, as described by Holland [42]. Each agent has a set of rules, similar to those of the SSMM. Each trinary rule has a sensory string, similar to that of the SSMM. A rule is implemented if the sensory string matches current conditions, exactly as described in Section 4.1.4. However, the set of sensors used by agents in the SFASM is more extensive than those in the SSMM, agents are able to detect short term trends in the price of the stock (e.g. rising or falling price). This enables technical trading to take place, where agents use the short-term market history to predict the next return from the stock.

The responses that are possible from the rules are also more sophisticated than those in the SSMM. Each rule has response parameters that enable a prediction of the next return to be made, based on absolute and relative return changes, exactly as per the SSMM. However, the simple restriction of these parameters to nine possible values does not occur; in the SFASM these parameters are reals lying within a given range. Each rule within a SFASM agent is therefore a more sophisticated version of the rules implemented in the SSMM.

The SFASM agents act as classifiers: each rule has an associated strength or fitness parameter. Each agent forms an expectation of the next return from the stock by taking a weighted average of the expectation of all rules that are activated by the current market conditions. The weights used are the fitnesses of the activated rules; rules with better predictive histories will have higher fitness. The expected next return of each agent is then passed to the marketmaker, exactly as per the SSMM. However, a single difference arises here: in the SSMM all agents are constrained to an identical risk function. This is not the case in the SFASM; each agent also passes a risk parameter to the marketmaker. This parameter is based on the variance of the set of predictions that its rules have made at that time step.

After the market maker has imposed clearing,the dividend is revealed, as per the SSMM. The fitnesses of the individual rules is now updated, based on a least-squares error function. At regular intervals agents update their rule set by applying a genetic algorithm, using a fitness based selection to remove the weakest members of the rule set, and replace them with the offspring of stronger rules via a combination of crossover and mutation.

The evolutionary algorithm is different in several respects:

1. In the SFASM, evolution takes place at a much slower rate than in the SSMM. In the SSMM the population is updated after every time-step, whereas in the SFASM the evolutionary algorithm is only applied every 250 or 1000 time steps, and asynchronously across agents.
2. In the SFASM it is not possible for agents to learn by copying the successful strategies of other agents. The rule-set in each agent is an isolated population; mixing between agents never takes place. Whilst agents can develop identical strategies, they must do so in isolation. In the SSMM, the copying of successful strategies between agents constitutes a major part of the evolutionary algorithm.
3. The SFASM implements a sexual reproductive algorithm, using the crossover operator, whereas the SSMM only uses an asexual reproductive operator. However, mutation is implemented in both models.

To conclude, the SFASM is a much more complex model. The implementation of the agents allows a much wider and more sophisticated range of agent responses to prevailing market conditions. The evolutionary algorithm is also quite different, and much more sophisticated. It does, however, appear odd that no facility to allow mixing between the rule-sets evolved in separate agents. This means that agents cannot choose to copy the behaviours of other agents, all behaviours must be evolved separately in independent agents.

The purpose of the models is however quite different. The SFASM was designed as an economic testbed, whereas the SSMM was designed to address issues of meta-stability. However, the grounding of the SSMM on the SFASM should lead to behavioural similarities between the two models. These will be discussed in Section 6.3.2.

4.2 Dynamics of the SSMM: General Issues

There are, however, a number of features of the expected behaviour of the SSMM that may be discussed before a detailed model of the behavioural dynamics of the market is built. The discussion of these more general features will inform the more detailed analysis presented in Section 4.3.

4.2.1 Fixed Points and Attractor Basins

Consider an evolutionary operator on the population consisting of fitness proportional selection plus mutation. In this case fitness will be assessed as the accuracy of an agent's prediction of the next price, using a mean-squared error measure (discussed further in Section 4.3.2). The fitness of an individual agent will then be some function of the composition of the entire population. How this might be formalised is discussed in detail in Section 4.3.

It is possible to write down the fitness of any particular agent at time t as a function of the vector ϕ, i.e. as a function of the composition of the entire market[3]. This would enable one to write down a matrix operator for the evolution of the market, and solve for the eigenvectors, i.e. the fixed points of the market[4].

This system is a Markov system, albeit a very complex one. The sensor string contains no historical information, so it does not appear possible for any technical trading based on trend analysis to take place. Arthur et al. [5] note that under this condition, the SFASM remains in a fundamental (h.r.e.e) trading regime. An initial expectation might therefore be that similar conditions would hold in the SSMM, the system is expected to remain in a fundamental trading regime, where the price of the

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[3] Although in practice this would be a complex and time consuming operation.

[4] In this case the state of the system can be written as a finite dimensional vector. In the infinite case one could write down a differential equation.

stock reflects its true or fundamental value.

If the time evolution of the system is followed, under any sequence of stock dividends, one might expect that the market would converge towards the h.r.e.e. price, the price that classical economic theory predicts that the market should adopt. Even if this is the case, and for example, the system exhibits rational (h.r.e.e) behaviour between periods of over or under-pricing, one should be wary of positing a single underlying causality to this behaviour. It is quite feasible that a single observed behaviour (such as an h.r.e.e regime) might result from more than one attractor in the space of population distributions, in a similar fashion to the multiple nucleus-shield combinations which Lomborg [56] observed in the iterated prisoners dilemma game[5].

This does not imply that there is necessarily a single attractor within the space of population distributions. There may be multiple stable population distributions, each of which gives rise to a fundamental trading regime. Meta-stability may still be present, in the form of transitions between these population distributions, caused by stochasticities inherent within the adaptive process.

Suppose there are a number of possible attractors, $\phi_1, \ldots \phi_m$, each of which is a population distribution across the N possible trading agents; each attractor will correspond to a particular distribution of the infinite population of traders between the possible rules[6]. Given a particular initial population distribution $\phi(0)$, and a given sequence of dividends D, the system will evolve towards one of the attracting states. Assume

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[5] See Section 1.3.2.

[6] There may appear to be a discrepancy here because it has previously been stated that there are a limited number of units of the stock available. As long as the ratio of stock units to trader numbers remains finite in the infinite limit, then the description of the system remains valid. If the market has a large enough population of traders compared to the mutation rate of traders, then it should behave as an infinite system would, i.e. sampling fluctuations in mutation and selection should have no effect on the evolution of the population.

that, as per a Hopfield net, that there is a time t_α corresponding to the maximal time for the system to reach a state from which its limit attractor is independent of the sequence D, i.e. the time after which the system will be so deeply within the basin of some attractor that escape is impossible, whatever the sequence of dividends from that time onwards. To affirm the existence of such a time t_α is merely to say that selection pressure is sufficiently strong that the system will enter an attractor basin, and once it is close enough to the attractor, it will be unable to escape, because it is close enough to an h.r.e.e. state, and will (in the limit) converge to the attractor.

One must be clear as to what it means for the system to be at, or close to an attracting point. One would not expect the agents to be identical, a stable market may consist of agents predicting in differing ways, and who (by the nature of their rule sets) are prepared to accept differing amounts of risk. Neither would one expect each agent to converge to a fixed holding in the stock, dependent upon the risk they are prepared to accept. Rather, one would expect trading to occur, albeit at low volumes, as traders update their optimal holdings of the stock under the influence of the run of dividends. Effectively, the stochastic sequence of dividends provides noise in the optimal holding algorithm for each agent, which is then reflected in low volumes of trading as agents update their positions.

4.2.2 Observable Dynamics with a Non-Evolving Population

Consider a population of n agents selected at random. In the absence of any initial bias towards any particular area of the genome space, the population will be uniformly distributed across the genome space. Given such a population, how will the price and trading volume of stock vary under the dividend series?

For the purpose of the analysis, place a partial ordering on the levels at which the various bits in the sensor string are triggered, i.e. $L_1 \leq L_2 \leq L_3 \leq L_4$[7]. The population can now be divided into three segments.

1. There will be a subset of the population, X whose rule is never activated. In order to be activated a rule must match the sensor string. Any rule which has, as part of the match string, one or more 0's followed by one or more 1's will never be activated, since under partial ordering of the sensor bit trigger levels, such a sensor string will never occur. This portion of the population can be estimated using standard probability theory; in the general case for a string of l sensor bits

   $$p(x \in X) = \sum_{i=1}^{l-1} p(\forall j < i : S_j \neq 0).p(S_i = 0).p(k > i : \exists k.S_k = 1) \qquad (4.13)$$

   Assuming that there is no differential expression of alleles across sites, i.e. $\forall i, j p(S_i = k) = p(S_j = k)$, this can be rewritten as

   $$p(x \in X) = \sum_{i=1}^{l-2} p(S_i \neq 0)^i.p(S_i = 0).\sum_{j=0}^{l-2-i} p(S_j \neq 0)^j.p(S_j = 1) \qquad (4.14)$$

   In the present case, where all alleles are equiprobable at every site, and where $l = 4$, $p(x \in X) = 11/27$.

   This proportion of the population will never match the sensor string, and will thus always return $E(p_{t+1} + d_{t+1}) = p_t + d_t$

2. There will be a second subset of the population, Y whose rules can be activated, but which does not respond to the particular sensor string presented. It is a simple task to estimate the subset of the population which will respond to a sensor string with k bits set.

   $$p(k) = p(S_i \neq 0)^k.p(S_i \neq 1)^{l-k} \qquad (4.15)$$

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[7] This ordering makes no difference to the result gained, but eases the effort needed to develop the analysis.

Under the current assumptions, the size of the subset of the population which is triggered is independent of the number of bits in the sensor string that is activated. One cannot easily estimate the probability that a trader is in Y, because not all traders have equal generality, e.g. 0000 will only respond to one signal, whereas #### will respond to any signal. We shall estimate Y as the subset of the population not in any other subset.

3. Finally there is a segment of the population, Z which is triggered by the sensor string that is presented. Equation 4.15 gives the probability of this happening given a sensor with the first k bits set. Note that the probability of a trader being activated is independent of the sensor string presented to the population.

$$p(x \in Z) = (\frac{2}{3})^l \tag{4.16}$$

With $l = 4$, $p(x \in Z) = 16/81$. This leads to an estimate of $p(x \in Y) = 32/81$ in the present case.

Note that the majority of the population will not have a rule activated at any particular time, the probability that a member of the population will not have a rule activated is $1 - (\frac{2}{3})^l$, which is a monotonically increasing function of l, so the larger l becomes, the smaller the proportion of active rules within the population.

Amongst the subset of rules that have been activated, one may easily show that there is a uniform distribution of expectations $E(p_{t+1} + d_{t+1})$ across the 9 different possible response strings. From this, one can calculate the moments of the distribution of responses to any price and dividend combination in the subset of the population whose rules are active, by consideration of all the possible cases, and making a maximal entropy assumption of a uniform distribution between possible responses.

$$\overline{E}_{x \in Z}(p_{t+1} + d_{t+1}) \quad = \quad \overline{c_0}(p_t + d_t) + \overline{c_1} \tag{4.17}$$

$$\sigma^2_{E_{x\in Z}} = \left(\frac{2}{3}\right)^l \frac{1}{n}\sum_{i=0}^{n}(c_0(p_t+d_t)+c_1-E(p_t+d_t))^2 \tag{4.18}$$

The design of the traders has already been discussed in Section 4.1.4. By definition, $\overline{c_0} = 1$ and $\overline{c_1} = 0$. This leads to the following expression for the expected next return:

$$\overline{E}(p_{t+1}+d_{t+1}) = p_t + d_t \tag{4.19}$$

To gain an expression for σ^2_E, recall that the active rules fall into 9 (equiprobable in the infinite limit) categories. By considering all the possibilities and simplifying, the following expression is gained.

$$\sigma^2_E = (\frac{2}{3})^{l+1}(C^2_0(p_t+d_t)+C^1_1) \tag{4.20}$$

This is an interesting result, because it deals with the expected behaviour of a large population of randomly selected agents. Whilst the agents' expectations of the return from the stock will vary, some predicting a higher return, and some predicting a lower return, the mean expectation (given in Equation 4.19) will be of an unchanged next return. This can be substituted back into Equation 4.6. In the absence of an evolutionary algorithm, the population distribution will remain unchanged. Here the price of the stock will fluctuate about a constant level, mediated by fluctuations in the dividend sequence. The long-term average of the actual return and the expected return will converge, because the dividend sequence has a well defined mean. Hence (following Arthur et al. [5]), the agents expectations are rational, and on average will be upheld by the market. The resulting price sequence will therefore be in rational expectations equilibrium: the resulting price is the h.r.e.e price.

The particular interest in this result is that it also corresponds to what one would expect from an efficient market where all available information about future returns is immediately incorporated into the price of the stock; the best prediction of tomorrow's price is today's price. Here a similar phenomenon is noted, not because the agents are capable of making good predictions which will be reflected in the price, but because of their absolute lack of predictive ability. This is because the lack of adaptation means that agents are unable to copy successful strategies.

Note also that the volume observable will be bounded from below by σ_E^2. In this case, a higher volume than the h.r.e.e. volume should be observed, because the population is not homogeneous, but has a distribution across expectations.

4.2.3 Existence of Multiple Fixed Points in the Population Space

In the above section, the collective dynamics of a non-evolving population have been explored. Here the population dynamics of the system under an evolutionary pressure will be considered, according to the simple asexual schema presented in Section 1.2.3.

Whilst one might expect to find one or more fixed points in the population space corresponding to the fundamental regime in the observers, no proof to this effect will be presented, although it is a reasonable suggestion. If the combination of mutation rate, selection pressure and dividend persistence is appropriately balanced, then the mean reverting behaviour will be sustained, and the (large) portion of the population that (for whatever reason) predicts that the return will remain constant will have high fitness.

In the following argument, one particular possible scenario is used as an example. This does not affect the generality of the argument; substitution of appropriate terms in other examples will lead to identical results. This particular example is chosen because it is easily comprehensible.

Consider a homogeneous population, whose response bits are all set, so that the population only responds if all sensory bits are set, i.e. $p_t > L_3$. Consider also that the price is such that the traders' rules will be activated. The argument will be developed as follows. First it will be shown that in the absence of mutation there may exist stable prices. From here it will be shown that a heterogeneous population may be stable under both selection and mutation.

Lemma 4.2.1 *For a homogeneous population of agents, there exist expected price levels corresponding to each possible set of rule bits, provided that the sensory bits of the population are appropriate to the expected price level.*

Proof.

The proof proceeds by solution for expected price levels. The appropriate sensory bit sets for a particular level will then be stated.

Consider a homogeneous population whose sensory bits are such that the rule fires. The expected next price plus dividend will be today's price plus dividend when

$$E(p_{t+1} + d_{t+1}) = c_0(p_t + d_t) + c_1 \tag{4.21}$$

Where c_0, c_1 represent the appropriate adjustment constants for the relative and absolute price change under the sensory bits of whatever the population's response bits are. Now, all agents will respond identically. Recall Equation 4.6

$$p_{t+1} = p_t = \left(\frac{\overline{E(p_{t+1} + d_{t+1}}}{R} - 1 \right) \frac{R}{1+r} \tag{4.22}$$

Where the homogeneous risk term is R. Substituting 4.21 into 4.22

$$p_{t+1} = \left(\frac{c_0(p_t + d_t) + c_1}{R} - 1 \right) \frac{R}{1+r} \tag{4.23}$$

At equilibrium, $p_{t+1} = p_t$; there is no temporal ambiguity, write the expected dividend as $\overline{d}$, and the expected equilibrium price at this dividend level as $\overline{p}$

$$\overline{p} = \frac{c_0\overline{p} + c_0\overline{d} + c_1 - R}{1+r} \tag{4.24}$$

Rearranging this equation gives a solution of $\overline{p}$

$$\overline{p} = \frac{c_0\overline{d} + c_1 - R}{1 + r - c_0} \tag{4.25}$$

Now this price is the expected price of the stock in a market of homogeneous agents whose sensors are active. This demonstrates the behaviour of the population in the fundamental regime; if the expectation is that the return will remain constant, the price will be dependent upon the dividend sequence.

The mean stock price levels, $\overline{p_{00}}, \ldots, \overline{p_{\#\#}}, \ldots, \overline{p_{11}}$ for homogeneous populations with appropriate sensor bits, and the relevant response bits may now be established. For each of the possible price equilibria,$\overline{p_{00}}, \ldots, \overline{p_{\#\#}}, \ldots, \overline{p_{11}}$, it is a simple matter to work out the set of possible sensor bits within the genotype which will activate the rule, and therefore the possible genotypes within a converged population.

