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Integrating Automata with Genetic Algorithms in order to provide Adaptive Operators

by

Anthony R.P. White

A thesis submitted to

the Faculty of Graduate Studies and Research

in partial fulfillment of the requirements for the degree of

Master of Computer Science

Ottawa-Carleton Institute for Computer Science

School of Computer Science

Carleton University

Ottawa, Ontario

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in order to provide Adaptive Operators**

submitted by
Anthony R.P. White, M.A.
A thesis submitted

in partial fulfillment of the requirements for
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Thesis Supervisor

Chairman, School of Computer Science

Carleton University

May 12, 1993

Abstract

Nature has conspired to cause change over time as a result of a changing environment. Life has shown itself to be highly successful in exploiting the characteristics of one generation and improving from one generation to the next. This process of environmental exploitation, called Evolution, has been described and studied using Genetics.

Genetic Algorithms are based loosely upon the principles of survival of the fittest and exploitation of genetic material from one generation to the next. Genetic Algorithms have shown themselves to be successful in solving a wide range of combinatorial problems. Genetic Algorithms have traditionally required the specification of a number of parameters that control the evolutionary process; two of these being related to the probability of applying the mutation and crossover operators.

This thesis proposes extensions to the classical Genetic Algorithm model. In the classical model, the aforementioned mutation and crossover operator probabilities are specified before the start of a Genetic Algorithm run and remain unchanged, a so-called static model. This thesis uses automata in order to allow the adaptation of these operator probabilities as the run progresses in order to improve quality of the solutions found. Favourable results have been achieved for a wide range of function minimization problems and these are described.

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I would also like to acknowledge the contribution of Prof. Oommen's teaching in the area of Automata Theory - material at the very core of this thesis.

Finally, but by no means least, I would like to thank my wife Nikki; without whose support, understanding and constant encouragement, very little would be possible.

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1 Introduction

Life seems capable of solving incredibly complex problems. Consider, for example, the human mind. Evolved over a long time span, it constitutes an incredibly efficient general-purpose design; being able to store a life time of experiences and knowledge all in a small volume with enviable recall capabilities. It is inconceivable that such a device could have appeared purely as a result of chance. Its intricate complexity seems to defy the idea that a sequence of random choices led to the current design. Can random processes be the *only* guiding force behind nature? Einstein certainly did not believe so when he said of Quantum Mechanics, "God does not play dice."

Biology is filled with examples of extraordinarily complex systems. The fertilization and development of the human fetus being amongst the most amazing. Here, thousands of genes regulate one another within individual cells causing an immune system to develop with remarkable adaptive properties and billions of neurons to be massively interconnected in networks which themselves possess learning behaviours ultimately allowing a child to master, and improve upon, the world in which he lives.

Again, it does not seem possible that these highly ordered systems have evolved by randomly changing the structure, or programming, of the previous generation. These intricate structures are maintained and duplicated through a precise balance of chemical and behavioral activities with a single element out of place causing degradation in the behaviour of the overall system. However, the keyword is structured, or

rather *hierarchical*. These systems did not immediately coalesce from a soup of genetic material but rather formed nuclei, with subsystems initially developing. The nuclei in turn forming clusters of nuclei; followed by clusters of clusters until we reach the levels of complexity that we see today.

What caused such order to develop? Since Darwin, biologists have seen natural selection as almost the only source of the order in evolution. However, Darwin could scarcely have suspected of the existence of self-organization: a recently discovered, innate property of some complex systems [Kauffman, 1991]. It is considered possible that biological order partially reflects the spontaneous order on which selection has acted. Selection has molded the native coherence of ontogeny, or biological development, even though it was not compelled to invent it. It is possible that the *capacity to adapt and evolve* is itself an achievement of evolution.

To understand how self-organization can be a force in evolution, the study and use of complex systems is necessary. Complex systems often exhibit the phenomenon known as "chaos". Chaos allows dynamic, non-linear systems that are orderly at first to become highly disordered over time with different starting conditions causing the system to behave in wildly varying ways. *Equally possible is that certain disordered systems "crystallize" into highly ordered systems.* Antichaos, it is believed, plays an important part in biological development and evolution. The self-regulating network of the genome (the complete set of genes in an organism) offers a good example of a system where antichaos may govern development. In fact, the interaction of Artificial Intelligence and Chaos Theory has recently been discussed in [Kiss, 1991].

Natural systems have often provided the inspiration for successful problem solving algorithms and this thesis is founded on one such analogy - the simulation of evolution using the genetic algorithm. Genetic algorithms draw upon the work of Darwin, and the study of Genetics. The genetic algorithm, due to Holland, is an example of a complex, non-linear system where an initially disordered system crystallizes to a highly ordered state through the mechanisms of *sexual reproduction, exploitation and survival of*

the fittest. Examples of both of these latter characteristics are available in abundance in Nature. Man has shown himself to be particularly adept at exploitation.

Genetic algorithms belong to the class of "weak" algorithms where the algorithm operates on a representation of the problem in question with no encoded domain knowledge¹; such as is the case in Explanation Based Learning. Further, genetic algorithms work with an encoding of the parameters of the problem rather than the parameters themselves and sexual reproduction is simulated by the exchange of genetic information using an operator which combines genetic material from the parents; redistributing it in the offspring. In Nature, the success of an individual is most usually measured by the ability to reproduce, having avoided predation. In the genetic algorithm, this is replaced by a function - called the fitness function - which is assumed to map onto the solution space.

The redistribution of genetic material in Nature, or rather the expression of features derived from the genetic encoding, is a dynamic process. Here, in one generation a particular encoding may result in a feature value X whereas in a subsequent generation the result may be Y. This arises as a result of the continual change in the dominance and recessiveness of alleles within the chromosome. In a Holland genetic algorithm, the redistribution process is static in that a successful redistribution of genetic material is not noted in such a way that future redistributions will tend to keep those genes together.

This thesis attempts to make the redistribution process adaptive by noting successful (and unsuccessful) redistributions of genetic material - rewarding success and penalizing failure. By doing this, the genetic algorithm becomes more like an evolutionary strategy [Schwefel, 1975], where two level learning is supported. This thesis draws together two pieces of previous work. Firstly, it builds upon the work of Syswerda; whose uniform crossover operator has been shown to be successful in a number of problem environments, despite the limitation noted above. Secondly, it uses Variable State Stochastic Automata - due to Oommen - in order to provide the adaptive redistribution of genetic material. This combination of mechanisms provides a more accurate analogy to

1. It is arguable that the fitness function constitutes domain knowledge.

the process embodied in Nature and is shown to be more effective than the static algorithm previously described.

1.1 Organization of this thesis

The overall aim of this thesis is to take the reader from no knowledge of genetic algorithms through to having sufficient knowledge to use these techniques in solving real optimization problems. This author hopes that by reading this document the reader will come to appreciate the power of evolutionary algorithms, such as the genetic algorithm.

This thesis is composed of nine chapters. Chapter 1 is this introduction. Chapter 2 describes the genetic algorithm in depth and consists of three subsections. It describes the genetic algorithm from a mechanical standpoint, starting with a section describing the classical genetic algorithm followed by a section that describes the design decisions, and problems which have to be solved when employing the genetic algorithms. The three subsections of this chapter provide essential definitions and describe the state of research in the areas of population selection techniques, problem representation, fitness function construction, operator specification and parameter selection. Chapter 3 provides an overview of genetic algorithm; elaborating on the biological metaphor and undertakes a survey of the wide range of applications that have been described in the literature. Chapter 4 undertakes an exploration of the theory underlying genetic algorithms, starting with the conventional schema analysis and ending with the theory of schema disruption and combination. Chapter 5 contrasts the genetic algorithm with other optimization techniques. It compares, in some detail, very fast simulated annealing with genetic algorithms. This chapter also discusses the similarities and differences between genetic algorithms and evolutionary strategies. Chapter 6 surveys previous work that has been undertaken in the area of adaptive operator probabilities in the context of genetic algorithms, highlighting both strengths and weaknesses of the approaches chosen. Chapter 7 introduces Automata theory, providing definitions, essential background theory and a description of Variable State Stochastic Automata (VSSA). Chapter 8 brings together genetic algorithms and VSSA in a framework which allows adaptive operator probabilities and introduces the adaptive uniform crossover operator and presents the results of using the adaptive crossover operator on an extended test bed of mathematical

functions. Finally, chapter 9 puts forward conclusions reached as a result of the study and proposes work which might be undertaken in order to extend the work and to justify the use of the adaptive uniform crossover operator in wider domains. It briefly describes how a operator similar in concept to the adaptive uniform crossover operator could be used to enhance the recently introduced genetic programming paradigm [Koza, 1990] with a view to automating the process of function definition.

2 Essential Genetic Algorithms

This chapter is composed of two distinct sections. It is designed to provide a working knowledge of the genetic algorithm and its components, followed by a detailed description of issues arising from genetic algorithms.

2.1 Genetic Algorithm Components

In general, an abstract task can be thought of as being a problem the solution to which can be found by searching some abstract space of solutions [Michalski, 1983]. As we are usually asking for the “best” solution, the task can be viewed as an optimization process [Holland, 1975].

Genetic algorithms (GAs) were originally proposed as a search technique for use in optimization problems. Many optimization problems are hard and although in specific cases algorithms of considerable importance have been developed for them, they are quite often not able to guarantee an optimal solution. Examples are the use of Simulated Annealing for wire routing and component placement problems [Kirkpatrick et al, 1983]. General techniques for the solution of NP-hard problems have not been forthcoming.

Genetic algorithms are stochastic search algorithms whose search methods model aspects of Darwinian evolution. As stated in [Davis, Steenstrup, 1987]:

“... the metaphor underlying genetic algorithms is that of natural evolution. In evolution, the problem each species faces is one of searching for beneficial adaptations to a

complicated and changing environment. The 'knowledge' that each species has gained is embodied in the makeup of the chromosomes of its members."

The basic principle behind genetic algorithms is to do what Nature does. The fitter the individual, the more likely it is to survive to be able to reproduce and thereby ensure that its genes survive to the next generation. While this section provides a brief introduction to genetic algorithms, more complete descriptions can be found in [Goldberg, 1989] and [Michalewicz, 1992].

Genetic algorithms use a vocabulary drawn from natural genetics. We talk about *individuals* (or *genotypes*) in a population. These individuals are sometimes also referred to as *chromosomes* or *strings*. Having individual and chromosome as synonyms in this context is a little confusing in that in man, for example, an individual is made of cells each of which contain 46 chromosomes. In genetic algorithms, a population consists of a set of single chromosomes. Chromosomes are made up of units called *genes* or *features* most often arranged in a linear formation or string. A feature is just a set of genes. Each gene controls the inheritance of one or more traits. The genes are said to express a given feature. Genes of certain features are located at specific locations on the chromosome - these are called *loci* or string positions. A feature which can have several values means that the associated genes can take on many values. The values which a gene can take are called *alleles*.

In the context of this thesis, each chromosome would represent a potential solution to an optimization problem. An evolution process run on a population of such chromosomes corresponds to a search through a space of potential solutions. The search process requires balancing two conflicting objectives: exploiting the best solutions at any point during the process and exploring the search space. Hill climbing is an example of a strategy which retains as much of the best solution to date as possible when moving to the next solution - only small perturbations are made and the results retained only if improvement is seen. Consequently, it neglects the exploration of the search space and only guarantees to obtain an optimal solution if the solution space contains a single peak. Random search, on the other hand, explores the solution space without

regard to the structure of the best solution to date nor to the region of the space where it was obtained. Genetic algorithms combine both solution exploitation and exploration of the search space in an extremely effective way.

Genetic algorithms have been used in a diverse set of optimization problems such as wire routing, travelling salesman problems, network link design [Coombs, Davis, 1987], [Davis, Coombs, 1987], adaptive control and many others. Consult [Michalewicz, 1992] for more details on optimization problems in the areas of scheduling, strategy formulation and transportation problems. Chapter 3 provides a description of a number of applications of genetic algorithms in the areas of Game Playing, Function Optimization, Neural Network Optimization, Design and Automatic Programming.

Genetic algorithms differ from more conventional search algorithms in that they work with a population of chromosomes (solutions) rather than a single chromosome (solution). Genetic algorithms also work indirectly, in that problem parameters are encoded before being manipulated by genetic operators. Finally genetic algorithms differ from most conventional search strategies in that they use probabilistic transition rules, not deterministic rules. As such they belong to the class of stochastic search algorithms.

Restricting the discussion to chromosomes represented as bit strings, each chromosome is the same length and each gene can take values drawn from $\{0,1\}$ - the so called binary alphabet. In this case, the chromosome is represented by a bit string and for a chromosome of length l , 2^l states can be represented. Generally, for an alphabet of cardinality m , m^l states can be represented¹.

Genetic algorithms are often characterized as algorithms that are better than hill climbing algorithms because they manipulate combinations of bit strings called schemata². If we consider the binary alphabet for the moment, the alphabet of associated schemata would

1. The principle of minimum alphabets states that we should use the smallest alphabet which makes sense for a particular problem and it is for this reason that a binary representation is most often chosen. However, this principle has most recently come to be questioned by genetic algorithm theorists.

