

Evolving Dynamical Systems: nearly neutral regions in continuous fitness landscapes

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The greater mystery, after all, is not the answers the scientists contrive, but the questions they are driven to pose. Why? Why this question rather than another? Why this search, hope, despair, rather than another? Why this ill-lit, nil understood, hobo path? And why the outrageous confidence, born of no evidence, to tred it? I do not know. But I know that this sense is not rare. What a strange pleasure it is to seek.

Stuart Kauffman

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Abstract

Neutrality arises from the many to one mapping between genotypes and phenotypes. Several studies have demonstrated that in the presence of selective neutrality evolution is qualitatively different from that on the more common rugged fitness landscapes which are often (implicitly) assumed by artificial evolution practitioners. Almost all of such work has been based on discrete genotype fitness landscapes. However, in many artificial evolutionary problems the most natural way to encode the parameters of the systems being evolved is using real valued genotypes. The notion of neutrality in continuous landscapes has been very little discussed.

Dynamical systems, with their parameter space as genotype and their dynamical behaviour determining fitness, generate a redundant mapping. In this sense, changes in parameter settings most of the times produce only slight changes in the dynamical behaviour; but for certain parameter values, even infinitesimal changes will cause the behaviour of the system to change radically.

In many real world evolutionary tasks, the fitness of the individuals is considerably related to the behaviour of the underlying system. It is the argument of this thesis that when evolving dynamical systems on such tasks, the evolutionary process may exhibit features which are reminiscent of neutral evolution. We explore the characteristics of the evolutionary process through the use of computer simulations on two families of landscapes. Special attention is paid to the existence and usefulness of regions of equal or nearly equal fitness in these continuous fitness landscapes.

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Chapter 1

Introduction

Traditionally, evolution has been considered as a gradual and continuous process of adaptation from the accumulation of small beneficial variations. This, in combination with our experiences in low-dimensional spaces, has generated a picture of fitness landscapes as rugged hilly terrains (Wright, 1932). Kimura's work, however, asserted that the great majority of changes at the molecular level caused no phenotypic changes, that is were neutral with respect to fitness and thus their fate was more frequently determined by random drift than by selection (Kimura, 1983). Relatively more recent developments in models of RNA secondary structure folding have renewed the interest in neutrality with the discovery of connected networks of genotypes mapping to common phenotypes, neutral networks (Schuster, Fontana, Stadler, & Hofacker, 1994). As a result, a very different picture of evolution is emerging: one of populations engaged not in hill-climbing but rather drifting along neutral networks, with sporadic jumps between networks (Barnett, 1997).

In artificial evolution, neutrality and neutral networks have been studied on discrete-alphabet spaces. From these studies many useful insights have been gained into the dynamics of evolutionary search on landscapes with neutrality (Barnett, 2002a). In many artificial evolutionary problems, however, organisms are encoded using real-valued genotypes. Yet the notion of neutral mutations has been very little discussed on real-valued landscapes and ideas from the discrete scenario do not carry on intuitively.

There is growing evidence that in artificial evolution and complex real-world engineering design problems involving many parameters (for example designing a controller for an autonomous agent), neutrality may arise from the fact that changes to a particular parameter may frequently produce no discernible contribution to fitness (Harvey, Husbands, & Cliff, 1993; Harvey & Thompson, 1996; Thompson, 1998; Smith, Husbands, & O'Shea, 2001a, 2001b; Smith, Philippides, Husbands, & O'Shea, 2002; Seys & Beer, 2004; Psujek, Ames, & Beer, 2004). Neutrality in both biological and artificial scenarios arises from a many to one mapping between genotype and phenotype or fitness. Dynamical systems can capture this redundant mapping when their parameter space is considered as the genotype space and their phase-portrait space as the phenotype or fitness.

The argument of this thesis is that when evolving dynamical systems on evolutionary tasks where the fitness of the individual is considerably related to the long-term behaviour or phase-

portrait of the underlying system, the evolutionary process may exhibit features which are reminiscent of evolution on neutral networks. But can ideas of neutrality and neutral networks developed for discrete-alphabet search spaces carry on to continuous spaces? How? **It will be the aim of this thesis to draw insights into the evolutionary process when evolving dynamical systems on such phase-portrait related continuous landscapes.** These questions and the answers presented herein are of particular relevance to the areas of artificial life and evolutionary robotics, with possible implications for evolutionary optimization problems as well.

We proceed to further understanding the structure of these continuous landscapes when evolving dynamical systems with the use of computer simulations of a very simplified evolutionary technique which has been employed as a good way to drift in neutral networks and with the use of a particular dynamical system model which has been increasingly used in a variety of contexts: continuous-time recurrent neural networks, as generic models of complex nonlinear dynamics. We basically explore the evolution of these systems in two different families of landscapes where the mapping from the genotype to the fitness ranges from directly related to the phase-portrait of the system to ones where the relationship is slightly more complex.

This work is organized as follows. We begin with an introduction to the notion of fitness landscapes and neutrality in biological and artificial evolution complemented with a review of the relevant work in this area in chapter 2. This is followed by an overview of dynamical systems and their importance for redundant mappings in evolution. In chapter 5 we explain the dynamical system models and the evolutionary methods and measurements that will be applied to these landscapes. Chapter 4 presents the results when evolving dynamical systems on the two different families of landscapes of increasing complexity between the relationship of phase-portraits and fitness. A chapter for the discussion of the results follows, providing the overall picture obtained from our research. The work ends with the conclusions, contributions and paths of future research. Appendix A contains the methods used to numerically compute equilibria and appendix B contains the source listing of the code used to compute all results in this work.

Chapter 2

Fitness Landscapes and Neutrality

This chapter will give a brief overview of the essential concepts relating to evolution: fitness landscapes, neutrality, and neutral networks. This will be complemented by a review of the relevant work in this area. Finally, an introduction to the notion of neutral regions in continuous landscapes will be provided.

2.1 Fitness Landscapes

The notion of *fitness landscapes* was introduced by Sewall Wright (1932) to aid the visualization of the relationship between the genotype and the fitness value of an individual or population. This abstraction, however, has been used with a variety of meanings. One source of ambiguity stems from the definition of the genotype space. Fitness landscapes are commonly depicted as continuous surfaces. However, in evolutionary biology such is only the case when analysing quantitative phenotypic traits (phenotypic landscapes) or when analysing the frequency of alleles in a population (gene frequency landscapes) in which case points in the surface denote different populations. At the molecular level, however, genotype space is used to represent the loci in the genome of an organism and it is represented by an n -dimensional hypercube, where n is the size of the genome, with numerical values associated to each of its vertexes as fitness. It is this ‘molecular’ notion of a genotype space which we will treat here.

In artificial evolution, as loci in the genome can either be drawn from a discrete alphabet or have numerical real values, fitness landscapes as hypercubes or continuous spaces, are both plausible (see figure 2.1). And unless you are a trained mathematician, it is very hard to visualize fitness landscapes of dimensions greater than three. For this reason, fitness landscapes as rugged terrains have permeated the minds of evolutionary biologists and artificial evolution practitioners alike. Adaptive evolution has been translated into a hill-climbing process, and shifts to higher peaks can only occur through fitness reductions as individuals traverse valleys or saddles. This picture carries with it an optimization conundrum: if selection pressure is strong enough, relative to the disruptive effects of genetic operators, to drag a population up a hill, it is also likely to be strong enough to hold it there! (Barnett, 1997).

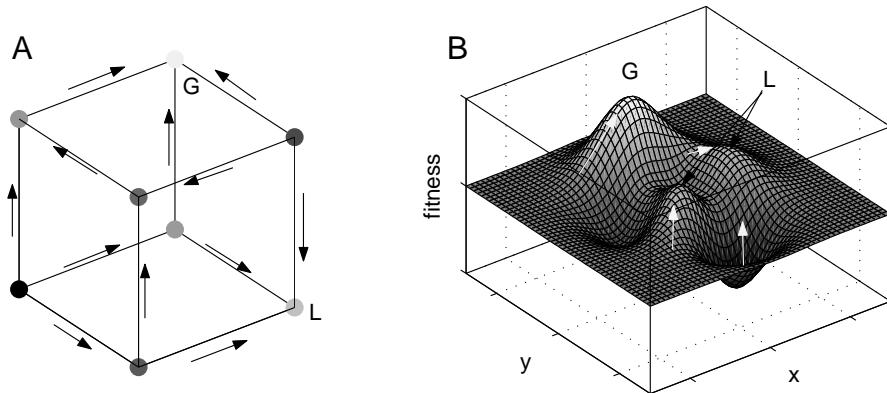


Figure 2.1: Sketch of fitness landscapes in artificial evolution for (A) discrete and (B) continuous genotype spaces. (A) 3D binary landscape as a cube: each axis denotes the value for one locus in the genotype, vertexes represent individuals, depicted as circles. The fitness is represented by the shade of the circle. (B) 2D continuous genotype with an added dimension for fitness: the x and y axis denote the real values for each loci in the genome, the vertical axis denotes fitness and each point in the 3-dimensional surface represents a possible individual and its fitness. In both landscapes, the arrows indicate the preferred flow of a population. Points L and G represent local and global optima respectively.

2.2 Neutrality

Motoo Kimura's neutral mutation - random drift hypothesis (or the *neutral theory* for short) asserts that the great majority of evolutionary changes at the molecular level are caused not by Darwinian selection but by random drift of selectively neutral or nearly neutral mutants (Kimura, 1983). The essential part of Kimura's theory is not so much that the molecular mutants are selectively neutral as that their fate is largely determined by random genetic drift. The importance of his theory is that genetic code can be constantly altered with no fitness disadvantage.

It is important to clarify that the theory does not deny the role of natural selection in determining the course of adaptive evolution. Rather, it assumes that only a minute fraction of DNA changes in evolution are adaptive in nature, while the great majority of mutations exert no discernible phenotypic influence and thus drift randomly through the species (Kimura, 1983). Therefore, that the theory of neutrality is not meant to replace the Darwinian theory of evolution as much as extend it.

2.3 Drift

While in a ‘perfect’ world, any differences in fitness, however small, would drive a gradual but perfectly regular directional change in the composition of the population; evolution is a stochastic process that is subject to sampling error.

Briefly stated, the composition of a population is given by three factors (Bell, 1996): (1) Historical: the composition of the previous generations from which it descends, (2) Selection: which tends to increase the frequency of some kinds of individual and decrease others and (3) Chance, when the difference in fitness is sufficiently small, the chance in composition caused by selection

may be smaller than the change caused by sampling error. Thus, a deterministic assumption (i.e. ignoring chance) is approximately true if the population is large and exact only if the population is infinite (Maynard-Smith, 1998).

For this reason, *genetic drift*, the consequences of random fluctuations in relatively small populations, has been a matter of concern to population geneticists; but one which has been frequently ignored by artificial evolution practitioners, despite the fact that population sizes in the latter tend to be rather small. Moreover, there is a common misunderstanding that this undirected process of variation reduces the effectiveness of selection and therefore retards or inhibits increase in adaptiveness.

2.4 Neutral Networks

Interest in selective neutrality has been re-kindled more recently by the identification of *neutral-networks* as connected networks of genotypes mapping to common phenotypes (and therefore equal fitness) in the context of RNA evolution (Schuster et al., 1994). Extensive computer simulations, based on RNA secondary structures have revealed that neutrality plays an important role in understanding the dynamics of evolution. Among other things, these studies have revealed a constructive role of random genetic drift - as actually improving substantially the search capacity of populations in sequence space.

Generic properties of neutral networks have been derived from the understanding of the relationship between the genotype (RNA sequence) and the phenotype (secondary structure) (Reidys, Stadler, & Schuster, 1997):

1. *More sequences than structures.* There are orders of magnitude more sequences than structures and hence, the map is many-to-one.
2. *Few common and many rare structures.* Relatively few common structures are opposed by a relatively large number of rare structures, some of which are formed by a single sequence only.
3. *Shape space covering.* The distribution of neutral genotypes - sequences that fold onto the same structure - is approximately random in sequence space. As a result, it is possible to define a small hypersphere which contains, on average, for every common structure at least one sequence that folds into it.
4. *Connectivity of neutral networks.* After a certain critical value, which depends on the degree of neutrality, that is the fraction of neutral neighbours, the space is said to be generically connected. Consequently, the phenomenon of percolation is known to occur, which basically means that the networks span the entire sequence space and are thus accessible through random drift (Schuster & Stadler, 2002).

Briefly summarized, neutral networks, depending on how *connected* they are, give access to virtually unlimited number of new phenotypes: the *constant-innovation property*. Consequently, they play an important role in adaptive evolution (Huynen, Stadler, & Fontana, 1996). Many other implications from the discovery of neutral networks have been discussed, including the evolution of complexity (Schuster, 1996), the origin of innovations (Crutchfield & Schuster, 2003) and the evolution of mutational robustness (van Nimwegen, Crutchfield, & Huynen, 1999).

2.5 Neutral Networks in Artificial Evolution

From abstract models of fitness landscapes with tunable neutrality, there has been substantial evidence that appropriate techniques for effective evolutionary search on landscapes with substantial neutrality differ quite radically from more traditional approaches to evolutionary search.

Much of this awareness has sprung from models of abstract fitness landscapes based on Kauffman's well known *NK* landscapes (Kauffman, 1993) with tunable genotype size N and tunable epistatic links K between genes. In Kauffman's model each gene contributes to the total fitness in a manner dependent on its allele and K others, providing thus tunable degrees of 'ruggedness' to the landscapes. Barnett introduced in (Barnett, 1997) an extension to the *NK* model, which adds tunable neutrality via the probability that a certain allele make no contribution to fitness, called the *NKp* model. Briefly summarized, the *NKp* family of landscapes demonstrates that the 'ruggedness' of a landscape can be of lesser significance than its neutral structure as regards evolutionary dynamics. Another very different model, also extended from Kauffman's *NK* model has been proposed in (Newman & Engelhardt, 1998) which has been referred to as the *NKq* model, in which the fitness contributions are drawn from integers between $[0, q]$. Thus, there are q discrete levels. Remarkably, from work on both models evidence has been found that:

1. Neutrality helps the population to find structures of high fitness without having to cross fitness barriers (sequences of lower fitness).
2. Evolution proceeds in jumps separated by epochs in which the fitness appears to change very little.
3. The population uses these epochs to diffuse across the current neutral network, allowing it to search a larger portion of sequence space for paths leading to networks of higher fitness.