Corollary 4.2.2 *There exist fitness neutral areas within the genotype space.*

Proof.

This follows from the fact that any 1 or 0 may be replaced by a # within the sensor bits, without altering the activation of a rule, if the dividend remains within a limited range[8]. Hence some of the fixed points in the population space do not correspond to unique sensor bit strings, but rather to connected[9] regions of the genotype space.

4.3 Formalisation of the Artificial Stock Market

Here a formalisation of the expected dynamics of the simple stock market model that has been put forwards in Section 4.1 is presented. The fundamental properties of the

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[8] i.e. small enough that the sensor string presented to the agents does not vary over time.

[9] Under 1-site mutation.

behaviour of the market, and of market observables (price, p_t, and trading volume, v_t) are considered from a statistical dynamics perspective in a large (i.e. effectively infinite) population, implementing the behavioural dynamics approach detailed in Section 3.1.1. From there, an argument is developed as to the expected finite population dynamics of the population, and of the observables of that population.

The population can be completely characterised by a $3^6 = 729$ dimensional vector of the frequencies of each possible genotype. However, as this is unwieldy to work with, a behavioural formalisation will be adopted, as put forward in Section 3.1.1. The formalisation described here could be generalisable to a more complex system. In this case, there are 9 possible behaviours that an agent can adopt. However, the system will be characterised by a 10, rather than 9 dimensional vector, in order to ease the formalisation of the mutation operator. The entries in the vector give the frequencies of each of the response classes within the population. Alternatively, the entries in the vector may be thought of as the probabilities of a trader lying in each of the response classes. Split the response of no price change into two, the first entry reflects the probability of a trader having a sensory string that does not match (describe this state as *unresponsive*), and the second being the probability that an agent has a sensory string that matches, and then predicts an unchanged next return. This formalisation is adopted to ease analytic tractability, otherwise it becomes difficult to estimate the transition probabilities in the mutation operator.

4.3.1 The Mutation Operator, $\mathcal{M}$

Assume that within each response there is a uniform probability of any genotype being found. Define the operator μ as the probability of a trader remaining in a responsive[10]

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[10] i.e. in any of the states apart from unresponsive.

return state, and the operator ν as the probability of moving from an unresponsive return state to a responsive state, under the action of the mutational operator. The underlying assumption used here is the 'mixing assumption' of Prügel-Bennett and Shapiro [70], which is discussed in Section 2.2.2. Under certain conditions, especially where the population size is small and the selection pressure is high, this assumption may be unwarranted; the population within any behavioural class may be clustered around some particular genotype. This point has already been raised in Section 3.1.2.

There are four possible transitions that maintain correctness: $0 \rightarrow \{0, \#\}$, $1 \rightarrow \{1, \#\}, \# \rightarrow \{\#, 1\}, \# \rightarrow \{\#, 0\}$. Given a # it is unknown *a priori* which of the two possible responsiveness maintaining mutational transitions is appropriate, but it does not affect the formulation, as all correctness maintaining mutations have the same probability, 2/3, of maintaining correctness. Hence a simple binomial gives the probability of responsiveness being maintained.

$$\mu = \sum_{i=0}^{i=l} (1-m)^{l-i} \left(\frac{2m}{3}\right)^{i} \binom{l}{i} \tag{4.26}$$

where l is the number of bits in the response string. The derivation of ν is a little more involved. In a similar manner to μ, each transition that transforms an incorrect allele to a correct one for the system to respond, has a probability of 2/3 of occurring during a mutation. For a mutation to turn an unresponsive genome to a responsive genome, two things must happen:

1. All incorrect alleles must be transformed to correct alleles.

2. All correct alleles must remain correct.

Given that there is at least one incorrect allele, the probability of i correct alleles is matrix operator

$$\mathcal{M} = \begin{bmatrix} 1-\nu & \nu/9 & \dots & & & & & & & \\ \beta & \mu\alpha_0 & \mu\alpha_1 & \mu\alpha_1 & \mu\alpha_1 & \mu\alpha_2 & \mu\alpha_2 & \mu\alpha_1 & \mu\alpha_2 & \mu\alpha_2 \\ \vdots & \mu\alpha_1 & \ddots & \mu\alpha_1 & \mu\alpha_2 & \ddots & \ddots & \ddots & \ddots & \ddots \\ & \mu\alpha_1 & \mu\alpha_1 & & \mu\alpha_2 & \mu\alpha_2 & & & & \\ & \mu\alpha_1 & \mu\alpha_2 & \mu\alpha_2 & & \mu\alpha_1 & \mu\alpha_1 & & & \\ & \mu\alpha_2 & \ddots & \mu\alpha_2 & \mu\alpha_1 & & \mu\alpha_1 & \mu\alpha_2 & & \\ & \mu\alpha_2 & \ddots & & \mu\alpha_1 & \mu\alpha_1 & & \mu\alpha_2 & \mu\alpha_2 & \\ & \mu\alpha_1 & \ddots & & & \mu\alpha_2 & \mu\alpha_2 & & \mu\alpha_1 & \mu\alpha_1 \\ & \mu\alpha_2 & \ddots & & & & \mu\alpha_2 & \mu\alpha_1 & & \mu\alpha_1 \\ & \mu\alpha_2 & \ddots & & & & & \mu\alpha_1 & \mu\alpha_1 & \end{bmatrix} \tag{4.32}$$

4.3.2 The Selection operator, $\mathcal{S}$

The fitness of an agent in with response i is given by

$$f(i) = \mid E_i(p_{t+1} + d_{t+1}) - (p_{t+1} + d_{t+1}) \mid \tag{4.33}$$

where a lower value of $f(i)$ indicates higher fitness.

Whilst the dividend at the next time step, d_{t+1} comes from a stochastic process, the price at the next time step, p_{t+1} does not; it is due to the interaction of the agents, in the form of their demand for the stock. This in turn is dependent upon the composition of the population, and their predictions of the next return. Recall the pricing equation, 4.6:

$$p_t = \left(\frac{\overline{E_t}}{R} - 1 \right) \frac{R}{1+r} \tag{4.34}$$

The expected return $\overline{E_{t+1}}$ may be written in terms of the composition of predictions in the population

$$\overline{E_{t+1}} = \sum_{i=1}^{N} E_{i,t+1}$$

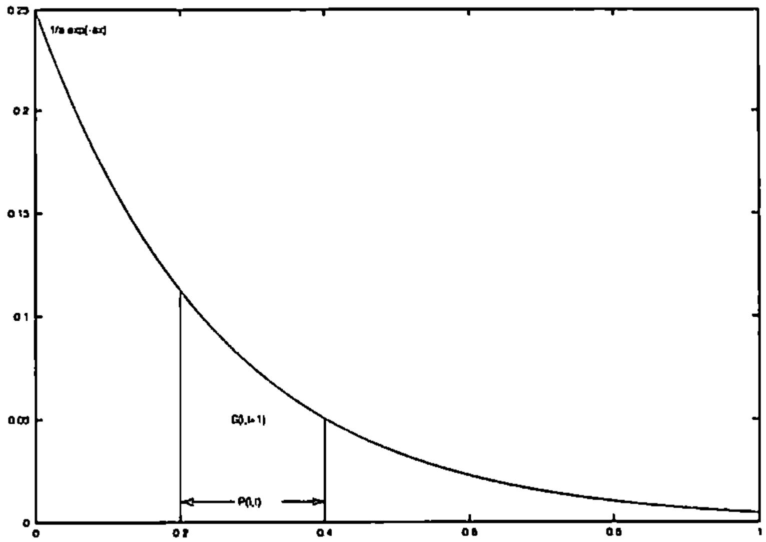

Figure 4.1: Roulette wheel selection scheme. The classes are ordered by descending fitness, and placed on the x-axis. The probability of selection of a given class is given by the corresponding portion of the area under a negative exponential function with selection gradient a. These areas must then be normalised to sum to 1.

$$\begin{aligned} &= \sum_{i=1}^{N} c_{0,i}(p_t + d_t) + c_{1,i} \\ &= \overline{c_0}(p_t + d_t) + \overline{c_1} \qquad (4.35) \end{aligned}$$

Substituting this term in 4.34 gives

$$p_t = \left(\frac{\overline{c_0}(p_{t-1} + d_{t-1}) + \overline{c_1}}{R} - 1 \right) \frac{R}{1+r} \qquad (4.36)$$

which explicitly shows the dependence of the next price upon the constants $c_{0,i}$ and $c_{1,i}$ as well as the distribution of the population between the response classes i.

The selection method used is a variant on the Boltzmann selection method, as used by Prügel-Bennett & Shapiro [69]. In the Boltzmann selection method, an exponential weighting is given to agent fitnesses; this exponential weighting gives the relative area of partitions in a roulette wheel which is used to select agents.

Here a variant on the Boltzmann selection scheme is used. Rather than directly use exponentially weighted agent fitnesses to construct a roulette wheel, the ordering of agent fitnesses is used to construct a roulette wheel. This might be described as Boltzmann selection on rank. The procedure is implemented as follows.

The population distribution P_t may be considered as a vector of the 10 response classes, with components $P_{t,i}$, where the response classes are in an order i, the ordering described in Section 4.3.1. Given that an agent may only respond in a limited number of ways (the 10 possible response classes), Equation 4.33 can be used to give the fitness of the response classes at any point in time. Because the fitness of each class is known, an ordering i^* can be constructed, arranging the response classes from lowest fitness (most fit) to highest fitness (least fit).

Figure 4.1 shows the nature of a roulette wheel selection scheme. The ordering of the classes by fitness determines the order in which they are assigned divisions in the roulette wheel, and the width of the roulette wheel division is determined by the position in the ordering and the frequency of that class within the present population. This is expressed mathematically in the following equation:

$$S_{t,i^*} = \frac{\lambda}{1 - e^{-\lambda}} \int_{\sum_{j=1}^{i^*} S_{t,j}}^{P_{t-1,i^*} + \sum_{j=1}^{i^*} S_{t,j}} e^{-\lambda x} \, dx \tag{4.37}$$

Here the integral term gives the relative size of division i^* of the roulette wheel, and the initial term before the integral is a scaling term to ensure that the divisions in the wheel sum to 1 (see Figure 4.1). If two or more fitness classes share the same fitness, the selection probability of these classes is determined by allocating them a single division in the roulette wheel, with a width determined by their joint probability, and then splitting this division according to their relative sizes.

Whilst this selection method is undoubtedly more complex to implement than the Boltzmann selection method, it has a single advantage: The Boltzmann selection method is directly dependent upon agent fitness; changing the fitness of an agent (or, as would be the case here, all agents in a particular response class) will change the fitness of every agent. This is not the case here, the selection operator is insensitive to small variations in the fitnesses of response classes, due, for example, to small changes in the dividend paid by the stock. What is of importance here, is the ordering of the fitness classes, from lowest to highest fitness. Given the values that c_0 and c_1 take, it is possible to enumerate all the possible orderings i^*, under various conditions of price and changing return.

4.3.3 The Evolutionary Operator

Finally, one can combine the effects of the mutation and selection operator. At a fixed point

$$P = \mathcal{MS}(P) \tag{4.38}$$

This equation is beyond reasonable analytic tractability. However, by making assumptions about the range in which $\overline{p}$ lies, one can fix the ordering i^* of the equivalence classes for fitness (given a matrix C of values $c_{i,j}$ which determines the response of each class). As stated above in Section 4.3.2, it is possible to calculate the ordering of the response classes for any price and next return.

Of particular interest are solutions which give stable price levels, i.e. population distributions for which the expected price lies within the range for which the ordering of the response classes is valid. This is because the SFASM [5] shows sustained over- and under-pricing regimes alongside a fundamental regime. Whilst one might expect to locate a fixed point in behaviour-space corresponding to a fundamental regime, the behaviour of the SFASM gives rise to the possibility that other fixed points in the behaviour space, corresponding to over and under-pricing regimes may in fact exist.

In practical terms, the procedure is to assume that the next return will be identical to the present return. This is an assumption that the effect of the dividend sequence is negligible[11]. Under this assumption, it is possible to calculate all the possible orderings of the response classes, and the price ranges across which they are valid. If a numerical solution for a fixed point in behaviour space can be found, its corresponding expected price can be calculated. This can then be checked to see if it lies within the price range for which that fitness ordering is valid.

At a fixed point in the behaviour, the population distribution P is fixed, hence the expected return will be fixed also. The ordering of the response classes i^*, may be written down: the fittest response classes will be those that predict no change; the other response classes will be arranged in equal fitness pairs, predicting equal but opposite price movements. The ordering of these pairs will, however, be dependent upon the expected price level of the fixed point. The selection pressure, λ, the mutation rate m, and the parameters of the agent coding (C_0, C_1, R) and of the market (r) are all fixed. Hence one can reduce Equation 4.38 down to ten simultaneous equations in ten unknowns, which we may be able to solve numerically using specialist software.

If the dividend is clamped at its mean value, then the numerical solution will give the stock price and trading volume at that dividend mean. This may then be compared to the trajectory of the system through the price–volume space.

4.4 Finite Population Dynamics

The system dynamics in the effectively infinite limit has been considered above. The population, whilst not infinite, is large enough that sampling fluctuations can be ignored. One can consider that under any given time series of dividends, the population

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[11] Occasionally, the dividend sequence may be capable of changing the fitness ordering i^* of the response classes, and triggering meta-stability.

will be undergoing deterministic transitions between consecutive states. It would indeed even be possible to rearrange the system in a continuous time form: the difference vector operator governing the evolution of the system would become a differential matrix operator. The difference system that is under consideration at present would be a Poincarré section of the differential form.

The move from an infinite to a finite population may have many effects. In Section 2.2.2 it was noted [69, 70] that a finite population can induce changes in higher order cumulants of order parameter distributions. This can alter the fixed points of the system (consider, for instance, Equation 2.37). Small finite populations can make sampling fluctuations important in determining the fixation of alleles within the population.

In a Markov system such as the SSMM, where the trajectory of the system is described by an operator with a one-step temporal dependence, acting on the population distribution, the differences between the finite and infinite population versions of the system are twofold. First, a stochastic element is introduced into the evolution of the system, and second, the system is constrained to a subset of all the possible states available to an infinite population. In this particular case, the formalisation of the system has no dependence upon population size; here the finite population case will be modeled as an infinite population with an additive noise term.

The stochasticity enters the system because for a finite system, especially a finite system with a small number of elements, the fundamental axiom of probability no longer applies. This means that it is no longer possible to derive (using the evolutionary operator) an expected population distribution for time $t+1$ given the population at time t, and assume that the population will take on this distribution. Rather, the expected population distribution at time $t+1$ must be treated as a probability distribution: in order to gain the population at time $t+1$ this distribution must be sampled from. The population distribution of the sample thus obtained becomes the population distribution for time $t+1$.

The main effect of this is the reduction of the stability of the system. To recap Section 3.3: Whilst the attractors of the system still are attracting, and the infinite limit dynamics are unchanged, there is now a finite probability that from any given point in the system, the next point obtained (via the evolutionary operator acting on the present population of traders, followed by the sampling process described above being applied) will not lie in the same attractor basin. In other words, one can nolonger talk of stability, only meta-stability. It is now only a question of time until the population shifts between attractor basins. We would thus expect to see the population of traders undergo catastrophic shifts between particular population profiles. Of course, one would not expect the population to retain any particular profile even during the meta-stable epochs, rather to retain a profile close to (and within the attractor basin of) the particular attractor.

This reduction in the stability of the system is augmented by positive feedback effects that are possible, due to the interactive nature of the population. Each trader determines their optimal holding based on a combination of private factors (such as the willingness to take risks) and a number of publicly available indicators (the last dividend posted and the current stock price). In turn, the stock price is governed by the supply and demand for the stock. Changes in the stock price can alter the response of traders, because the conditions that trigger their rules may alter. This in turn affects the demand for stock by agents, which influences the price. The positive feedback here may in some circumstances trigger avalanches of market and evolutionary activity.

If the population of traders is restricted to some finite number, S say, then each element of ϕ is restricted to a value $i/S, i \in \{0, \ldots, S\}$, and still subject to the normality condition. The sampling process described above will guarantee that the population will always lie on the lattice. However, there is no such restriction on any of the attracting fixed points within the system. It may not be possible for the population to ever gain the attractor, because the attractor does not lie on the lattice.