2. The terms schemata and schema are used interchangeably.

be $\{0,1,\#\}$, where the # symbol indicates unknown. Figure 1 shows a schema and two possible strings which are examples of it. A schema represents a class of strings.

Figure 1 Examples of schema

The first important question to answer when using genetic algorithms is how do I encode the important parameters in my optimization problem? *The degree of success in using genetic algorithms is strongly linked to solving the representation problem well.* For example, choosing a representation where the genes describing a particular feature are not contiguous in the chromosome generally leads to poor genetic algorithms performance.

The next problem to resolve when encoding a problem in genetic algorithms form is to provide a *fitness function*. The fitness function takes the chromosome and generates a single value which represents the utility of a particular solution. The fitness function is analogous to the objective function found in Operational Research. In some domains such as function optimization, the fitness function is obvious - it is the function itself. In others, such as the partitioning of m objects into k classes, the fitness function is less obvious and requires considerable thought. The ideal fitness function should, as far as is possible, provide an accurate mapping between the utility of the solution in the real world and the modelled world such that the relative fitness values of potential solutions are accurately captured. As an example of a poor fitness function consider a function in which the fitness of solution A is less than the fitness of solution B while the real world utility of solution A is greater than that of solution B. Such a fitness function could never hope to find an acceptable optimal solution. This is discussed in a later section.

Having resolved the representation and utility mapping problems, all that remains is the mechanics of the genetic algorithm itself. The genetic algorithm can best be described by the program below:

```

Program GeneticAlgorithm()
Begin
  initializePopulation();
  evaluatePopulationFitness();
  while notFinished() do
    Begin
      for i:= 0 to populationSize by 1 do
        Begin
          offspring1 := randomRouletteWheel();
          offspring2 := randomRouletteWheel();
          if random() < crossoverProbability then
            newOffspring := crossover(offspring1, offspring2);
            newPopulation[i] := mutate(newOffspring[0]);
            newPopulation[i+1] := mutate(newOffspring[1]);
          End
          population := newPopulation;
          evaluatePopulationFitness();
        End
      End
    End
  End
End

```

The various procedural elements of the program are described in the following sections.

2.1.1 initializePopulation

The initializePopulation procedure is quite simple; we create a population of chromosomes where each chromosome is a binary vector of l bits. All l bits for each chromosome are initialized randomly.

Program control parameters are: *lengthOfChromosome* and *populationSize*.

2.1.2 notFinished

The notFinished function returns true if the number of trials does not exceed a program threshold, and the fitness of the best individual is less than a program threshold.

Program control parameters are: *maxTrials* and *fitnessThreshold*.

2.1.3 evaluatePopulationFitness

The evaluatePopulationFitness procedure uses the fitness function referred to above in order to compute the fitness of each chromosome in the population. These values are stored as part of the population.

2.1.4 random

The random function returns a number in the range (0,1).

2.1.5 randomRouletteWheel

The randomRouletteWheel function is used to choose which chromosomes from one generation should be reproduced in the next one. This is done by calculating an imaginary roulette wheel where each chromosome has a probability of selection calculated from:

$$p(i) = \frac{f(i)}{f_{avg}}, f_{avg} = \frac{1}{\text{populationSize}} \sum_{i=0}^{\text{populationSize}} f(i)$$

This is called fitness proportional selection. Viewed as a roulette wheel, for a population of five chromosomes, Figure 2 might be visualized.

Figure 2 Population Roulette Wheel

In order to generate the new population, the imaginary roulette wheel is spun a total of *populationSize* times and each time wherever it stops, that chromosome is reproduced in the new population. Referring to Figure 2, chromosome 5 should be reproduced in the next generation. In fact, chromosome 5 occupies approximately 40% of the roulette wheel and we would expect in the neighborhood of that percentage of the new population to be chromosome 5. Obviously, several chromosomes will appear multiple times in the new population and it is just this mechanism - survival of the fittest - that causes highly fit members of the population to dominate subsequent generations.

2.1.6 crossover

The crossover procedure takes two chromosomes as input and generates two new chromosomes as output. The crossover operation occurs by selecting a position between 1 and $l-1$ in the first string. This identifies two substrings A_1 and A_2 , where A_1A_2 is the same as the original string A . The same position is used for string B , generating the

substrings B_1 and B_2 . The crossover procedure returns the strings A_1B_2 and B_1A_2 . Graphically, this procedure is shown in Figure 3:

Figure 3 Crossover in action

In the above figure, $\oplus$ is meant to represent the crossover operator. As can be seen from the above example, completely different chromosomes can be returned as a result of the action of this procedure. It should also be noted that the crossover procedure occurs under the control of a program parameter - *crossoverProbability*.

2.1.7 mutate

The mutate procedure allows modified alleles to be introduced to the new population after crossover. The mutate procedure takes a chromosome and *for each bit* executes the following:

```
if random() < mutationProbability then
    toggleBit();
```

The mutation of an input chromosome occurs under the control of a program parameters - *mutationProbability*. The mutation operation ensures that the population maintains some diversity as we proceed from generation to generation.

2.1.8 Summary

As can be seen from the above, genetic algorithms are simple procedures which rely on a survival of the fittest mechanism drawn from the Darwinian view of

evolution. The procedure can be seen to be evolutionary as elements of each chromosome are exchanged and carried forward into the next generation - this being the purpose of the crossover operator. The crossover operator works by identifying building blocks which are exchanged and that these building blocks tend to grow as we close in on a global optimum. Now, having seen the way the crossover operator works, it is obvious why genes of particular feature should be grouped contiguously in the chromosome.

Genetic algorithms thus possess the crystallization property described earlier. They combine elements of random search (as they can search multiple promising areas of the solution region) with a use of current solution knowledge (through the reproductive mechanism). In fact, if the *crossoverProbability* is set to zero and the *mutationProbability* is set to a very low value, the genetic algorithm reduces to a hill climber strategy. If, on the other hand, the *mutationProbability* is set to a very high value, the genetic algorithm reduces to a random search strategy.

2.2 Formalism

A genetic algorithm can be formulated as an 8-tuple

$$GA = (P^0, \lambda, l, s, \rho, \Omega, f, t)$$

$$P^0 = (a_1^0, \dots, a_\lambda^0) \in I^\lambda$$

initial population

$$\lambda \in N$$

population size

$$l \in N$$

length of individual

$$s: I^\lambda \rightarrow I^\lambda$$

selection operator

$$\rho: I \rightarrow \Omega$$

operator determination function

$$\Omega \subseteq \{ \omega: I \times I^\lambda \rightarrow \Gamma \times I \}$$

genetic operator set

$$f: I \rightarrow R$$

fitness function

$$t: I^\lambda \rightarrow \{0, 1\}$$

termination criterion

P^0 is the initial randomly generated population and λ is the number of individuals representing one generation (i.e. the number of offspring produced in a single generation). l is the length of the representation.

The selection operator s produces an intermediate population P' from the population P^t by the generation of copies of P^t according to the probability distribution:

$$\Gamma \ni p_s: \quad l \rightarrow [0, 1]$$

$$p_s(a_i^t) = f(a_i^t) / \sum_{j=1}^{\lambda} f(a_j^t)$$

In other words, proportional selection. This leads to the expectation of individual a_i^t to occur $\eta = \lambda p(a_i^t)$ times in generation $t+1$ ¹.

After the selection phase has taken place the available genetic operators are applied. The application of genetic operators can be thought of as a mapping $\rho: l \rightarrow \Omega$ which determines an operator $\omega_i^t \in \Omega$ for each individual $a_i^t \in P^t$ which will be applied to this individual $\rho(a_i^t) = \omega_i^t \quad \forall i \in \{1, \dots, \lambda\}$. The operator which is applied to the intermediate population is generally, in fact, a composite of the crossover and mutation operators.

2.3 Genetic Algorithm Design Issues

There are two extremely important influences in genetic search: population diversity and selective pressure. These factors are strongly related. An increase in the selection pressure decreases the diversity of the population, and vice versa. Strong selection pressure promotes the convergence of the genetic search process; a weak selection pressure can render the search procedure ineffective. Whitley [Whitley, 1989] observes:

“it can be argued that there are only two primary factors (and perhaps only two factors) in genetic search: population diversity

1. This will be shown in Chapter 4.

and selective pressure [...] In some sense this is just another variation on the idea of exploration versus exploitation that has been discussed by Holland and others. Many of the various parameters that are used to 'tune' genetic search are really indirect means of affecting selective pressure and population diversity. As selective pressure is increased, the search focuses on the top individuals in the population, but because of this 'exploitation' genetic diversity is lost. Reducing the selective pressure (or using a larger population) increases 'exploration' because more genotypes and thus more schemata are involved in the search."

Thus when casting a problem in a form such that it can be solved using a genetic algorithm, a number of questions have to be answered and design decisions made. These decisions are addressed in the following sections.

2.3.1 Representation

Traditional genetic algorithms work with a fixed representation i.e. strings of a user-defined length. All members of the population have the same length and contain the same features which are to be represented in the problem. To use the language of genetics, the phenotype to genotype mapping has to be determined. The encoding essentially takes one of two forms - binary or non-binary. In determining an encoding for a problem, the statement, "binary or non-binary" means choosing the units of genetic material which can be manipulated by the set of genetic operators¹. *The choice of representation strongly determines the ease with which the genetic algorithm will be able to solve the target problem.*

2.3.1.1 Alphabet Choice

Binary representations are often used in the solution of genetic algorithm problems. When binary representations are used, each object variable encoded in the bit string is represented using the {0,1} alphabet. A mapping, which is usually one to one² between the object variable and encoded string, is then defined.

1. Obviously, when running genetic algorithms on a computer, the ultimate representation is a sequence of bits.

2. Unless synonyms are required.

The $\{0,1\}$ ¹ alphabet is most often used because of the belief in the principle of Minimum Alphabets, which can be stated [Goldberg, 1989, page 80]:

“The user should select the smallest alphabet that permits a natural expression of the problem.”

Recently, in [Antonisse, 1989], the principle of Minimum Alphabets has been questioned and empirical evidence for the efficient searching of spaces with higher cardinality alphabets or direct manipulation of schema can be found in [Deugo, Oppacher, 1992], [Belew, 1990]².

Antonisse argues that:

“The more expressive alphabet is seen to carry much more power in an informationally equivalent environment. More expressive languages seem, then, to provide finer-grained tools for the construction of adaptive plans.”

This work has subsequently led to an interest in more obvious encoding, such as floating point [Janikow, Michalewicz, 1991]. From their empirical studies at least, they find that:

“... the floating point representation is faster, more consistent from run to run, and provides higher precision (especially with large domains where binary encoding would require prohibitively long representation). At the same time its performance can be enhanced by special operators to achieve high (even higher than that of the binary representation) performance accuracy.”

The binary representation maps naturally to bits on a computer, but often a byte is used to represent a single allele for reasons of processing efficiency³ - bit manipulation operators are not then required. Binary alphabets allow the mutation operator to be defined very simply; in fact as the (probabilistic⁴) toggling of a single bit.

1. This alphabet is the smallest alphabet that can be used in a genetic algorithm.

2. Direct manipulation of schema, although attractive, does come at some price in that the fitness of partial solutions to the underlying problem must be obtained. It is unclear whether this is an attractive addition to genetic search. See, for example, [Goldberg, et al, 1991].

3. This is so on the GENEsYs system build by Bäck.

4. Certain implementations choose to toggle the bit, if mutation occurs. Other implementations choose to flip a coin in order to determine whether the allele will be a 1 or a 0. The implementations are equivalent if the latter implementation has double the probability of mutation of the former.

The importance of this mapping from problem to genetic representation cannot be overstated, as inefficient or inadequate mappings will ensure that the crossover and mutation operators will be unable to find an optimal solution. For this reason, the principle of Meaningful Building Blocks has been proposed. This can be stated as in [Goldberg, 1989, page 80]:

“The user should select a coding so that short low-order schemata are relevant to the underlying problem and relatively unrelated to schemata over other fixed positions.”

Stated another way, *related bits should be grouped together*. This principle arises as a consequence of the design of the crossover operator. We will return to this point in a later section.

2.3.1.2 Encoding Strategy

Once an alphabet has been chosen, what remains is to map the object variables onto the target alphabet. The simplest of all encoding strategies is the binary encoding strategy where the ordinal value of the object variable is mapped directly onto a number of bits. This is shown schematically in Figure 4.

Figure 4 Binary coding example

While this works well for problems in a symbolic space, where the mapping is straightforward; in problems where floating point values are to be represented the choice is less obvious.

Studies have been performed upon the effect of representation and hidden bias in genetic algorithm encodings [Caruana, Schaffer, 1988]. In [Caruana, Schaffer, 1988], results

clearly demonstrate that Gray coding for function optimization - where real values are being manipulated - result in superior genetic algorithm performance. Figure 5 shows the above example using Gray coding.

Figure 5 Gray coding example

It can be seen from the above figure that flipping a multiple bits causes the decoded value to represent the preceding value (usually if the high bit is flipped) or the succeeding value (usually if the low bit is flipped)¹. By using Gray encoding, single bit flipping (mutation) produces a value one above or one below the original value. Put another way, single bit mutations move the decoded value by the same extent regardless of the bit mutated. Table 1 shows the gray codes for the integers 1-15.