Neutral evolution has not been restricted to biological and abstract computational models. There has been gathering evidence that neutrality is prevalent in many real-world evolutionary engineering design problems. The rationale behind this has been mainly that, in complex real-world problems, with many parameters, neutrality may arise from the fact that changes to a particular parameter may frequently produce no discernible contribution to fitness.

In the field of evolutionary robotics, awareness has been raised of the importance of genetic drift when evolving 'neural' network controllers for autonomous visually guided robots in (Harvey et al., 1993; Harvey, 1995). In fact, throughout their work evolving such systems, suggestions are made regarding 'hyper-spatial bypasses' or 'ridges' when referring to the structures of high dimensional fitness landscapes (before the term neutral-networks was coined). Similarly, evidence has been found in (Smith et al., 2001a, 2001b, 2002) of landscapes with neutrality in addition to qualitatively different evolutionary dynamics when evolving another form of robot controller based on neuron-modulating properties of diffusing signalling gas (GasNets).

In the field of evolutionary hardware, when evolving the configuration for a silicon chip on a tone-recognition task it is suggested that neutral networks are crucial for the effectiveness of the search process (Thompson, 1998; Harvey & Thompson, 1996). The evolutionary pathway is analysed showing that the population is genetically highly converged and yet travels far through genotype space. The cause for such aspect of neutral evolution was found to reside in the use of 'junk' genotype, creating a redundant genotype-phenotype mapping.

On the other hand, there has been an amount of work directed towards ‘adding’ neutrality. This work has been mainly directed at purposely engineering redundant mappings and then evaluating the usefulness of the neutrality which arises from it (Shipman, Shackleton, & Harvey, 2000; Shackleton, Shipman, & Ebner, 2000; Jakobi, 2000). In a similar fashion, some (very few) attempts have been made of introducing neutrality to real-valued search spaces by adding binary dimensions to the search space (Zendric-Ashmore, 2003).

2.6 Continuous Fitness Landscapes

Almost all of this work has been based on discrete-alphabet genotypes. Currently, little research has been carried out on real-valued search spaces, regardless of the fact that many artificial evolutionary problems have ‘natural’ real valued parameters. It would be possible to deploy a discrete encoding for a problem with such continuous parameters via binary or Grey coding scheme, but it is not clear why one might one to do so.

Neutrality and neutral network ideas do not carry on intuitively to continuous search spaces. The main reason behind this is that, in the discrete case a particular genotype has a closed set of possible one point mutation neighbours. From those, a proportion will be neutral.

Conversely, in a real-valued search space, an individual has an infinite number of neighbouring points to mutate to, generally given by a hypersphere around the n -dimensional point in genotype space. Although, similar to the discrete case, a proportion may be neutral. In the continuous case it will be statistically impossible to mutate to such equally fit neighbouring points. Mainly because exactly equal points in the surrounding area come to represent an infinitesimal proportion of the complete volume, much like contour lines in a three dimensional surface (see figure 2.2 A).

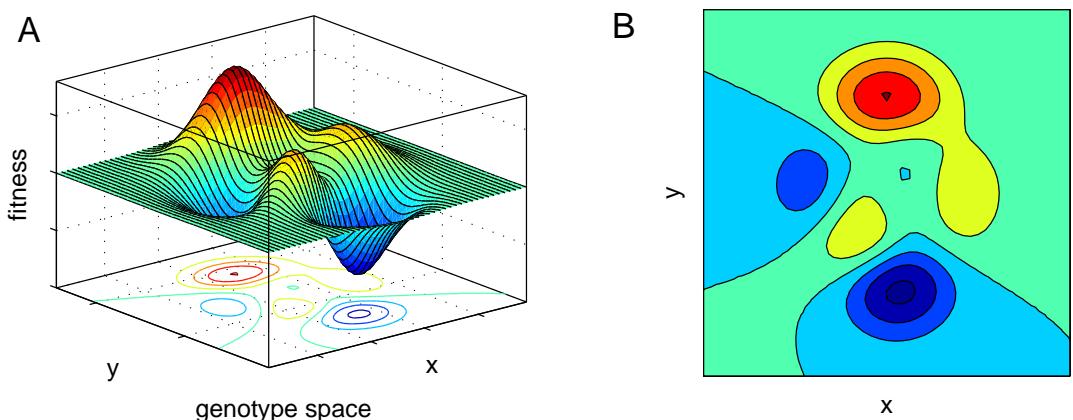


Figure 2.2: Notion of neutral regions in continuous fitness landscapes.

In the case that fitness is quantized, however, one can imagine neutrality as the space between

the contour lines (figure 2.2 B). A notion of a *neutral region* can, then, be proposed as the points in an area (hypervolume in higher dimensions) with *equal* fitness. Indeed, the computational discrete models of landscapes with neutrality intrinsically deal with a finite set of numerical fitness and thus implicitly regard neutral networks as points with exact equal fitness.

However, in many (possibly most) real-world continuous search space scenarios, fitness will most likely be on a continuum. For this reason, the notion of neutral regions in continuous landscapes will necessitate taking into account sufficiently small variations in fitness such that two individuals with similar fitness are regarded as (*nearly*) neutral.

From Ohta's nearly neutral theory of molecular evolution (Ohta, 1992), we know that for the behaviour of alleles to be mainly controlled by random drift, it is not necessary that they be strictly neutral, that is, completely equivalent with respect to fitness. What is required is that the magnitude of their selective advantage or disadvantage does not exceed, roughly speaking, the reciprocal of twice the effective population size (for details see (Ohta, 1992; Kimura, 1983)).

On the other hand, due to intrinsic or even exogenous variations (e.g. environmental variations), there simply may not exist a deterministic fitness value for each possible genotype. In this case, fluctuations induce variations in fitness such that genotypes with similar average fitness are not distinct at the level of selection. Differences in fitness are simply washed out and selection cannot act on them. Thus (near) neutrality may be induced either by many genotypes coding for a given phenotype with a unique fitness, by sampling error from small population sizes or by 'noise' in the fitness evaluations of individuals.

Chapter 3

Dynamical Systems

This chapter will give a very brief review of the essential concepts and terminology of the qualitative theory of dynamical systems which will be needed to understand the rest of this work. This will be followed by their relevance to evolution and neutrality, complemented by related work.

3.1 Essential Concepts and Terminology

A dynamical system is characterized by a set of *state variables* and a *dynamical law* that governs how the values of those state variables change with time. In a continuous-time dynamical system, the dynamical law is given in terms of a set of differential equations which will depend on the state variables and some set of fixed *parameters*. The set of all possible values of the state variables constitutes the system's *state space*.

3.1.1 State Space and Phase Portraits

Starting from some initial state, the sequence of states generated by the action of the dynamical law is called a *trajectory* of the system. The set of all such trajectories through every point in the state space is called the *flow*. In the qualitative theory of dynamical systems one is usually interested in the geometrical or topological structure of the entire flow (Hale & Kocak, 1991).

Of particular interest is the possible long-term behaviour of a dynamical system (Beer, 1995a). The state of some systems will converge to *limit sets*. A limit set is a set of points that is invariant with respect to the dynamical law. An *attractor* is a *stable* limit set which is of particular importance. It has the property that all trajectories passing through all nearby states converge to the attractor. The set of initial states that converge to a given attractor is termed its *basin of attraction*. Those proportions of the trajectories which do not lie on the attractor itself are called transients. *Repellers* are limit sets that are *unstable* (Abraham & Shaw, 1992).

Attractors are important because they govern the long-term behaviour of any physical system. Regardless of the initial state, a physically embodied dynamical system will always be found near an attractor after transients have passed (Beer, 1995a). Due to their instability, repellors can only be observed by starting a dynamical system on a repellor and then never perturbing it. Real-world systems are *noisy* and thus they could never be found on a repellor.

In general, the state space of a dynamical system will contain multiple attractors, each surrounded by its own basin of attraction. A global characterization of this space is called the *phase portrait* of the system (Abraham & Shaw, 1992).

3.1.2 Parameter Space

We need another fundamental idea from dynamical systems theory: *parameter space*. A point in parameter space reflects a specific combination of all parameter values and thus to a fixed set of basins of attraction and attractors in the corresponding state space of the dynamical system or phase portrait. Most dynamical systems are *structurally stable*, that is, for most parameter settings; small changes in the parameter values will produce small changes in the flow. Limit sets and basins of attraction may deform and move around a bit, but the new flow will be qualitatively similar to the old one. However, at certain parameter values, dynamical systems can become *structurally unstable*, so that even infinitesimal changes in parameter values can cause drastic changes in the flow, producing phase portraits that are qualitatively different from the original. For example, a basin may contract to nothing, or a new basin might appear. These qualitative changes in the types of limit sets are called bifurcations (Hale & Kocak, 1991). The values of parameters at which bifurcations occur therefore divide parameter space into disjoint volumes.

Finally, recommended tutorial introductions to dynamical systems theory are (Strogatz, 1994; Abraham & Shaw, 1992; Hale & Kocak, 1991).

3.2 Relevance to Evolution and Neutrality

Dynamical systems, their parameter space and phase-portraits are of relevance to this work because in many real world evolutionary design problems it is the case that one is attempting to synthesize a dynamical system (for example a dynamical neural network for a robot controller) capable of particular dynamical behaviours, in a process which is constrained to altering the real-valued parameters of the system. The question that we are asking is: in the case that the approach taken to alter the real-valued parameters is an evolutionary one, can the redundant mapping from the dynamical system's parameter space to its phase-portrait affect the evolutionary dynamics? In other words, during evolving, are most changes to the parameters (nearly) neutral? Neutral or nearly neutral would come to represent in the language of dynamical systems: movement in parameter space without crossing a bifurcation. Furthermore, we ask, in the case that such redundant mapping is available, and consequently small changes to the parameter space frequently lead to only slight changes in the phase-portrait, how can one take notice of it? Will it be, as in the discrete case, a matter of exact neutrality? How does this affect the evolutionary dynamics when evolving dynamical systems?

W. R. Ashby first introduced the idea of adaptive walks in parameter space of a dynamical system toward parameter values corresponding to a dynamical system with ‘good’ attractors. Although he was thinking of physiological and neural adaptation (as opposed to evolutionary adaptation), he attempted to capture the central problem of adaptation in a system with many interacting parts (Ashby, 1960).

Kauffman in (Kauffman, 1993) discusses very similar ideas in discrete dynamical systems in the context of evolution. In particular, he analyses Boolean dynamical networks and as he is gen-

erally referring to landscapes as purely rugged terrains, he comes to the conclusion that landscape structure varies from correlated to very uncorrelated as Boolean systems pass from ordered to chaotic behaviour. His remark is that the ruggedness of a fitness landscape is governed in part by how closely intertwined bifurcation surfaces are. If they are closely interwoven, landscapes are very rugged.

Beer in (Beer, 1995a) proposes a dynamical systems approach to understanding adaptive behaviour (following the Cybernetic tradition), with the underlying theme that behaviour must be seen as emerging from the ongoing interaction between an agent's nervous system, its body and its environment. For this reason his work has involved synthesizing dynamical system models to produce particular dynamical behaviours. For this his approach has been an evolutionary one. In recent work, from evolving dynamical neural network to synthesize central pattern generators for walking behaviours (Seys & Beer, 2004), the evolutionary dynamics has been observed to have relatively well-defined regions of similar fitness which they have referred to as 'phases'. Evolving populations are seen to spend some time on such phenotype-static epochs and then jump to levels of higher fitness. In a similar fashion and in the same context in (Psujek et al., 2004) particular unique ranges of fitness have been associated with the architecture of the dynamical system's network as well.

Finally, recent work in (Barnett, 2002b) evolving similar dynamical neural networks, this time to solve a logic gate, using real-valued genes, evidence is provided of regions of similar fitness at different levels (plateau-like) from three-dimensional projections of the higher dimensional landscapes. In (Izquierdo-Torres, 2004) evidence supporting this picture is provided from the study of the distribution of fitness effects of mutations on a similar model, where most genetic changes caused only slight effects in fitness and only some caused major ones.

Chapter 4

Methodology

In this chapter we describe the dynamical system model, the fitness landscapes and the evolutionary technique and measurements. This will be used to gain insight into the evolutionary process when evolving dynamical systems on distinctly phase-portrait-related continuous landscapes.

4.1 Continuous-Time Recurrent Neural Networks

As a generic dynamical system model in which to study evolutionary processes we resource to continuous-time recurrent neural networks (CTRNNs) for several reasons:

1. CTRNNs are complex nonlinear dynamical systems which are universal dynamics approximators (Funahashi & Nakamura, 1993). In other words, given any dynamical system where the variables change smoothly, we can in principle find a CTRNN, with enough nodes, that will approximate its dynamical behaviour to any desired degree of accuracy.
2. CTRNNs are being applied to a wide variety of problems. Among others, within the autonomous agents community, there is a growing interest in the use of dynamical neural networks for controlling the behaviour of agents (Beer, 1995a).
3. The approach to tuning the parameters of CTRNNs has been, for the most part, an evolutionary one (Harvey, Husbands, Cliff, Thompson, & Jakobi, 1997). They are commonly evolved using real-valued genotypes, providing a family of continuous landscapes of tunable dimensionality and complexity.

A neurobiological interpretation has been given to CTRNNs (Beer, 1995b), where a unit in the network is associated with a biological neuron. This view will be orthogonal to the aims of our work. We are interested in CTRNNs as a generic complex nonlinear dynamical system: simple enough to be computationally and analytically tractable; yet powerful enough to be capable of modelling any dynamical behaviour. Accordingly, we will refer to the units of the network as nodes and not neurons. CTRNNs are networks of model nodes of the following general form (for details see (Beer, 1995b)):

$$\dot{y}_i \equiv \frac{1}{\tau_i} \left(-y_i + \sum_{j=1}^N w_{ji} \sigma(y_j + \theta_j) + I_i \right) \quad i = 1, 2, \dots, N \quad (4.1)$$

where y is the state of each node, τ is its time constant ($\tau > 0$), w_{ji} is the strength of the connection from the j^{th} to the i^{th} node, θ is a bias term, $\sigma(x) = 1/(1 + e^{-x})$ is the standard logistic activation function, I represents a constant external input, and N is the number of nodes. In simulation, node activations are calculated forward through time by straightforward time-slicing using Euler integration.