To conclude, the finite population dynamics of the simple neo-classical market described above are expected to show meta-stable periods where the population lies close to[12] one of the infinite limit attractor profiles. These meta-stable periods will be separated by catastrophic changes, where the population rapidly shifts between meta-stable profiles. Note that in the system described above, one would expect all the attractors to produce similar market behaviour; a tracking of the fundamental value of the stock by the market. In the finite case there may be fluctuations of the price around the fundamental value associated with the failure of the system to actually reach, and stay at the attractor. There may also be transient fluctuations in stock price and trading volume associated with the catastrophic transitions between meta-stable epochs.

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[12] Under some convenient metric.

Chapter 5

Simulation Results

5.1 Introduction

In the previous chapter, a simple model of an artificial stock market has been put forward. The model is a simplified version of the Santa Fe Artificial Stock Market, which has been cut down to try to aid analytic tractability. This has involved retaining only those agent sensors that track the present price of the stock, removing any historical dependencies from the model. The adaptive process within the agents has also been altered, individual trading strategies now compete with each other across the entire population. The replacement strategy has also been altered to asexual cloning plus mutation. This (in the limit of an infinite population) is equivalent to a diffusion process across a potential field. In the previous chapter, an analysis of this simplified stock market model has been put forward and statistical dynamics approximations based upon behavioural order parameters have been used reduce the dynamics of the system to a tractable number of dimensions.

In this chapter, the results of a computational implementation of this model will be presented, in order to allow an evaluation of the analytic approach put forward. This chapter is organised as follows. First there is a qualitative discussion of the behaviours observed in the model. Next there is an examination of the dynamics of the model; comparisons are made between the observed dynamics of the model, and the dynamics predicted under the analytic formalisation given in Chapter 4. In this discussion the effects of population size upon the dynamics of the model are discussed.

5.2 Overview of the Qualitative Features of the Simple Stock Market Model

Recall the basic premise of this study, put forward in Chapter 1: various studies of systems involving the interaction of adaptive agents appear to show sudden transitions between behavioural regimes. These transitions appear to be the result of sampling fluctuations in a finite population under an adaptive pressure. The stochasticies implicit in the exploratory element of adaptation are compounded by the positive feedbacks implicit in the exploitative element; these two combine to magnify the instability of the system, so that sampling fluctuations remain significant in quite large populations. In a stock market model, such as the SFASM [5], three basic behavioural regimes are observed: a fundamental regime where the price of the stock agrees with that predicted by classical economic theory; an over-pricing regime; and an under-pricing regime. The transitions between these regimes appear to be sudden, and without obvious cause. It is posited that the transitions between these basic regimes are caused by sampling fluctuations within a finite population, compounded by external shocks to the system in the form of an AR(1) process dividend sequence. A simple model of an artificial stock market has been constructed to try to further examine and understand these phenomena.

5.2.1 Implementation Details

The market consists of a population of N adaptive agents trading against each other. At time t they produce demands for stock at time $t+1$, given knowledge of the current market conditions, expressed in terms of four binary sensors (see Section 4.1.4 for details). The activation levels of these sensors $S_1, \ldots, S_4$ are set at $0.5, 0.7, 0.9$ and 1.1 respectively, unless stated otherwise. All agents have a uniform risk aversion R set at $R = 1.3$, unless stated otherwise. The agents' predictions are based upon the two response bits of their genome, response parameters to bits $0, \#, 1$ are set at $c_0 = 0.9, 1.0, 1.1$ and $c_1 = -0.5, 0, 0.5$ respectively. The dividend d_t is based upon an AR(1) process, with mean $\overline{d} = 10$, and autoregressive constant $\rho = 0.95$, the driving random variable being Gaussian, i.i.d. (all samples taken from independent identically distributed random variables) with zero mean and variance $\sigma^2 = 0.074$. The bond has a price of 1.0 and pays an interest of 0.1. The selection process operates every $t_s = 1$ time period, replacing the entire population with a new population drawn from a random sample of the old population under a roulette wheel selection scheme, where individuals within the population are ranked by mean squared prediction error, and assigned selection probabilities according to a negative exponential distribution, with selection constant $\lambda = -0.01$. The new population is then subjected to mutation, with an independent mutational probability at every site in each member of the population, $m = 0.03$.

Simulations were conducted at a variety of population sizes, with 10, 20, 50, 100, 200, 500 and 1000 agents in the market. At all population sizes a total of 20 replications of each simulation were performed.

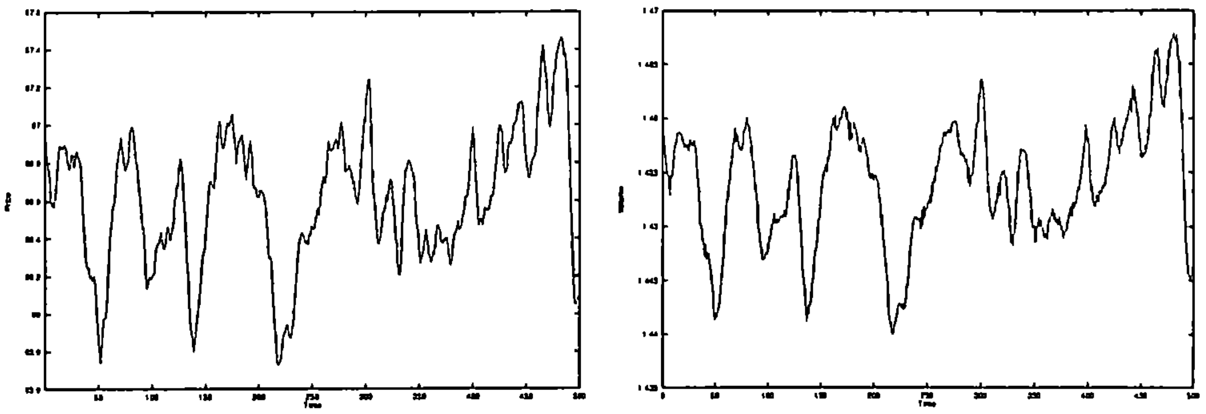
The results shown in this section are selected to give the reader a feel for the behavioural dynamics of the system, and to point out in a qualitative fashion the salient features which will be analysed in a quantitative fashion in later sections. Unless specifically stated otherwise, the results shown are typical of the dynamics of a population of the described size.

5.2.2 Market Dynamics in Small and Large Populations

Consider first Figure 5.1. This shows the dynamics of a population without a driving adaptive force. In this, and all other references to a non-adaptive population, the population size is 1000 agents; a larger population should have a behaviour closer to the infinite limit dynamics (especially in the non-adaptive case). In all other cases the population is adaptive. Because the population remains constant, the dynamics here are driven only by changes in the dividend series. The distribution of the threshold levels on the sensors is sufficiently wide that changes in the dividend series do not cause the active sub-population of adaptive agents to vary.

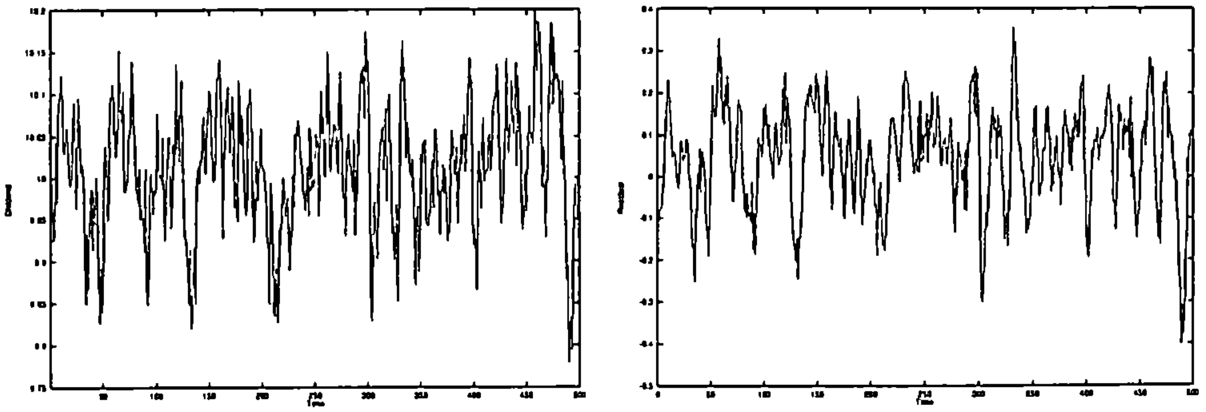
Now consider the behaviours of adaptive populations across a range of population sizes. Whilst simulations have been carried out at a number of differing population sizes, here time series are shown for large ($N = 1000$), medium ($N = 100$) and small $N = 10$ populations, in order to illustrate the behaviour of the SSMM across a range of magnitudes of populations. Figures 5.2, 5.3, 5.4 and 5.5 show these times series.

First consider system behaviour for a large population (Figure 5.2). As population size increases, the behaviour of the system approaches the expected behaviour in the infinite limit. As the population size increases the dynamics of the price-time series more closely match the dynamics of the dividend time series. Within an infinite population, one would expect the price of the stock to reflect the dividend at any point in time, and thus the price series to follow the dividend series (Section 4.3.3). This is not completely the case here, although major shocks in the dividend series are reflected in the price



Price

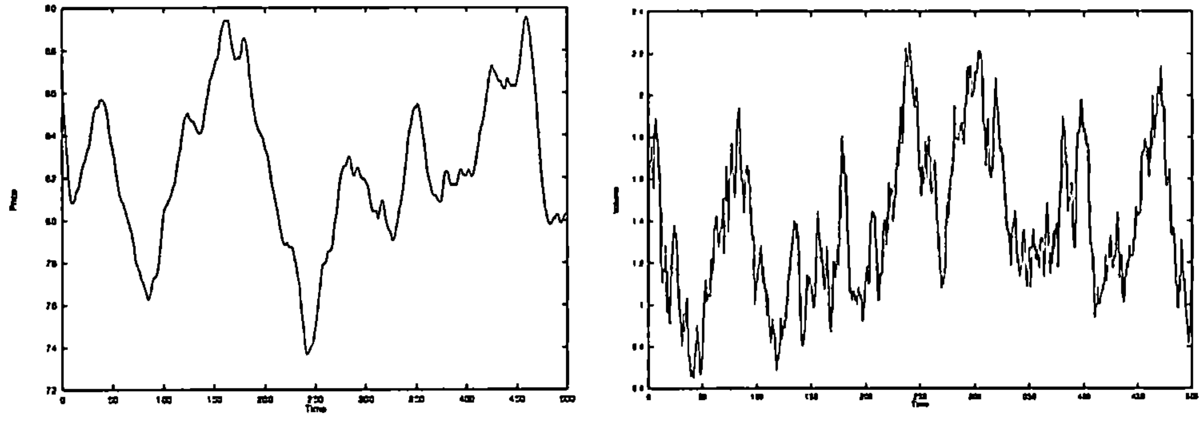
Volume



Dividend

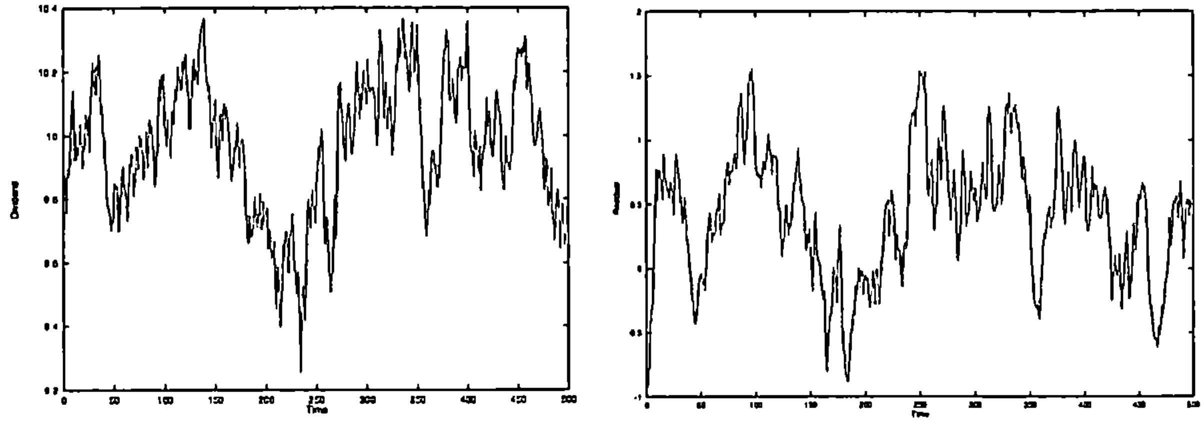
Residual

Figure 5.1: Time Series for the SSMM, with a population of 1000 agents. There is no adaptive pressure in this case, the population remains unchanged throughout the run. The four series shown are all taken from a single run of the model. Clockwise from Top Left, they show Stock Price, Trading Volume, Residual and Stock Dividend.



Price

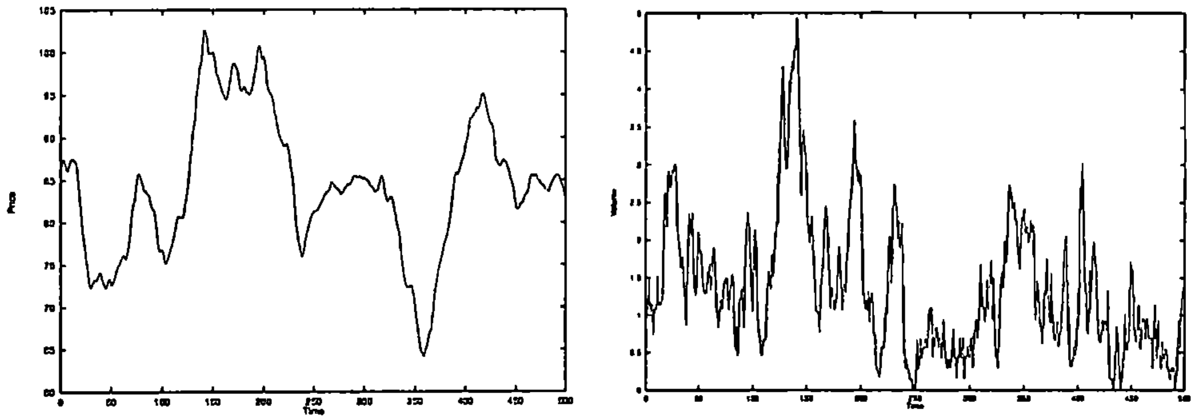
Volume



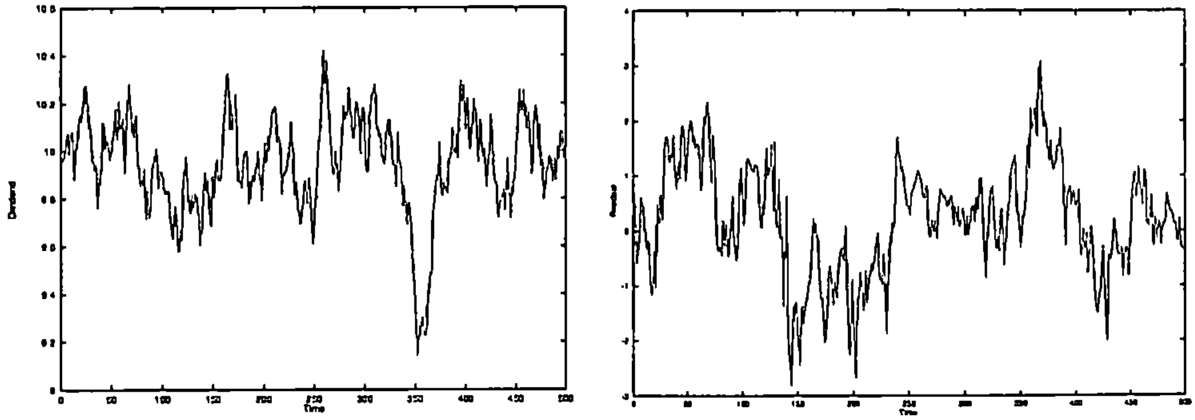
Dividend

Residual

Figure 5.2: Time Series for the SSMM, with an adaptive population of 1000 agents.