Table 1 Binary and Gray Codes

Value	Binary Code	Hamming Distance	Gray Code	Hamming Distance
0	0000	-	0000	-
1	0001	1	0001	1
2	0010	2	0011	1
3	0011	1	0010	1
4	0100	3	0110	1
5	0101	1	0111	1
6	0110	2	0101	1
7	0111	1	0100	1

1. Assuming a toroidal structure to the object values.

Table 1 Binary and Gray Codes

Value	Binary Code	Hamming Distance	Gray Code	Hamming Distance
8	1000	4	1100	1
9	1001	1	1101	1
10	1010	2	1111	1
11	1011	1	1110	1
12	1100	3	1010	1
13	1101	1	1011	1
14	1110	2	1001	1
15	1111	1	1000	1

The binary encoding can make search difficult for genetic algorithms because the Hamming distance between adjacent values is not constant. Actually, *it can be as large as the number of bits in the representation*. However, the similarity exploited by the genetic algorithm is schema similarity; the genetic algorithm's recombination operators implicitly assume that genetically similar strings have similar performance. It is expected that the effectiveness of the genetic algorithm will improve when the Hamming distance between encoded values has a similar functional form to that of the distance between values in the problem domain. This is certainly the case in Table 1.

For this reason - the lack of a Hamming cliff - Gray coding is generally preferred over Binary coding in function optimization.

2.3.2 Reproductive Scheme

A reproductive scheme consists of two components: the sampling method and whether the whole population or some subset of the population is replaced during a single generation.

When the whole population is replaced during a generation this is called a generational scheme. In a generational scheme, the set of parents is fixed until n offspring have been reproduced from that set of parents and then the parents are discarded. Parents, therefore, live for a single generation. When a subset of the population is replaced in any given

generation, the scheme is called steady state. In a steady state scheme, only a few members of the population are changed and thus parents can live for many generations before dying.

Steady state schemes are now receiving more attention in the genetic algorithm literature as they are thought to have advantages such that (a) schema fitness versus percentage in the population works out properly as the fixed point of the system, and (b) good members of the population float to the top of the list¹ where they are protected from deletion, and that (c) poor members of the population sink to the bottom where are more likely to be deleted.

Various reproductive schemes, or sampling mechanisms, have been investigated for genetic algorithms in order to improve upon the basic roulette wheel scheme. The roulette wheel, or fitness proportional reproductive scheme has the disadvantage that highly fit members of the population can quickly dominate, or crowd out, weak members of the population leading to premature convergence.

Although a partial solution is to allow raw fitness to be scaled - see section 2.3.3.1 - the choice of scaling mechanism and scaling coefficients implies that new genetic algorithm parameters need to be chosen that are certainly problem specific. Reproductive schemes, on the other hand, offer a more robust mechanism for the prevention of premature convergence.

In the earliest study [DeJong, 1975], several variations on the basic scheme were investigated. The first variation - the elitist model - enforced the preservation of the best individual in the population. The second variation - the expected value model - reduces errors due to poor sampling. In this variation, the number of offspring generated in the next generation is computed using:

$$n(i) = f(i) / f_{avg} \quad f_{avg} = \frac{\sum_{i=1}^{populationSize} f(i)}{populationSize}$$

1. assuming some form of population ranking.

where $n(i)$ represents the expected number of copies of an individual that are to be reproduced in the next generation. As offspring are reproduced using the standard roulette wheel, the $n(i)$ is reduced by 0.5 or 1. When $n(i)$ falls below zero, that individual is not a candidate for further selection.

In the elitist expected model, the best chromosome is guaranteed to be reproduced, while all other selections are performed using the expected model algorithm. In the crowding factor model, a newly generated individual replaces one from the parent generation - the parent being selected based upon its similarity to the offspring. In this scheme, a hamming distance measure is typically used in order to determine similarity. The crowding factor determines the set of individuals which are considered to be similar to the offspring and are therefore candidates for replacement. Replacement of an individual from this set is done randomly, or using the proportional fitness mechanism.

Brindle [Brindle, 1981] proposed other alternatives for selection schemes: deterministic sampling, remainder stochastic sampling without replacement, stochastic tournament, remainder stochastic sampling with replacement, and stochastic tournament. Empirical studies showed improvement over the basic fitness proportional mechanism, and in particular, the remainder stochastic sampling with replacement method was shown to have superior properties. This scheme uses the following:

$$n(i) = \text{floor}\left(f(i)/f_{avg}\right) \quad f_{avg} = \frac{\sum_{i=1}^{\text{populationSize}} f(i)}{\text{populationSize}}$$

In this scheme, a certain number of individuals are guaranteed in the next generation as given by $n(i)$. The remaining offspring compete, using a roulette wheel mechanism, according to the fractional value, $n(i) - f(i)/f_{avg}$. The remainder stochastic sampling with replacement method is arguably the most popular sampling method used by genetic algorithm practitioners today.

Selection methods based upon ranking, rather than fitness, have also been studied [Baker, 1985], [Whitley, 1989a]. Baker, in particular, uses an adaptive mechanism in order to

control premature convergence. This is described at length in Chapter 6, section 6.1.1 along with other mechanism for the avoidance of premature population convergence.

Unfortunately, ranking selection schemes violate the Schema Theorem¹ and so theoretical support for their optimal allocation of trials does not exist. However, the aforementioned studies have indicated that they prevent scaling problems (see section 2.3.3) and provide better control over the selection pressure implicit in the genetic algorithm.

A comprehensive review of sampling mechanisms, and their complexities, can be found in [Baker, 1987] and a taxonomy of selection schemes can be found in [Bäck, Hoffmeister, 1991].

2.3.3 Fitness Function

The fitness function in a genetic algorithm represents the abstraction of the real world objective function. *The choice of fitness function is the single most important design decision made in a genetic algorithm.* Poor choice of fitness function will ensure poor genetic algorithm results. If the fitness function does not map to the real world objective function such that equivalent trends are seen in each function, the genetic algorithm will be unlikely to find a global optimum easily. The fitness function is actually an abstraction of the environment of the problem to be solved.

Often, the objective function can span a wide range of values, both negative and positive. As a result, it is consequently necessary to map the underlying natural objective function to a fitness form through one or more mappings. For example, given an objective function $g(x)$, which is a cost function that we wish to minimize, a useful fitness function might be:

$$f(x) = k_{max} - g(x) \quad g(x) < k_{max}$$

$$f(x) = 0 \quad otherwise$$

1. See Chapter 4.

Alternatively, when trying to maximize a function which can take both negative and positive values, an appropriate fitness function might be:

$$f(x) = k_{min} + h(x) \quad h(x) + k_{min} > 0$$
$$f(x) = 0 \quad otherwise$$

The fitness function, then, should be as direct a mapping as possible from the objective function. However, the fitness function must also take into account the properties of the selection algorithm as with proportional selection it is possible for one or two highly fit members of the population to dominate during reproduction and thereby cause other, less fit, members not to be reproduced at all. As a consequence, certain bit patterns get lost and the population can converge too quickly before the genetic algorithm has had the opportunity to explore a reasonable proportion of the search space.

For this reason, two modifications to the basic genetic algorithm have been proposed. Firstly, fitness scaling is possible. This is described in the next section. Secondly, reproduction strategies other than those based upon relative fitness values have been investigated. This was previously described in section 2.3.2.

In more recent work on genetic algorithms, reproductive strategies other than fitness proportional selection have tended to be preferred over fitness scaling mechanisms as a means of controlling population diversity loss.

2.3.3.1 Scaling

Scaling of the fitness function is undertaken in order to regulate the number of copies of any one string that will be reproduced to the next generation. If left to normal roulette wheel selection, extraordinary individuals could easily take over a very large proportion of the population in a single generation. This is *highly* undesirable as it causes premature convergence. Empirical scaling studies were first performed by Bagley [Bagley, 1967], and Rosenberg [Rosenberg, 1967]. Scaling attempts to retain diversity in the population but still provide sufficient

evolution pressure such that significant numbers of highly fit individuals will be reproduced in a subsequent generation once they emerge during the course of a genetic algorithm run.

Several scaling procedures have been studied. Linear scaling takes the unscaled, or raw fitness, and generates a fitness defined by:

$$f = Af' + B$$

where A and B are scaling coefficients and f' is the raw fitness. Typically, A and B are chosen such that: $f_{avg} = \dot{f}_{avg}$ in order that the average members of the population contribute one member, on average, to the next generation. Similarly, the maximum fitness can be constrained, $f_{max} = \dot{f}_{max}C$, where C is the expected number of copies of the fittest members in the next generation. Typically, C lies between 1.2 and 2.

This form of linear scaling has the effect of ensuring that superfit members of the population do not generate a large number of copies of themselves in the next generation. Although linear scaling works well, it can generate negative fitness values¹. This occurs when the population contains mostly highly fit members but a few inferior members remain.

Forrest [Forrest, 1985] proposes the use of population variance in pre-scaling raw fitness values:

$$f = \dot{f} - (\dot{f}_{avg} - c \cdot \sigma)$$

where c is a constant between 1 and 3 and negative fitness values are truncated to zero. Fitness scaling can then occur without danger of negative results.

1. Which are arbitrarily truncated to zero.

Power scaling has also been suggested [Gillies, 1985]. In this scaling procedure, the raw fitness is raised to some positive power, as shown below:

$$f = f^k \quad k > 0$$

For $k > 1$, the fitness range is stretched, meaning that higher than average fitness individuals will get substantially more than one offspring on average. For $k < 1$, the fitness range is shrunk, meaning that inferior individuals will not be crowded out during the reproduction phase.

2.3.4 Operators

Operators in genetic algorithms are used to manipulate one or more strings in a population in order to produce one or more offspring. In a conventional genetic algorithm, the crossover and mutation operators have been applied sequentially, as outlined in the Program GeneticAlgorithm() on page 10. A wide range of problem-specific operators have been defined for particular problem domains. Specifically, the Travelling Salesman Problem and problems involving permutations have necessitated specialized operators. Examples of specialized operators can be found in [Whitley et al., 1989b], [Oliver et al., 1987]. Also, the specialized operators used by Davis - see section 6.4 Adaptive Operator Selection on page 106 - are examples of specialized operators.

In the next three sections, three classes of operator are described. These operator classes are widely used by genetic algorithm researchers today.

2.3.4.1 Crossover

Putting aside the specialized operators alluded to above, two distinct classes of crossover operator have been described in the literature. These are multi point crossover and uniform crossover.

Single point crossover - shown schematically in Figure 3 Crossover in action on page 13 - is a special case of multi-point crossover. In multi-point crossover, with the number of

points in the crossover being n , n points are selected in the parent string. Each crossover point, plus the two ends of the string, define $n+1$ intervals. Multi-point crossover then proceeds by allocating the first interval from parent 1 to offspring 1, the second to offspring 2, the third to offspring 1 and so on. This is shown schematically in Figure 6.

Figure 6 An example of three-point crossover

DeJong [DeJong, 1975] observed that multi-point crossover operators tended to degrade online and offline performance and he attributed this to poor survival rates of second order schemata. However, it is easier to understand by consideration of the number of unique operators which are potentially involved in genetic search. With n -point crossover there are $\binom{l}{n}$ different ways of picking the n points. As a result, when n is increased, each operator is less likely to be picked during a particular cross, and less structure can be preserved. With more mixing and less structure, these more complex operators become more like random shuffle and fewer important schema can be preserved. However, two-point crossover (and n for that matter) does avoid the representational bias which results in single point crossover - which tends to avoid mixing alleles as we move from the centre to the end of the string.

This appears to be a more important effect than the previous argument, as two-point crossover has empirically been shown to exhibit superior performance when compared to single-point crossover in a number of environments [Eshelman, et al., 1989]¹[Syswerda,

1. This paper also discusses other forms of crossover, for purposes of comparison. Multi-point and uniform crossover operators remain the two classes of operator most often used in genetic search.

1989]. In situations where multi-point crossover is used, two-point crossover seems to be most favoured in the literature.

Uniform crossover due to Syswerda [Syswerda, 1989] avoids the representational bias implicit in multi-point crossover by considering each bit in turn. Thus, starting at bit 1, the two parents' bits are exchanged with probability 0.5^1 , similarly at bit 2 and so on. The expected number of bits to be exchanged is thus $l/2$, with l being the length of the string. The uniform crossover algorithm is shown schematically in Figure 7.

Figure 7 An example of uniform crossover operator

In [Syswerda, 1989] the uniform crossover operator is shown to have superior performance when compared to one and two-point crossover on a wide range of problems. Syswerda argues that although schema are being destroyed at a faster rate in the uniform crossover operator when compared to single or two-point crossover, schema are also being created at a far faster rate. Based upon his empirical results, it would appear that the latter effect dominates - although a comprehensive theory remains to be developed.

The improvement of the uniform crossover operator over multi-point crossover provides the motivation for its choice as principal candidate for the addition of an adaption mechanism using automata. Also, as Figure 8 clearly shows, 0.5 is not the optimal setting for the uniform crossover operator probability in all cases and lends support to the idea that adaption should improve the performance of the uniform operator.

1. This value is not always optimal. See for example Figure 8. The choice of this parameter is made in the range 0-0.5, as the "function" describing the performance of the uniform crossover is clearly symmetric about 0.5. A simple symmetry argument - exchanging the two parents - proves this.