Of particular interest when evolving these dynamical systems are networks in which the sigmoidal activation function of each node is centred over the range of net inputs that it receives. This corresponds to networks whose nullclines intersect at their exact centres, and will be referred to as centre-crossing networks (Beer, 1995a; Mathayomchan & Beer, 2002). They are defined by setting the bias of each node in the network to:

$$\theta_i = -\frac{I_i + \sum_{j=1}^N w_{ji}}{2} \quad (4.2)$$

4.1.1 Parameter Space as Genotype Space

The property of neutrality in the dynamics of evolution is greatly determined by the genotype-phenotype mapping of the model being evolved. Our model represents the common encoding and mapping scheme used in the artificial life and evolutionary robotics literature, where the genotype is real-valued and maps almost directly to the parameters of the CTRNN. The genotype, \underline{G} , is a vector of $N^2 + 2N$ real numbers which can take any value ($g_i \in [-\infty, \infty]$), where N is the number of nodes in the network. The weights and biases in the network are given directly by the real-valued genes: g_i for $i = 1, \dots, N^2 + N$. The time constants are exponentially mapped by: $\tau_i = e^{|g_i|}$. Additionally, τ is forced to be at least ten times bigger than the integration time-step. The rationale behind the exponential mapping is to ensure that both big and small time-constants are easily accessible in parameter space. Forcing it to be above a certain threshold relative to the integration time-step ensures that it will not generate undesired errors in the Euler integration.

4.1.2 Phase Portrait as Phenotype

A phenotype can be defined in multiple ways. In particular, when evolving dynamical systems three obvious levels of phenotype can be accounted for:

1. Phenotype as configuration of the parameters of the system. For the case of CTRNNs the weights, biases and time-constants of the nodes.
2. Phenotype as dynamical behaviour (or phase-portrait) of the dynamical system.
3. Phenotype as the adequacy of the system in the task at hand (evaluated fitness).

Arguably, many other levels of phenotype can be defined as well. For the reasons discussed in the previous chapters, in our work the notion of phenotype is to be centred on the dynamical behaviour or phase-portrait of the system.

4.2 Landscape Models

In order to study the possibilities of redundant mappings arising from the evolution of dynamical systems we introduce two evolutionary scenarios which differ in their directness of the mapping between the phase-portrait and the fitness.

4.2.1 Phase-Portrait Landscapes

The first evolutionary scenario deals with landscapes at the most abstract and direct level. The mapping to fitness corresponds to a one-to-one ranking of the distinct phase-portraits of a dynamical system. This model is important because it allows us to better understand the relationship between the dynamical system's parameter (genotype) space and its phase-portrait (fitness) space. This scenario represents a *family of landscapes*, defined as the set of different orderings of the possible phase-portraits. Thus, the cardinality of the family will be given by the number of distinct phase-portraits that the system can exhibit. Accordingly, each N -node CTRNN has its own family of landscapes.

In order to simulate evolution on these landscapes we would like to automatically categorize the distinct phase-portraits of the CTRNN. The ideal would be to have an explicit expression for the general solution of the nonlinear sets of equations describing how the trajectories of the CTRNN solve in time from a given initial state. Unfortunately, no elementary expression for the solution exists even in the simplest cases.

In dynamical systems theory, the normal equivalence relation is that of topological conjugacy. Roughly speaking, two dynamical systems are topologically conjugate (have the same phase-portrait) if the phase-portrait can be continuously deformed into the phase-portrait of the other without producing any bifurcations (Beer, 1995a). As we would like to quantitatively classify the distinct dynamical behaviours for our evolutionary simulations, we resource to a categorization based on the number and type of equilibrium points. Even though many of the phase-portraits will be uniquely identified, there will be cases where two different phase-portraits have the same number and global type of equilibria. For the purpose of our work this drawback is not a major one.

One node CTRNN

The behaviour of scalar systems are constrained to points as limit sets, which maybe either stable (single-point attractor) or unstable (single-point repellor). A single node, in the absence of a self-connection, would decay exponentially to the external input (I) and thus only a phase-portrait with an attractor would be possible. The presence of the self-connection endows this simple system with an additional phase-portrait: two attractors whose basins of attraction are separated by an unstable equilibrium point. This portrait occurs when the self-connection is large enough to maintain the state of the node activated through positive feedback (Beer, 1995b). Figure 5.1 depicts both 1-node phase-portraits possible, which we will refer to as unistable and bistable, respectively.

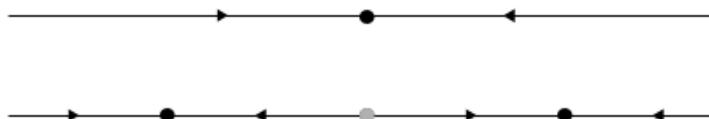


Figure 4.1: Phase-portrait catalogue for 1 node with a self-connection. Black circles represent stable equilibrium points, and the grey circle represents an unstable equilibrium point.

The family of *1-node Phase-Portrait Landscapes* is, thus, proposed as assigning an ordering

on the two portraits possible with a unique numerical fitness. Naturally, this family contains only two possible landscapes: one where bistable systems are ranked higher than unistable ones, and vice versa. Either way, this family of landscapes can be imagined as comprised of two big flat regions. A *neutral region* is, then, defined as the three-dimensional volume in parameter space (w , θ and τ) whose points represent unistable or bistable dynamical systems.

In order to classify the phase-portraits we compute the number and type of equilibrium points from the one node CTRNN as given by:

$$\dot{y} = f(y; w; \theta; I; \tau) \equiv \frac{1}{\tau} (-y + w\sigma(y + \theta) + I) \quad (4.3)$$

Equilibrium points represent constant solutions of Equation 5.3 and correspond to zeroes of f . The zeroes of f are clearly independent of τ . The stability of an equilibrium point is given by the sign of:

$$\frac{\partial f}{\partial y} \equiv f'(\bar{y}, w, \theta) \equiv w\sigma'(y + \theta) - 1 \quad (4.4)$$

where $\sigma'(x) \equiv \sigma(x)(1 - \sigma(x))$. A given equilibrium point \bar{y} of Equation 5.4 is stable if $f'(\bar{y}, w, \theta) < 0$ and unstable if $f'(\bar{y}, w, \theta) > 0$ (Hale & Kocak, 1991). For details on the computational method used to obtain the roots see appendix A.

Two node CTRNNs

Planar dynamical systems are subject to a few more limit sets, including saddle-nodes and limit cycles. In particular, 2 node CTRNNs are capable of many more interesting phase-portraits with distinct global and local behaviours including attractive combinations of limit cycles with attractors. The range of dynamical behaviours in 2 node CTRNNs has been systematically studied in (Beer, 1995b). The 2 node categorization is simplified to the number and global type of equilibrium points as in table 5.1. We will, nevertheless, refer to this classification as the available phase-portraits for the rest of the work.

Analogously, the family of 2-node landscapes is proposed as assigning each of the 10 phase-portraits possible a unique fitness ordering. The number of different landscapes is given by the permutations of rank-ordering; thus, this family contains more than 3 million possible landscapes! (i.e. $10!$). The *neutral regions* would similarly correspond to points in space (8D hyper-volumes) generating a dynamical system with the same phase-portrait. In the following chapter, we proceed to study the generic properties of the complete family of landscapes, without loss of generalization, by not assigning particular rank orderings, but studying them abstractly.

In order to classify the phase-portraits we compute the number and type of equilibrium points from the 2 dimensional CTRNN as given by:

$$\begin{aligned} \dot{y}_1 &= f(y; w; \theta; I; \tau) \equiv \frac{1}{\tau_1} (-y_1 + w_{11}\sigma(y_1 + \theta_1) + w_{21}\sigma(y_2 + \theta_2) + I_1) \\ \dot{y}_2 &= f(y; w; \theta; I; \tau) \equiv \frac{1}{\tau_2} (-y_2 + w_{12}\sigma(y_1 + \theta_1) + w_{22}\sigma(y_2 + \theta_2) + I_2) \end{aligned} \quad (4.5)$$

Unlike the one node case, intersecting the curves along which either $\dot{y}_1 = 0$ or $\dot{y}_2 = 0$ in state space (y_1, y_2) is much more complicated because the nullcline expressions may have as many as three disjoint ranges of y_1 values (Beer, 1995b). It is more convenient to study Equation 5.5 in

Name	Attractors	Repellors	Saddle Nodes	Limit Cycles
1	1	0	0	0
1lc	0	1	0	1
3a	2	0	1	0
3b	2	0	1	0
3lc	1	1	1	1
5a	3	0	2	1
5b/5c	2	1	2	0
5lc	2	1	2	1
7	3	1	3	0
9	4	1	4	0

Table 4.1: Names and global configuration of the two-node phase-portraits used for classification in this work - adapted from (Beer, 1995b). The names for each portrait reflect its number of equilibrium points. In the case of 3 and 5 equilibrium points an additional letter is used to distinguish between distinct phase-portraits having the same number of equilibrium points. The suffix *lc* represents the presence of a limit cycle. Note: even though phase-portraits 5b and 5c are different as they have the same number and global type of equilibrium points they are classified under the same category.

the synaptic input space (J_1, J_2) of the nodes. The synaptic input is just the input that it receives from the other nodes. Thus, $J_1 \equiv w_{21}\sigma(y_2 + \theta_2)$ and $J_2 \equiv w_{12}\sigma(y_1 + \theta_1)$. Assuming that the cross-connections are non-zero, Equation 5.5 can be re-written as (Beer, 1995b):

$$\begin{aligned} J_1 &= \frac{1}{\tau_2} \left(J_1 - \frac{J_1^2}{w_{21}} \right) \left(\frac{w_{22}}{w_{21}} J_1 - \ln \left(\frac{J_1}{w_{21} - J_1} \right) + J_2 + I_2 + \theta_2 \right) \\ J_2 &= \frac{1}{\tau_1} \left(J_2 - \frac{J_2^2}{w_{12}} \right) \left(\frac{w_{11}}{w_{12}} J_2 - \ln \left(\frac{J_2}{w_{12} - J_2} \right) + J_1 + I_1 + \theta_1 \right) \end{aligned} \quad (4.6)$$

By setting these expressions equal to 0 and solving for J_1 and J_2 , respectively, we obtain the following expressions for the nullclines in synaptic input space:

$$\begin{aligned} J_2 &= \ln \left(\frac{J_1}{w_{21} - J_1} \right) - \frac{w_{22}}{w_{21}} J_1 - I_2 - \theta_2 \\ J_1 &= \ln \left(\frac{J_2}{w_{12} - J_2} \right) - \frac{w_{11}}{w_{12}} J_2 - I_1 - \theta_1 \end{aligned} \quad (4.7)$$

The intersections of the nullclines in Equation 5.7 give the equilibrium points of the 2 node CTRNN.

The common notion about solving systems of nonlinear equations is that there are no good general methods (Press, Teukolsky, Vetterling, & Flannery, 1992). In order to find all common points, which are the solutions of our nonlinear equations, we will have to map the full zero contours of both functions. This basically requires finding all the points of intersection of 2 nonlinear systems of equations. This is very computational demanding (see appendix A for method to numerically computing equilibria). It is easy to see why we stopped calculating equilibria at this

early dimension. In higher dimensional scenarios, we would need to find points mutually common to N unrelated zero-contour hypersurfaces, each of dimension $N - 1$. Numerically computing all possible equilibria becomes virtually impossible.

4.2.2 Attractor Landscapes

Categorizing the fitness of the CTRNNs directly from its phase-portraits is a very abstract scenario and ultimately fitness values are quantised. For the second part of our work we will turn to a model landscape whose genotype-fitness mapping is less direct. The main idea is to produce a model landscape in which to study the evolutionary dynamics of CTRNNs in relation to their dynamical behaviour but in the presence of a continuous fitness function. For this reason, we introduce a family of tasks which we will refer to as *Attractor Landscapes*. It is intended to represent a ‘generic’ scenario where, from a dynamical systems perspective, a successful solution depends on the number of attractors of the system.

Briefly stated, the model asks a dynamical system to categorize a pattern of inputs composed of high or low signals which are fed through the external input of a number of the nodes. The categorization is achieved by the settling of the system into a particular attractor state for each different pattern of inputs. An important aspect of this model is that it considers circuits with (very simple) time-varying inputs. *Phase-portraits landscapes* allow us to study the dynamics of autonomous circuits (i.e. circuits whose inputs are fixed to constant values). Nonautonomous systems are important mainly because it allows taking into account the possible interactions between the system and its environment (in the example of robots, this would correspond to one that has sensors). Ahead we explain the model using the simplest case of the model and later we extend it to its generic form.

Say we have a 1-node CTRNN with a self-connection. For an evaluation trial the activation of the node is initialized at random. Then the dynamical system is integrated forward through time for an initial period of stabilization (T_s) where no external input is presented. After which, an external input is given with a positive or negative signal for a duration of T_i units of time. The CTRNN is, then, evaluated by the difference between a target output (λ) and the average of the sigmoided activation of its node over T_e units of time (i.e. long enough so that it remains settled into its target attractor). A fitness trial is considered when the process described above is performed for both positive and negative signals.

Let us define the *dimension of the external input* as the number of different signals that the CTRNN will be subject to and label it α . In the simplest case described above $\alpha = 1$. For $\alpha = 2$, the CTRNN receives signals on two of its nodes. The *signal* can have two possible values (positive or negative). Consequently, the number of different pattern of inputs will be given by 2^α and it will require at least the same amount of different attractors from the CTRNN to receive near full fitness. Naturally, the CTRNN must have at least α nodes as well¹.

Having explained the smallest cases, let us formally define a fitness trial by:

¹Interestingly enough, an α task requires a potential for 2^α attractors for full fitness and similarly an α -node CTRNN can maximally have the same, 2^α , number of attractors!

$$f = 1 - \left[\frac{\sum_{j=1}^{2^\alpha} \sum_{i=1}^{\alpha} \sqrt{(\lambda_{ij} - \bar{y}_{ij})^2}}{2^{\alpha-1} \alpha} \right] \quad (4.8)$$

where α is the number of nodes receiving external inputs and being evaluated; \bar{y}_{ij} is the averaged sigmoided activation over the evaluation period for the corresponding pattern of inputs j and node i ; λ_{ij} is the target output which can be 1 or 0 depending on whether the external input presented, I_{ij} , is positive or negative, respectively.

Ultimately, the fitness function is given by the worst f over a number of trials (γ). On each trial the initial activations of the CTRNN are randomized over each node's bias term by $[\theta - \beta, \theta + \beta]$, where β is a random variable uniform in $[0, 1]$. Additionally, white noise with a Gaussian random variable with mean 0 and standard deviation 0.01 is added throughout the simulation on the external input signal and the activation of the nodes. An integration time step of 0.1 is used, an initial stabilization period of $T_s = 10$ units of time, input is then presented for $T_i = 10$, and the activations are evaluated over a longer period of $T_e = 30$. Accordingly, the fitness function ranges from -1 to 1.

