Our understanding of how the many forms of life on this planet came to exist has gone through many guises in recorded history. The earliest explanations utilised creation myths and have manifested in various forms in our religious beliefs. As understanding of our environment increased more scientifically grounded theories began to establish. One of the earliest and well-known scientific theories of merit was that of Charles Darwin. He used contemporary observations of natural processes to argue that evolution by natural selection was the driving force of creation. Today we hold a much more detailed and accurate knowledge of our origins, in terms of evolution, with the discovery of genetic structures such as Deoxyribonucleic acid (DNA), the multiple mechanisms of the cell and statistical theories of populations. We can also make educated guesses about how evolution may have begun, with self-replicating polymer molecules or reversible chemical reactions. We can even travel back through evolutionary time identifying key adaptations and changes by exploring both the genealogies and phylogenies of species. With every new insight natural evolution becomes increasingly wondrous in its complexity.

The beauty in evolution could be arguably placed on its ability to produce what appears to be highly improbable from a relatively simple process, certainly when compared to our own engineering feats. This alone forms a justifiable reason to attempt to simulate evolutionary processes within computational machines. From this concept an entire
research field has been born which uses simulated evolution as an optimisation or search process and, as many have argued, a tool for design and creation [17].

This introductory chapter describes the advances and limitations that have been uncovered from the simulation of evolution, outlining the motivation, objectives and importance of the work contained in this thesis.

1.1 Evolutionary Computation: The simulation of evolution like processes

Natural evolution is an incredibly complex and dynamical system that we are still grasping to understand. For every question answered several are raised. However, one thing we have undoubtedly learned is that evolution has built for itself this complex natural system and as such there must be some simple underlying process upon which it is based. Finding computational systems that utilise this underlying process of evolution for our own gain could be considered to be the goal of the field of Evolutionary Computation.

Commonly, the underlying process of evolution is described as a population based stochastic search algorithm and, as such, it is perfectly valid to argue that evolution is, in fact, nothing more than a simple search process, a statement that few would dispute. This raises a question. Why should such a simple search process be of such vast importance to both nature and science?

The answer to this question is in what evolution has clearly achieved. What is so impressive about natural evolution is how it has adapted the very system upon which it operates to form a remarkable eco-system interacting on many levels from the molecular to populations of individuals, each consisting of many billions of cells. Simulating evolution may open the door to a realm of many nature inspired techniques since evolution is at the core foundation of nature.
1.1.1 Limitations of Evolutionary Algorithms

The vast majority of research in evolutionary computation has been heavily tied to prior work on search algorithms and the problem sets and theories upon which they are based. This has been a doubled edged sword for simulated evolution.

The most common task for which simulated evolutionary systems are utilised are those of optimisation of mathematical and engineering problems. The most successful of these are implemented with the problem in mind. Just like other search algorithms the success of simulated evolutionary systems are heavily problem dependent. The No Free Lunch Theorem [137] highlights this issue. It states:

“...for any algorithm, any elevated performance over one class of problems is exactly paid for in performance over another class.”

Therefore, any algorithm adapted to solve one particular set of problems will perform less well on all other problem sets since, in order to implement domain knowledge into an evolutionary system, constraints have to be applied. This establishes that there is no truly universally optimal search strategy. So the real problem becomes knowing how to construct a search algorithm which is optimal for a given class of problem when little domain knowledge is known.

1.1.2 Why Computational Embryogeny?

The term *embryogeny* refers to the natural process by which the genetic representation within the single initial cell (zygote) controls the development of that cell to form a functioning multi-cellular organism. This process allows an extraordinarily complex organism (phenotype) to be produced from a relatively simple set of genetic instructions (genotype). This can be achieved because the zygote cell divides to produce additional cells that continue to proliferate to eventually produce every cell within the organism. All
of these cells originated from the zygote cell and all contain the same genetic information. Therefore, differences in the behaviour of cells within an organism, as a result of this genetic information, must be derived from the state of the cell and its environment. However the state of the cell and its environment can also depend upon the actions of cells. This forms a complex interaction between the phenotype and genotype and results in an extremely complex mapping between the two representations.

A commonly used argument to justify the simulation of an embryogeny-like process is to point to the issue of scalability in relation to phenotype size for evolution [102, 18, 124]. In a typical evolutionary algorithm the representation used to transform the genotype into a phenotype is either a direct (one-to-one mapping) or indirect (many-to-one mapping). This may lead to an association of size between the genotype and phenotype. For a direct encoding, larger phenotypes result in larger genetic search spaces that may be more difficult for evolution to find optima within. Since modelling embryological processes introduces a complex (indirect) mapping between the genotype and phenotype this association of size no longer exists.

A second argument is that nature is very good at maintaining a system that is undergoing perpetual change with cells constantly dying and being replaced. These natural systems demonstrate high levels of robustness and self-repair and work has begun to try to build robust characteristics into man-made systems [101, 102].