Figure 8 f₅ performance for varying uniform crossover probability

Note: the results obtained for f₅ were gathered over 100 runs of 10,000 trials using a population of 50, probability of mutation 0.001 and fitness proportional reproduction. The information plotted is the best-at-trial at 10,000 trials.

2.3.4.2 Mutation

Mutation is often considered to be a “secondary” operator by genetic algorithm practitioners and is often ignored by the genetic programming community. However, Bäck and others from the Evolutionary Strategy community have shown that complex problems can be solved using just mutation. Similarly, Ray [Ray, 1991] has shown that complex behaviour can result from the action of the mutation operator alone without the need for sexual reproduction¹. The mutation operator works on a single string. The role of mutation

1. i.e. crossover

in genetic search is two-fold. Firstly, mutation provides a local search capability as it makes small changes in the structure of the offspring. Also, the diversity of the population is increased by the action of the mutation operator.

Research have been undertaken to make the mutation operator depend upon the diversity of the population and this is the subject of section 6.1.2 Diversity Maintenance using Entropy on page 99.

In its simplest form, the mutation operator toggles bits as it moves along the bit string. However, in higher cardinality alphabets the mutation operator requires more specification in that a mapping is required for each possible value. For example, in the situation where floating point values are being mutated, a mutation increment is usually defined and either added to, or subtracted from, the current value. In [Ray, 1991], mutation takes the form of a counter being incremented by two or zero when one was indicated, or a copy instruction was incorrectly interpreted along with the more conventional bit flipping.

2.3.4.3 Inversion

The inversion operator was originally proposed by Holland [Holland, 1975] as a means by which an initially poor problem representation could be improved through genetic search. The inversion operator works on a single string. Under inversion, two points are chosen at random along the length of the string and the string is cut at those points. The ends are then exchanged. This operation is shown schematically in Figure 9.

Figure 9 An example of the inversion operator

It is not clear how the inversion operator is helping in the search for a new representation - it looks as though bits are just being shuffled about. In fact, Bagley [Bagley, 1967 pg. 168] states:

“The inversion results ... were somewhat [sic] disappointing. The most obvious effect of inversion is the large increase in the length of the runs. Recall that one of the consequences of inversion is a decrease in the effective crossover rate since crossover is inhibited between parts of the chromosomes which are not locus homologous. As we have seen, a lower crossover rate has an adverse effect on the simulation and it is this effect that was predominant in our results. The desirable consequence of inversion, which is the appearance in the population of gametes whose geographical gene linkages reflect combinations ... was not observed.”

Although Cavicchio used an inversion operator in a pattern recognition detector design task [Cavicchio, 1970], very few genetic algorithm implementations tend to use the operator today. It is believed that the more powerful two-point and uniform crossover operators, along with improved population reproduction strategies, have rendered the operator obsolete.

2.3.5 Parameter Settings

The genetic algorithm requires the setting of a number of parameters. These are the probability of mutation, the probability of crossover, and the population size. While the values presented here are not “cast in stone” they provide a reasonable starting point for investigations involving genetic algorithms.

For functions in the test bed, from f_1 to f_{10} , [Schaffer, et al., 1989] reasonable performance has been obtained using:

Table 2 Genetic algorithm parameter setting defaults

Variable	Meaning	Value
p_m	Probability of mutation	0.005-0.01
p_c	Probability of crossover	0.75-0.95
N	Population size	20-30

For function optimization at least, it seems that Gray coding should be used in conjunction with the remainder stochastic sampling with replacement method for population reproduction in a generational genetic algorithm. A uniform crossover operator seems to show most promise for high performance across a wide range of problems.

3 Overview of Genetic Algorithms

3.1 Overview

This chapter consists of two distinct sections. First, the historical and biological motivations for genetic algorithms are discussed. Second, a review of the applications of genetic algorithms is presented. The principal purpose of this chapter is to highlight the diversity of applications which have chosen to employ genetic algorithms and to detail the design decisions that have been made during their use in the chosen problem domain.

3.2 Motivations

Machine Learning can be viewed as a problem of searching in some abstract solution space [Mitchell, 1982] where learning occurs through the process of identification of better and better solutions.

It is particularly interesting to note that both of the most promising approaches to the design of algorithms for Machine Learning have as their metaphor naturally occurring systems. Connectionist algorithms draw for their inspiration on the neural structure of the brain and attempt to emulate how neurons in biological systems allow organisms to adapt to their environment. Amongst the most prominent connectionist scientists would be Hopfield, Kohonen and Grossberg. Similarly, models of simulated evolution are attempts to mimic the way in which species become adapted to their respective environmental niches. The question answered by studying simulated evolution can be stated as, "How does evolution produce increasingly fit organisms in environments which are highly uncertain for individual organisms?" Amongst the most notable

scientists attempting to answer this question are Holland, Maynard Smith and more recently Ray.

It is generally believed that complex life systems have evolved via Darwinian evolution where the principal force behind evolutionary change is selective pressure applied by an ever-changing environment. Darwin's seminal work, "The Origin of Species" [Darwin, 1859] not only represented a revolution in scientific thinking but also the triumph of scientific method over religious doctrine. It is important to note that it appears¹ that there can be intelligent behaviour without a designer.

The above observation tends to support the view that symbolic approaches to learning tend to be simulating learning at the meme² [Dawkins, 1986] level - or rather cultural learning - where knowledge is passed from one generation to the next in used to improve Society in the next generation. For example, the knowledge embodied in an Explanation Based Learning system forming the Domain theory could be said to consist of memes which have been derived from a previous system and passed from computer to computer or brain to computer.

It has also been noted that evolution has occurred in a hierarchical fashion with less complex organisms, or structures, forming the basis for increasingly complex systems. Our own brain is a remarkable example of such an evolutionary process. The brain is the result of thousands, perhaps millions, of years of evolution. Simple vertebrates had only a simple nervous tube, or spinal cord. This was sufficient for survival. That tube evolved to receive sensory information through various nerve fibres and to send motor signals to contract the animal's primitive muscles. Soon it became apparent that it is easier to move in a single direction rather than many directions and, as such, it was more important to know what is happening in the direction of movement than any other. As a result the frontal part of the spinal cord which was receiving signals from the preferred direction of movement became more important than other signals. This portion of the spinal cord its sensory capabilities and the brainstem - the precursor of the human brain - came into

1. If one is to assume no divine guidance in the evolutionary process.

2. A term used by Dawkins in order to describe knowledge replicators which can be propagated from brain to brain, computer to computer, or brain to computer as examples.

being. New challenges from an ever-changing environment induced further development in the motor and sensory systems. The brainstem grew in order that functionality could be controlled in a better, more direct, way. The frontal part of the brainstem was enlarged by the addition of two cerebral hemispheres. The back (or posterior) part of the brain evolved into the cerebellum. The cerebellum acquired the abilities of data analysis and decision making. In short, the relatively simple nerve tube evolved into the seat of human intelligence.

The importance of this extended example is to demonstrate the following points. Firstly, systems of ever-increasing sophistication and complexity have evolved. Building blocks are designed and are used as subsystems in higher order systems. Secondly, evolution occurs on many levels simultaneously. As higher order systems appear, the building blocks do not remain “frozen” but can continue to evolve in their own right.

Genetic algorithms offer an entirely different approach to Machine Learning when compared to symbolic learning. If the problem of feature expression is set aside for the moment (as this is not understood in Nature) genetic algorithms can be seen as a class of Machine Learning algorithm in which no “designer” is needed, but where intelligent behaviour can be observed.

The field of genetic algorithms - an abstract form of simulated evolution - is generally accredited to John Holland, although its beginnings can be traced back to biological simulations of the early 1950's. In [Holland, 1975], the Darwinian notions of evolution via a survival of the fittest mechanism are integrated with modern notions of Genetics, in a mathematical framework, in order to provide a robust search algorithm that is now called the genetic algorithm. Excellent texts describing genetic algorithms in depth can be found in [Goldberg, 1989], [Davis, 1987, 1991] and [Michalewicz, 1992]. It was Holland's observation that adaptive processes are fundamentally optimization processes but that unified study had previously not been possible owing to the complexity of the structures being modified and the uncertainty of their performance in the chosen problem domain. Moreover, that an efficient adaptive process must exploit elements of its past experience in order to continue to improve.

Holland also observed the failures of the symbolic approaches to Machine Learning. In [Michalski et al, 1986], he observed:

“The systems [expert systems] are brittle in the sense that they respond appropriately only in narrow domains and require substantial human intervention to compensate for even slight shifts in domain.”

One of Holland’s principal goals in designing improved algorithms for Machine Learning was that the resulting algorithms be *robust* and be able to perform in noisy environments. He observed the importance of building solutions *hierarchically* - starting with small fragments and combining them in ever more complex patterns. This was considered crucial to the success of genetic algorithms as the theory in Chapter 4 proves.

A parallel development, called evolution strategies, can be traced back to experiments undertaken at the Technical University of Berlin in 1964 [Rechenberg, 1973] and formalized by Schwefel [Schwefel, 1975]. Evolutionary strategies first saw application in the area of Numerical or function optimization and were applied to functions of continuous variables. In this, the “European” approach, less emphasis has been placed upon the biological metaphor - although the term biological is found in the title of the original 1964 paper - while in the “American” approach the terminology used in genetic algorithms still reflects its natural origins. Concerns continue to be expressed in the literature whenever an “unnatural” operator, or contrived selection technique are proposed [Goldberg, 1989 pgs 153-154]. The biological metaphor is considered to be very important when talking about genetic algorithms.

Fortunately, with increasing communication between researchers in the evolutionary systems and genetic algorithm camps and the coordination of conferences in Europe and North America, an attempt to provide a taxonomy of algorithms has been attempted. In [Bäck et al, 1991], definitions and terms are introduced which show that a genetic algorithm can be *broadly* classified in terms of evolutionary strategies. Essentially, the genetic algorithm can be seen as being an evolutionary strategy in which (a) a uniform representation is used for all features of the problem and (b) applies its operators in an unchanging¹ way during the course of the algorithm run. Chapter 5 describes the

similarities and differences between evolutionary strategies and genetic algorithms in considerably more detail. It is introduced here in order to provide an historical perspective on the genetic algorithm.

In the next section applications of genetic algorithms are presented. The spectrum of problem classes that have seen the application of genetic algorithms is considerable and underscores the claim as to the power of this class of algorithm.

3.3 Applications of Genetic Algorithms

Genetic algorithms have been used in a very wide range of problem solving situations. The four international conferences on genetic algorithms have seen a wide range of application areas using genetic algorithms and it is not possible to describe those application areas here. The application areas described here are:

1. game playing
2. function optimization
3. neural network optimization
4. design
5. automatic programming

Although this does not represent a comprehensive view of the application areas that have chosen to adopt genetic algorithms as a solution technique, it does indicate the diverse nature of the application areas themselves. Selected applications from these areas are described in the next five sections.

3.3.1 Game Playing

The Artificial Intelligence community has long considered game playing as a fertile test bed for the application of Machine Learning techniques and it is no surprise that genetic algorithms have been used here. Essentially, the aim is to develop better and better strategies as a result of learning from experience.

1. This is true of a traditional Genetic Algorithm. In this thesis, and in other areas of the literature, dynamic operators have been utilized. This will be discussed further in Chapter 6.

The term "genetic algorithm" appeared long before its association with Holland in 1975. Bagley's work [Bagley, 1967] consisted of devising a test bed of game-playing tasks modelled after the game of hexapawn. Hexapawn is played on a 3x3 chessboard where each player starts with three pawns and tries to reach the other side of the board. Bagley chose to vary the abilities of a player by allowing search to a given number of moves. He called this the "task depth".

Bagley devised genetic algorithms to search for parameter sets in game evaluation functions; comparing them to correlation algorithms¹. Correlation algorithms were found to require a strong match between the nonlinearity of the game and the nonlinearity of the correlation algorithm. However, Bagley's genetic algorithm seemed much less sensitive to game nonlinearity and performed well over a wide range of task depths.

The genetic algorithm proposed by Bagley strongly resembles the Holland genetic algorithm in that reproductive, crossover and mutation operators are constructed. However, rather than the monoploid representation favoured in Holland genetic algorithms, a diploid representation was used in order to encode the concept of dominance. Bagley also used a non-binary encoding for his problems; something which tends not to be done in modern genetic algorithms.

Bagley's work is doubly relevant to this thesis in that he observed the need for "self contained controls" and was conscious of the problems of fitness scaling. He believed that at the start of a genetic algorithm run fitness should be scaled in order to ensure that no single individual be allowed to dominate the population. However, later in the run fitness should be scaled in order to take advantage of small differences in the fitness values. He also suggested encoding the probability of mutation and crossover in the chromosome themselves. However, his thesis did not present results of suggested experiments.

The prisoner's dilemma is a classic problem of conflict and cooperation. In this game, two players have a choice of cooperating with the other or defecting.

1. Correlation algorithms are learning procedures modelled after the weight-changing algorithms of that time. See for instance, [Friedberg, 1958], [Samuel, 1959, 1967]; [Uhr, Vossel, 1961]

Depending on the two players' decisions, each receives a payoff according to a payoff matrix such as shown in Table 3.