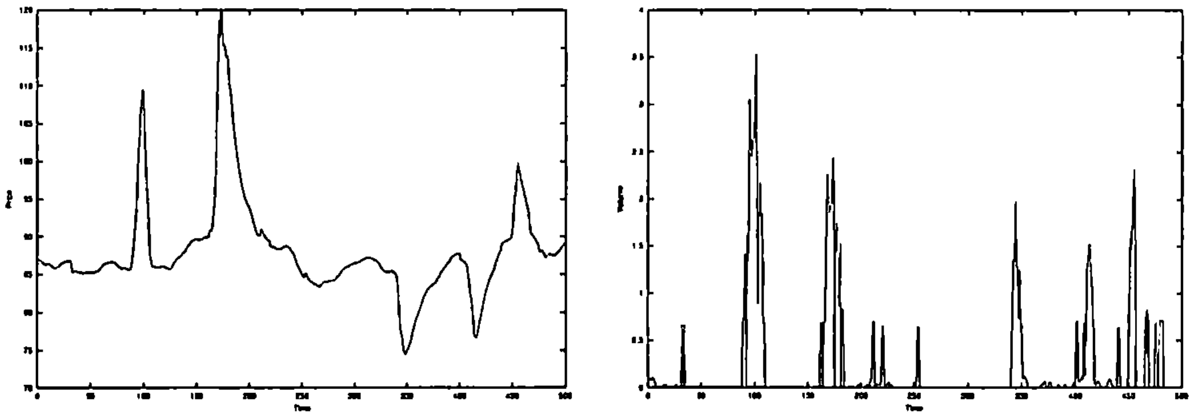


Price Volume



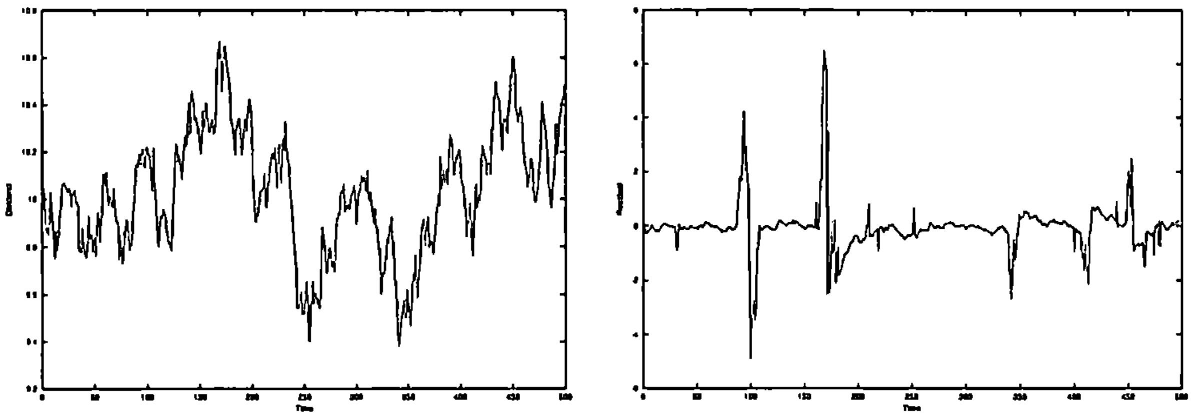
Dividend Residual

Figure 5.3: Time Series for the SSMM, with an adaptive population of 100 agents.



Price

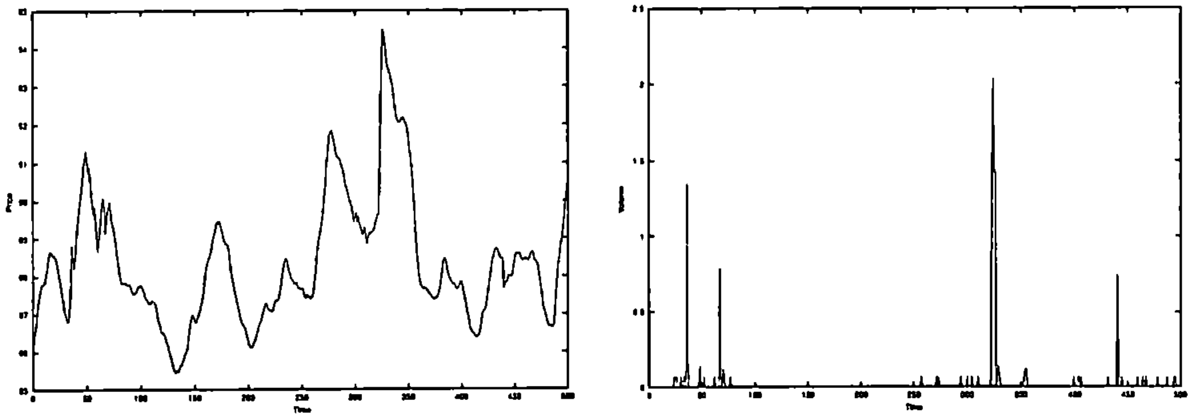
Volume



Dividend

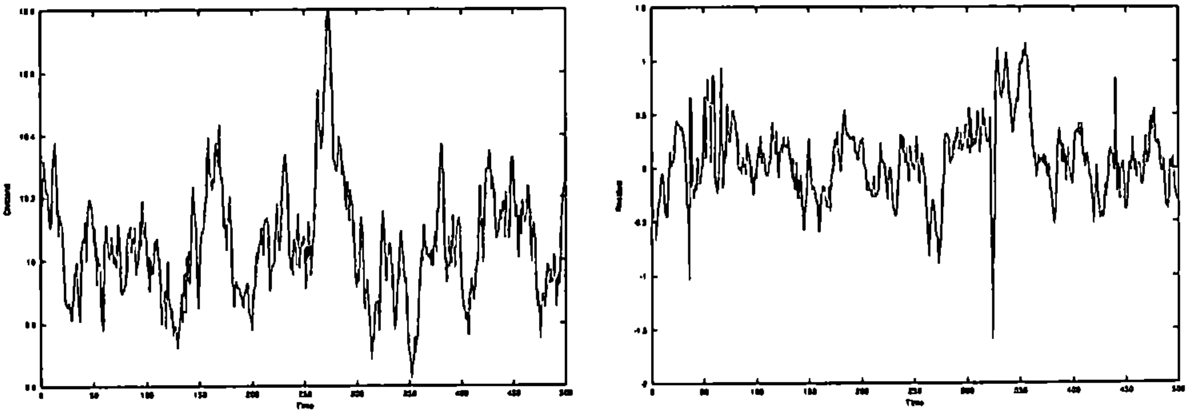
Residual

Figure 5.4: Time Series for the SSMM, with an adaptive population of 10 agents. Here repeated bubble and crash events, in both upward and downward directions can be seen. These bubble and crash events are taken as separate regimes from the fundamental regime, and their existence provides evidence of meta-stable behaviour.



Price

Volume



Dividend

Residual

Figure 5.5: Time series for the SSMM, with an adaptive population of 10 agents. In contrast to Figure 5.4, no bubble and crash events are observed here. The stock price approximates the dividend sequence, albeit with more noise than is observed in a larger population, such as in Figures 5.2 and 5.3.

series.

In the case of a small population, a very different picture (Figures 5.4 and 5.5) is seen. Here the population has been reduced to 10 individuals. In Figure 5.5 the price sequence follows the dividend sequence in an approximate manner. Sampling fluctuations in the population distribution obscure the dependency of the price sequence on the dividend sequence. In contrast, in Figure 5.4 bubble and crash events are seen, where the price sequence accelerates away from the fundamental regime, either in an upwards (over-pricing) or downwards (under-pricing) direction. This is followed by a crash where the price of the stock suddenly reverts back to the fundamental regime. The cause of such events will be studied further in Section 5.3.4. These events have been observed in a number of runs of the SSMM at small population sizes. Whilst they are most clearly visible and occur most often in the smallest population size (4 occurrences in 20 runs at population size 10), they have also been seen at population sizes 20 (2/20 runs) and 50 (1/20 runs).

These are interesting phenomena because there is no historical information included within the sensory information available to agents. Arthur et al. [5] claim that in the absence of such historical information, technical trading phenomena such as over- and under-pricing regimes are not possible. These claims will be evaluated in Section 6.3.2, in the light of the results presented here.

The interpretation that will be placed upon these phenomena is that they are driven by stochastic fluctuations within the population. Such a fluctuation can move the system out of a fundamental regime into an over- or under-pricing regime. This mispricing regime will persist until either a second fluctuation shifts the population into another regime, or the price of the stock reaches a level at which demand is limited by the agent's risk function. At this point any agents predicting an unchanged price will suddenly be favoured, and the demand will slacken, precipitating a price crash. This phenomenon can be seen in the price boom centred around $t \simeq 170$. Note also the apparent linkage between price and volume. Informally, the volume appears low when the price is at a median level; increases in trading volume correspond to price trends away from this level. These linkages will be interpreted in terms of fundamental, over- and under-pricing regimes in a following section (5.3.3).

Within a medium sized population (Figure 5.3), a combination of both effects are seen. The price sequence follows the dividend sequence for much of the experimental run, but there are periods when this dividend following behaviour is not seen. For instance, in the period $t = 100 \ldots 230$ an over-pricing regime is observed. This appears to be an example of the meta-stable phenomenon that is postulated.

A comparison between the market's behaviour with large and small population reveals several major differences. First, the range of variation of the time series appears to be inversely correlated with population size: the price range and volume range is much greater in a small population (Figure 5.10) than in a large population (Figure 5.2). Second, the small population appears to exhibit far greater behavioural changes than the large population: i.e. the rate of change of all the time series is greater in the small population than the large population. Again, these issues will be explored in greater depth in a later section.

5.3 The Market as a Dynamical System

In a previous section (4.3), a statistical dynamics formulation of the dynamics of the SSMM has been put forwards, and the component parts of the evolutionary process implemented (asexual reproduction with mutation) have been examined. This formulation enables the market to be considered as a dynamical system in a 10 dimensional space of population distributions; the components in each dimension representing the proportion of the population exhibiting each of the 10 (mutually exclusive, and therefore orthogonal) possible behaviours. This presents the possibility of using numerical methods to solve for the simple fixed points of the system.

$$P^* - \mathcal{MS}(P^*) = 0 \tag{5.1}$$

Before attempting such a solution, the statistical dynamics formulation was validated, using information theoretic methods.

5.3.1 Cross-Entropy validation

It is important to confirm the accuracy of any proposed formalisation before a computationally intensive numerical solution is proposed. In this case, a simple method is available. The cross-entropy (sometimes known as the I-divergence or Kullback-Lieber distortion) provides an error measure[1] for estimates of probability distributions. It is given by

$$D_{CE} = \int_{-\infty}^{\infty} p(x) \ln \frac{p(x)}{q(x)} dx \tag{5.2}$$

where p is the true probability distribution, and q is the estimated probability distribution. In the discrete case, over N partitions, this reduces to

$$D_{CE} = \sum_{i=1}^{i=N} p_i(x) \ln \frac{p_i(x)}{q_i(x)} \tag{5.3}$$

The cross-entropy is positive definite if $p \neq q$, and zero if and only if $p \equiv q$.

---

[1] As the cross-entropy is not symmetric it cannot be a metric.

In pure information-theoretic terms, the cross-entropy can be interpreted as the additional information rate needed to transmit a signal whose symbols have probability distribution p, if only an estimate q of their distribution is available.

Given a sequence of behavioural class population distributions from the simulations, the theoretical formalisation of the system can be validated by comparing the formalisation's prediction for the population distribution at the next time step, with the actual population distribution, using the cross-entropy measure. The hypothesis underlying this thesis is that sampling fluctuations in finite populations modulate the dynamics of populations of interacting adaptive agents: as the population size increases, one would expect the mean cross-entropy to tend to zero, because the sampling fluctuations will decrease, becoming zero at the infinite population limit.

The existence of this convergence can be used to validate the mathematical and computational formalisation of the system. If the mean cross-entropy does not converge to zero as population size increases, then there is a divergence between the model behaviour and the prediction of that behaviour. This indicates either a problem with the mathematical formalisation of the system, or in the computational implementation of that formalisation to be used in finding a numerical solution.

Here the distribution of the population between the response classes in the prediction is used as p and the actual distribution is used as q in the equation for the discrete case (Equation 5.3). The mean cross entropy based on every step (500 steps implies 499 predictions) of a single run has been used to produce the results shown in Figure 5.6. By contrast, in Figure 5.7, the results are taken across a set of 5 runs at each population size.

It should be noted that the convergence of the model's behaviour and the analytic formalisation is no guarantee of the accuracy of the analytic formalisation: it is possible

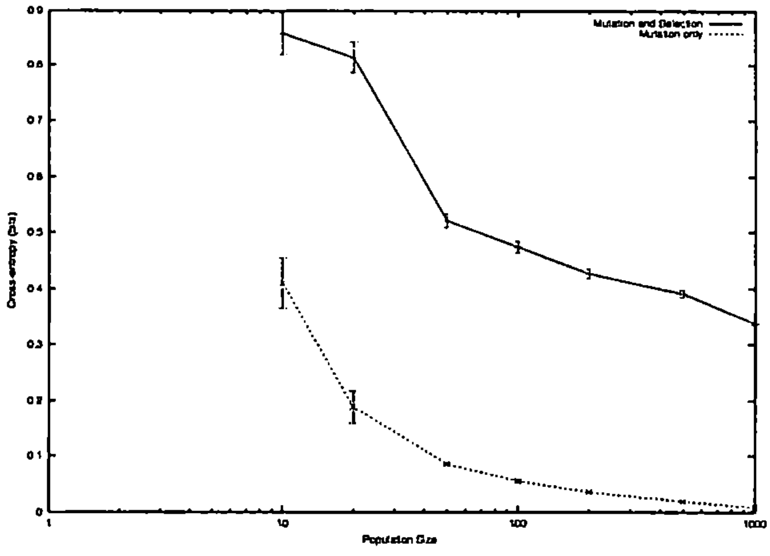


Figure 5.6: Cross-entropy vs. Population size in a previous (incorrect) formalisation of the SSMM. Two data-sets are shown, for the mutation operator alone, and for selection plus mutation. The non-convergence of the latter indicates that the selection operator is incorrectly formulated.

that the formalisation is incorrect, but fails to make predictions which are contradicted by the model.

Figure 5.6 shows the cross-entropy convergence in a previous (incorrect) formalisation of the SSMM. Clearly, under mutation and selection the cross-entropy does not converge to zero as population size increases. Further checking, by examining the cross-entropy of the mutation operator alone, reveals that the mutation operator converges to zero with increasing population size, and therefore is most likely correct. The assumption was made that the error lay in the selection operator, either in the formalisation, or in the coding of the formalisation for use in a numerical solution. Further detailed checking revealed an error in the coding.

Figure 5.7 shows the cross-entropy convergence of the coded formalisation used in finding numerical solutions to Equation 5.3. The convergence to zero indicates that the formalisation and coding is probably correct.

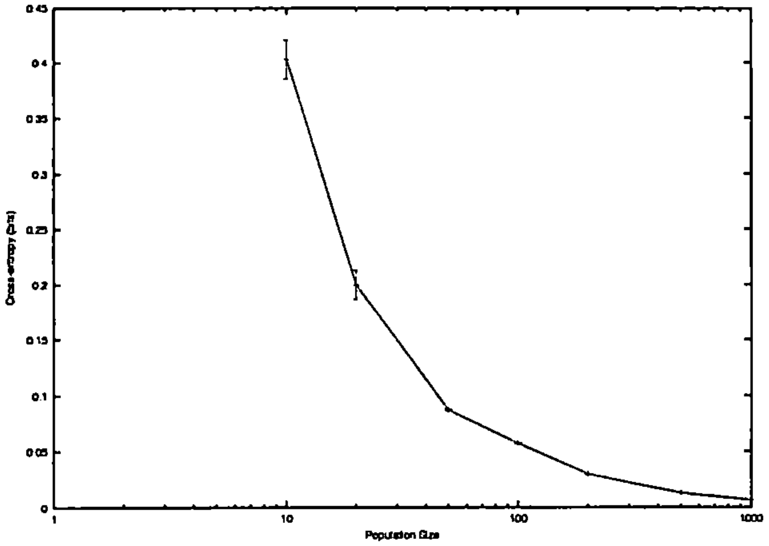


Figure 5.7: Cross-entropy vs. Population size in the thermodynamic formalisation of the SSMM.

5.3.2 Fixed points of the Thermodynamic Formalisation of the SSMM

Using a multidimensional simplex method within the GNU Octave computational package, numerical solutions to Equation 5.3 were found. Despite many attempts from various starting points within the population distribution space, only a single fixed point could be found. This point, $P^{\mathcal{MS}}$ corresponds to the fundamental value of the stock. In order to better understand the nature of this fixed point, an examination of the fixed points of operators $\mathcal{M}$ and $\mathcal{S}$ may be helpful.