Briefly stated, this family of landscapes is the result of evolving N -node CTRNNs to have at least α attractors, and to be capable of moving from one attractor to the other as a result of a time-dependent set of inputs.

Finally, in an attempt to provide a ‘real-world’ interpretation we can suppose that: (1) an agent with 2 sensors is controlled by a 2-node CTRNN, (2) external input signals are ‘different pattern of lights/sounds an agent is exposed to from its environment’, (3) the agent has two motor output (i.e. wheels) to its side which are controlled by each of the nodes. The wheels can be anywhere from off (0) to on (1) as given by the sigmoided activation of each node. The agent’s sensor can be non-activated (0), or positively and negatively activated (1 or -1 respectively). A successfully evolved agent would correspond to one that after sensing positive signals for a duration of time, moves forward and maintains movement until another pattern of signals is received. This would correspond to being on a particular attractor and similarly for other pattern of inputs. The complexity of behaviours obviously increases with the α dimension and needless to say there are as many different interpretations as ones imagination may account for.

The model has fundamentally two tunable parameters which we will discuss briefly ahead: First, the dimension of external input, α , defines the complexity of the task. Second, the number of nodes, N , tunes the dimensionality of the search space. Additionally, three parameters of the model affect different forms of noise: (1) the randomization of the initial activations, β , (2) the number of trials per fitness, γ , and (3) the standard deviation of the white noise, σ^2 .

4.3 Evolutionary Dynamics

This section introduces the measurements that will be used to gauge the dynamics of our evolutionary models and the evolutionary technique employed.

4.3.1 Evolutionary Algorithms

The evolutionary technique used consists of a simple 1+1 population with a random mutation strategy, or *Netcrawler* (Barnett, 2001). The hill-climber is initially dropped into genotype space

according to a uniformly distributed random vector in $[-k, k]$. The individual is then mutated, and unless the new individual is worst fit than the original, this one is replaced by the newer. For simplicity, the original individual will be referred to as the *netcrawler*; and the individual generated from a mutation of the original individual will be referred to as the *mutant netcrawler*.

This technique has been originally designed as an optimum way to drift along discrete-alphabet fitness landscapes with substantial neutrality featuring neutral networks. The reason for this is, basically, that the *netcrawler* can randomly drift through sequences of equal fitness in genotype space, diffusing through the current neutral network, until a mutation leads it to a network of higher fitness, in which case it jumps to a different neutral network, and so on, repeatedly.

It is important to note that the *netcrawler* can only drift through search space along *equally* fit neighbours. In our implementation of the technique, when fitness is on a continuum and the fitness function is noisy (i.e. for the Attractor Landscape), fitness is evaluated every time the *netcrawler* is compared with a new mutation. This, in turn, allows for random drifting to take place between individuals of nearly-equal fitness due to fluctuations in fitness. In (Izquierdo-Torres, 2004) we experimented with a different variation to the original *netcrawler* technique for the case of deterministic fitness evaluations. There, the *netcrawler* was allowed to be replaced by individuals with (tunable) ranges of slightly worst fitness (note that noise makes this variation unnecessary).

Mutation

Mutation operators in binary genotypes generally consist of 1-point mutations (or similar N -point mutation operators). In real-valued space, the mutation operator changes significantly. As the genotype is a point in the N -dimensional hyperspace, where N is the size of the genome, the most convenient mutation operator is one that displaces the individual with equal probability to any point in the surrounding space. For this reason, the mutation operator used is a Gaussian distributed vector displacement with mean 0 and standard deviation $\sigma^2 = 0.1$.

4.3.2 Evolutionary Measurements

Our approach for drawing insight into the evolutionary process is based on the movement of the *netcrawler* in both its fitness and in genotype space an evolutionary run. Despite the lack of measurements for neutrality in continuous landscapes, several indicators have been introduced which provide a meaningful idea of the coupling between phenotypic and genotypic convergence.

At the fitness level, the fitness of the *netcrawler* and of the mutation (*mutant netcrawler*) is measured. The fitness of the mutant is a good indicator of the structure of the landscape surrounding the *netcrawler* at a certain time.

As regards genotype space, the *diffusion coefficient* is an estimate of the velocity at which the population is moving in genotype space, as given by the squared Euclidean distance of the *netcrawler* in adjacent generations. In practice, the diffusion coefficient is more fruitfully presented as an average over several generations, this will be referred to as the *lagged diffusion coefficient*, and it serves as an estimate of the distance travelled by the *netcrawler* in a certain time lapse. This is given by a lagged squared Euclidean distance between the *netcrawler* at generation i and k generations prior. In our experiments a time lag $k = 500$ was used.

Additionally, in the quantised fitness landscapes provided by the *Phase-Portraits Landscapes*

a variation of the *netcrawler* is used to perform *neutral walks*. In this case, the individual mutates to a new point in genotype space as long as its fitness remains unchanged.

Finally, it is important to remark that, in this study, particular evolutionary runs will be preferred over averages over many runs. For the simple reason that averages effectively smooth the fitness epochs during evolution.

Chapter 5

Simulation Results

In this section the results taken from evolutionary runs using the experimental design described in the previous chapter are given. The notion of *neutral* and *nearly neutral regions* in continuous search spaces when evolving dynamical neural networks is interpreted and discussed in two different scenarios ranging from completely abstract ranked phase-portraits to slightly more complex real-world-related-task landscapes.

5.1 Phase-Portraits Landscapes

This first section deals with landscapes at the most abstract level, where the mapping from the phase-portrait to the fitness is direct. These experiments are important because they allow us to better understand the relationship between the dynamical system's parameter space and phase-portrait space.

5.1.1 A Single Node with a Self-Connection

We begin with the simplest CTRNN: a single node with a self connection. We are interested in the statistical properties of this family of landscapes, in its general form. In particular, the proportion of distinct phase-portraits from randomly generated individuals is of crucial importance to evolutionary dynamics for it offers a quantitative characterization of the landscape structure. Figure 4.1 shows the proportion of both phase-portraits from randomly generated individuals for two different ranges of parameters.

As can be observed, genotype space is dominated by unstable systems. Interestingly enough, when the search is biased exclusively on centre-crossing circuits then the proportion of randomly generated bistable systems increases significantly. Although the time constant is a crucial factor in the behaviour of a system, we know from section 5.2.1 that only the weight and bias are involved in determining the equilibrium points. Such low dimensional space allows us to study the structure of this family of landscapes exhaustively from a simple two-dimensional projection (see figure 4.2).

Evolution in 1-node Phase-Portrait Landscapes

Predicting the duration of the epochs of random drift while the population is diffusing in regions of neutral fitness until a new region is found tends to be very problematic, largely due our poor

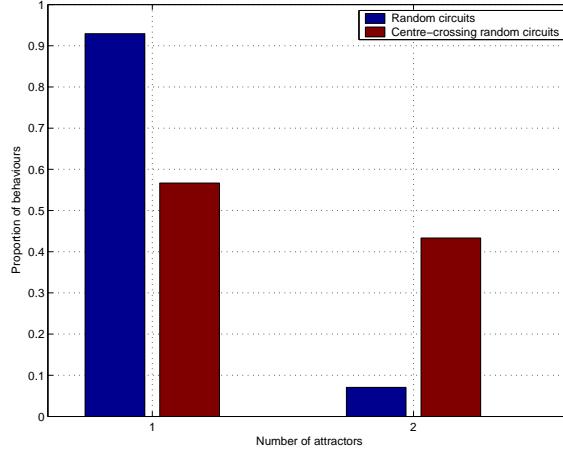


Figure 5.1: Proportion of unstable (1) and bistable (2) behaviours from randomly generated 1-node CTRNNs (blue) and randomly generated centre-crossing 1-node CTRNNs (red) with parameters drawn uniformly at random ($w, \theta \in [-30, 30]$) with a fixed time-constant, $\tau = 1$.

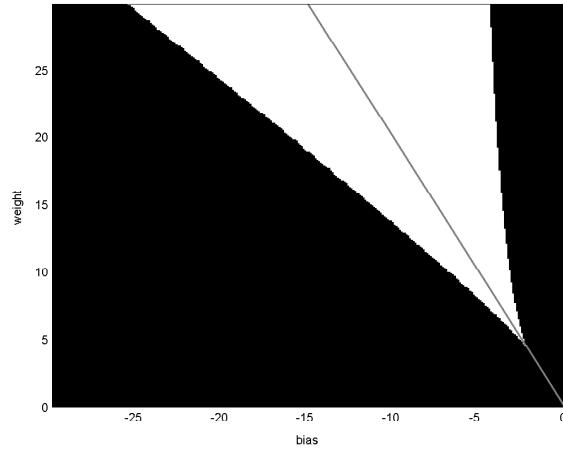


Figure 5.2: 2D projection of the phase-portrait landscape for the one node with a self-connection dynamical system. Black area represents regions of genotype space which produce systems that are unstable. Similarly, white area represents bistable systems. The grey line represents centre-crossing networks.

understanding of neutrally drifting populations (Derrida & Peliti, 1991). In order to obtain a better idea of the likeliness of reaching one region from anywhere else in the other region we performed 1000 evolutionary runs with the *netcrawler*, starting from uniformly random points in genotype space ($w, \theta \in [-30, 30]$) and terminating when the other region or a maximum of 100000 mutations are reached. From this experiment the following results were obtained: Out of the 1000 walks, 934 started in the unstable region and the rest in the bistable one. From the unstable region, only 21.73% of the times the netcrawler managed to reach the bistable region below the maximum number of mutations. For the walks in which it reached the other region it did so with an average 72807 mutations and standard deviation 38168. On the other hand, from the bistable area, it reached the other region 98.53% of the times, on those times it took an average 11053 mutation on average, with standard deviation 15540. These results provide us with a further understanding

of how evolution may proceed in this simplest family of landscapes.

The simplicity of the behavioural possibilities in the one node CTRNN in addition to the low dimensional genotype space besides offering us a very concrete notion of what the *neutral regions* are and how they can be related to both genotype and phenotype space, it leaves us with little more to explore at the moment. We will come back to evolution of the simplest CTRNN when analysing *Attractor Landscapes*.

5.1.2 Two Node Networks

Two node CTRNNs provide a more ideal level of complexity to analyse neutral regions in continuous search spaces for several reasons: (1) the behavioural dynamics possible are much richer; (2) dimensionality of the space is of intermediate complexity, far more interesting than 2 and 3 low dimensional spaces but neither unmanageably large; (3) the computational task of automatically categorizing dynamical behaviours is just on the borders of tractability.

Statistical Properties of 2 node CTRNN Phase-Portrait Landscapes

This higher dimensional space is already much harder to grasp at once. For this reason we are interested in its statistical characterization. In particular we ask how are the *neutral regions* distributed and connected in genotype space. To begin, we first explore 3 dimensional projections of this family of landscapes. Figure 4.3 depict projections of this family of landscapes, where the x and y axis represent dimensions of genotype space (self-connections and biases, respectively) and colour represents phenotype space (phase-portraits) as given by the legend in table 4.1.

1	1lc	3a	3b	3lc	5a	5b/5c	5lc	7	9
1	2	3	4	5	6	7	8	9	10

Table 5.1: Phase-portrait legend for figure 4.3

Although projections (A) and (B) (from figure 4.3) of the 2-node phase-portrait landscape provides us with much insight into how changing certain parameters we can generate certain dynamical systems with particular behaviours. Their low-dimensionality leads us into thinking that certain regions may be locally isolated from each other. In projection C, a different perspective on genotype space is provided: in a very small range of biases ($\theta_1 \in [-4.5, -3.5]$, $\theta_2 \in [-3.5, -2.6]$) a statistical sampling of the possible phase-portraits from variations in the self-connections and one of the cross-connection, endow us with further insight into the high dimensional structure of these landscapes: with many different phase-portraits laying relatively close to each other in different dimensions.

In order to analyse the statistical properties of this space more systematically, we randomly generated 1 million CTRNNs and observed what phase-portrait they generated, for different ranges of parameters: (A) between $[-7, 7]$ and (B) between $[-14, 14]$. Similarly, for randomly generated centre-crossing CTRNNs (C and D) (see table 4.2 and figure 4.4).

As in the simpler one node with a self-connection, the *two node CTRNN Phase-Portrait Landscapes* is vastly dominated by networks which generate unstable dynamics. Furthermore, it is fair to characterize the landscape as having *few very common portraits and many uncommon ones*. We can also appreciate from this experiment that certain regions of the landscape, in particular