Table 3 Payoff matrix for the Prisoner's Dilemma

Decision	Cooperate	Defect
Cooperate	(R=6, R=6)	(S=0, T=10)
Defect	(T=10, S=0)	(P=2, P=2)

In the above table, R represents reward, S represents sucker, T represents temptation and P represents penalty. The object of the game is to maximize the reward received by the player over a series of rounds. As can be seen in the above table, the maximum, single round reward is received in the situation where one player cooperates and the other defects.

The first genetic algorithm solution to the Prisoners' dilemma was due to Axelrod [Axelrod, 1985, 1987]. Axelrod's idea was to have the genetic algorithm search for improved strategies capable of playing the iterated form of the game. In order to do this, Axelrod allowed decision rules to be based upon the behaviour of the other player in the previous three moves. In order to code a particular strategy, Axelrod coded the sequence of actions as a three letter string. Thus PPP represents the situation where both prisoners defect on the three moves while TTP represents the scenario in which one prisoner defects twice, and then cooperates while the other prisoner cooperates on all three moves. A possible 64 alternatives exist.

Actually, the problem is more complex in that behaviour is unknown at the beginning of the game. Axelrod added a further six bits in order to capture the pregame assumptions of behaviour. Pregame behaviour, as Axelrod showed, was extremely important in determining the efficacy of the chosen strategy.

Strategies were evolved by having a population of candidate strategies play against a set of eight opponents taken from his computer tournaments. The success of a particular strategy was measured over a game of 151 moves and the point score at the end of the game used as a measure of the value of the strategy. In performing

this experiment using randomly generated initial strategies, Axelrod obtained strategies that were superior to the previous best solution of "tit for tat"¹. As Axelrod [Axelrod, 1985] observed:

"This is a remarkable achievement because to be able to get this added effectiveness, a rule must be able to do three things. First, it must be able to discriminate between one representative and another based upon only the behavior the other play shows spontaneously or is provoked into showing. Second, it must be able to adjust its own behavior to exploit a representative that is identified as an exploitable player. Third, and perhaps most difficult, it must be able to achieve this discrimination and exploitation without getting into too much trouble with the other representatives. *This is something that none of the rules originally submitted to the tournament were able to do.*

These very effective rules evolved by breaking the most important device developed in the computer tournament, namely to be "nice," that is never to be the first to defect. These highly effective rules always defect on the very first move, and sometimes on the second as well, and use the choices of the other player to discriminate what should be done next. The highly effective rules then had responses that allowed them to "apologize" and get to mutual cooperation with most of the unexploitable representatives, and they had different responses which allowed them to exploit a representative that was exploitable."

Axelrod demonstrated, with his use of genetic algorithms, that intelligent behavior that was not part of the initial problem setup could emerge naturally through an evolutionary process.

Another example of genetic algorithms applied to game playing can be found in [Deugo, 1989]. Deugo provides a framework for the integration of Case Based Reasoning with Rule Based Reasoning and allows for the modification of cases using genetic algorithms. While the thesis provides a general framework for synthesis of Case Based Planning and genetic algorithms, its application to the game of checkers is of interest here. In Deugo's work the basic unit being manipulated is a case which represents a checker strategy. Each

1. In the "tit for tat" strategy, a player merely uses his opponents last move as his own in the next round.

case has a collection of frames and a strength value. The checker case is just a sequence of moves experienced during the progress of a checker game.

Genetic algorithms are used in the Simple Classifier System for Cases (SCSC) in order to improve the quality of strategies which are stored in the case library. The system works by playing a number of simulated games which cause a library of cases to develop. At predefined points during the learning process cases which have been used successfully during the previous game playing cycle have had their value increased and so are preferentially reproduced in a modified case library to be used in the next game playing cycle.

The results of this thesis clearly show that integrating genetic algorithms with a Case Based Reasoning system can result in improved performance of the CBR system and that behaviour not originally present in the case library, nor in any single acquired case, can emerge.

The Tower Of Hanoi is a well known problem, where rings of differing sizes are initially stacked in increasing dimension on one peg and the goal is to move them to another peg where the rule that a larger dimension ring can never be placed on top of a smaller dimension ring. The Tower Of Hanoi problem can be classed as either a game of strategy or a puzzle. As such it has frequently been of interest to the Artificial Intelligence community as a test bed for problem solving algorithms. Cardoso [Cardoso, 1991] proposed solutions for a general number of rings using neural networks trained using the backpropagation algorithm. More recently, Margarita [Margarita, 1993] has used genetic algorithms to solve the Tower of Hanoi problem.

Margarita's approach to the Tower of Hanoi problem is interesting because it provides an extended discussion on the importance of the fitness function and demonstrates how genetic algorithm effectiveness is *strongly* influenced by function design¹. To quote Margarita:

1. Again the argument with respect to domain knowledge rears its ugly head.

"The fitness landscape is the most important problem to consider when tuning a genetic algorithm. Ideally, the fitness function should have values monotonically increasing when going from one position to the next until reaching the final configuration. In other words, the fitness function applied to the optimal strategy should exhibit an increasing shape from the first move to the last so as to avoid the local maxima and surely converge to the final position during the evolutive process."

Margarita studied a relatively simple problem; that of 5 rings and a possible 6.18×10^{14} strategies¹. While a number of representations are proposed, and the relative merits discussed, the representation used is one in which the string comprises the moves in the strategy. The coding of a single move is of the form (D_s, D_d) , where the subscript *s* stands for start and the subscript *d* stands for destination, and *D* the ring to move. The code used for D_s and D_d is not based upon the absolute dimension but on their relative dimension. Considering just three rings - three possibilities exist - an alphabet represented by (1,2,3) is therefore sufficient. The three rings present are of differing dimensions, so with no empty peg, it is always possible to label a smallest, intermediate and largest ring. Similarly, if there is one empty peg (or two), the peg is defined as corresponding to the biggest ring (always bigger than the biggest ring). This encoding is shown in Table 4.

Table 4 Tower of Hanoi coding scheme

Code	Move	Meaning
1	(Min, Max)	Move the smallest ring on the top of biggest.
2	(Min, Intermediate)	Move the smallest ring on the top of the intermediate.
3	(Intermediate, Max)	Move the intermediate ring on the top of the biggest.

By using this encoding, a string can *never* represent an infeasible strategy. The coding of a single action does not depend upon the previous action. This is important because it ensures that no infeasible solutions are explored and that no modifications are required to the crossover and mutation operators in order to

1. Number of strategies is given by 3^p , where $p = 2^n - 1$. Minimum number of moves is given by p .

avoid the generation of illegal strategies. It can thus be seen that an effective representation, such as this one, can be used to significantly reduce the size of the search space which is explored. It can also be observed that this representation is only effective because the number of moves required to solve the Tower of Hanoi problem¹ is encoded in the problem itself and that the final solution represents the set of moves required to solve the problem.

It has been argued, with some vigour in [Rice, 1993] and by others, that strategies are not developed by this type of solution to the Tower of Hanoi problem in that generalization has not taken place. He argues that a higher-order representation, as embodied in Genetic Programming, is required in order to solve the n-ring Tower of Hanoi problem.

The investigation of fitness function choice provides the most interesting aspect of this paper. The three functional forms are shown below:

$$F = \frac{\beta (n_2^2 + n_3^2)}{n_1 + 1} + 1$$

$$F = 1 + \beta n_p$$

$$F = \sum_{i=1}^n A(i, p) \times 10^{(n-1)}$$

In the above equations, n_i is the number of rings present on the pegs numbered 1, 2 and 3; β is an experimental parameter; p is a peg number; $A(i, p)$ is a matrix with a number of rows equal to the number of rings in the problem and with a number of columns equal to the number of pegs that code the position of the

1. The minimum number of moves for an n-ring Tower of Hanoi problem is $2^n - 1$.

board. This last fitness function takes into account not only the number of rings on the destination peg but also the correct position of the rings, assigning a weight proportional to the dimension of the rings.

It is interesting to note that Margarita criticizes the non-monotonic nature of his fitness functions and attributes the *relative* lack of success in finding an optimal strategy to their relative poverty in describing the actual fitness landscape. Actually, in most simulations, the genetic algorithm found a winning strategy in a number of steps far from the optimal one but also far from the allowed one - from one to a half to three times the optimal length although five times the optimal length was allowed.

3.3.2 Function Optimization

Function optimization has most often been used as an area where modifications to the basic genetic algorithm have been proven by evaluating potential changes against a test bed of functions.

The earliest systematic work on function optimization and a use of genetic algorithms is found in Hollstein [Hollstein, 1971]. Hollstein's work concerned itself with optimizing functions of two variables using a variety of breeding schemes using animal husbandry and horticulture as their metaphor with the traditional operators of crossover, mutation from genetics.

The selection methods investigated by Hollstein are shown in Table 5. The mating preference methods can be seen in Table 6. In order to test the effects of combinations of selection scheme and mating method, Hollstein used a function test bed of 14 functions.

The computer runs used strings of 16 bits where two 8 bit strings were encoded as either a binary unsigned integer or a Gray-coded integer.

Table 5 Selection schemes used in Hollstein's study

Scheme	Description
Progeny testing	The fitness of offspring controls subsequent breedings of the parents.
Individual selection	The fitness of an individual controls its future use as a parent.
Family selection	The fitness of the family controls the use of all family members as parents.
Within-family selection	The fitness of individuals within a family is used in order to control the selection of parents for breeding within a family.
Combined selection	Here, two or more of the above selection methods is combined to form a hybrid scheme.

As has been seen earlier, Gray codes provide the advantage that adjacent integers differ by a single bit. Hollstein also discussed the use of hash coding¹ but did not present any results.

Table 6 Mating methods used in Hollstein's study

Scheme	Description
Random mating	All mates are equally likely to mate with one another.
Inbreeding	Related parents are intentionally mated.
Line breeding	A "uniquely valuable" individual is bred with a base population and their subsequent offspring selected as parents.
Outbreeding	Individuals with markedly different phenotypic characteristics are selected as parents ^a .
Self-fertilization	An individual breeds with itself.
Clonal propagation	An exact replica of an individual is formed.
Positive assortive mating	Like individuals are bred with other like individuals ^b .
Negative assortive mating	Unlike individuals are bred. See footnote a.

1. One of $(2^l)!$ coding permutations is generated and used repeatedly.

- a. This is the antithesis of work done by [Todd, Miller, 1991].
- b. This is similar to the work done by [Todd, Miller, 1991].

In all of Hollstein's work a population of 16 was used. He observed that this was too small a population and recommended that significantly larger populations be used in future investigations of this kind. He noted that recurrent inbreeding and crossbreeding were the most robust of all breeding plans that he tried and that Gray codes provided some improvement over the unsigned integer representation. This, he argued, was due to the natural way single bit mutations mapped to an integer increment or decrement.

DeJong's thesis [DeJong, 1975] is considered pivotal in the history of genetic algorithms. This thesis is considered important because it combines the schemata theorem with very carefully constructed computer experiments. DeJong constructed a test environment of five problems in function minimization; taking care to include functions which had the following six characteristics:

1. continuous/discontinuous
2. convex/nonconvex
3. unimodal/multimodal
4. quadratic/nonquadratic
5. low-dimensionality/high dimensionality
6. deterministic/stochastic (or noisy)

Actually, the five functions used in his study form the first five functions encoded in the GENESYs¹ system and can be found in Appendix A. Function optimization was chosen for his study of genetic algorithm performance in order to (a) remove the problem of choosing a problem representation; thereby avoiding the problem of introducing representational bias into the study and (b) the fitness function is the function itself (possibly scaled). DeJong was interested in characterizing the effectiveness of various genetic algorithms and introduced the concepts of on and off-line performance. On line performance represents the ongoing performance of the genetic algorithm whereas off line performance represents the convergence level for the algorithm.

1. GENESYs (due to Back) is a derivative of the GENESIS (due to Grefenstette)

DeJong's studies investigated six reproductive plans, found in Table 7.

Table 7 DeJong's Reproductive plans

Plan Name	Plan Description
R1	Roulette wheel reproduction. Individuals reproduce in proportion to their fitness relative to the average fitness of the population.
R2	Elitist model. Best structures are preserved.
R3	Expected value model. The expected number of off-spring are created in the next generation.
R4	Elitist expected value model. A combination of R2 and R3.
R5	Crowding factor model. When an individual reproduces, a similar (as measured by the number of bits the same) individual is randomly selected to die.
R6	Generalized crossover model. This is equivalent to a multi-point crossover operator.

The majority of investigations occurred using the R1 reproductive scheme with conventional single point crossover and mutation operators.

3.3.3 Neural Network Optimization

The training of neural networks has been shown to be a hard problem, and the selection of an appropriate architecture for the task domain to be a black art. Even small networks can behave in ways that defy comprehension; multi-layer, non-linear networks have no intuitive interpretation. No comprehensive analytical or algorithmic solutions are in sight and empirical results have shown to be limited in terms of their generalizability. Many different classes of architecture for neural networks have been documented and for a good overview the reader should consult Simpson [Simpson, 1990].