Fixed points of $\mathcal{M}$

$\mathcal{M}$ is a simple matrix operator, which transforms one probability distribution into another probability distribution. There is no temporal or historical dependencies in $\mathcal{M}$, thus the system $P_{t+1} = \mathcal{M}P_t$ forms a Markov system within any sensory regime, and can be solved by standard methods. There is only one fixed point for this system,

$P^{\mathcal{M}}$, which is approached asymptotically.

Fixed points of $\mathcal{S}$

The operator $\mathcal{S}$ at first glance appears to be much more complex in nature than $\mathcal{M}$. It has a highly non-linear dependency upon the probability distribution that it acts upon. In this case, however, the initial appearance is deceiving: $\mathcal{S}$ has easily found fixed points. In Section 4.3.2 it is shown that there is a *stable price* for any population; the price at which the demand will match the supply, and the price will remain constant. A fixed point of $\mathcal{S}$ necessarily corresponds to a stable price level. At this stable price level, a partial ordering will exist on the behavioural classes; as one might intuitively expect, the two behavioural classes *UR* and ##, which predict an unchanged price plus dividend, will have the highest fitness: The system will converge to some combination of these two classes.

Under a pure selective force, this system is in essence very similar to a Polya Urn[2] scheme [26], although it differs in that the population is fixed. Intuitively, this is likely to lead to the extinction of one of the two high fitness classes, due to stochastic fluctuations within a small population. However, this effect is likely to become less important as the population size grows.

There are thus an infinite number of fixed points to $\mathcal{S}$; any point which lies on the line $P_{UR} + P_{\#\#} = 1$ is a fixed point.

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[2] In a Polya Urn scheme, an urn filled with red and black balls has balls repeatedly drawn out, and replaced with two balls of the same colour. It can be shown that the ratio of red/black balls always converges, but that the convergence ratio follows a β–distribution.

Behaviour	$P^{\mathcal{S}}$	$P^{\mathcal{M}}$	$P^{\mathcal{MS}}$
UR	0.91940	0.835031	0.855626
00	0.00000	0.018330	0.015868
0#	0.00000	0.018330	0.018659
01	0.00000	0.018330	0.015884
#0	0.00000	0.018330	0.015488
##	0.08060	0.018330	0.016903
#1	0.00000	0.018330	0.015214
10	0.00000	0.018330	0.015085
1#	0.00000	0.018330	0.016281
11	0.00000	0.018330	0.014993

Table 5.1: Fixed points of the thermodynamic approximation of the SSMM, under selection ($P^{\mathcal{S}}$), mutation ($P^{\mathcal{M}}$), and selection followed by mutation ($P^{\mathcal{MS}}$). Note that the fixed point of the selection operator is the closest point of approach of the solution line of $\mathcal{S}$ to $P^{\mathcal{MS}}$ under a Euclidean metric.

Fixed points of $\mathcal{MS}$

Table 5.1 shows the closest fixed point (under a Euclidean Metric) of the set of fixed points of $\mathcal{S}$ to the fixed point of $\mathcal{MS}$ found using a simplex method, as detailed above. Inspection of the solutions in Table 5.1 suggests the possibility that the fixed point of $\mathcal{MS}$ might be a linear combination of the fixed point of S given above and the single fixed point of M, that is to say that it might lie on the normal connecting the line describing the set of fixed points of $\mathcal{S}$ to the fixed point of $\mathcal{M}$. A simple search locates the closest point on the normal to $P^{\mathcal{MS}}$, and indeed this point is close (distance 0.013771 under a Euclidean metric) to $P^{\mathcal{MS}}$.

From this, and the fact that the simplex process used to find $P^{\mathcal{MS}}$ terminates due to limitations of machine arithmetic[3], one might assume that the difference is due to the termination of the simplex process.

In fact, this turns out not to be the case: a simplex method, starting from the closest point on the normal from $\mathcal{S}$ to $P^{\mathcal{M}}$ also converges towards solution $P^{\mathcal{MS}}$. Hence the fixed point does not lie on the normal between the fixed point of the mutation operator, and the fixed point of the selection operator. This may be due to the extreme non-linearity of the selection operator.

Given the population distribution $P^{\mathcal{MS}}$, the stock price and volume traded at this fixed point may now be calculated. Substitution into Equation 4.6 gives the equilibrium price, and hence through Equations 4.2 and 4.7 for volume may now be made. Tables 5.2, 5.3 and 5.4 show the basic statistics of the price and volume distributions observed across five repetitions of the market simulation at each adaptive population

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[3] The simplex method used in involves the calculation of a normal to a high dimensional plane. When the points that define the plane become very close (as the simplex converges), limitations in the accuracy of the machine arithmetic become significant.

Pop. Size	Mean	Std. Dev.
10	93.205	22.009
20	83.760	7.053
50	87.414	12.961
100	85.604	6.677
200	83.104	4.834
500	84.071	4.303
1000	83.013	3.151
unadaptive	86.609	0.035
analytic	86.600	

Table 5.2: Statistics of the stock price distribution.

size (a total of 2500 samples), in a non-adaptive population of 1000 individuals, and the values at the fixed point P^*.

It might initially appear that given the above tables of statistics (Tables 5.2, 5.3 and 5.4), a t-test could be applied to check the hypothesis (H_0) that a population shares the same underlying observables (price, volume, residual) as the analytic population. However, such a test is only valid for a set of independently drawn samples. This is not the case presented here; the observables at adjacent time steps are not independent of each other, the dependencies are examined in the previous chapter. The t-test statistic is given by

$$t = \frac{\overline{x} - \mu}{\hat{\sigma}/\sqrt{n}} \tag{5.4}$$

where $\mu, \hat{\sigma}$ are respectively the mean and standard distribution of the parent distribution, $\overline{x}$ is the mean of the sample and n is the sample size.

Due to the dependence between samples taken, it is problematic to estimate t. All

Pop. Size	Mean	Std. Dev.
10	0.958	2.233
20	0.860	1.134
50	1.603	1.139
100	1.714	0.890
200	1.118	0.619
500	1.177	0.324
1000	1.295	0.275
unadaptive	1.451	0.065
analytic	1.301	

Table 5.3: Statistics of the trading volume distribution.

Pop. Size	Mean	Std. Dev.
10	-0.667	3.198
20	0.380	1.222
50	-0.095	1.530
100	0.156	0.913
200	0.443	0.722
500	0.279	0.568
1000	0.431	0.371
unadaptive	0.049	0.121
analytic	0[4]	

Table 5.4: Statistics of the residual distribution.

the above statistics are based on 5 runs of the simulation under each condition, with a run length of 500. Therefore, one can certainly place bounds of $5 < n < 2500$. This is of limited value, effectively constraining t to a range of 2 orders of magnitude. At the lower limit ($n = 5$), the null hypothesis (the simulation observable is drawn from the same distribution as a population with the analytic value) is confirmed in every case. At the upper limit, the alternative hypothesis (the simulation observable is drawn from a different population) is confirmed in every case except that of a non-evolving population.

Note however, that across all runs under all conditions, an identical sampling schedule is followed, namely to sample at each time step. Clearly there is a correlation between the statistics at adjacent time steps, but an assumption of consistent bias is made: it is assumed that the identical sampling schedule on each run implies that all runs are equally biased. Therefore, the approach taken will be to consider the trend of the t-scores across population size under an adaptive condition. The hypothesis of this thesis is that sampling fluctuations cause meta-stability, and thus transitions between the fundamental regime, and various meta-stable regimes (describable as over- and under-pricing regimes). In the system examined here, these meta-stable regimes can be shown to lie in pairs equally spaced above and below the fundamental regime. One might therefore expect that over a statistically significant time period, the statistics of the observables might tend towards those of the fundamental regime as population size increases, because the stochastic fluctuations become smaller as population size increases. Therefore, the t-scores will be examined for evidence of a downward trend which might indicate that the statistics of the observables are converging towards those of the fundamental regime as population size increases. This is shown in Figure 5.8. It would be difficult to claim any clear trends in the t-scores across population size; if anything, a claim of an upward trend in the t-scores in the price and residual observables might be more defensible.

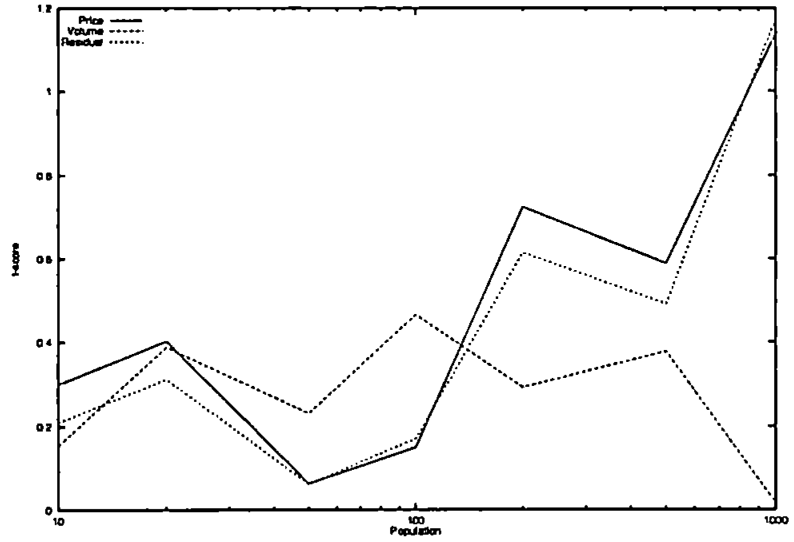

Figure 5.8: Normalised t-scores of the observable series across the range of population sizes for the price, volume and residual series. Here the t-scores have been normalised for a sample size of 1, at any estimated independent sample size, they will be a constant multiple of the value shown.

What interpretation should be placed upon theses statistics? There is no clear evidence to support the hypothesis that the statistics of any adaptive population studied are consistent with those of an infinite population at the analytic fixed point $\mathcal{P}^*$ condition (which corresponds to the fundamental regime). The evidence is equivocal, but if anything tends to support the alternate hypothesis.

This conclusion leads to an interesting disparity: in Section 5.3.1 it was shown that as population size increases the one-step analytic prediction of the next population distribution converges towards the simulation value. Yet in this section, evidence has been presented that the system does not converge to the one analytic point that has been found using numerical methods. It is certainly possible that other attractors in the system exist apart from a fundamental regime attractor. The system may be converged about some other attractor, which most likely has a more complex structure than a simple fixed point. This point will be discussed further in the next chapter (Section 6.1.2).

5.3.3 Phase Portraits of the SSMM

In Section 4.3, the correspondence between population distributions at the fixed points, and the stock price and trading volume has been explored. Following from this, an examination of the system's trajectories in price-volume space are presented in Figure 5.9.

Inspection of the phase portraits in Figure 5.9 quite clearly shows that as the population size increases, the volume of the phase space swept out by the trajectory is reduced. This is because the fluctuations in the population caused by the stochasticities inherent in the adaptive process become smaller as the population size increases. Because the underlying fitness landscape is itself a function of the population distribution, smaller variations in the population distribution are unlikely to move the population out of the fundamental basin of attraction and into one of the other basins, corresponding to a meta-stable regime.

Note also the 'V' shape to the phase portraits, especially with intermediate population sizes ($n = 20 \ldots n = 200$). The lowest point in the 'V' corresponds to the theoretical fixed point. Physically, this corresponds to low volume trading around the fundamental value (the fixed point) with higher volume trading being associated with movements away from that fixed point.

The 'V' shape in the phase portraits is explained by the formalisation presented in Section 4.3. A fixed point in the population distribution space necessarily corresponds to a fixed point in the stock price: the population will be converged onto some combination of the unresponsive class and the unchanged return predicting class, with all other

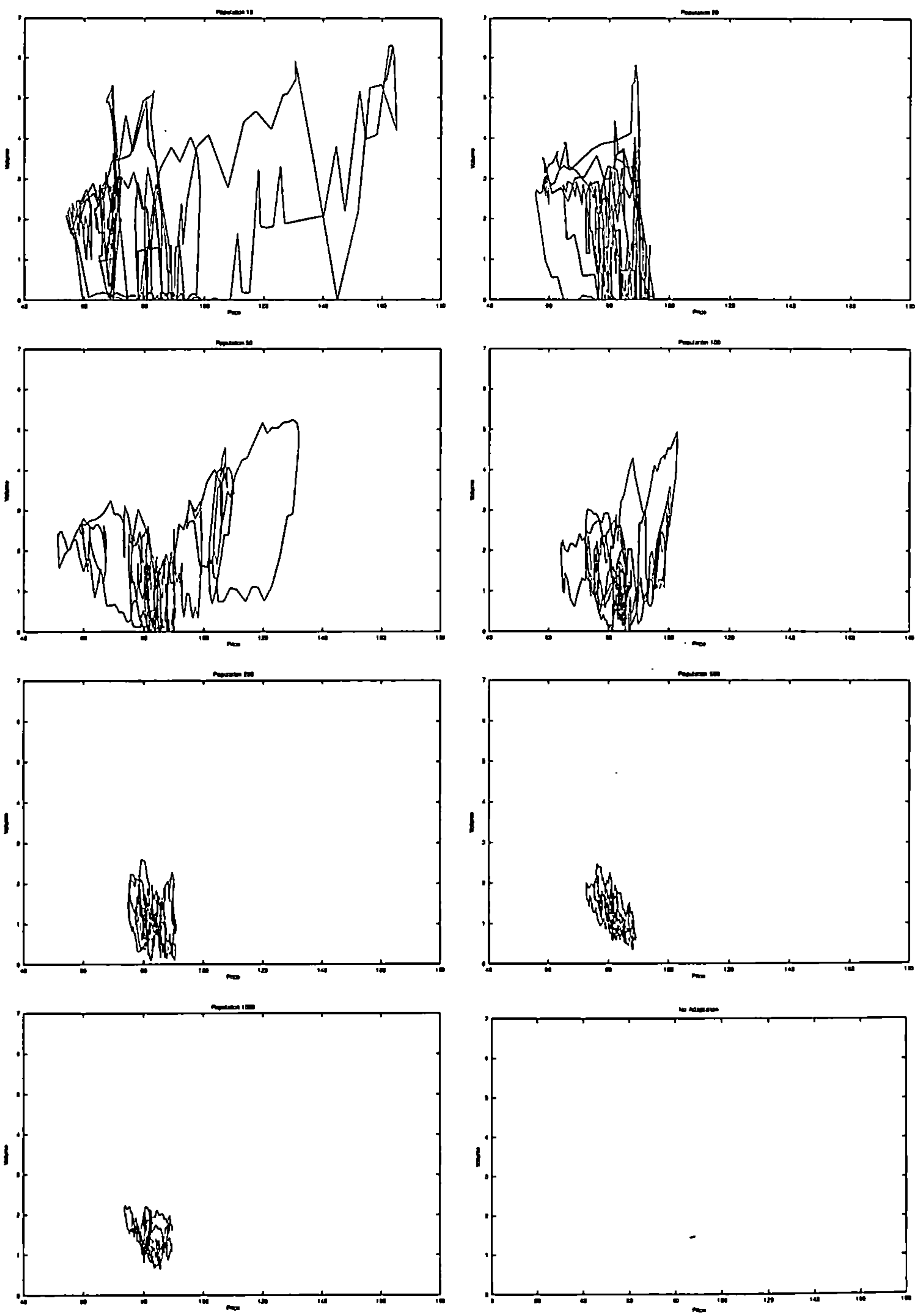

Figure 5.9: Phase portraits in price-volume for the SSMM. Population sizes are given in the individual graphs. All phase portraits are to the same scale.

classes having low frequencies, maintained by the mutational operator.

This is predicted by the analytic formalisation. In Section 4.1.3 it was noted that the volume of stock traded (Equation 4.7) is bounded from below by the standard deviation of agent demands for stock. As the population moves away from the fundamental price, the variance in demands for stock is likely to increase. If agents expect an increased or decreased next return, then the unresponsive segment of the population will settle for a respectively decreased or increased demand, because of the price change. This will increase the variance of the population, as the mean demand is fixed (and indeed sets the clearing price). Hence one would expect an increased trading volume away from the fundamental price, leading to a 'V' shaped phase portrait.