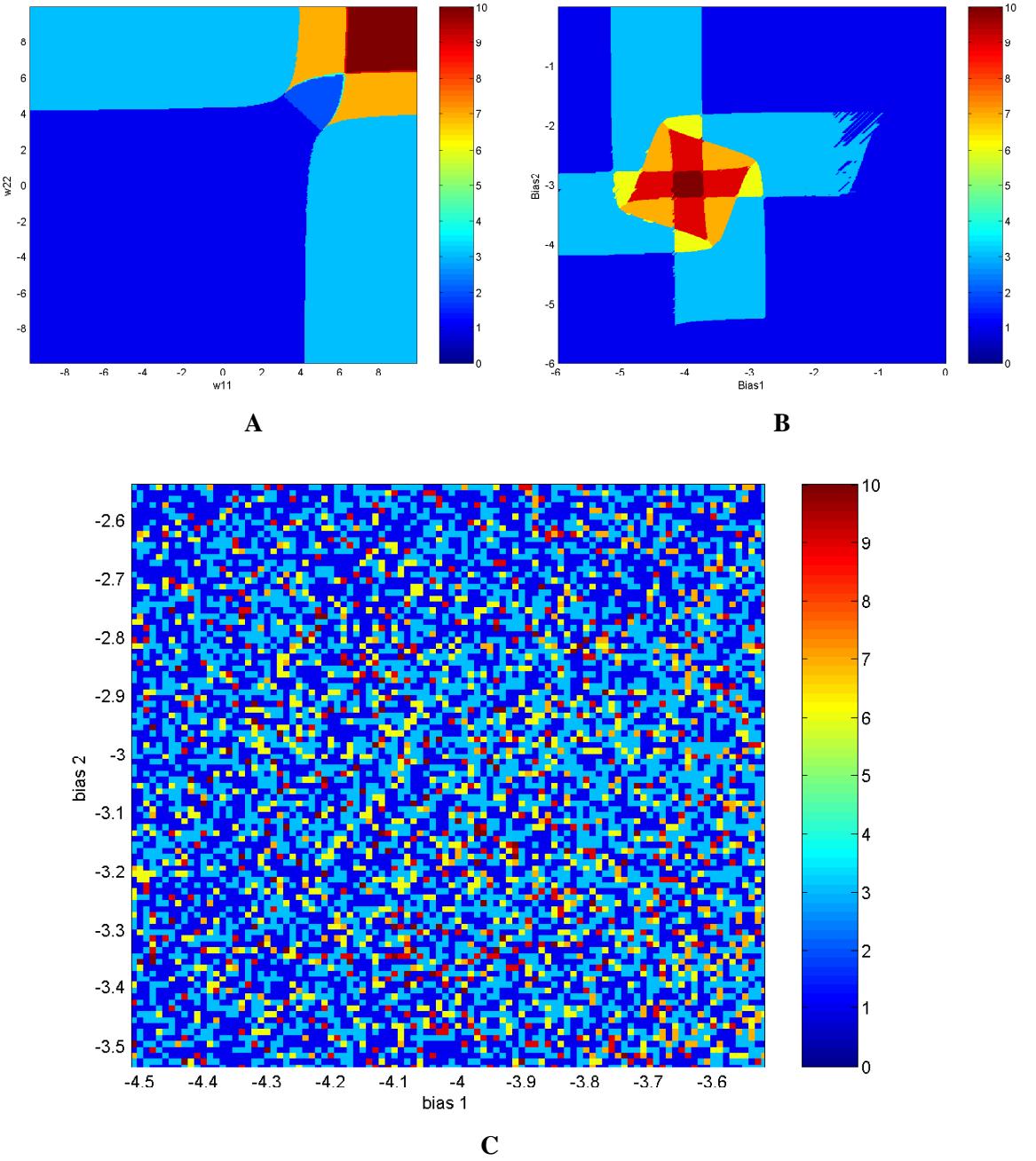


Figure 5.3: Slices through the 9-dimensional phase-portrait landscape for the 2-node CTRNN. (A) The x and y axis represent the self-connections $w_{11}, w_{22} \in [-10, 10]$, biases are varying so to produce centre-crossing circuits. All other parameters are fixed ($w_{12} = -1, w_{21} = \tau_1 = \tau_2 = 1$). (B) Biases on the x and y axis $\theta_1, \theta_2 \in [-6, 0]$. All other parameters are fixed ($w_{11} = w_{22} = 7, w_{21} = -1, \tau_1 = \tau_2 = 1$). (C) Behaviour space covering: Biases on the x and y axis $\theta_1 \in [-4.5, -3.5], \theta_2 \in [-3.5, -2.6]$. Self connections are drawn uniformly between [3, 5] and w_{21} is flipped between -1 and 1 with 50% chance. The rest of parameters fixed ($w_{21} = \tau_1 = \tau_2 = 1$). On all figures, colour represents distinct phase-portraits as given by the phase-portrait legend in table 4.1.

the region of centre-crossing networks (as can be seen from figure 4.4 B and B'), seem to have a relatively higher probability of generating more of the uncommon phase-portraits. This is im-

	1	1lc	3a	3b	3lc	5a	5b/5c	5lc	7	9
A	97.607	0.089	1.5126	0.0087	0.0006	0.004	0.001	0	0.0002	0
B	95.155	0.1924	1.0188	0.0401	0.0018	0.0018	0.0054	0.0004	0.0005	0
C	60.596	4.5595	32.662	0.0099	0.0006	0.0377	0.6409	0.0372	0.0152	0.0113
D	41.002	7.4874	26.768	0.2274	0.013	0.1313	1.0326	0.0414	0.0518	0.0641

Table 5.2: Percentages of randomly generated CTRNNs grouped per phase-portraits. Parameters drawn from: (A) uniformly random between $[-7,7]$; (B): uniformly random between $[-14,14]$; (C): uniformly random centre-crossing between $[-7,7]$; and (D): uniformly random centre-crossing between $[-14,14]$

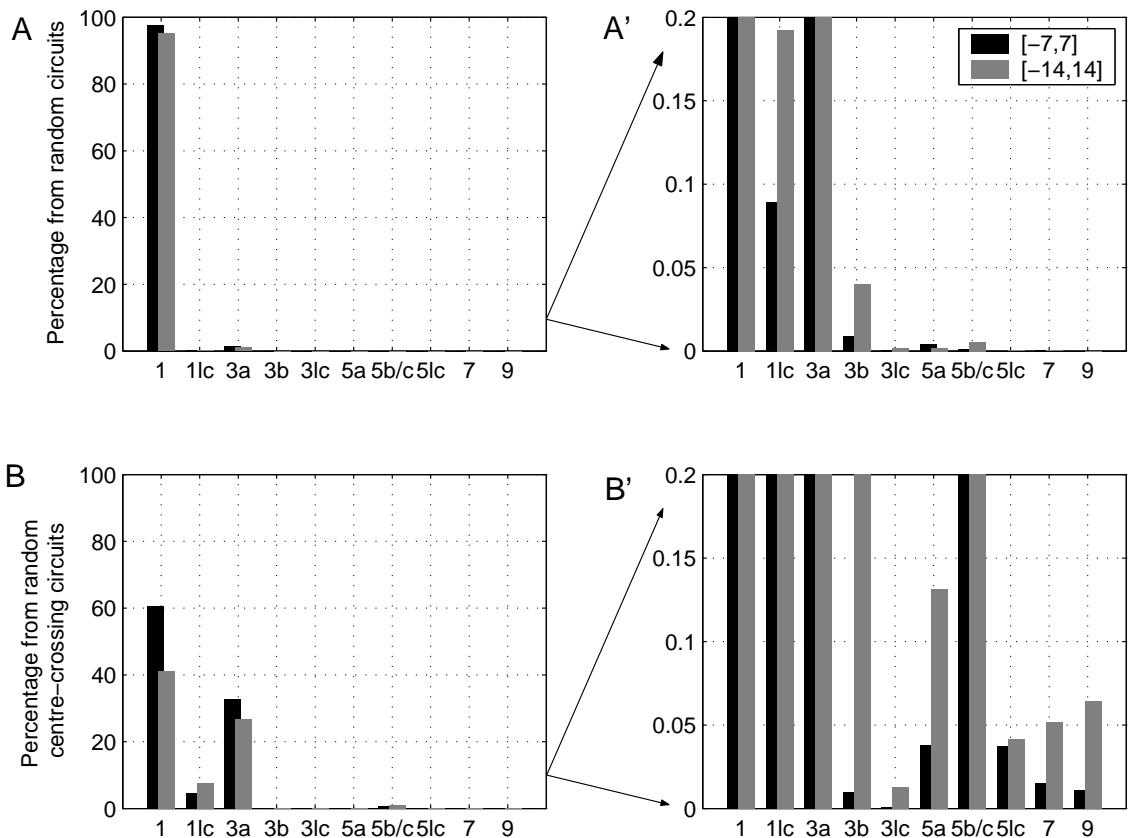


Figure 5.4: Percentage of distinct dynamical behaviours from 1 million randomly generated circuits (A) drawn uniformly from $[-7,7]$ (black bars) and $[-14,14]$ (grey bars). Similarly, for randomly generated centre-crossing circuits (B). The second column shows a close up of the histograms to appreciate some of the smaller values.

portant because this region could potentially serve as a place where many ridges connect any phase-portrait to any other.

Evolution in Two node CTRNN Phase-Portrait Landscapes

Again, without losing generalization, by studying if a single individual can evolve (via a sufficiently small mutation rate $\sigma^2 = 0.1$) from any one neutral region to any other we are exhaustively studying the properties of evolving on any of the $10!$ possible landscapes in this family. Such is the experiment presented ahead: a *netcrawler* is dropped into a point in space generating a par-

ticular phase-portrait (see table A.1 for the starting points for each portrait) and proceeds to move neutrally through genotype space until finding regions producing distinct behaviours. 200000 mutations are performed from each region. Once a new region is encountered the *netcrawler* is re-placed at its starting position. In table 4.3 the number of times region B is reached from region A is given by the number in column B and row A.

	1	1lc	3a	3b	3lc	5a	5b/5c	5lc	7	9
1	199976	3	21	0	0	0	0	0	0	0
1lc	54615	142121	2125	954	184	0	1	0	0	0
3a	26056	2803	151198	16074	455	205	3207	1	1	0
3b	307	7432	1248	107895	211	26	78249	28	4576	28
3lc	47613	1936	70130	57704	17437	58	5115	6	1	0
5a	469	0	82024	1	0	102613	14549	0	344	0
5b	4464	586	37849	29982	123	7988	106685	171	12148	4
5lc	11845	323	81526	11219	187	17640	48982	-	1207	0
7	1	167	253	7511	86	332	86230	122	-	3575
9	0	2	2	523	8	1	35229	50	73713	-

Table 5.3: Connectivity of phase-portraits in parameter space. The number of times (out of 200000 mutations) region B is reached from region A is given by the number in column B and row A. Numbers in bold represent places of reciprocal non-connectivity.

Table 4.3 suggests that the regions generating distinct phase-portraits in the 2 node family of landscapes are largely connected, 78.9% of the connections exist between any one region to any other. Perhaps more importantly, only 2 pairs of regions came out as being reciprocally unconnected, they appear in bold on the table. This is important because it suggests that when evolving on these 2node CTRNN landscapes, one can virtually go from any one region in genotype space to any other, without the need to bypass third regions of possible worst fitness. The sketch of highly connected neutral regions is depicted in figure 4.5, with the implication that local optima are unlikely.

Results up to this point have yielded the notion that the volumes of the different neutral regions are considerably disparate. This obviously affects evolution on these landscapes, for the genotypic movement required to diffuse effectively on each region varies accordingly. An *adaptive mutation rate* has been proposed in the neutral-networks literature as a way to optimally search through such landscapes. As our landscape is comprised of only ten different regions, we use the adaptive mutation rate in the next experiment to exhaustively study the ideal mutation rates to go from each region to every other. The experiment consist of evolving with the *netcrawler* from region A to region B with an adaptive mutation rate, which attempts to maintain a proportion of all mutations neutral in a window of the last 100 mutations. We use a proportion 1/e of neutral mutations which was observed to work well in a certain family of discrete landscapes in (Barnett, 2002a). Nevertheless, not much relevance is given to the particular rule, but more importantly to the relative differences in mutation rates that are achieved for diffusing on each of the regions. Figure 4.6 shows the average adaptive mutation rate over a maximum of 100000 mutations when performing the *netcrawler* to reach every region from every other. The result observed is that it

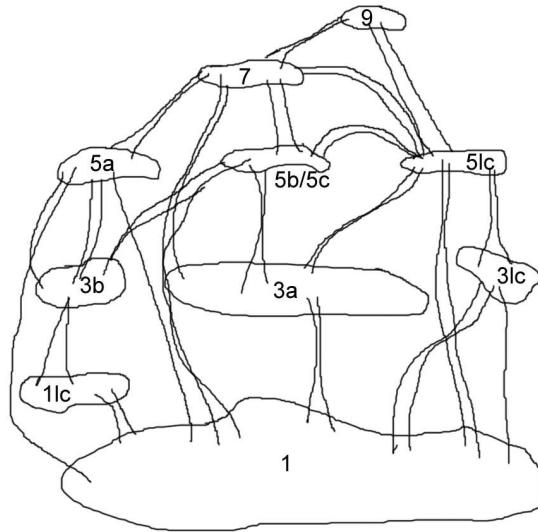


Figure 5.5: Sketch of phase-portrait connectivity

takes very different mutation rates to maintain the sort of exploration/exploitation balance provided by the adaptive mutation rule in each of the different neutral regions.

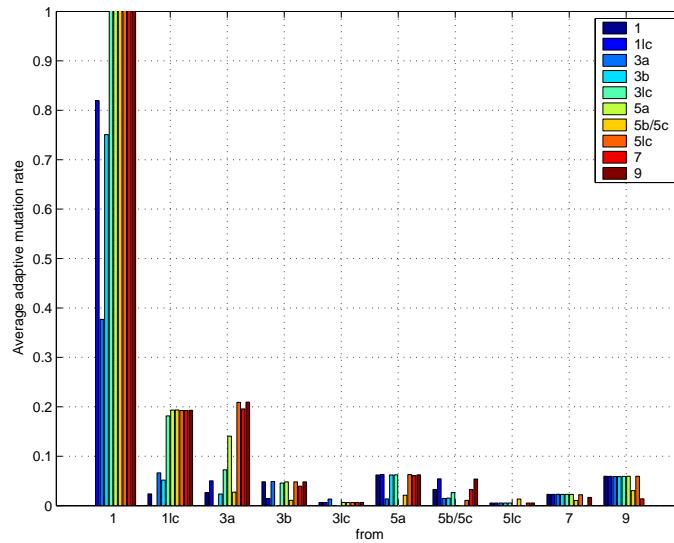


Figure 5.6: Dimension of neutral regions in 2-node CTRNN phase-portrait landscapes. Starting from each distinct behaviour, as depicted by the x axis, mutations are performed at a rate such that $1/e$ proportion of them are neutral, until arriving at a different behaviour. The average adaptive mutation rate is given for every pair of behaviours, depicted by the coloured bar.

Evolution in a Two node CTRNN Phase-Portrait Landscapes

Next, we used the netcrawler to evolve on an arbitrarily chosen landscape from the 2 node phase-portrait family as given by the fitness ranking in table 4.4. The differences in the *neutral dimensions* (or volumes of the regions in parameter space generating similar phase-portraits) of each of the regions suggest that a good way to evolve through these regions would be using an adaptive mutation rate. In figure 4.7 a comparison between evolutionary runs using (I) two different fixed

mutation rates and (II) an adaptive mutation rate with a $1/e$ neutral rule for the arbitrary ranking are shown.