Genetic algorithms have been used to design neural network architectures and determine the weights associated with the links between neurons. The application of genetic algorithms to the problem of neural network design is appropriate for a number of reasons. Firstly, the space of possible architectures is very large and analytical results do not exist for the selection of an architecture appropriate to

the task. As a result of the size of the space of possible architectures, published accounts of architecture investigation have tended to deal with simple configurations. No effective, general search techniques have been forthcoming. Network parameters also show strong interaction - implying highly nonlinear behaviour - giving rise to local minima which tend to deceive heuristic search and elementary optimization techniques. Equally importantly, most applications have to deal with noisy data which can cause the failure of even the highly robust backpropagation algorithm¹.

A number of issues present themselves when using genetic algorithms for neural network design. Firstly, the problem of representation needs to be addressed. In the case of fixed architecture, how many bits are required in order to represent the weights in the network effectively? In the case of a dynamic architecture, what data structures can be manipulated genetically in order to design the most effective neural network for the task domain? Secondly, what adaptations of the genetic operators are necessary for the genetic manipulation of neural networks. These questions, and steps towards answering them, can be found in [Harp, Sumad and Guha, 1989].

The genetic neural network design problem can be broken down into two categories. These are genetic algorithms that attempt to generate the weights for a given architecture (*the static problem*) and genetic algorithms which induce the architecture as well (*the dynamic problem*). The second class of problem is naturally considerably harder. The first problem has received considerably more attention than the second for that reason. So far,

1. As shown previously, the genetic algorithm has shown itself to be particularly effective at dealing with noisy data. For example, the DeJong's function test bed includes noisy functions.

only feed forward network design has been attempted. The basic architecture for genetic algorithm design of neural networks is shown in Figure 10.

Figure 10 Genetic Algorithm Design of Neural Networks

Both categories of design problem use the above methodology.

3.3.3.1 The Static Problem

In the static problem, genetic search attempts to replace learning (such as the Backpropagation algorithm) as the mechanism for finding weights in fixed architecture neural networks. Here, the bit string representation for the neural network is straightforward and easy to implement. For example, [Miller and Todd, 1989], [Whitley and Hanson, 1989] and [Montana and Davis, 1989] have compared genetic search to gradient descent learning for particular network designs and problem domains.

Early work in this area concentrated on the recombination of binary encoded strings to predict weights in small neural networks. However, results were mixed and found difficult to extrapolate to problems requiring more than 300 bits. It is

believed that the reason for limited success was due, in part, to the existence of multiple symmetric weight-set solutions. Restated, this says that the solution space contains multiple maxima and the crossover operator is constantly forcing us to move towards different peaks in the solution space - oscillation then occurs.

However, work by Whitley, et al [Whitley et al. 1991] appears to have overcome this problem. Firstly, in their implementation of the genetic algorithm for neural network prediction they use real-valued weights instead of binary encoding and that the crossover operator only works on weight boundaries. In a sense, they are no longer working with a binary alphabet but rather the alphabet of real numbers. Secondly, a much higher mutation rate is used, this being necessary owing to the significantly reduced exchange of genetic information between population members during crossover. An example of crossover on real-valued boundaries is shown in Figure 11.

Figure 11 Crossover on real-valued boundaries

This is in direct contrast to a more traditional genetic algorithm where the mutation operator is considered a “secondary” operator and in some work, [Koza, 1990], ignored altogether.

Finally, a small population (typically 50) is used in the genetic search. This, the authors state, has been found to reduce the exploration of multiple solutions which are representationally dissimilar. By relying more on mutation than on the more powerful crossover operator, the genetic algorithm becomes more of a genetic hill climber. During the genetic search process, the size of the population is gradually reduced until a single population member remains. This is in stark contrast to a conventional genetic algorithm in which the population size remains constant¹.

1. The author also chose to use a variation on the GENITOR algorithm [Whitley, Kauth, 1988].

In [Whitley et al, 1991] a genetic algorithm is used to generate a network which controls an inverted pendulum, or broom-on-a-cart and the results contrasted with those generated using an Adaptive Heuristic Critic (AHC) network¹. The genetically engineered networks were shown to have better average worst and best performance when compared to the traditionally-trained AHC networks. Although search time was considerably reduced by decreasing the populations size during the course of genetic search, it had the unfortunate side effect of increasing the probability of failing to find a solution.

3.3.3.2 The Dynamic Problem

Automatic mechanisms for node creation and/or destruction in neural networks, occurring naturally during the learning phase, are a relatively new phenomenon [Ash, 1988]. This is because the problem of generating both weights and architecture of a neural network is *considerably* harder than the static problem. This is so because of the difficult representation issues involved. At least three distinct approaches have been documented [Harp, Sumad and Guha, 1989], [Kitano, 1990] and [Koza, 1990, pgs 81-88]. The focus of the work of Harp et al is the generation of the architecture of the neural network, the weights being computed using the Backpropagation algorithm. Between each generation of the genetic algorithm, a neural network builder takes the candidate strings and builds a neural network which is subsequently trained using the Backpropagation algorithm. As the authors noted, automatic weight generation could be included in their representation by encoding the weights directly in the bit string. In [Harp, Sumad and Guha, 1989] a bit string representation as shown in Figure 12 is proposed.

Figure 12 Overview of neural network bit string representation

1. See [Anderson, 1989] or [Sutton, 1984] for details on Adaptive Heuristic Critic networks.

The bit string is composed of several segments called areas. Each area contains two structures, an Area Parameter Specification (APS) and a Projection Specification Field (PSF). These areas contain information on its connectivity to other areas and information on the area itself. A more detailed view of the structure of an area is shown in Figure 13 below.

Figure 13 Area and Projection Specification field detail

The markers in this representation enable (a) a modified crossover operator to generate new networks that are structurally viable and (b) there is a well-defined mapping to a neural network. Harp et al limited the crossover operator to genetic exchange at area borders only.

Each substring within a given area consists of a number of bits between 0 and 4 - in their experiments 3 was always chosen. Parameters are Gray scale encoded in order that values close in the chosen domain are close in bit string representation. An area has a total size which determines the number of units an area will have. This ranged from 0 to 7. Eta and Eta slope are used to govern the initial learning rate used by the backpropagation algorithm and are designed to represent 8 values in the range 0.1 to 12.8.

The APS total size parameter represents the number of neurons in the area of the neural network; the value being interpreted as $\log_2$.

The APS is used to define the sizes of the various areas in the associated projection specification field. Being a three dimensional neural network representation, the three "Dimensional share" values are required. Dimensionality was included in this "general" representation in order to support the discovery of neural network architectures usable in vision pattern recognition problems.

Each PSF indicates the target area - two modes of addressing being supported. Firstly, *absolute* addressing can be specified; in which case the linkage is to the area indicated by the target address value. Secondly, *relative* addressing can be specified in which case the linkage is to the area specification address plus the value indicated in the target address structure¹ of the PSF. Relative addressing is considered necessary in order to limit the destructiveness of the crossover operator.

The radii structures in the PSF allow units in an area to project only to a localized group of units in the target area. This feature, the authors believe, allows the target units to have localized receptor fields, which is common in biological neural networks and extremely important from the viewpoint of hardware implementation.

The connection density structure provides a measure of the connectivity of neuron between areas. Eight values are provided, ranging from complete connectivity to 30% connectivity.

1. The semantics of zero are the next area.

Harp et al, do not consider this representation ideal. In [Harp et al, 1989] they state:

“The genetic operators tend to rip apart distant connections on strings; it is useful to cluster interacting genes to increase the likelihood that successful combinations will travel together.”

Although this thesis does not consider the neural network design problem in detail, the above quote almost begs to have the adaptive crossover operator applied to the above problem in order to have the adaptation identify which genes are interacting strongly and ensure crossover of these tightly-coupled genes.

Harp et al describes the representation applied to the 4x8 digit recognition problem and shows that the genetically engineered networks are considerably better than generating networks randomly.

Another approach to the neural network design problem has also concentrated upon architecture determination. This approach, due to Kitano [Kitano, 1990], owes its inspiration to Lindenmayer systems, or L-systems [Lindenmayer, 1968, 1971]. Kitano's approach differs considerably from Harp et al, in that the architecture of the neural network is not *directly* encoded in the bit string but rather in a graph generation grammar which is used to generate the neural network architecture.

Kitano criticizes the previous genetic algorithm-based approaches to neural network design for two reasons. Firstly, results on the scalability of their approaches have not been forthcoming. In fact, Kitano demonstrates the scalability problems for a simple encoder/decoder problem using the approach documented in [Miller and Todd, 1989]. Accuracy of the neural network designs is shown clearly to degrade significantly with increasing network size. Secondly, that the implementations are biologically infeasible as they imply that connectivity information is encoded in DNA¹.

1. Kitano is of the school that considers the biological metaphor extremely important. Also, neural network interconnections in the brain shown a high degree of local variation but a low degree of global variation i.e. global functionality is more or less constant in the human brain. See, for example, Broca's map of the functionality of the human brain.

Kitano's graph generation scheme is defined as $L = (SN, SE, MN, ME, RN, RE, \omega)$. The meaning of the various symbols is shown in Table 8.

Table 8 Graph Generation Scheme Symbols

Symbol	Meaning
SN	A set of symbols representing the state of a node.
SE	A set of symbols representing the state of an edge.
MN	A set of 2x2 matrices with symbols for nodes assigned at diagonal elements and a symbol for an edge assigned at a non-diagonal element
ME	A set of 2x2 matrices with 0 and symbols for edges
RN	Rewriting rules for nodes.
RE	Rewriting rules for edges.
ω	Initial graph.

By application of the graph generation system, a strong¹ representation of the neural network [Miller and Todd, 1989] is generated. This is demonstrated in Figure 14 and Figure 15.

Figure 14 Demonstration of Graph Generation Grammar for XOR

1. A strong representation is one in which the nxn adjacency matrix is represented by the bit string

Figure 15 Graph generation rules for 2-2-1 XOR network

The encoding of graph generation rules in a chromosome consists of a variable portion and a constant portion with crossover and mutation operations being limited to the variable region of the string. The constant portion of the string represents the left hand side of a graph generation rule, the variable part the generated production. An example is shown in Figure 16.

Figure 16 Chromosome encoding grammar

The constant part does not change, and the 16 rules that rewrite symbols for non-differentiated cells into symbols for differentiated cells are encoded here. Each rule consists of five alleles (as shown in the figure above). For the variable region, symbols are generated for each position in the chromosome in the range A to p . The initial chromosome fragment is fixed to be S , the initial graph, in order that the initial graph can always be evolved (i.e. a rule exists which transforms the initial graph).

The chromosome rules are used to generate neural networks by the process of rewriting symbols until no further symbols can be rewritten i.e. the adjacency matrix is computed.

The results of using this representation on 4-x-4 and 8-x-8 encoder/decoder problems indicated superior accuracy and scalability when compared to [Miller and Todd, 1989]. Kitano attributes this to three things. Firstly, the grammar encoding method generates more regular patterns than the direct encoding method. This is extremely attractive from a biological perspective as considerable regularity is observed throughout the brain. Secondly, the grammar encoding method is better able to preserve the meaningful subcircuits which are discovered during the genetic algorithm. This latter point is in direct contrast to the direct encoding method where connectivities are distributed throughout the chromosome. Reuse of a useful neural network fragment is not possible. Finally, the grammar encoding method requires considerably shorter chromosomes when compared to the direct encoding method - where the adjacency matrix is directly manipulated.

Finally, in [Koza, 1990], the problem of neural network architecture and weight determination has been approached. In all of Koza's work, LISP S-expressions are manipulated using a genetic algorithm with special crossover and mutation operators. In the neural network design domain, the function set that Koza uses consists of $F = \{P, W, +, -, *, /\}$. The function P is the linear threshold processing function. The function W is the weighting function used to give a weight to a signal going into a P-type node. It is, in fact, multiplication. The set of terminals that is used consists of $S = \{D_1, D_2, \dots, D_n, R\}$. The D_i represent the input signals and R is a random number. An example of Koza's representation for a neural network and its conventional representation is shown in Figure 17.

While the genetic algorithm is applied in a conventional way, the manipulation of the LISP S-expressions that represent neural networks require special rules of construction. The root of the tree has to be an L-node, or list node. Immediately below this node, one or more P nodes must be present. At a level below a P node, W nodes must be present. At the level below a weighting node, it is possible to have an arithmetic operator, an input signal, a random number or another P node. The neural tree is generated by applying these rules

recursively until a depth limit is reached, or a full tree is generated. The leaves of the tree are always floating point values or input signals.

Figure 17 Genetic Programming and Neural Networks

As can be seen, this representation does not place any limits on either the architecture or weights of neural network connections. This representation and use of genetic algorithms provides the most general mechanism for neural network induction documented to date. The learning associated with the neural network takes place exclusively by genetic search from one generation to another.

The crossover operator takes two members of the population and, selecting nodes of the same type, exchanges subtrees. This is actually unnecessarily restrictive but did not appear to degrade¹ the results of the genetic search. By selecting nodes of the same type for crossover, we guarantee to generate a structurally correct neural network. Similarly, the mutation operator selects a node within the tree at random and replaces the node with a randomly generated subtree subject to the previously described rules.

Koza has used the above representation and modified genetic operators in order to design neural networks that solve the XOR problem² and the two bit adder problem. His results, using no mutation, and an initial population of 500, indicate that there is a 99% chance of

1. [White, 1992] confirmed these results by use of GASTE. A more generalized crossover operator was used in GASTE.