This corresponds to the phenomenon observed by Arthur et al. [5]:

> "We find that if our agents adapt their forecasts very slowly to new observations of the market's behaviour, the market converges to a rational expectations regime. Here 'mutant' expectations cannot get a profitable footing; and technical trading, bubbles, crashes and auto-correlative behaviour do not emerge. The efficient market theory prevails.
>
> If on the other hand we allow the traders to adapt to new market observations at a more realistic rate, heterogeneous beliefs persist, and the market self-organises into a complex regime. A rich "market psychology" –a rich set of expectations–become observable. Technical trading emerges as a profitable activity, and temporary bubbles and crashes emerge from time to time. Trading volume is high, with times of quiescence alternating with times of intense market activity... ...over the period of our experiments, at least, individual behaviour evolves continually and does not settle down. In this regime the traders' view is upheld."

5.3.4 Analysis of a 'Bubble and Crash' phenomenon

The SSMM is a highly simplified version of the artificial market whose features are described in the above quote, but important common features are present. In large populations within the SSMM technical trading is not possible because the stochastic sampling in selection and mutation becomes less important. The dominant force becomes stability, the agents tend to predict that the price will remain constant, and the price fluctuations are dependent upon the dividend fluctuations. On the other hand, as the population size becomes smaller, stochastic fluctuations have greater and greater effects within the population. Small numbers of mutant agents can effect the predictive trend of the population towards an upward or downward prediction. This can become strong enough that these mutant agents are rewarded, and can take hold within the population[5].

If this mutant takes hold, then the price will continue to rise until it reaches a maximal level sustainable by a homogeneous population of the fit mutants. At this point the price will no longer rise, and the mutant population becomes vulnerable to invasion by another mutant. A self-reinforcing crash follows, as the price returns towards the rational-expectations regime. This can be seen most clearly with a population of 10 (see Figures 5.10 and 5.11, where a pronounced bubble appears in time interval $t = 350 \ldots 400$, with a corresponding peak in trading volume accompanying it. Analysis of the actual population in this period shows this (Figures 5.13 and 5.11). Before $t = 360$ the price is stable at approximately the rational expectations price of $p = 87$. In the period $t = 360$ to $t = 380$, the population balance shifts rapidly towards a population that predicts an upward price trend (Figure 5.13). Correspondingly, the stock price rises (Figure 5.11). At $t = 380$ the price peaks.

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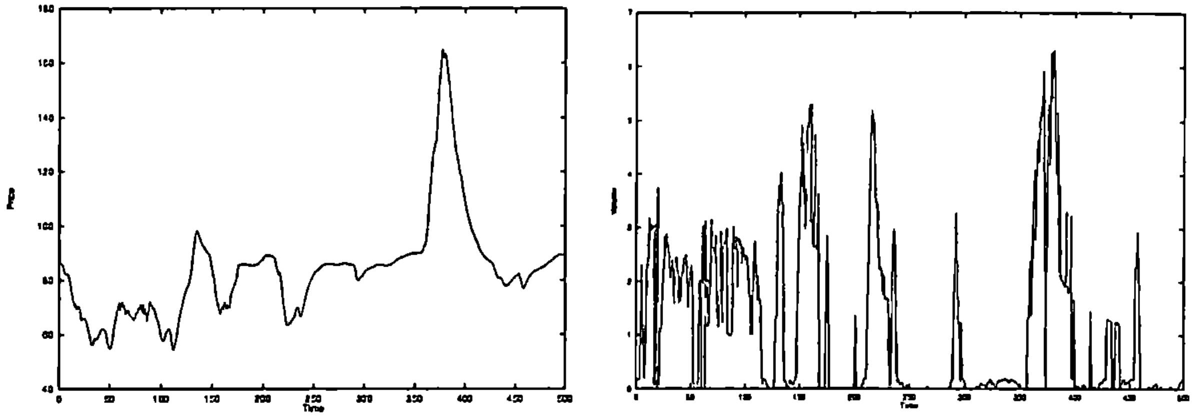
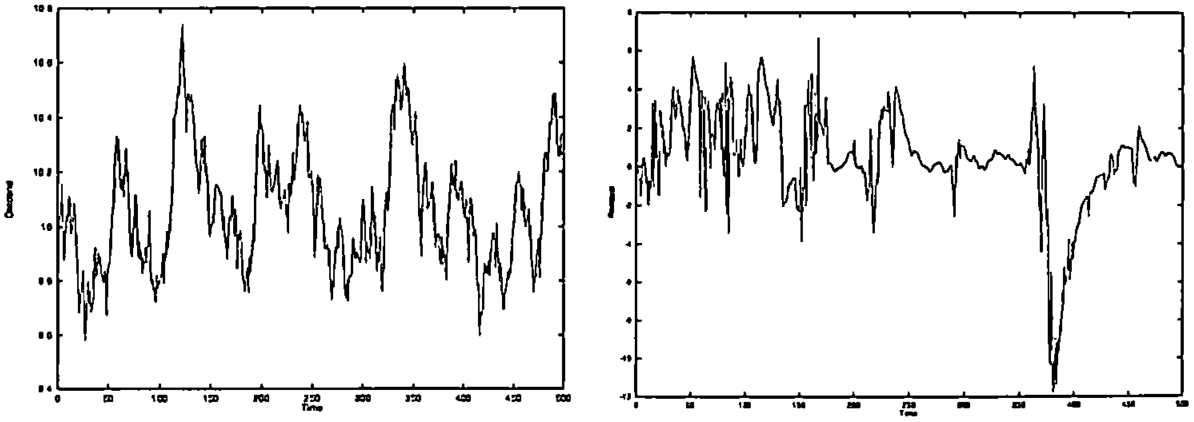
[5] Although this will not always happen. Section 2.1.6 discusses the mathematics of this process.



Price Volume



Dividend Residual

Figure 5.10: Time series for the SSMM, with an adaptive population of 10 agents. Here a single bubble and crash event is seen, centred about time $t = 400$.

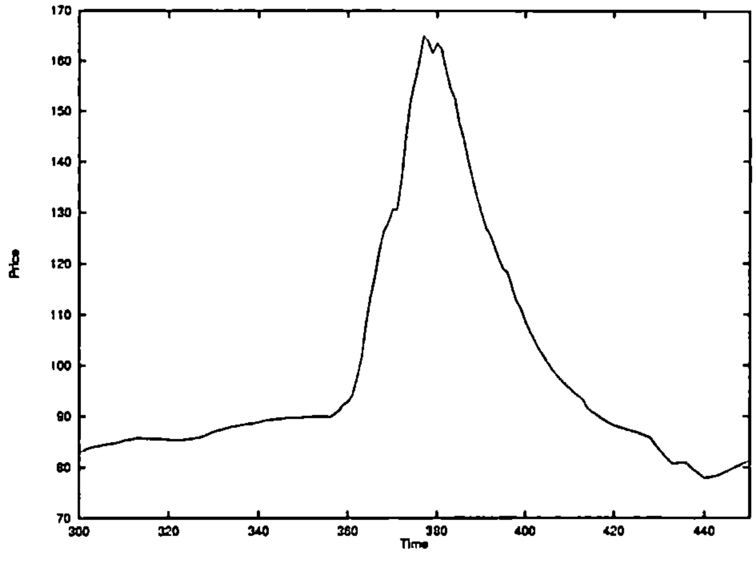


Figure 5.11: Stock price in the bubble described in the text. The population dynamics during this bubble are shown in Figure 5.13. This figure is an enlargement of the price time series in Figure 5.10.

Figure 5.12 shows the situation clearly, with a further expansion of scale on the x-axis. Two price time series are shown, the *actual price*, i.e. the price that the marketmaker fixes, given the demand functions of the population of agents, and the *stable price*, the price that, given the population distribution and the dividend, is sustainable by the population (Equation 4.36. Whilst the actual price is lower than this price, the stock price will rise because demand exceeds supply. Once this price is reached, the demand matches supply, and the portion of the population that predicts an upwards trend loses its fitness advantage. Agents that predict a stable price or a downward trend can now gain a foothold in the population, and their presence reduces the demand, and thus the stable price. The price falls, increasing the fitness of agents predicting a downwards trend. The balance of the population now shifts; the downwards predicting agents take over the population from $t \simeq 378$ onwards. Once the price has dropped sufficiently, they in turn lose their selective advantage to agents predicting a stable price; this occurs at $t \simeq 400$.

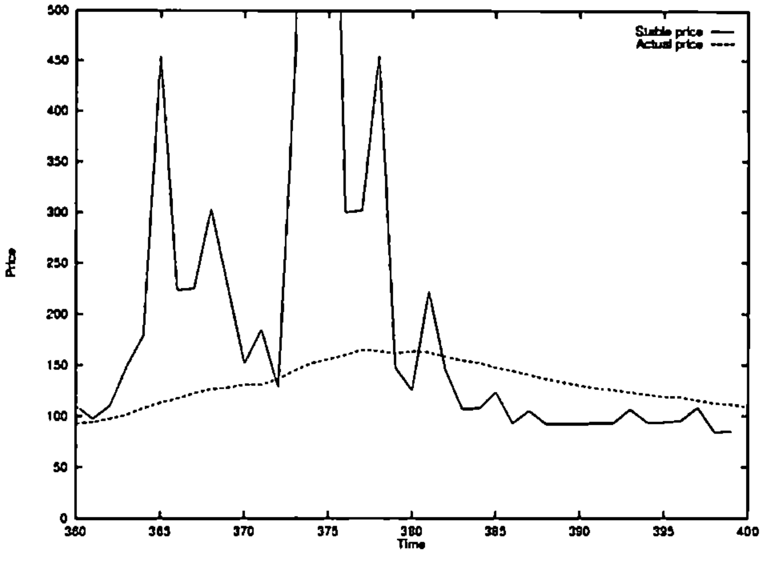


Figure 5.12: Actual and stable stock price series in the range $360 \leq t \leq 380$. The actual price is always moving towards the stable price (which is dependent upon the composition of the population).

The population dynamics underlying this bubble and crash can be observed in Figure 5.13. Immediately prior to the appearance of the $t = 350 - 400$ bubble, the population distribution is stable, dominated by agents predicting an unchanged next return. The onset of the bubble corresponds to a shift in the population distribution: agents predicting a rising return from the stock dominate the market. This shift in population is interpreted as a meta-stable shift between attractors in the population space. This new population remains stable itself for approximately 20 trading epochs, until the agents' demand for stock is limited by their risk functions. At this point supply matches demand and the price stabilizes. The population is now invaded by agents predicting a stable or lower return. The system shifts attractor once more, and the price drops. It is debatable as to whether this regime change should be characterised as a meta-stable event. Certainly its existence can be predicted, and for a given population distribution, the price at which it will occur can be predicted. However, the population distribution is always influenced by the stochasticities inherent in the adaptive process. Finally, as the price returns to the fundamental price another transition between attractor basins occurs; agents predicting an unchanged return dominate the population once more.

There is a second interesting phenomenon here. Note that during the crash phase, as the price drops, the population is dominated by agents predicting a falling return. However, these agents predict an absolute fall in price only, as can be deduced from comparing the bottom pair of figures in Figure 5.13. Given the rate of decrease of the return from the stock, one would expect that the fittest class of agents would be those predicting large drops in stock return; in these simulations the relative response bit has a much greater influence on the prediction than the absolute response bit. However, during the crash phase, the population is dominated by agents whose response bits are #0. Agents with a falling return predicting relative response bit (classes 00, 0#, 01) do enter the population, but are unable to become established within it.

Another interesting feature that should be noted is the fact that the stock price moves smoothly to the peak price, and then back down again. During this 'bubble and crash' event the active subset of the population changes, because the set of activated sensors changes, both as the price rises and then again as it falls. Yet this change in the active population has no effect on the progress of this transient event. This indicates that the population is well mixed: the distribution of response bits in the newly activated and de-activated segments of the population is similar. If it were not, one might expect to see a loss of momentum in the upwards price, because an unmixed population would be expected to have a maximal entropy distribution, which would no support such a high stock price.

To summarise, technical trading is observed in the SSMM, in the form of self-reinforcing predictions of price increases or decreases. Due to the intense selection pressures, fit mutants spread quickly through the population; in small populations

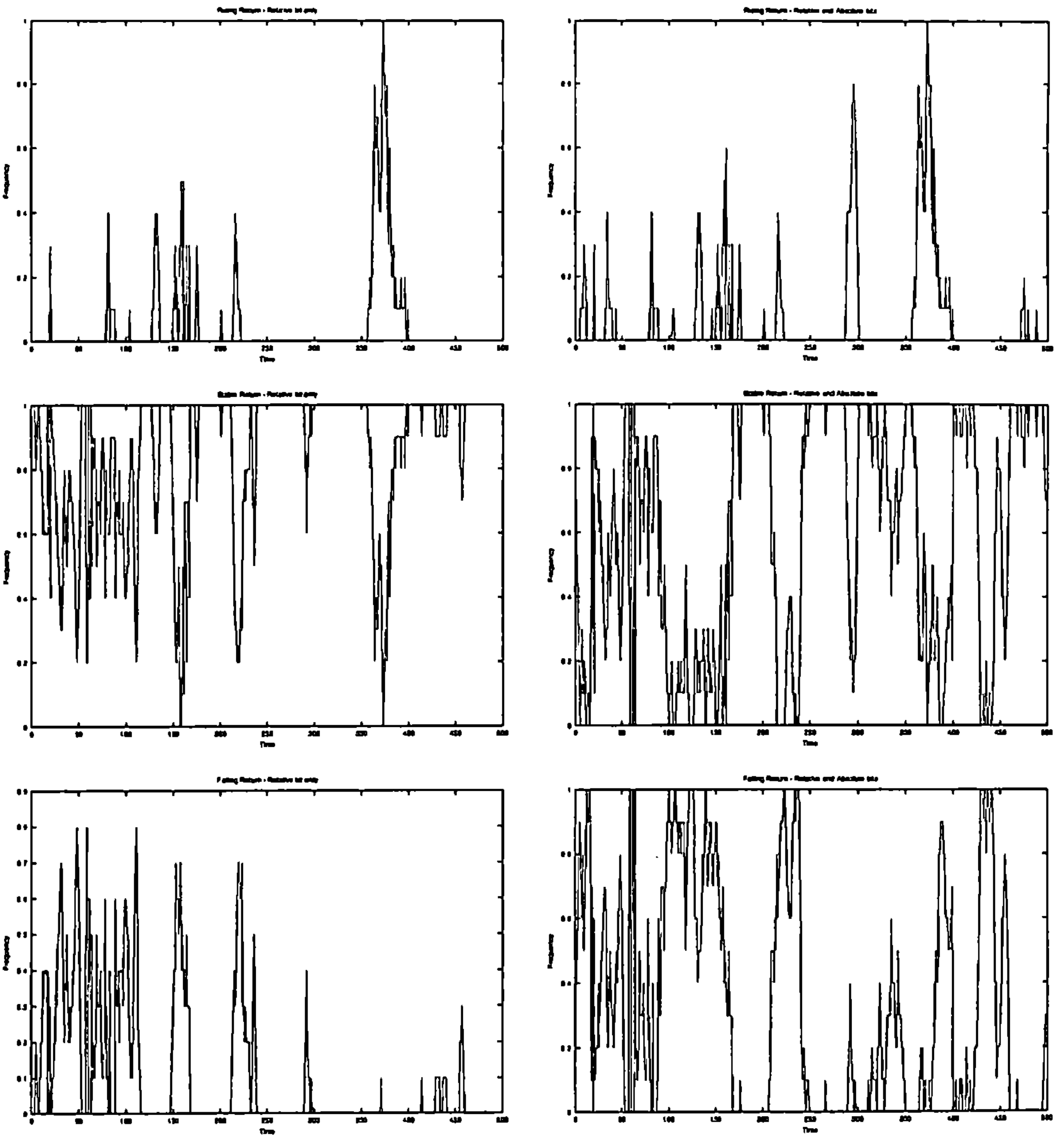


Figure 5.13: Composition of the population during the bubble in the population: 10 run discussed in the text. The 10 behavioural classes have been further reduced to 3 classes, corresponding to upwards, stable and downwards price pressures, to aid clarity. The left hand set of figures conflate fitness classes based on the relative price change response bit, the right hand set based on both bits. From top to bottom, upwards, unchanged and downwards return predicting segments of the population are shown. See also Figure 5.10.

these have a marked effect on the system dynamics. However, these self-reinforcing trends sow the seeds of their own downfall; even those agents predicting an upward trend have a limit on the price they are prepared to pay. When the price rises too high, demand drops off, the trend no longer continues and selective advantage is lost. A self-reinforcing crash follows.