1	1lc	3a	3b	3lc	5a	5b/5c	5lc	7	9
1	2	3	4	5	6	7	8	9	10

Table 5.4: Arbitrary ranking of the phase-portraits

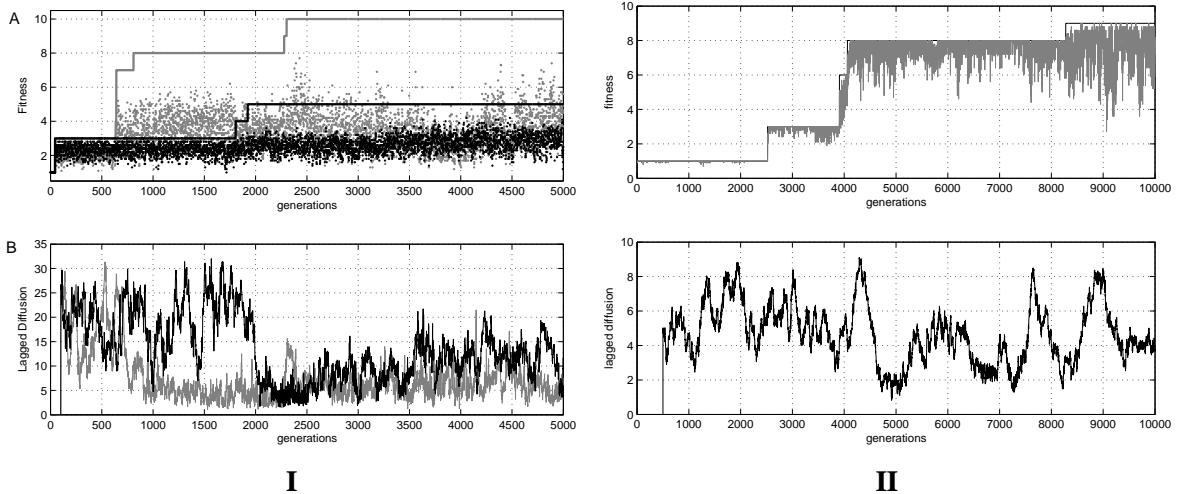


Figure 5.7: Evolutionary runs for an arbitrary ranking on the 2 node CTRNN phase-portrait landscape (Table 4.4). On top row figures, solid lines represent best fitness. Dots represent the fitness of the mutant netcrawler. Bottom figure depicts the movement of the netcrawler through genotype space. Column (I) shows evolutionary runs using two different fixed mutation rates: 1 (grey) and 0.1 (black). Column (II) shows an evolutionary run using an adaptive mutation rate with the $1/e$ neutral rule.

The evolutionary runs show that when using fixed mutation rates, as the netcrawler is forced to diffuse equally on large and small regions either too much time is spent on one region (black) if the mutation is small, or jumps across all other regions of space if the mutation is too big. On the contrary, with the adaptive mutation rate, the individual is able to traverse each neutral region until more adequately.

Three node CTRNNs already have too many distinct phase-portraits to rank and work with. Similarly, numerically computing all the points of intersection for the three nullsurfaces becomes much more computationally prohibiting. We may, arguably, intuit that as the number of behaviours and dimensionality of the landscape increases, the probability of two regions connecting simply increases as well.

5.2 Attractor Landscapes

In the previous section we dealt with exactly neutral regions. Such scenario is very abstract and assumes that the fitness function is an engineered phase-portrait-recognizer with pre-made plateaus from a ranked fitness. In more real-world problems it will be the case that the fitness function is

not quantised, but continuous as well as the genes. Yet, very likely it will be highly related to the phase-portrait of the underlying dynamical system. The *Attractor Landscape* is meant as a generic model to study such evolutionary processes.

5.2.1 $\alpha = 1$ Landscapes

The $\alpha = 1$ attractor landscape is the simplest scenario and it requires that the dynamical system recognize two different signals presented as time-dependent external input by settling onto a different attractor for each signal.

In the case that a one node CTRNN is evolved to solve the task, the landscape will be highly related to the *1 node phase-portrait landscape* for the case when the bistable behaviour has a higher ranking than the unstable one. The main difference is that, no longer will the neutral regions be perfectly flat plateaus. This time it will be more like two layers of hilly terrains on different levels. An interesting combination and interaction between ruggedness and neutral regions (now more appropriately referred to as *nearly neutral regions*).

Although fitness is on a continuum, the behaviour of the dynamical system can be simplified to four (i.e. $(2^\alpha)^{(2^\alpha)}$) different possibilities (see table 4.5). From these, we can expect 3 broad possible distinct fitness regions: (1) Unresponsive behaviour, as given by column 1 and 2, will receive fitness near 0; (2) the opposite behaviour to that being evolved for is represented by column 3, and will receive fitness near -1; finally (3) a successful behaviour will receive fitness near 1.

External Input (target output)	activations			
	1	2	3	4
-1 (0)	0	1	1	0
1 (1)	0	1	0	1

Table 5.5: Behavioural possibilities as given by the activation of the output node in the simplest $\alpha = 1$ *Attractor Landscapes* case for each of the external input signals.

We first evolved one node CTRNNs on this landscape using the netcrawler and observed the characteristics of the evolutionary process. From the evolutionary run depicted in figure 4.8 (A) and the exhaustive 3D projection of the landscape in figure 4.8 (B) we can appreciate that the fitness of the netcrawler proceeds in a manner very much reminiscent of neutral or metastable evolution: an initial period of slight (if any) increase in fitness, followed by a very rapid jump to a region of higher fitness.

There are two crucial aspects of this process that we would like to point out. First, from the fitness of the mutant netcrawler (grey dots) we obtain a very clear picture of the *nearly neutral regions* around the near zero and near one fitness levels. Secondly, from the movement of the netcrawler through genotype space, we can observe that at the start of the run, even when phenotypically the netcrawler seems to be static, its dynamics in genotype space are very different: traversing the space.

In figure 4.9 (A) we show the behaviour of a successfully evolved one node CTRNN on this scenario. The bistable phase-portrait of the system is clearly identifiable. Equally noticeable is how the external input is able to kick the system into one or the other attractor depending on the external input. In figure 4.9 (B) an analysis of the nullclines of different CTRNNs in

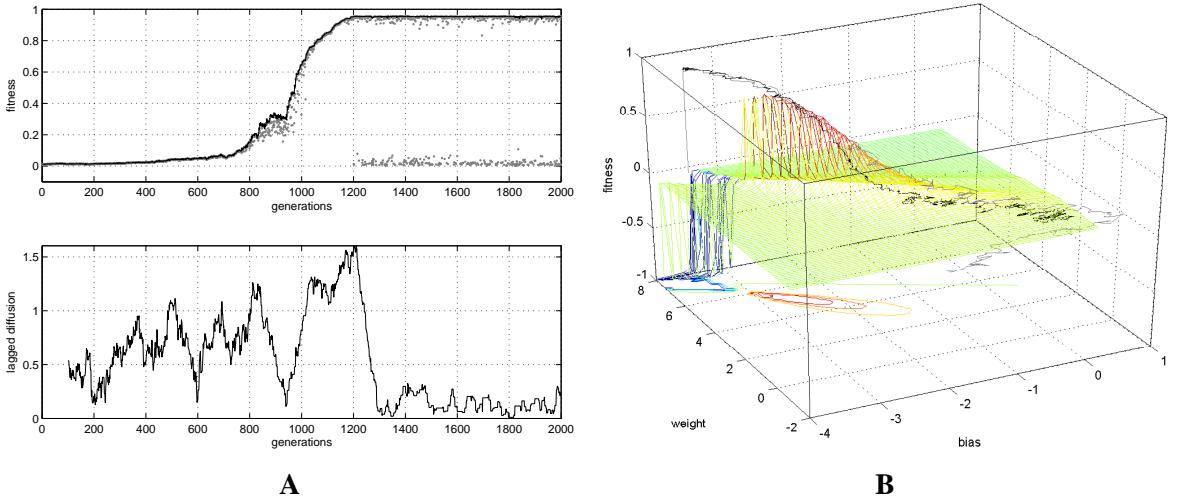


Figure 5.8: (A) Evolving 1 node CTRNN on the $\alpha = 1$ attractor landscape. Black line represents best fitness. Grey dots represent the fitness of the mutant netcrawler. The bottom figure represents the movement of the netcrawler through genotype space ($\beta = 1, \gamma = 20$). (B) Exhaustive 3D slice through the 4D $\alpha = 1$ landscape. The x and y axis represent values in genotype space (w and θ) and the vertical axis denotes fitness.

relation to their fitness is depicted. This analysis is useful because it provides a clearer picture of how most changes to the parameters of the system do not affect its behaviour (and therefore its fitness). For a small number of parameters, however, it undergoes radical changes in its behaviour (corresponding to undergoing a bifurcation), which in turn leads to a rapid jump in the individual's fitness. The external input pushes the nullcline up (or down depending on the sign of the signal). So a successful solution must: (1) have a fold, (2) be near centre crossing and (3) have a fold which is not too wide, otherwise the external input is not able to push the nullcline sufficiently up or down. Folds which are the right size, allow time for the system to switch between having one attractor or the other.

At this point, it's important to note the role of *noise* as given by: (1) white noise in the external input signals and node activations, and (2) random initialization of the node activations at the start of each fitness trial. The importance of such noise is twofold: (1) the evolved behaviour becomes robust to perturbations and (2) the fitness function becomes non-deterministic, that is, the same individual will very likely score differently every time it is evaluated. Consequence (1) is a good thing for obvious reasons. Consequence (2) provides the possibility that individuals be replaced by slightly worst individuals by chance. The benefit of this is slightly more subtle. As we are evolving with a hill-climber, which only diffuses neutrally for *exactly* neutral neighbours then in a non-noisy environment with a deterministic fitness evaluation evolution would be very susceptible to becoming stuck. As this is not the case, we end up with a netcrawler who is actually able to randomly drift through *nearly-neutral regions*.

However, can there be too much noise? Would certain levels of noise actually deteriorate the search? One parameter that tunes noise is the number of evaluation trials (γ). In order to gain insights on the effect of too much noise in this simplest landscape, we explored particular

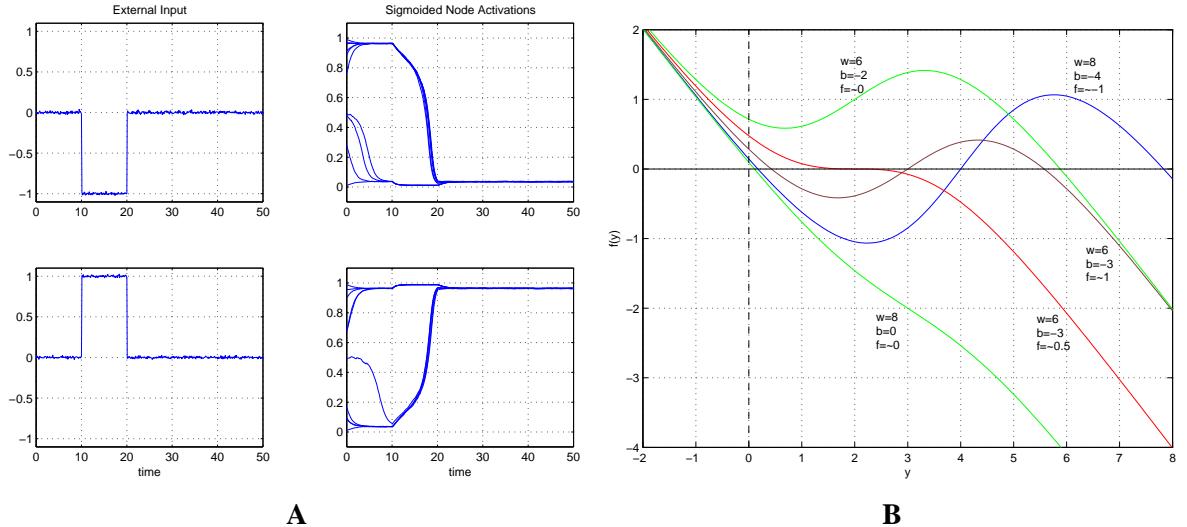


Figure 5.9: (A) Behaviour of a successfully evolved 1 node CTRNN on the $\alpha = 1$ task. Column to the left shows the external input. Each row depicts the different pattern of signals - in this case 2. Column on the right shows the sigmoided activation of the node. The behaviour is shown for several initial random activations. The horizontal axis depicts units of time. (B) Understanding the relationship between the parameters, the dynamical behaviour and the fitness in the Attractor Landscape. Lines depict the nullclines for CTRNNs. The colours represent the fitness according to the colours in the previous landscape graph (figure 4.8 B). The parameters (w, θ) and corresponding fitness are shown next to each line.

evolutionary runs using different number of trials per fitness ($\gamma = 1, 4, 10$). The runs correspond to evolving 2 node CTRNNs on the $\alpha = 1$ task. As can be seen in Figure 4.10, too much noise does indeed result, in failure to find regions of higher fitness, or failure of maintaining adaptive mutations for any decent period of time. Interestingly enough, in all three cases, the individual continues to move in genotype space relatively in the same way.

5.2.2 $\alpha = 2$ Landscapes

The number of behavioural possibilities in the $\alpha = 2$ case is already too big to present exhaustively on this page, with $4 (2^2)$ different patterns of signals to be recognized, but $256 ((2^2)^{(2^2)})$ distinct possible behaviours. Nonetheless, this range of possible behaviours can become categorized into only 9 subgroups following a similar interpretation than that of the $\alpha = 1$ scenario. Briefly stated, there are those who recognize one, two, three or all four of the patterns successfully, then there are those ‘agents’ who do exactly the opposite and finally there are those which react similarly for all inputs, or randomly. The first group will obtain fitness near 0.25, 0.5, 0.75 and 1, respectively. Similarly the second group will have negative values, and the unresponsive ones will have near zero fitness.

In figure 4.11, we show an evolutionary run when evolving a 2 node CTRNN on this landscape. Again, evolution proceeds very much reminiscent of evolution on neural networks. For this particular run, around the first 1000 generations were spent on the near zero region of fitness, this was followed by a rapid jump towards near half fitness, where the netcrawler spends a relatively

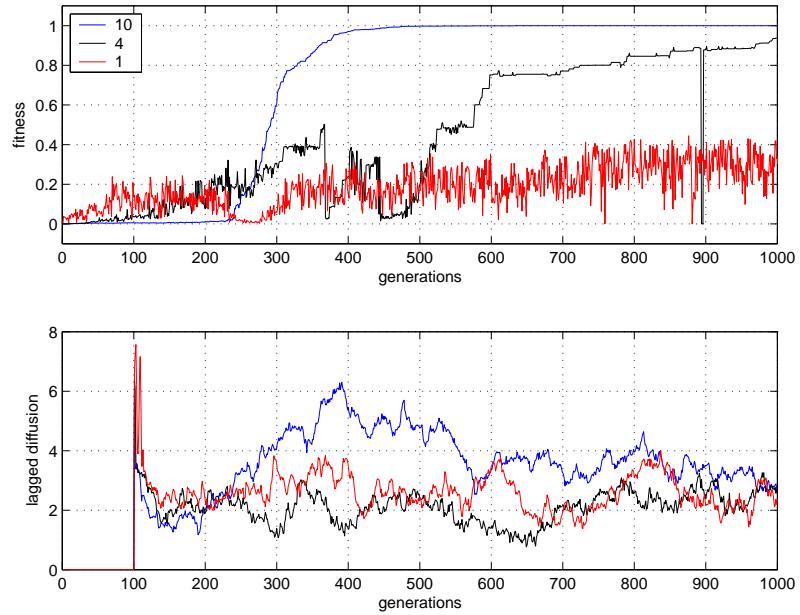


Figure 5.10: Effects of noise: varying the number of trials per fitness (γ). Three evolutionary runs on the $\alpha = 1$ *Attractor Landscapes* with a 2 node CTRNN. Top figure shows the fitness of the netcrawler. Bottom figure shows the movement of through genotype space.

long epoch (150000 generations) of more or less phenotypic stasis, but, nevertheless, with much movement through genotype space, and indeed with several drops to regions of lower fitness which were rapidly regained. Finally, the individual reaches the near highest fitness, relatively rapidly with one big jump and then while in the optimum genotypic movement decreases considerably. We know that noise plays an important role for it allows drifting through nearly neutral regions in the landscape. So, what happens if fitness is only evaluated once an individual comes up? That is, when the individual's fitness is deterministic (no noise). An evolutionary run is depicted (blue line in figure 4.11) for such case. In this case, phenotypic convergence would (and indeed does) lead to genotypic convergence!