2. The XOR problem is considered a "hard" problem for the backpropagation algorithm to solve and is famous due to its analysis by Minsky and the effect this analysis had on neural network research in the 1960s.

generating a 100% correct individual within 3 independent runs of 50 generations - *a very impressive result*¹.

3.3.4 Design

A wide range of design problems have been solved using genetic algorithms. In this section, design in the area of telecommunications is considered.

Communication network design is a difficult process. A wealth of literature has been devoted to the subject, with the development of a large number of heuristic algorithms being proposed. Books by Kleinrock [Kleinrock, 1975], Tannenbaum [Tannebaum, 1981] and Bertsekas and Gallager [Bertsekas and Gallager, 1987] provide excellent sources for such material.

A related problem class is that of optimization of network operational parameters in order to minimize average network delay. In a DPN² network, traffic is routed deterministically from a particular source to any given destination. However, many equivalent paths may exist from which to choose. Without explicit human intervention the network will make less than optimal routing choices as a result of having an incomplete view of the network. The manual specification of preferred path service data for a DPN 100 network presents such an optimization problem and traditionally has been seen as a time consuming process. Preferred path service data is used in a DPN 100 network in order to balance the utilization of available trunk capacity and to route traffic in such a way as to reduce network delay. In a large network, with many equivalent paths from which to choose, this optimization problem becomes infeasible for manual solution. The probability of being able to balance the utilization of the backbone network by making primary path selections manually is low and the time taken to do it prohibitively high.

An algorithm based upon hill-climbing techniques has been implemented in order to solve this problem. The algorithm used to compute primary neighbor selections is based upon first generating a feasible (unbalanced) solution - the

1. By restricting the choice, and range, of random numbers used in the genetic search, and employing elitist reproduction strategies this can be further improved [White, 1992].

2. Copyright Northern Telecom

Minimum Link algorithm [Chou and Frank, 1972] - and then perturbing this solution in order to provide a more balanced network - the Flow Deviation algorithm [Fratta et al, 1963]. This hill climbing algorithm continues until either no more improvement can be seen or a given number of iterations are completed.

Unfortunately, the hill climbing approach does not guarantee the generation of a globally optimal solution. Being a hill climbing algorithm, if the space of feasible solutions contains many local maxima, the algorithm will most likely converge to the top of a local peak rather than find the global maximum. This is a highly undesirable characteristic of the algorithm.

The purpose of primary neighbor selection is to try and balance the utilization of trunk capacity within the network by making choices for preferred path amongst equivalent paths.

The primary neighbor problem (PNP) cannot feasibly be solved manually for large networks with a reasonable number of paths from which to choose. For example, in a large european network, approximately 2^{64} networks can be defined by choice of primary neighbor. This european network is relatively small; consisting of 34 modules and 62 trunks. Even evaluating one network per second, a total of 5.8×10^{11} years would be required to test all possible combinations for primary neighbor selection. Obviously, a solution strategy is required in order to search the solution space more efficiently. The process of specifying routing parameters using a genetic algorithm is shown diagrammatically in Figure 18 below.

Figure 18 The Genetic Algorithm Primary Neighbor selection process

One of the overriding concerns in choosing a representation for this problem was that the representation not allow the expression of infeasible solutions. For example, if only two possible choices exist for primary neighbor selection and the representation allows for four this would be an error. In other words, the representation only defines the space of feasible solutions.

By requiring the above, it became necessary to choose a non-binary alphabet for chromosome expression. Consider two nodes, PM DK1 and PM CH2. PM DK1 has two primary neighbor selections, each with two choices. PM CH2 also has two primary neighbor selections, one with two choices, the other with three choices. Thus if we were to use a binary alphabet for expression of the (partial) solution, PM DK1 would require 1+1 bits while PM CH2 would require 1+2 bits. However, in the latter case, while only three possibilities exist, the representation allows for four. *An infeasible solution is allowed by the representation.*

A natural representation is to use an alphabet which depends on the number of choices to be made for a particular PM and then modify the mutation operator appropriately. So, using the previous example, PM DK1 uses a {0,1} alphabet for the choices available to it while PM CH2 uses a {0,1} alphabet for the two choice primary neighbor node and a {0,1,2} alphabet for the three choice primary neighbor node.

It is also important to realize that the representation can only be computed once the routing tables have been created for the network as it is only at this point that the number of possible primary neighbors is known. The overall representation for the chromosome to be used in the genetic algorithm is then derived as follows:

```

for each node in the network do:
  if node has primary neighbor choices
    Begin
      representation[i].source := nodeIndex;
      for each source choice do
        representation[i].choices := numberOfChoicesForSource;
    End
  end if
end for

```

The `representation[i].choices` information is used in order to (a) generate an initial population and (b) used during mutation in order to ensure that the value for a specific gene is changed to a legal value. The maximum number of choices at any point is `maxTrunkGroups` (31), which can be encoded in 5 bits. Hence, the physical size of the chromosome in bits is just the number of nodes for which primary neighbors can be defined (source to destination) multiplied by five.

Note: The physical implementation of the representation is still a bit string. It is only the logical implementation of the chromosome which uses variable, possibly non-binary alphabets.

The crossover operator needs to be modified such that crossover only occurs on five bit boundaries.

The modification to the mutation operator is a little more complex due to the variable alphabet used throughout the chromosome. The code fragment below applies to the `i`th gene in the chromosome.

```
if random() < mutationProbability then
    geneValue := randomRange(representation[i].choices);
```

The above code fragment modifies the `geneValue` to be in the range of zero to `representation[i].choices - 1`. Note that the value may go unchanged as the function `randomRange()` returns an integer chosen using a uniform distribution. This is a little different to the previous definition in which a different value was guaranteed. Actually, the difference in practical terms is resolved by increasing the `mutationProbability`.

The fitness function for the primary neighbor problem needs to be able to take into account constraints specified by the user. Certain trunks might need to be utilization limited and solutions generating values in excess of these thresholds

be considered highly unfit. For this reason a penalty must be added to those chromosomes which exceed user specified thresholds. In the equations below, this is represented by the penaltyFitness_j and the *penalty* value in the same equation is an algorithm or program parameter.

It might be useful for networks with primary neighbor selections which violate user defined constraints to have a non-zero fitness i.e. they can appear fitter than some networks which have highly unbalanced trunk utilization values. This is designed into the fitness function included here and can be controlled through the setting of the *penalty* parameter. The ConstraintUtil_j values are also program inputs. For trunk groups that are not utilization limited, the ConstraintUtil_j value would be set to 100 in order to ensure a zero penalty term. The $\text{Util}_{ij} > \text{ConstraintUtil}_j$ term returns 1 if true, 0 if false, so that the term $(\text{Util}_{ij} > \text{ConstraintUtil}_j)$ penalty returns either 0 or penalty.

The index j in the above equations refers to the j th chromosome in the population. The 0.01 figure in the final equation is a rounding term only and ensures that the fitness of any chromosome lies in the range (0,100). In the equations below, all utilization values are measured in the range (0,1).

The results obtained by implementing this search strategy compared to the hill climbing method proved that the genetic algorithm did not tend to be trapped into

$$\text{penaltyFitness}_j = \sum_{i=1}^{\text{totalTrunks}} (\text{Util}_{ij} > \text{ConstraintUtil}_j) \times \text{penalty}$$

$$\text{Util}_{\text{avg}} = \sum_{i=1}^{\text{totalTrunks}} \text{Util}_{ij} / \text{totalTrunks}$$

$$\text{rawFitness}_j = \sum_{i=1}^{\text{totalTrunks}} \text{abs}(\text{Util}_{\text{avg}} - \text{Util}_{ij})$$

$$\text{totalRawFitness}_j = \text{rawFitness}_j + \text{penaltyFitness}_j$$

$$\text{fitness}_j = 1 / (\text{totalRawFitness}_j + 0.01)$$

producing a local minimum. Other use of the genetic algorithm in the area of Telecommunications can be found in [Coombs, Davis, 1987], [Davis, Coombs, 1987] and [Pan, Wang, 1991].

3.3.5 Automatic Programming

It has long been a dream that one day computers will generate programs automatically. As such, a number of attempts to generate programs automatically using genetic algorithms have been made. Not all of these efforts have concentrated on the development of a LISP or other such program representation. Finite state machines have also been chosen as the following paragraphs show.

An early evolutionary programming attempt used small finite state machines [Fogel et al, 1966]. In this work, sequential symbol prediction tasks were performed by searching through a space of small finite state machines. The purpose of the machines was to identify patterns in symbol sequences which were presented to them. Fogel et al. used only selection and mutation operators in their work and performed only single mutations in moving from parent to offspring. This, essentially random, search of the space of finite state machines proved to be inadequate for all but the smallest problems. No structured recombination operators were present in their evolutionary programming efforts.

The single-step mutation operator had an interesting description [Fogel et al, 1966, pg. 14-15]:

“An offspring of this machine is then produced through mutation; that is, through a single modification of the parent machine in accordance with some mutation noise distribution. The mode of mutation is determined by the interval within which number selected from a random number table lies. The intervals are chosen in accordance with a probability distribution over the permitted modes of mutation. Additional numbers are then selected in order to determine the specific details of the mutation. Thus the offspring is made to differ from its parent either by an output

symbol, a state transition, the number of states, or the initial state.”

The lack of structured recombination and an acknowledgment that the work applied to small finite state machine problems tended to see this work ignored by the A.I. community. Further evidence for the limitation of a “structured hill-climbing” approach to the induction of finite automata can be found in [Tomita, 1982].

However, a related piece of work due to Zhou and Grefenstette [Zhou, Grefenstette, 1986] uses the full power of a genetic algorithm in order to induce descriptions of finite automata. These automata learn to parse a regular expression which is presented to them via positive and negative examples - an NP complete problem [Gold, 1978]. The automata thus learn on the basis of incomplete information. The automata are assumed to have a maximum of 8 states and are capable of parsing strings composed of a binary alphabet. The search space considered was large (10^{22}) thus answering one of the limitations implicit in Fogel et al’s work.

The representation used was of the following form:

$$((X_1, Y_1, F_1), (X_2, Y_2, F_2), \dots, (X_8, Y_8, F_8))$$

where each (X_i, Y_i, F_i) represents the i th state of the automaton. X_i and Y_i correspond to the destination states of the 0 and 1 transition respectively. F_i is represented by three bits: the first two of which indicating whether or not there exists an arrow coming from the i th state, and the final bit determines whether the state i is a final state. Hence, the string representation for this problem is $(3+3+3)*8 = 72$ bits. The search space is thus 2^{72} in size. Small finite automata were preferred over larger solutions as suggested in [Michalski, 1983] in order to induce parsimonious solutions.

The results of this work are quite convincing, even given the fact that the size of the automaton which can be generated is small (being only eight states). Correct finite state automata were developed after a small number of generations. The paper contrasts the genetic approach with random search and *clearly* demonstrate that random search fails to identify the finite state automata. The scalability of

this work is uncertain. This author has worked directly with a more natural representation - that of graphs [White, 1992]. A modified crossover operator, exchanging strongly connected components in parent graphs, and a mutation operator which either added or deleted a node, allowed equivalent finite state machines to be generated. However, the approach did not scale well.

Other work in the area of induction of finite state automata (FSA) can be found in [Jefferson et al., 1991], [Collins and Jefferson, 1991]. In this work, finite state automata are again encoded in bit string format; in this case several hundred bits long. The purpose of the Jefferson work was to develop an FSA capable of following a trail - a foraging problem. The trail has a series of turns, gaps and jumps that get more and more difficult as the trail progresses. The experiment was an attempt to see if it is possible to produce artificial organisms that exhibit a relatively complex behaviour (embodied in the FSA), and to do so by evolutionary methods, with no built in design bias and with no learning.

Table 9 Binary-coded State Transition Table

Old State	Input	New State	Action
00	0	00	01
00	1	01	11
01	0	01	01
01	1	11	11
10	0	10	10
10	1	11	11
11	0	10	10
11	1	10	11

The "ant trail" problem, as it is often referred to, used a 453 bit encoding allowing for a possible 32 states and 4 possible actions (move forward, turn left, turn right, do nothing) with 2 possible outcomes (food present or no food present).

The genome that encodes the FSA can be seen in Table 9. The bit string encoding this organism consists of the initial state and the last two columns. The first two columns need

not be encoded because they are in canonical order. The encoding is highlighted by heavy lines in the above table.

This study is particularly interesting in that the authors were particularly conscious of possible bias that could be introduced into their experiments by “appropriate” choice of genetic operators. Hence, the crossover operator which was used in the experiments was standard; being applied blindly to all positions of the bit string without regard to the boundaries of semantic units. The mutation operator was applied equally to all members of the population and mating performed randomly with reproduction according to a standard roulette wheel strategy. The fitness function in this work presented itself naturally from the environment itself; namely, the number of pieces of food found in a bounded number of moves¹.

Figure 19 Champion FSA

Various successful FSA's developed, one of which is shown in Figure 19. The finite state machine is a complex one, and Jefferson et al go to great lengths to demonstrate that such a structure could not have evolved by purely random means. They conclude that

1. The authors were not interested in parsimonious solutions, so the time factor was not included in the fitness calculation. In nature, a more efficient forager would be favoured. In this regard then, the simulation is somewhat limited.

evolutionary influences caused such an FSA to develop. From an initially random population of FSAs, with an average ability of 3¹ and including a large percentage of totally incompetent foragers, the population evolves to levels of sophistication observed in the above FSA. In short, the population evolves behaviours that were initially not present in the population suggesting that "evolution has had the effect of "compiling" knowledge of this environment into the structure of the organism."