5.4 Internal and External Shocks to the System

In Section 5.3 the dynamics of the SSMM have been considered. The movement of the market in response to a fluctuating population has been examined, and the resulting bubbles and crashes have been explained. In Lemma 4.2.1, the dependence of the market dynamics upon the dividend sequence has been laid bare. In this section, the relationship between the population dynamics and the dividend sequence will be considered, and the relative importance of the stochasticity in the dividend sequence and the stochasticity of the finite population will be examined. In simple terms, here the relative importance of internal and external shocks to the system will be considered.

In order to perform this analysis, the cross-entropy validation method described in Section 5.3.1 will be employed. This method allows the magnitude of internal shocks to the system to be measured; comparison of the cross-entropy time series and the price time series; and of the dividend time series to the price time series, using a correlation analysis. This should allow conclusions to be drawn about the relative importance of internal and external shocks in determining the dynamics of the system.

Clearly, a correlation may easily be taken between stock price and dividend, establishing the relationship between the price time series and the dividend time series. To establish a correlation between price movement and cross-entropy is more tricky, as cross-entropy is a measure of the internal sampling fluctuations within the population,

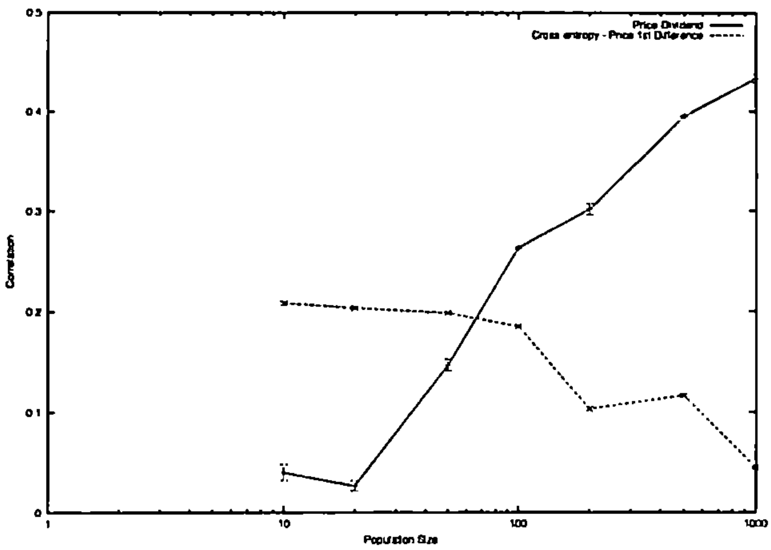


Figure 5.14: Correlation coefficients between price and dividend, and between the absolute price first difference and cross-entropy.

and is always positive. By taking the first difference of the price series, we have a measure of the *change* in stock price. The absolute value of this first difference can then be correlated against the cross-entropy series. The results of such a comparison are shown in Figure 5.14.

This figure shows that for small populations, internal sampling fluctuations are more highly correlated with the movements in the price series than the dividend sequence is. As the population size grows, not only does the mean cross-entropy fall, as discussed in Section 5.3.1, but also the correlation between cross-entropy and price fluctuations decreases. As this happens the correlation between the dividend and price series increases. The conclusion is that for small populations, the driving force in the population dynamics is internal: sampling fluctuations inherent in the adaptive process play an important role in determining system dynamics. In larger populations this is no longer the case; the system is driven by external forces (in this case the dividend sequence); internal fluctuations are insignificant in comparison. There lies an intermediate zone where the dynamics of the system are dependent upon both internal and external fluctuations.

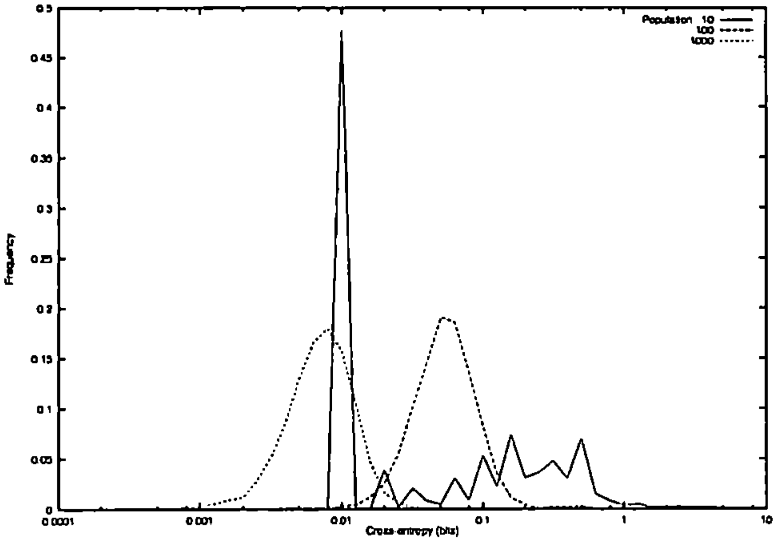


Figure 5.15: Distribution of cross-entropic shocks in small, medium and large populations.

Given that in small populations a correlation between cross-entropy and system dynamics does exist, what distribution do such shocks take? In Figure 5.15 the distribution of cross-entropic shocks is given for small, medium and large populations. Note that the more 'spiky' distribution in the small ($n = 10$) population is an artifact. In a smaller population, the range of possible population distribution is more limited; this constrains the cross-entropy to a more limited range of values, resulting in a 'spiky' distribution. From the distributions shown in Figure 5.15, it is clear that the cross-entropy follows a distribution which, if not Gaussian, is at least single-peaked with a well-defined mean. That is to say, it is not a negative exponential distribution, which would correspond to power-law dynamics of internal shocks. Whilst the shocks obey a distribution, there is certainly a characteristic scale to shock events. This is much as one would expect: the internal shocks to the system are caused by sampling fluctuations within the adaptive process. There is no opportunity for such stochastic fluctuations to be affected by the dynamics of the system; hence one would one expect to find the internal shocks obeying a power law distribution.

In a similar fashion, one would not expect to find the magnitudes of external shocks to obey a power law distribution, as the experimental design constrains the dividend sequence to an AR(1) process, driven by a Gaussian random variable.

5.4.1 Dynamics of Populations of Agents with Unequal Influence

At this point it should be stressed that the populations described consist of agents with equal influence: all agents have the same resources, and the same effect on supply and demand for the stock. In a real stock market, traders vary in their resources, as well as their risk functions, and the sensory information they have access to, or choose to utilise to help their decision making. If agents have heterogeneous effects on the market dynamics, then a large market may be effectively dominated by the actions of a few powerful traders. In these cases, even if the market contains a very large number of traders, then the stochastic fluctuations in the adaptive processes governing the actions of the few more powerful agents can have a large effect on the dynamics of the market. A powerful example of this can be seen in the effect of George Soros and his Quantum Fund in bringing about the exit of Sterling from the European Exchange rate mechanism on 'Black Wednesday' in 1992. Here a single powerful agent was able to force a run on a currency despite the intervention of central banks (also powerful agents). This is in no sense a claim about the decision methods used by any particular player in the world stock markets. Instead it is merely an observation that a few extremely powerful players can exert a strong influence on the market, even when the total number of players is extremely large.

Chapter 6

Discussion and Conclusions

In this chapter the results obtained in Chapter 5 will be discussed in the light of the general points put forwards in Chapter 3, and the theoretical predictions made in Chapter 4.

6.1 The Analytic Formalisation of the SSMM

The work presented has consisted of two elements, an experimental method, consisting of a computational implementation of a system of interacting adaptive agents (the SSM-M), and an analytical component, which attempts to model and explain the behaviour of the experimental system. In this section the success of the model will be examined.

To recap, the computational implementation consists of a population of interacting adaptive agents. Each agent consists of a single classifier rule having a six site trinary genome. Thus there are 729 different possible genomes. The implementation adapts via selection followed by mutation on the population (asexual reproduction). The population can thus strictly be seen as a discrete time, discrete space dynamical system in 729 dimensions. The analytical model of the system has only 10 dimensions, corresponding to the nine possible behavioural responses of an agent to the current macroscopic system state, with one response (##) split between two response classes to facilitate analytic tractability.

There are two aspects to the modeling of the SSMM that need to be considered.

1. Does the specific statistical dynamics formalisation that has been adapted as an analytical model adequately capture the dynamics of the SSMM?
2. Are the methods used to examine the analytic model sufficient? If not, in which areas are they inadequate?

6.1.1 Adequacy of the Analytic Formalisation

Consider first, whether the analytic model does capture the dynamics of the SSMM. In Section 5.3.1 a cross-entropic approach was used to validate the analytic model developed in Chapter 4. The validation demonstrated conclusively that, as an infinite population was approached, the one step prediction of the population at the next time step, and the actual population converged. It was pointed out that this is no conclusive guarantee that the analytic formalisation was correct, but it is highly unlikely that this might be so. One must therefore conclude that the analytic formalisation does capture the dynamics of the SSMM, at least as population size increases. The equation

$$P_{t+1} = \mathcal{M}\mathcal{S}p_t \tag{6.1}$$

adequately expresses the dynamics of the system.

Furthermore, analysis of the individual events within particular simulation runs, such as the 'bubble and crash' regime discussed in Section 5.3.4 is possible. In this instance, it was possible to explain the timing of the transition from the upwards 'bubble' to the downwards 'crash' in terms of the changing demand caused by the adapting population. The population converged on a distribution of agents predicting increased stock prices. This led to a price increase, which was ultimately halted because the population was unable to sustain such price rises. This led to a change in the adaptive dynamics, and a corresponding crash.

Overall, it would be fair to describe the analytic formalisation as having good short-term predictive power, in that it can accurately predict the population distribution at the next time step, provided the population size is large enough. The formalisation also possesses good explanatory power, in that it can be used to explain the dynamics of major events within the time series, once they have occurred.

6.1.2 Adequacy of the Analysis of the Analytic Formalisation

In Section 5.3.2, an analysis of the formalisation put forwards in Chapter 4 was presented. It had been hoped to find the attractors of this system. Unfortunately, the system proved not to be amenable to an analytic solution, therefore numerical solutions were sought using a multidimensional simplex method.

Only one solution was found. The stable price of this solution corresponds to the fundamental, or rational expectations regime. It was unsurprising that such a solution was found: Blume & Easeley [13] prove analytically that in a simple adaptive investment model, the fundamental regime is an attractor. Arthur et al. [5] also claim that a rational expectations regime in an attractor in the SFASM, which the SSMM is based upon.

There is, however, no evidence to support the hypothesis that an adaptive population in the SSMM lies within this rational regime. Across the statistics of all observables, there is no evidence that as population size increases, the system converges towards a fundamental regime. The only condition under which the system converges to such a regime is a non-adaptive one. Here it is possible to show analytically that the population will remain in a rational expectations regime. This is confirmed empirically.

Why does an adaptive population not converge on the fundamental regime? Arthur et al. [5] discuss the existence of a complex regime where rational expectations are not upheld. In this case, the dynamics of the population may be self-reinforcing, giving rise to persistent variation from the fundamental regime, described as over- and under-pricing regimes. The population here is driven by its own internal feedbacks, possibly triggered by stochastic fluctuations. This will be discussed in Section 6.2.

This is not an adequate explanation; the numerical methods used predicted the existence of a fixed point corresponding to a fundamental regime. Such a fundamental regime was indeed observed, although only in a non-adaptive condition. In the previous section (Section 6.1.1) the adequacy of the model has been discussed, and it has been concluded that it is sound. The salient question, therefore, is why the analysis of the formalisation fails to predict the existence of the attractors that the system falls into?

The analytic method used to locate attractors is the simplex method (Section 5.3.2), which is used to find solutions of an equation of the form

$$x - f(x) = 0 \tag{6.2}$$

by a gradient descent method across the vertices of a simplex. This should be expected to find any fixed points of the system. It cannot, however, be expected to find limit cycles or strange attractors, which take more complex forms, having a periodicity strictly greater than one. If the attractors of the system are not simple fixed points, then a numerical method will not find them. One could, of course attempt a numerical solution for a period k map

$$x - f^k(x) = 0 \tag{6.3}$$

but, given the computational load, and the fact that k is unknown, this approach was rejected. Also, if more complex attractors, such as strange attractors exist, such an approach will still fail. In Section 3.2.5, the work of Friston [31] in describing the attractors of complex interacting systems was discussed. Following this, it is considered likely that a system of interacting adaptive agents such as the SSMM may possess such complex attractors.

Certainly, over short time periods, interesting dynamical phenomena are observed, such as the 'bubble and crash' phenomenon discussed in Section 5.3.4. The Friston model [31] (following Kelso [47]), which describes a complex interactive system possessing attractors with complex form, where the system can move between sub-manifolds of the attractor surface. Such a description may be relevant here, in Section 5.3.4 this phenomenon was explained by the model in terms of the population moving towards a price attractor that itself moved in response to the population distribution.

To conclude, the analysis of the dynamics of the SSMM appears inadequate. This is primarily due to the complexities inherent in the formalisation. The system is multidimensional and highly non-linear, which limits the feasibility of an analytic solution for the attractors of the system. Not only that, but it appears to possess attractors with a complex structure which are unlikely to be discovered by a numerical method.

6.2 Dynamical Regime and Population Size

In Section 3.3 it was argued that three dynamical regimes exist, which were labelled stable, meta-stable and unstable. To recap, the stable regime would exist in the limit of large populations: here, external shocks (in this case the dividend sequence) should provide the driving force for the population. The second regime was described as meta-stable. The conditions under which this regime was postulated to exist were dependent upon the population size, observational timescale and schedule, and the strength of the exploitative and explorative operators. Finally, a third regime, described as unstable, was postulated to exist. Such a regime would be characterised by extremely small populations where the stochasticities inherent in the exploitative and exploratory operators (internal shocks) become the driving force for the dynamics of the population.

Here the evidence for such a characterisation, based on the SSMM presented in Chapters 3 and 4 will be reviewed. Such evidence as exists has two components: a qualitative component based upon the observation of the market evolution presented in Section 5.2, and a quantitative component based upon the cross-entropy approach detailed in Section 5.4.

In Section 6.1.2 the adequacy of the analysis of the formalisation produced in Chapter 4 was discussed. There appear to be multiple regimes within the system, whilst the fundamental, or rational expectations regime is an attractor, the system appears not to converge towards it under with an adaptive population of any size. This implies that other attractors may well exist. One might also consider the 'bubble' phenomenon discussed in Section 5.3.4. This may be the result of the system switching between attractors, or alternatively it may result from the type of complex dynamics discussed by Friston [31] and Kelso [47], where a system remains within a single attractor, but varies it position within that attractor, because the control parameter is modulated by the system itself.

Ultimately, it is unclear as to whether the dynamics of the system are best described as transitions between a number of separate attractors, or as the switching of the system between sub-manifolds of a single attractor. Indeed, both descriptions may be correct, depending upon the level at which the system is viewed. In the former case, one might wish to describe the system as meta-stable, following the convention of Kelso [47] and Friston [31]. In the latter case, further evidence is provided by the discussion of the role of shocks to the system put forwards in Section 5.4.

Figure 5.14 shows that the system is dominated by the effect of internal shocks (i.e. stochastic fluctuations) in small populations, and that the effect of these internal shocks decreases with increasing population size. Simultaneously, as population size increases, there is an increasing dependence upon external shocks to the system; in this case a direct correlation between stock price and dividend. One would expect this, the variance of the population distribution due to sampling fluctuations to scale as $\sqrt{n}$. As population size increases, the population takes longer and longer to switch between alternate attractor basins, because the smaller stochastic fluctuations make it more and more difficult for it to stray from the attractor.

Arthur et al. [5] associate low volume trading with a rational expectations regime, and higher volume trading with a complex regime. Rapid switching between these conditions is certainly observed in small populations, for example, in Figure 5.10. This may be interpreted as evidence of regime switching within the system. On the other hand, such behaviour is observed more rarely, if at all in larger population systems. This is seen is Figures 5.3 and 5.2.

Clearly, if the population size is sufficient, and one does not wait a sufficient amount of time, the system will not have undergone a stochastic jump across the population space sufficient to move it between attractors. In this case, the population will tend to be practically classified as behaviourally stable. Conversely, if the population is sufficiently small, the population will be completely driven by internal shocks (i.e. stochastic fluctuations). Here the population may be unable to remain in any attractor basin for a significant length of time, and the behaviour will be classed as unstable.

In the case of the SSMM, this latter behavioural pattern has not been observed. However, meta-stability is certainly observed in small and medium sized populations, and stability in large populations. It is predicted that for a larger population, meta-stability would be observed in a sufficiently long observational window.