Additionally, in figure 4.12 we show the behaviour of a successfully evolved 2 node CTRNN on the $\alpha = 2$ task. We can see how the node activations settle into different attractors for each pattern of signals, regardless of the initial states of the network.

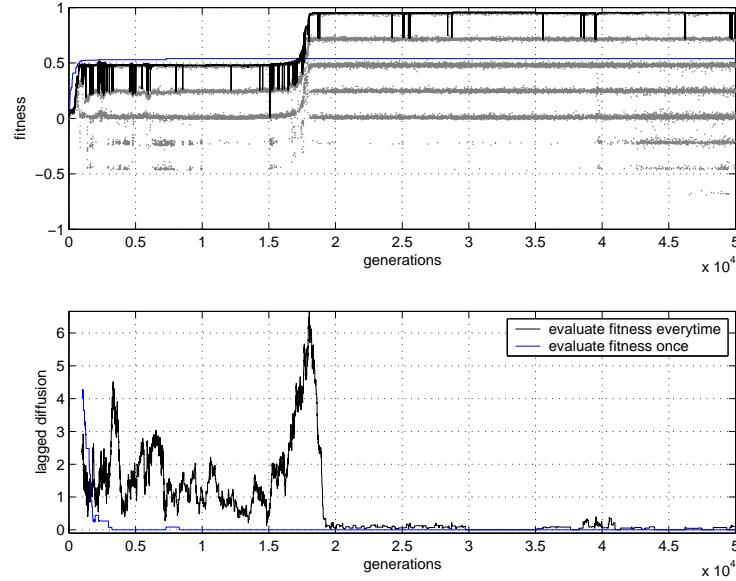


Figure 5.11: Evolutionary run on the $\alpha = 2$ *Attractor Landscapes* with a 2 node CTRNN. Black line represents best fitness. Grey dots represent the fitness of the mutant. Bottom figure shows the movement of the *netcrawler* through genotype space. On both figures the blue line represents an evolutionary run when evaluating fitness only once (no noise).

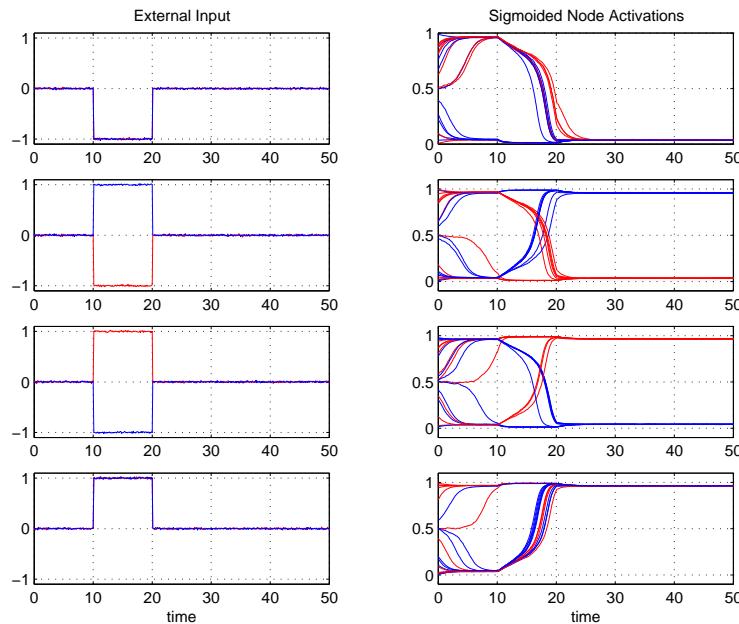


Figure 5.12: Behaviour of successfully evolved 2 node CTRNN on the $\alpha = 2$ *Attractor Landscapes*. The column to the left shows a particular pattern of signals presented as external input to the system. Each row depicts the different pattern of signals - in this case 4. The column to the right shows the sigmoided activations of the 2 output nodes when presented with the external input to its left. The behaviour is shown for several initial random node activations and white noise through the simulation. The horizontal axis depicts units of time.

5.2.3 Generic Attractor Landscapes

We can generalize, that the α landscape has a total of $2(2^\alpha) + 1$ nearly neutral regions. It will be comprised of 2^α regions above 0 corresponding to the CTRNN recognizing each possible pattern of signals. Similarly, it will have the same number of nearly neutral regions below zero. Finally, it will have a nearly neutral region around zero comprised of non-responsive/non-sensitive dynamical systems with very probably either unstable dynamics or random/chaotic behaviour.

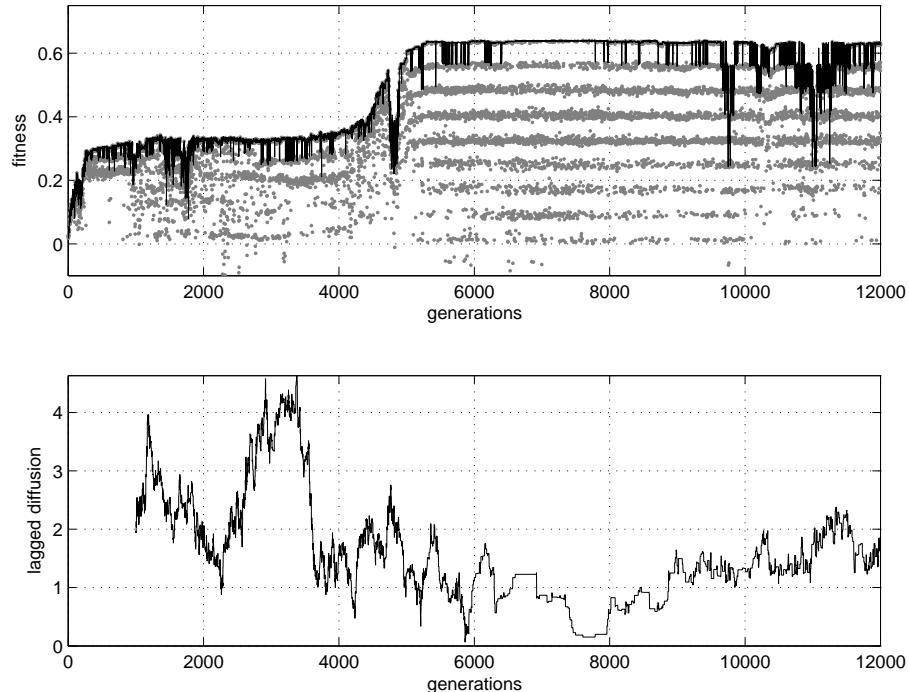


Figure 5.13: Evolutionary run for the $\alpha = 3$ *Attractor Landscape* with a 3 node CTRNN. Black line represents best fitness. Grey dots represents the fitness of the mutant. The bottom figure represents the movement of the *netcrawler* through genotype space.

In figure 4.13, as a last example, we can appreciate that as we increase the complexity (α) of the task the landscape begins to present many more (nearly) neutral regions closer to each other. The difficulty of the task, then, can be regarded as avoiding a gradient downhill as a result from falling on regions of lower fitness ever closer. Evidently, noise plays a crucial role. Similar to observations in the simpler landscapes, we can still observe the characteristic features of the evolutionary processes described before, mainly (1) long epochs of phenotypic stasis followed by periods of rapid changes (where the individual moves to a region of higher or lower fitness) and (2) ongoing movement through genotype space, regardless of phenotypic stasis.

Chapter 6

Discussion

Several studies have demonstrated that in the presence of selective neutrality evolution is qualitatively different from that on the more common rugged fitness landscapes which are often (implicitly) assumed by artificial evolution practitioners. These studies, however, have been mostly limited to evolution using discrete-alphabet genotypes. In this work we have explored the dynamics of evolving dynamical systems, in particular continuous time-recurrent neural networks, using real-valued genes, paying special attention to the possible existence of connected regions of points with selective neutrality (nearly neutral regions).

When evolving dynamical neural networks it is common to speak of the phenotype as the architecture or configuration of the network. If one attempts to define neutrality in the mapping from the real-valued genotype to the configuration of the network, then, no change, no matter how small, will be considered neutral. Given that any mutation will trivially cause changes in the network. In this sense, the genotype-phenotype mapping is one-to-one, and thus neutrality (at this level) is not possible. Immediately, two ideas arise as possibilities to ‘introduce’ neutrality in such real-valued search spaces: First, the discretization of the real-valued genotype into a binary or similarly discrete alphabet. Even though this is possible, there is no good reason why one would want to limit the range of possible dynamical systems from its genotype encoding. Secondly, attempts to introduce neutrality may come from engineering a redundant genotype-phenotype mapping. For example, adding genes that produce no change to the architecture. It is not intuitive why this should work, for it seems that a sort of No-Free-Lunch Theorem (Wolpert & Macready, 1997) would apply. That is, adding dimensions to the search space will perhaps improve some things but deteriorate others and ultimately make no difference in the search.

From the qualitative theory of dynamical systems, we know that for the majority of changes in the parameter settings of a dynamical system only small changes in their dynamical behaviour will be produced, moving attractors around a bit, but leaving the overall phase-portrait of the system qualitatively unchanged. However, at certain parameter values, infinitesimal changes cause a drastic change in the behaviour of the system and ultimately produce a phase-portrait that is qualitatively different from the original. Therefore, if one accounts for the phenotype as the phase-portrait or dynamical behaviour of the system, then (near) neutrality may exist! It is phenotype at this level which we explore in this work.

This first part of our work deals with landscapes at the most abstract level, where the mapping to fitness is a ranking of the distinct phase-portraits of a dynamical system. Ahead we summarize the observations made from evolving on this family of landscapes:

1. Few very common portraits and many uncommon ones.
2. Neutral regions of very different volumes (possible benefits of using an adaptive mutation rate).
3. Many phase-portraits in a small region of parameter space (particular importance in centre-crossing regions).
4. Highly connected neutral regions (possibility to go from one region to any other without crossing regions of lower fitness).

Although evolution on this *Phase-Portrait Landscapes* allows us to gain insight into the particular structure of the dynamical system's parameter space, a major limitation of this model is that fitness is quantised. In real-world evolutionary problems, however, it is much more likely that fitness will be on a continuum. Yet, hopefully it will still be related to the phase-portrait of the dynamical system!

In the second part of our work we introduce a family of landscapes which allow us to study the evolutionary dynamics when evolving CTRNNs with fitness on a continuum. The *Attractor Landscapes* are meant as a generic model to study evolution on continuous landscapes of tunable complexity, where successful solutions depend on the long-term behaviour of the system. We summarize the observations made from evolving on this family of real-valued landscapes:

1. These landscapes are characterized by regions of similar fitness which have certain correspondence with the phase-portraits of the dynamical systems being evolved.
2. A notion of nearness (or noise) is crucial to be able to navigate through such regions of nearly-equal fitness.
3. Evolution proceeds in a manner reminiscent to evolution on neutral-networks in two ways: (a) metastable evolution, long periods of stasis interrupted by rapid jumps to different fitness and (b) phenotypic convergence not resulting in genotypic convergence.
4. Noise has been observed to play a big role when studying these continuous landscapes with phenotype as dynamical behaviour. Furthermore (and possibly more worrying), the boundaries between nearly neutral regions becomes smaller as the complexity (α) increases.

There are many implications from the insights drawn from this work, particularly for the fields of artificial life, adaptive behaviour and evolutionary robotics. The main reason being that: (i) very often real value genotype encodings are used to describe complex systems and (ii) the fitness of an organism under evolution is generally more or less related to its dynamical behaviour. With this in mind, there exists the possibility that an artificial organism, with some pattern of behaviours which influences its fitness, be able to evolve to potentially any other organism possible (with a different patterns of behaviours) without having to go through regions of lower fitness (non-adaptive behaviour), regardless of its genotype encoding! Likewise, much of the work that has been addressed towards neutral networks in discrete or combinatorial landscapes may be of relevance for that subset of continuous landscapes which exhibit nearly neutral regions as well.

We have analysed the evolution of dynamical systems in a completely abstract level and in a model task with fitness on a continuum straightforwardly related to the attractors of the dynamical systems. But what happens in complex real-world evolutionary problems? Does some of what we have observed carry on? In other words, do the redundant genotype to phenotype mappings which are common when evolving dynamical systems with fitness related to the dynamical behaviour, influence the evolutionary search on problems in which fitness is related in much more complex ways to the attractors and phase-portraits of the system? This question is crucial to the artificial evolution practitioner. Obviously much work remains to be done!

Chapter 7

Conclusions

The purpose of this work has been to *gain insights into the evolutionary process when evolving dynamical systems on landscapes where the fitness of an individual is considerably related to the dynamical behaviour or phase-portrait of the system*. We have explored the evolutionary dynamics of evolving dynamical systems. In particular, we have evolved continuous-time recurrent neural networks via computer simulations, in two different families of landscapes where the relationship between the phase-portrait of the dynamical system and its fitness increases in complexity.

The contributions that this work has made are the following:

- Discovery of highly connected regions of points representing parameters of dynamical systems generating similar pattern of behaviours.
- Generation of a model to study (near) neutrality in continuous landscapes arising from the evolution of dynamical systems where the fitness is highly related to their long-term behaviour: *Attractor Landscapes*.
- Identification of a different process of evolutionary dynamics than that of rugged hilly terrains when evolving on such landscapes. Evolution proceeds in a manner more reminiscent of neutral evolution.
- Finally, this work has drawn attention to the importance of taking into consideration nearly-neutral ranges of fitness and noise when identifying (and possibly taking advantage of) neutral regions on continuous landscapes.