Whilst these are valid arguments for the use of a computational model of embryogeny they do not alone form the argument used to justify this work. Evolutionary biologists commonly state that nothing in biology makes sense except in the light of evolution [42]. Evolution is highly involved with biological mechanisms such as embryogeny and this involvement has fundamental consequences. This work investigates such consequences by simulating evolution with a computational model of embryogeny.
1.2 Thesis Objectives

Natural evolution is about searching for adaptations in order to survive in a constantly changing environment. Of course, in nature, these adaptations can occur at many levels from the single gene to entire populations of individuals. Adaptation can consist of rapid successful genetic changes, common in many forms of bacteria, to changes in phenotypic behaviour, such as the ability of humans to develop new skills and technologies. On the other hand, simulated evolution is very constrained in how it can be allowed to adapt by the representations that are used.

It can be argued that nature has evolved techniques, such as multi-cellular organisms and the complex unfolding of genetic information, in order to provide new, and more successful, ways of adapting in order to ensure survival. I believe that striving to achieve these same capabilities through simulated evolution may be an extremely fruitful direction of research.

There are two approaches that can be taken. Firstly, a more open ended approach to evolution can be attempted. Tierra is a simulated evolutionary system developed by Thomas S. Ray [113] in which individuals compete for energy (processor time) and resources (memory). What makes Tierra different from other simulated evolutionary approaches is that there is no objective or fitness evaluation procedure explicitly defined. A successful individual is one that remains and propagates within the population. Systems such as this have been shown to evolve individuals with increasingly complex interactions, however this growth in complexity diminishes over time as the system ceases to produce novel adaptations. This represents a much more biologically plausible approach to the simulation of evolution. However, the major issue with this approach from the engineering perspective is the lack of direction. There is no pre-defined fitness evaluation function and so there is no way to direct the evolutionary process to some target solution.
The second approach, and the one utilised in this work, is to try to integrate some of the adaptations that nature has made in a bid to find a use for them in a simulated evolutionary framework. The advantage of this approach is that the ability to explicitly define an objective function is retained while enabling us to observe the change in behaviour that newly inherited features cause in a simulated evolutionary system. However, this requires careful, and often extremely difficult, untangling of these adaptations from the biological and physical framework in which they developed. Both of these approaches are fraught with difficulties due to limitation in our understanding of nature.

The introduction of biological evolutionary developmental growth processes to simulations of evolution is becoming an increasingly popular direction of research in the evolutionary computation field. However, the majority of the work in this area has been to identify how it can be of benefit in terms of increasing the scope of the complexity for potential solutions. The following statement outlines the overall objective of this thesis:

To investigate the effects of a computational model of embryonic growth and its interaction with an evolutionary search process with the aim of identifying useful characteristics such as robustness, scalability and modularity.

1.2.1 Core Hypotheses

Given the aforementioned arguments for the potential benefits of a computational model of embryogeny, this thesis will test the following hypotheses concerning the properties of such a process:

- A computational model of embryogeny within a simulated evolutionary framework will produce robust behaviour when exposed to perturbations.
- A computational model of embryogeny within a simulated evolutionary framework will be scalable in terms of the size of solutions produced.
• A computational model of embryogeny within a simulated evolutionary framework will produce individuals which are inherently modular in their structure.

• The source of these traits of robustness, scalability and modularity is a result of the interaction between the computational model of embryogeny and simulated evolution.

1.2.2 Thesis Structure

The remainder of this thesis is structured as follows.

In chapter 2, the background material that has both helped to inspire and direct this research is presented as a wide body of material to which this thesis contributes. The chapter has been split into three major sections. The first acts as an introduction to the field of evolutionary computation and its various successes and failings. The second gives a broad overview of developmental biology, concentrating in detail only in relevant areas due to the enormity of this field of research. The third section describes how concepts from developmental biology can be used within a simulated evolutionary framework in an attempt to overcome some of the problems associated with evolutionary computation.

Chapter 3 describes a new computational model of biological development, or more precisely embryogeny, for use with search processes such as simulated evolution. This is the culmination of several years of work to find an appropriate representation and describes how problems with previous models and simulations have been overcome. Although the model acts as a fundamental core that can be extended to a range of potential problems, a specific case study is presented. This pattern formation problem highlights the capabilities of the model and provides the tools and results upon which the remaining body of this thesis is based.

Chapter 4 investigates how such a model exhibits characteristics of robustness in various forms. This includes the ability to self-repair, self-regulate and be resistant to
noise and discusses how these characteristics are inherently supported by the model.

Chapter 5 looks at aspects of scalability and complexity within various aspects of the model. Scalability is often used as an argument for the introduction of such a complex mapping process. This chapter investigates whether this argument is justified and how this relates to the system’s ability to produce complex solutions.

Chapter 6 is a discussion of the prevalence of modularity, in both nature and man-made engineering, and its effects on a system. The potential for existence of modularity in the model is analysed in various forms and the relationship between the various structures utilised in the mapping process is examined.

Chapter 7 looks at the performance of the evolutionary approach taken in this work and compares it to other search techniques. Observations are made about how the various forms of search affect the various traits observed from the computational model of embryogeny and how the computational embryogeny affects the process of search.

Chapter 8 reviews and outlines the significance of the observations and results obtained through the work presented in this thesis. Suggestions to how this thesis should be evaluated as a body of work are given and potential future directions of work are discussed.

1.3 Publications related to this work

A number of papers have been published as a consequence of the work that has culminated in this thesis [23, 24, 22, 25]