To conclude, stability, meta-stability and instability are generic properties of systems of interacting adaptive agents. The dynamics of the system, and the cases in which these three regimes are observed in, appear to have a high dependence upon both the adaptive regime and the nature of the interaction. In the system studied, there is a smooth transition between instability, meta-stability and stability as population size increases. This may not be the case for all systems, as there may exist systems which demonstrate sharp bifurcations between these regimes.

6.3 Critique: Plausibility vs. Analytic Tractability

In this section, wider issues concerning the study of populations of interacting adaptive agents will be discussed. In particular the success of the SSMM will be examined, both as a model of a stock market, and as a model of a population of interacting adaptive agents.

6.3.1 The success of the Simple Stock Market Model

Recall Section 4.1.1. The SSMM was motivated by three core design issues: analytic tractability, simple dynamics, and a well understood problem. At this point the success of the model in terms of these three design criteria will be reviewed. Other design issues have been easily implemented on the model, and will not be discussed further here.

First, consider the analytic tractability of the SSMM. A statistical dynamics formalisation of this system has been constructed, and this has led to the identification of a fixed point. However, as has been discussed in a previous section (Section 6.1.2), there is no clear evidence that the system converges on this fixed point in any adaptive condition. On the other hand, the analytic formalisation adopted successfully predicts the short term behaviour of the system. The root of the discrepancy has been identified as the inadequacy of analytic methods available.

As discussed in Chapters 2 and 3, there are strong links between the analysis of this system, and other dynamical and evolutionary systems. In particular, the analysis is based on the statistical dynamics analysis of the Royal Road GA [78]. The meta-stability analysis that followed has links to the analysis of noise in non-linear dynamical systems, particularly the work of Knobloch & Weiss [52]. Despite this, it cannot be said that the dynamics of this system are completely understood either from an experimental or an analytic viewpoint. Despite the dimensional reduction, the reduced system still has a relatively high number of dimensions (11, including time), and this is one of the main problems in analysis. At present there appears little hope of finding improved analytical techniques which would allow a deeper analysis of the system. In particular, the following questions remain unanswered:

1. What is the nature of the complex regime that an adaptive population appears to reside in?
2. Are the 'bubble and crash' phenomena, discussed in Section 5.3.4 best characterised as an alternate attractor (or attractors), or as the sub-manifold of a single attractor.
3. However one might wish to characterise the regimes existing within the system, what is the distribution of waiting times between transitions between these regimes? How is this distribution dependent upon population size, exploitation and exploration rates?

Given that these questions remain unanswered as yet, the SSMM cannot be judged as an overwhelming success from the point of view of analytical tractability. The SSMM has good explanatory and predictive power on a short term basis, but fails to fulfill expectations with regard to the larger and more general issues.

Second, consider the criterion of simple dynamics. The rationale guiding the experimental design within this thesis was to try and identify a system with a limited number of identifiable dynamical regimes. A stock market model was chosen, because the evidence in existing work, for example Arthur et al. [5] showed the existence of over- and under-pricing regimes accompanying the fundamental regime. It was anticipated that the reduced complexity of the SSMM, as compared to the SFASM would lead to a combination of simple dynamics, and a more easily analysable system. These beliefs have proved to be only partially upheld. Certainly, a number of easily identifiable regimes exist; it has been possible to distinguish between a fundamental regime and a complex regime. 'Bubble and crash' events have also been identified which only occur in the complex regime, and may or may not form a third regime. The problem of analytic tractability is again paramount. Whilst the fundamental regime is understood to be an attracting fixed point of the formalisation, no analysis of the complex regime has been possible, and its nature is not understood at all. Similarly, it has been possible to perform an analysis of the behaviour of the system during a 'bubble and crash' event. However, it is unclear what the relation of this type of event is to the complex regime, because the complex regime is not understood.

Third, a model of a well understood problem was desired. The SSMM is a gross simplification of the Santa Fe Institute artificial stock market (SFASM), and is governed by the same market structure, clearing method and timing sequence. However, the simplifications occur in agent structure: the agents are heavily simplified, incapable of the sophistication of decision making that they have in the SFASM. There is also a difference in that the SFASM does not allow agents to copy each other's strategies directly, whereas this occurs in the SSMM. The SSMM is far more reactive than the SFASM; in practice the evolutionary pace is far quicker. This aids the observation of the meta-stable phenomena that have been sought. With a large population, the SSMM displays similar behaviour to the SFASM without historical information, converging towards the fundamental pricing regime. This is confirmation of the correct operation of the SSMM. However, the existence of over- and under-pricing regimes for small populations is not predicted by Arthur et al. [5]. This is due to the difference in adaptive structure between the two models: In the SFASM, the evolutionary pace is much slower, and more importantly, agents choose the predictive rules that they use based upon their past performance. In the SSMM, each agent has a single rule, and these are all implemented. This makes the SSMM much more responsive to stochastic variations; the slow evolutionary pace ensures that agents are likely to already possess good predictors; new predictors are only likely to affect agent's demand once they have proved their predictive ability 'off-line', or if novel conditions prevail. This latter option is made less likely by the former; the appearance of novel conditions is damped by the predilection of agents to choose tested predictors. The suggestion is that the structure of the SFASM without historical information damps the stochasticity inherent in the system, making the system appear stable.

6.3.2 Meta-stabilty in the SSMM and SFASM

In an earlier discussion (Section 5.2.2) it was noted that Arthur et al. [5] claim, on the basis of theoretical considerations and the results that they present, that technical trading is not possible unless the agents are able to respond to historical information. Therefore the system should remain in a fundamental regime if the agents have no historical sensory information available to them. Is this claim consistent with the behaviour of the SSMM presented here?

Initially, it would appear that the observed meta-stable behaviour in the SSMM, consisting of a fundamental behaviour regime punctuated by bubble and crash events in both upwards (over-pricing) and downwards (under-pricing) directions, invalidates the claim made by Arthur et al. On closer inspection, this may not actually be the case. As has been discussed above (Section 6.3.1), the fact that meta-stable events are not observed in the SFASM in the absence of historical sensory information may be due to the different evolutionary algorithm and slower pace of adaptation in the SFASM. This does not, however, explain how meta-stable phenomena which appear to be technical trading, can arise in a system where agents do not have direct access to historical information.

Arthur et al. [5] explain how bubble and crash regimes can arise via a mutually reinforcing subset of the population. Their reasoning is mirrored in the explanation of bubble and crash regimes in the SSMM discussed in Section 5.3.4. However, their experimentation shows that in the SSMM, what they describe as a 'complex' regime, where bubbles and crashes can occur, cannot arise without the existence of technical trading bits in the agents' sensors, which give short term historical information about market behaviour.

A possible explanation for the apparent inconsistency between the claims of Arthur et al. [5] and the behaviour of the SSMM is that information on the short term history of market behaviour is actually available to the agents in the SSMM. The evolutionary pace of this model is high, the population quickly responds to changing trends in the market. Moreover, every agent has but a single rule, and the evolutionary algorithm allows agents to imitate the successful strategies of other agents. In some sense, the distribution of the population between the response classes gives historical information about recent market behaviour. Responses that are widespread within the population are associated with successful prediction, and therefore give information about recent trends in stock pricing. Hence technical trading is possible in the SSMM, and is observed as bubble and crash regimes. The manner in which these regimes are dependent upon the evolutionary algorithm has already been discussed in Section 5.3.4.

6.3.3 The Big Issue: Modelling Systems of Interacting Adaptive Agents

The SSMM has proved to be a valuable testbed for ideas concerning the evolution of interacting adaptive systems. It has demonstrated the feasibility of statistical dynamic approaches to the problem, despite the substantial non-linearities involved at a very basic level. It has illustrated the existence of meta-stability as an important dynamical regime in finite populations, and has enabled the examination of a basic adaptive system, namely asexual reproduction followed by mutation, which encapsulates exploitation with global choice, plus random exploration. This is one of the simplest, and most analytically tractable adaptive schemata.

The demonstrated meta-stability can be applied back into many of the systems discussed in Section 1.3. There is now a good case for describing the regime changes observed in these systems as a result of meta-stability due to the stochastic nature of adaptation in finite populations. The generic nature of meta-stability in finite populations can be used to inform the design of interacting systems of adaptive agents, especially distributed adaptive control systems. Further work is necessary in order to further understand these systems, especially the waiting times in particular states, and the probability of transition from any given state to any of the other states. The question is, where on the continuum between analytic tractability and implementational plausibility should future work be pitched?

The discussion above (especially Sections 6.1 and 6.3.1) has shown the great practical difficulties in analysing even highly simplified versions of real-world systems. The SSMM is a simplified model of an artificial stock market, which in turn is restricted to a single stock, with no external fluctuations save the stock dividend. Even so, analysis has proved difficult; the practically important questions of waiting times have remained unanswered, and are likely to remain so.

The approach that has been taken in this thesis has been to try and build a model of an entire system. Whilst the model rests on some basic assumptions, most notably the maximal entropy assumption of Prügel-Bennett and Shapiro [69], the approach has been holistic in that it attempts to integrate all aspects of the system into the model. The central question that must be addressed is whether such an approach is worthwhile. Certainly it is a valid approach; it has enabled predictions to be made which have been tested against the empirical system in computational simulations. The problem is that this is a very labour-intensive approach: the computational simulations are fairly large, and they are time-consuming to write and debug[1]. The analytic formalisation that has been developed is an extension of the method adopted by van Nimwegen et al. [79], and is certainly applicable to other systems. The devil, as always, is in the detail, although it is hard to see how the operators $\mathcal{M}$ and $\mathcal{S}$ could be easily used in another system, as they are tailored to the detail of the operation of this system.

The system that has been studied in this thesis is essentially a 'toy' system; in many respects it is an oversimplification of a real stock market. It still does maintain important aspects of the behaviour of a real stock market though. However difficult it

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[1] To be fair, the writing of the computational simulation was treated as a learning exercise in a new language (Java), and this slowed up progress. However, once the model was written, the Java GUI allowed the system behaviour to be easily and quickly explored over a wide range of parameters.

may have proved, the analysis of the working of this system has been made possible by the complete access to information that is a feature of computational models. In the computational simulations there is complete access to every aspect of the system: there are no unknowns. This is not the case with a real-world system as it is very rare that the dynamics of the system are completely understood and in many cases the agents themselves do not understand the causes of their actions. As has been discussed in Section 1.1.2, the combination of a number of agents all acting in goal-directed manners, although with differing beliefs and goals, can underlie the exploratory operator.

Do 'big' models, such as the SSMM fulfill any useful role? Do they have 'added value' above smaller models which only claim to model specific aspects of complex systems. In many cases they do, because they allow the range of dynamics of a system to be explored. Should they be used as the basis of analytic models? Probably not: the effort that goes into the model of a specific system may yield results about that system, but is likely not to be easily generalisable to other systems. Smaller, more restricted models may have a more canonical nature, and be more easily applied to a wider range of systems.

This is not a rejection of the work presented in this thesis. The model (both analytic and computational) was built with a specific purpose: to examine and further understand the phenomenon of meta-stability in finite populations of interacting adaptive agents, and its relationship with the stochastic fluctuations inherent in such processes due to the adaptive operators. It has succeeded in that it has contributed to the understanding of such systems. Based on that knowledge, new directions for research in this area may be proposed, and the current model, having served its purpose, is abandoned.

It is suggested that future work should be directed very much more towards simpler systems which are likely to be more analytically tractable. If anything, the SSMM is too complex. Further levels of system abstraction would aid tractability, and allow additional approaches to be taken, including symbolic dynamics, spin glass approaches, and improved thermodynamic approaches. A second advantage of simpler systems is that they will allow easier comparison of different adaptive approaches. There is very little understanding of the interaction of exploration and exploitation, and the interplay between these fundamental forces in many adaptive algorithms. The use of simple systems will make this task easier. Questions along this track that remain unanswered (some of these are extremely fundamental questions within adaptive theory) include

1. What is the role of the crossover operator in GA theory? Nimwegen et al. [78] speculate that in the Royal Road GA, crossover allows good genotypes to spread through the population faster than would be the case under asexual reproduction. Prügel-Bennett and Shapiro [69] claim that the effect of crossover is problem dependent, as the representation used will determine the amount of mixing that is inherent in the crossover operator. What is the action of crossover in an interacting population? What level of stochasticity is inherent in crossover, and how will it effect the meta-stability of the population's behaviour?

2. More generally, how do different adaptive schemata affect the behavioural meta-stability of the population?

3. Is it possible to alter the strength of the explorative and interactive components of adaptation in order to manipulate the stability of the system, and its reaction to changing environmental conditions? In the case of a distributed adaptive control system, is it possible to optimise the system's response to a range of environmental conditions given constraints on required stability and reaction speed?

Additionally, there is a strong case for studying interacting adaptive systems with a spatial component: either those set within a spatial environment, such as problems in situated robotics, or those in which an interaction topology exists, such as network problems. These are two very important class of system from a practical standpoint. The latter system may also have additional behavioural complications, such as the presence of spatial co-ordination effects, similar to those noted in physio-chemical complex systems such as the Belousov–Zhabotinski reaction [27]. Here, local stochastic fluctuations give rise to globally co-ordinated behaviour. It is important to examine such systems in adaptive agents. Can global co-ordination of agent behaviour result when local interactions are influenced by local adaptation, which in turn feeds back from local agent performance?

In addition, it is expected that power-law dynamics [8] will result from the imposition of a topography on agent interactions. This type of dynamics is very common in such systems, ranging from avalanches in sandpiles [9] through to extinction events in food webs [63]. An understanding of the likely global impact of local events is essential for the successful implementation of such systems.

6.3.4 Further Work: The Spatial Minority Game

In the light of the above discussion, a spatial minority game is presented. This is a co-ordination problem between adaptive agents, based upon the work of Arthur [3] and Zhang [88, 18], as discussed in Section 1.3.3. The spatial co-ordination is played between agent on a one-dimensional torus. This allows easy control of the locality of interaction and exploitation. As yet, there is little work on this game, but it is hoped that it possesses a sufficient level of abstraction to allow a deep analysis of its workings.

This game has a number of advantages over an artificial stock market for the analysis of the dynamics of interacting adaptive systems. First, the interaction is much simpler, and therefore much easier to model. Second, the interaction is more explicit: precise control can be exerted over the interactive radius, plus the length and specificity of the game history that agents have access to. This is in contrast to the SSMM where, although the agents directly have only access to the previous price, this has a deterministic relationship to the previous price and population. The model of the system as a Markov process is effective, but it is difficult to conceptualise.

Third, finer control over the evolutionary process in a spatial minority game is possible. As in the SSMM, it is possible to alter the evolutionary algorithm, not only in terms of mutation and selection rates, but also the nature of the evolutionary operators. In addition, in a spatial game it is possible to alter the spatial factors in the evolutionary process, such as the radius within which the exploitative process takes place.

Fourth, a spatial minority game has strong conceptual links to spin-glass systems (a well studied class of physical systems which explain the low temperature behaviour of paramagnetic materials). The language of spin-glass systems includes concepts such as frustration (the inability of all particles to reach their desired state), and makes full use of entropic and thermodynamic concepts. There is the opportunity to use the analyses developed for such systems to explain the dynamics of adaptive systems in spatial networks.

6.4 Conclusion

The SSMM has proved to be an interesting testbed for interacting adaptive systems. However, the study has suffered from the excessive complexity of the system, which has limited the depth of the analysis which has been possible.

The existence of stable, meta-stable and unstable regimes within adaptive systems has been demonstrated. Even within large populations, the stochasticity inherent in the exploratory and exploitative processes has been shown to have a significant effect on the evolution of the system. In addition, the system has been shown to undergo a transition from being driven by internal shocks (stochastic fluctuations) to external shocks (environmental fluctuations) as population size increases.

In modelling terms, the success of a statistical dynamics approach based on reducing the system to a manageable number of behavioural states, in conjunction with a master equation approach to state transitions, has been confirmed, although the SSMM lies at the upper limit of tractability. Whilst the limited analysis possible has precluded a full understanding of this system, and many of the interesting questions have been left unanswered, it has provided a foundation from which further work on interacting adaptive system may proceed.

> "Er muss sozusagen die Leiter wegwerfen, nachdem er auf ihr hinaufgestiegen ist.[2]" [85]

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[2] He must so to speak, throw away the ladder after he has climbed up on it.

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