Finally, we make mention of that which we have not dealt with in this work, not because we feel they are not important, but because they would have introduced further complexity to the already complex issue at hand. For this no apologies are made, we only hope that the caveats presented ahead open new avenues of research for the future:

- Much work has gone into understanding the properties of discrete landscapes with neutrality. This work has taken only a first small step in investigating these issues in real-valued landscapes. Most of the features that have been identified in the former deserve careful treatment in real-valued landscapes featuring nearly neutral regions.
- We have limited our study to the use of a population of 1+1 evolutionary technique. Work on the dynamics of (larger) populations is an important part of understanding the evolutionary process in the landscapes described herein.

- This work has not set out to identify a best strategy or set of parameters for exploiting nearly neutral regions in continuous spaces. Further understanding of the properties of these landscapes will enable such work.
- Finally, in this work we have only been interested in a subset of the continuous landscapes arising from the evolution of dynamical systems. We have not set out to study the set of all continuous landscapes - an abstract model of random continuous landscapes with tunable ruggedness and tunable neutrality is, indeed, much needed.

Even though this thesis is complete, it is not a complete thesis. All of the issues presented in this work deserve further development. They are presented here in full knowledge of this fact. Nonetheless, if this work raises awareness of the need for further understanding evolutionary dynamics on continuous fitness landscapes with neutrality, then its objectives will have been fulfilled.

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Appendix A

Numerically Computing Equilibria

This additional chapter gives further detail into the numerical mechanism used in this work in order to calculate the number and type of equilibrium points present in a one-node and two-node CTRNN with particular parameters and ultimately classify the dynamical behaviour or topological features of the phase-portrait of such dynamical systems.

Scalar Dynamical System

The one node CTRNN is given by:

$$\dot{y} = \frac{1}{\tau}(-y + w\sigma(y + \theta) + I) \quad (\text{A.1})$$

Equilibrium points represent constant solutions of Equation A.1 and correspond to zeroes of f . The zeroes of f are clearly independent of τ .

The stability of an equilibrium point is given by the sign of:

$$\frac{\partial f}{\partial y} \equiv f'(\bar{y}, w, \theta) \equiv w\sigma'(y + \theta) - 1 \quad (\text{A.2})$$

where $\sigma'(x)$ is often written as $\sigma(x)(1 - \sigma(x))$.

A given equilibrium point \bar{y} of Equation A.2 is stable if $f'(\bar{y}, w, \theta) < 0$ and unstable if $f'(\bar{y}, w, \theta) > 0$ (Hale & Kocak, 1991).

For classifying the dynamical behaviours of the one node CTRNN we approximate the roots of Equation A.1 by computing \dot{y} for $K = 1000$ values of $y_i \in [-50, 50]$ increasing y by a sufficiently small step, $k = 0.1$. An equilibria is considered to be in the range between y and $y + k$ when the signs of \dot{y} and $y + k$ are different. Having identified the ranges where the roots are laying we proceed to close in our initial approximations by partitioning the current space into half and choosing the region where the signs remain different. This is repeated successively until the root is bracketed in a region at least smaller than 0.001, determining the precision to which the equilibria is found. Very close roots are a problem, especially if the multiplicity is an even number. In this case, there may be no readily apparent sign change, and so the notion of bracketing a root becomes difficult (Press et al., 1992). Nonetheless, for our experiments $k = 0.1$ was found to find most roots.

For each of the roots \bar{y} found, if $f'(\bar{y}, w, \theta) < 0$ is classified as stable equilibria and if $f'(\bar{y}, w, \theta) > 0$ is classified as unstable equilibria. The case when $f'(\bar{y}, w, \theta) = 0$ is called degenerate or nonhyperbolic and they are exceptional and thus not taken into consideration. Finally, with the number and type of the equilibria found the algorithm classifies the behaviour into the distinct available phase-portraits of the system.

Planar Dynamical Systems

The 2 dimensional CTRNN is given by:

$$\begin{aligned}\dot{y}_1 &= \frac{1}{\tau_1} (-y_1 + w_{11}\sigma(y_1 + \theta_1) + w_{21}\sigma(y_2 + \theta_2) + I_1) \\ \dot{y}_2 &= \frac{1}{\tau_2} (-y_2 + w_{12}\sigma(y_1 + \theta_1) + w_{22}\sigma(y_2 + \theta_2) + I_2)\end{aligned}\quad (\text{A.3})$$

is already considerably more complex. The common notion about solving systems of nonlinear equations is that there are no good general methods. In this two dimensional case, the zero contour boundaries are of interest to us. The solutions that we seek are those points (at least there will be one) that are common to the zero contours of J_1 and J_2 . In order to find all common points, which are the solutions of our nonlinear equations, we will have to map the full zero contours of both functions. basically requires finding all the points of intersection of 2 nonlinear system of equations. Contrary to the scalar system, the classification of behavioural possibilities in the 2 node CTRNN will not be exhaustive for the reasons explained earlier - again we simplify the problem to finding the number and type of equilibria.

Unlike the 1 node case, intersecting the curves along which either $\dot{y}_1 = 0$ or $\dot{y}_2 = 0$ in state space (y_1, y_2) is much more complicated because the nullcline expressions may have as many as three disjoint ranges of y_1 values (Beer, 1995b). It is more convenient to study Equation A.3 in the synaptic input space (J_1, J_2) of the nodes. The synaptic input is just the input that it receives from the other nodes. Thus, $J_1 \equiv w_{21}\sigma y_2 + \theta_2$ and $J_2 \equiv w_{12}\sigma y_1 + \theta_1$.

$$\begin{aligned}J_1 &= \frac{1}{\tau_2} \left(J_1 - \frac{J_1^2}{w_{21}} \right) \left(\frac{w_{22}}{w_{21}} J_1 - \ln \left(\frac{J_1}{w_{21} - J_1} \right) + J_2 + I_2 + \theta_2 \right) \\ J_2 &= \frac{1}{\tau_1} \left(J_2 - \frac{J_2^2}{w_{12}} \right) \left(\frac{w_{11}}{w_{12}} J_2 - \ln \left(\frac{J_2}{w_{12} - J_2} \right) + J_1 + I_1 + \theta_1 \right)\end{aligned}\quad (\text{A.4})$$

By setting these expressions equal to 0 and solving for J_1 and J_2 , respectively, we obtain the following expressions for the nullclines in synaptic input space:

$$\begin{aligned}J_2 &= \ln \left(\frac{J_1}{w_{21} - J_1} \right) - \frac{w_{22}}{w_{21}} J_1 - I_2 - \theta_2 \\ J_1 &= \ln \left(\frac{J_2}{w_{12} - J_2} \right) - \frac{w_{11}}{w_{12}} J_2 - I_1 - \theta_1\end{aligned}\quad (\text{A.5})$$

The intersections of $\bar{J}_2(J_1)$ and $\bar{J}_1(J_2)$ give the equilibrium points of Equation A.3.

We proceed to finding the equilibrium points of a particular CTRNN by limiting our search in:

$$\begin{aligned}J_1 &\in (\underline{\phi}_1, \bar{\phi}_1) \\ J_2 &\in (\underline{\phi}_2, \bar{\phi}_2)\end{aligned}\quad (\text{A.6})$$

where if $w_{21} < 0$ then $\underline{\phi}_1 = w_{21}$ and $\bar{\phi}_1 = 0$ otherwise $\underline{\phi}_1 = 0$ and $\bar{\phi}_1 = w_{21}$. Similarly, if $w_{12} < 0$ then $\underline{\phi}_2 = w_{12}$ and $\bar{\phi}_2 = 0$ otherwise $\underline{\phi}_2 = 0$ and $\bar{\phi}_2 = w_{12}$ where we know the $\ln(x)$ is well defined.

We then reduce the problem to calculating the intersection of two lines in sufficiently small grids of the whole space where we know both nullclines are crossing. Each sub region, (i, j) , of the grid is given by:

$$\begin{aligned} J_1 &\in (x_i, x_{i+1}) \\ J_2 &\in (y_j, y_{j+1}) \end{aligned} \quad (\text{A.7})$$

for $i = 1, \dots, N$ and $j = 1, \dots, N$, where $x_i = \underline{\phi}_1 + (ik_1)$, $y_j = \underline{\phi}_2 + (jk_2)$, $k_1 = (\bar{\phi}_1 - \underline{\phi}_1)/N$, $k_2 = (\bar{\phi}_2 - \underline{\phi}_2)/N$, and N is the number of regions in which each axis will be partitioned. For the work herein described $N = 500$. Generating N^2 sub regions in the initial grid.

We know when the \dot{J}_1 nullcline is crossing area (i, j) when either:

$$\begin{aligned} ((\dot{J}_1(x_i) < y_j) \wedge (\dot{J}_1(x_{i+1}) > y_{i+1})) \vee \\ ((\dot{J}_1(x_i) > y_{j+1}) \wedge (\dot{J}_1(x_{i+1}) < y_{j+1})) \end{aligned} \quad (\text{A.8})$$

For obvious reasons of efficiency, we discard at once those regions where the \dot{J}_1 nullcline does not cross and proceed only for those who meet the above criteria, reducing the initial N^2 area of search tremendously.

We proceed by finding out if the \dot{J}_2 nullcline crosses the (i, j) area as well. This criterion is met with a similar requirement as the previous one, on the different axis, as given by either:

$$\begin{aligned} ((\dot{J}_2(y_j) < x_{i+1}) \wedge (\dot{J}_2(y_{j+1}) < x_i)) \vee \\ ((\dot{J}_2(y_j) < x_i) \wedge (\dot{J}_2(y_{j+1}) < x_{i+1})) \end{aligned} \quad (\text{A.9})$$

In the regions that we know both nullclines are passing by we approximate lines for each of the them:

$$\begin{aligned} J_1 &\equiv y = m_1 x + b_1 \\ J_2 &\equiv y = m_2 x + b_2 \end{aligned} \quad (\text{A.10})$$

$$(\text{A.11})$$

as given by:

$$\begin{aligned} m_1 &= \frac{J_1(x_{i+1}) - J_1(x_i)}{x_{i+1} - x_i} \\ m_2 &= \frac{y_{j+1} - y_j}{J_2(y_{j+1}) - J_2(y_j)} \\ b_1 &= J_1(x_i) - m_1 x_i \\ b_2 &= y_j - m_2 J_2(y_j) \end{aligned} \quad (\text{A.12})$$

from where we obtain the point of intersection (x, y) by equating A.10 and A.11 straightforwardly given by:

$$\begin{aligned} x &= \frac{b_2 - b_1}{m_1 - m_2} \\ y &= m_1 x + b_1 \end{aligned} \quad (\text{A.13})$$

We consider such point an actual equilibrium of the system only if (x, y) lays inside the original sub region from A.7.

Having the number of equilibria and their approximate positions in synaptic input space we map the points back to state space with the mapping (Beer, 1995b):

$$\begin{aligned}\bar{y}_1 &= \sigma^{-1}(\bar{J}_2/w_{12}) - \theta_1 \\ \bar{y}_2 &= \sigma^{-1}(\bar{J}_1/w_{21}) - \theta_2\end{aligned}\quad (\text{A.14})$$

At this point we have the overall number of equilibria and location of equilibrium points in state space. Finally, for classifying the dynamical behaviours we would also like to consider if the equilibria are stable, unstable or saddle nodes. For this we resource to the eigenvalues of $Df(\bar{y})$, the Jacobian matrix of f evaluated at \bar{y} (Beer, 1995b):

$$\begin{aligned}\lambda_1, \lambda_2 &= \frac{w_{11}\sigma'(\bar{y}_1 + \theta_1) - 1}{2\tau_1} + \frac{w_{22}\sigma'(\bar{y}_2 + \theta_2) - 1}{2\tau_2} \\ &\pm \frac{1}{2}\sqrt{\left(\frac{w_{11}\sigma'(\bar{y}_1 + \theta_1) - 1}{\tau_1} - \frac{w_{22}\sigma'(\bar{y}_2 + \theta_2) - 1}{\tau_2}\right)^2 + \frac{4w_{12}w_{21}\sigma'(\bar{y}_1 + \theta_1)\sigma'(\bar{y}_2 + \theta_2)}{\tau_1\tau_2}}\end{aligned}\quad (\text{A.15})$$

An equilibrium point \bar{y} of Equation A.3 is *stable* if $\text{Re}[\lambda_1], \text{Re}[\lambda_2] < 0$, *unstable* if $\text{Re}[\lambda_1], \text{Re}[\lambda_2] > 0$, and a *saddle* if $\text{Re}[\lambda_1]$ and $\text{Re}[\lambda_2]$ have opposite signs (Hale & Kocak, 1991) (local behaviour, information about how the trajectories proceed to the equilibria, is dismissed for simplicity).

We then determine if the CTRNN's dynamical behaviour has a limit cycle only on those cases when an unstable equilibrium is found. This is done simply by starting the CTRNN displaced slightly from the unstable point and integrating the trajectory of the system forwards in time (time step = 0.1) for an initial stabilization period ($T_s = 100$ units of time) to allow for the system to stabilize into its attractors. The system is, then, evaluated again for a second period of time ($T_e = 100$) in which the rate of change both nodes is accumulated at each time step. If the accumulated value is greater than a sufficiently small value ($c = 0.01$) then the trajectory has fallen into a limit cycle, otherwise, based on its lack of movement, it has receded into a point attractor.

Finally, we categorize the CTRNN's dynamical behaviour into 10 possible distinct sets of number and global type of equilibria according to table 5.1, which also relates our simplified classification with the original catalogue of distinct phase-portraits of 2 node CTRNNs in (Beer, 1995b)¹

¹A few more 2-node phase-portraits have been discovered since the original catalogue was published.

Name	w_{11}	w_{12}	w_{21}	w_{22}	θ_1	θ_2
1	3	-1	1	3	-2	-1
1lc	4.5	-1	1	4.5	-2.75	-1.75
3a	5.25	-1	1	5.25	-3.4	-2.5
3b	6	-1	1	6	-3.5	-2.6
3lc	5.5	-1	1	5.5	-3.233	-1.75
5a	5.5	1	1	5.5	-3.4	-3.1
5b	6.5	-1	1	5.7	-3.75	-2.35
5lc	6	-1	1	5.5	-3.617	-1.72
7	6.3	-1	1	6.3	-3.75	-2.65
9	6.5	-1	1	6.5	-3.75	-2.75

Table A.1: Starting points used for exploring connectivity of regions in the *2 node CTRNN phase-portrait landscapes*. Points taken from work in (Beer, 1995b)