This led the authors to draw the conclusion that it is computationally feasible to produce artificial organisms that exhibit complex behaviour using evolutionary strategies.

More conventional approaches to automated programming have been less forthcoming. This is due - in no small part - to the fragile nature of programming languages themselves. Considering a program to be a string of symbols, a single missing piece of punctuation can completely change the meaning of a program and probably ensure that it is syntactically incorrect. The usual genetic operators of mutation and crossover are *disastrous* for traditional programming languages.

However, undeterred, Fujiki [Fujiki and Dickinson, 1987] generated programs using a simplified form of Lisp in order to solve the problem of the Prisoner's Dilemma (see section 3.3.1) and were effective in reproducing Axelrod's work. The significance of this work is in the application of the genetic algorithm to the generation of real source code. Fujika and Dickinson's work shows that the genetic algorithm can be used to find optimal solutions to less than trivial problems when a proper set of productions are used.

Cramer [Cramer, 1985] used a subset of a simple algorithmic language PL - a pseudo-assembly language - in order to produce two input, single output, multiplication functions. Cramer attempts to preserve potentially useful code in the population from destruction by the crossover and mutation operators by dividing the program into blocks. These blocks are exchanged as units, in the crossover operation and the mutation operator restricted to areas of the program which are "non-catastrophic." Unfortunately, the real problem in attempting to

1. meaning 3 units of food were gathered in the time allotted

evolve such a program is in the construction of a fitness function. If we consider the space of all possible programs, the space is largely flat with a few peaks scattered on the landscape. To put it another way, most programs are absolutely useless or are gibberish! A fitness function was developed which gave credit for partial solutions but this was, of course, highly domain dependent. More recently, [Harvey, 1991] appears to have resolved the problem of the “stark” landscape by indentifying “useful” program elements in a general way, but his descriptions are far from clear to this author.

By far the most promising application of genetic algorithms to the problem of automatic programming can be attributed to Koza [Koza, 1990]. For a detailed description of genetic programming, the reader is referred to [Koza, 1992]. Programs, in the genetic programming paradigm, are represented as LISP S-expressions¹. The LISP S-expressions are manipulated in their parse tree formulation using the crossover and mutation operations which now have special forms.

The crossover operator now takes a subtree from one parent and exchanges it with the subtree rooted at the same location in the other parent. The mutation operator picks a node and replaces the subtree rooted at that node with another randomly generated subtree. An example is shown in Figure 20.

Figure 20 Genetic Programming Crossover Operation

1. This author has manipulated an alternative parse tree formulation using the GASTE system. See [White, 1992]

Genetic Programming is a rapidly expanding area of research interest and Koza has already shown that it can be applied in a wide range of program induction problems. Programs have been produced genetically for problems in such diverse areas as:

- induction of decision trees
- mathematical discovery of relationships
- evolution of emergent behaviour
- discovery of game-playing strategies
- planning and
- sequence induction

3.4 Summary

The examples described in this chapter represent a cross section of the work that has been undertaken using genetic algorithms. As the previous five sections have shown, areas as diverse as function optimization, neural network design, automatic programming and game playing have seen the successful application of genetic algorithms.

Traditionally, genetic algorithms in function optimization have been used in order to investigate the sensitivity of the genetic algorithm to changes in operator design and the parameters which determine their application. This strategy has been continued in this thesis, where function minimization tasks on a standard test bed of functions has been chosen in order to demonstrate the benefits of combining automata and genetic algorithms.

Game playing was included in order to demonstrate that "programs" with no notion of strategy could evolve same by the application of a genetic algorithm and, very importantly, could identify hitherto unknown strategies. Applications of genetic algorithms in the area of automatic programming demonstrated three things. Firstly, that behaviour required for successful survival could develop under evolutionary pressure. Secondly, that correct generalized solutions could develop on the basis of a small number of examples. Finally, that the genetic algorithm could be successfully applied to an infinite data structure - the parse tree of a program - in order to induce the descriptions of computer programs.

The application of genetic search in neural network design has moved quickly from the naive representation where the adjacency matrix representation is directly manipulated by the genetic algorithm to richer representations, such as those proposed by Kitano and Koza. Although genetic search has clearly demonstrated that neural network design can be achieved, scalability remains an issue. It remains to be seen as to the prospects of their approaches in real world problems.

Automated programming remains the philosophers' stone of Machine Learning and it is here that genetic algorithms have shown considerable promise in the genetic programming paradigm. Koza, in his widely influential thesis, has shown that genetic programming can be applied to a wide range of program induction tasks - two of which are briefly described in this chapter. The problem of hierarchical learning - learning to identify program subunits which become part of the set of functions manipulated by the genetic algorithm - remains an open one and we will return to this point later in final chapter of this thesis.

Genetic algorithms have not been confined to the academic community. They have been widely used in engineering circles as the section on design implies. As such, engineering users have concerned themselves with obtaining optimal solutions where conventional techniques such as hill climbing have failed.

However, in all of the above implementations of genetic search, concerns have been raised as to the art involved in selecting algorithm parameters that allow the algorithm to obtain an optimal solution in a reasonable amount of time.

Hence the motivation for this thesis.

4 Genetic Algorithm Theory

The purpose of this chapter is to provide a mathematical framework that can be used to explain why genetic algorithms work. In this chapter the Schema Theorem is developed, along with equations that describe schema disruption for two classes of crossover operator.

4.1 The Schema Theorem

The theoretical foundations of genetic algorithms rely on a bit string representation of solutions, and on the notion of a *schema*. A schema is a template allowing exploration of similarities amongst chromosomes. A schema can be derived by augmenting the *don't care* symbol (#) into the alphabet of genes. A schema represents all strings - a hyperplane in the search space - which match it on all points other than the #.

Figure 21 Examples of schema

Figure 21 shows an example of a schema and the class of strings which it represents. Schema with no #'s represent only one string. Generally, schema with r #'s represent 2^r strings. Similarly, strings of length l are matched by 2^l schemata. For strings of length l ,

there are 3^l schemata and in a population of size n , between 2^l and $n \cdot 2^l$ different schemata may be represented.

Different schemata have different properties. There are two important attributes of interest for schema. Firstly, the *order* of a schema is important. The order of a schema, denoted $o(S)$, is the number of 0 and 1 positions in the schema i.e. the number of fixed positions in the schema. This measure defines the *generality*¹ of the schema. The defining length is also equal to the length of the string minus the number of *don't care* positions in the string. Referring to Figure 21, we see that the defining length of the example schema is 3. The number of strings represented by the schema is thus:

$$n(S) = 2^{l - o(S)}$$

Thus, the lower the order of a schema, the more general the schema and the larger the dimension of the set of strings that the schema represents. The order of a schema is useful in calculating the probability of survival of the schema for mutations.

Secondly, the *defining length* of a schema is the distance between the first and last fixed string positions i.e. it determines the compactness of the information that is stored in the schema. Referring once again to Figure 21, the defining length of the schema is $\delta(S) = 5 - 1 = 4$. The larger the defining length of a schema, the less compact the information stored in the schema. The defining length of a schema is required in order to compute the probability of survival of a schema during crossover.

As shown in Program GeneticAlgorithm() in Chapter 2, the genetic algorithm can be seen as a process of selection, combination², mutation and evaluation; with the process being repeated until either a number of trials have been performed or a fitness threshold has been reached. If we define the number of strings matching a given schema in the population at

1. or specialty.

2. the exchange of genetic information between two parent strings via the crossover operator.

some time t as $m(S, t)$, and the fitness of the schema at time t as $F(S, t)$, then the schema fitness is given by:

$$F(S, t) = \sum_{i=1}^p f_i(S, t) / p$$

where $f_i(S, t)$ is the fitness of the i th string in the population which is an example of the schema, and there are p such strings in the population at time t .

During the selection stage, an intermediate population of strings is constructed using fitness proportional reproduction. Each string is copied into the intermediate population with a probability given by:

$$p_i(t) = f_i(S, t) / F_{total}(t) \quad F_{total}(t) = \sum_{i=1}^n f_i(S, t)$$

Since for an average string matched by a schema S , the probability of its selection is equal to $F(S, t) / F_{total}(t)$, and the number of strings matched by a schema S is $m(S, t)$, the number of strings matching a given schema in the selected population is then given by:

$$m(S, t+1) = m(S, t) \cdot n \cdot F(S, t)$$

or this can be written:

$$m(S, t+1) = m(S, t) \cdot F(S, t) / F(t) \quad F(t) = F_{total}(t) / n$$

Thus the number of strings in the population grows as the ratio of the fitness of schema to the average fitness of the population. Put another way, "above average" schema receive an increasing number of strings in the next generation while "below average" schema receive decreasing numbers of strings in the next generation.

If we assume that $F(S, t) = (1 + \epsilon) F(t)$, then the growth of schema from one generation to another can be written as:

$$m(S, t + 1) = m(S, t) \cdot (1 + \epsilon)$$

which, if we assume ϵ remains a constant, is a simple geometric progression and can be solved to give a closed form for $m(S, t)$.

$$m(S, t) = m(S, 0) \cdot (1 + \epsilon)^t$$

That is, above average schema receive an exponentially increasing number of strings in the next generation. The above equation is often called the reproductive schema growth equation.

However, just reproducing highly fit schema from one generation to another would achieve nothing, as no new solutions are produced during this process. This is the purpose of the crossover and mutation phases of the genetic algorithm.

Considering single-point crossover only, if a crossover site is selected randomly from among the $l-1$ possible sites, the probability that a schema S will be destroyed is given by:

$$p_d(S) = \frac{\delta(S)}{l-1}$$

and that the probability of survival is consequently:

$$p_s(S) = 1 - \frac{\delta(S)}{l-1}$$

If the probability of crossover is given by p_{cvt} , the probability of survival is given by:

$$p_s(S) = 1 - p_{cvt} \cdot \frac{\delta(S)}{l-1}$$

Actually, the above equation is an underestimate of the survival probability of any given schema. This arises from the fact that even if a crossover site is selected between fixed positions in a schema, there is still a chance that the schema will survive. This can occur when the parents exchange genetic information in such a way that the affected schema positions do not change their bit string values. A trivial example of this occurs when two identical parents are mated - crossover does not disrupt any schema in this case. The previous equation is then rewritten:

$$p_s(S) \geq 1 - p_{cvt} \cdot \frac{\delta(S)}{l-1}$$

and the reproductive schema growth equation can be rewritten:

$$m(S, t+1) \geq m(S, t) \cdot F(S, t)/F(t) \left[1 - p_{cvt} \cdot \frac{\delta(S)}{l-1} \right]$$

The above equation tells us that the expected number of strings matching a schema S in the next generation still grows exponentially, **but that the smaller that schema, the more likely it is to survive**. Hence the justification for the building block hypothesis stated in chapter 2.

The next operator to be considered is mutation. The mutation operator randomly changes a single position within a chromosome with probability p_m . The effect is a toggle of a bit from one to zero or vice versa. In order for a schema to survive, all of the bits in the schema must remain unchanged. Since the probability of the alteration of a single bit is

p_m , the probability of a single bit survival is $1-p_m$. A single mutation is independent of any other mutation, so the probability of a schema S surviving a mutation is:

$$p_s(S) = (1 - p_m)^{o(S)}$$

and since $p_m \ll 1$, this probability can be approximated by the first two terms of the binomial expansion:

$$p_s(S) = 1 - p_m \cdot o(S)$$

and that the reproductive schema growth equation can be rewritten to include the effect of mutation as:

$$m(S, t + 1) \geq m(S, t) \cdot F(S, t) / \bar{F}(t) \left[1 - p_{covr} \cdot \frac{\delta(S)}{l - 1} - p_m \cdot o(S) \right]$$

This final equation embodies the Schema theorem which states:

Theorem 1 (Schema Theorem). *Short, low-order, above-average schemata receive exponentially increasing trials in subsequent generations of a genetic algorithm.*

and a intermediate result of this theorem is that genetic algorithms explore the search space by short, low-order schemata which are used for information exchange during crossover:

Hypothesis 1 (Building Block Hypothesis). *A genetic algorithm seeks near optimal performance through the juxtaposition of short, low-order, high-performance schemata, called the building blocks.*

This hypothesis suggests that the problem of finding a “good” coding for a genetic algorithm is critical for its performance and that related bits should be “close together” in

the string. Alternatively, we can restate this problem as one in which we want to identify those bits that should always be kept together during crossover. *This is a crucial observation in this thesis, as it is exactly the purpose for which adaptive uniform crossover has been designed.*

The real value of the genetic algorithm comes from its ability to process large numbers of schemata in a single generation. Holland calls this *implicit parallelism* [Holland, 1975]. Even though n structures are processed in any one generation, the genetic algorithm processes something like n^3 schemata. This can be shown as below.

Consider a population of n binary strings of length l . If only schemata that survive with a probability greater than p (a constant) are considered, and simple crossover with only a small mutation rate are allowed, we admit only those schemata with an error rate $\epsilon = 1 - p$. Hence, only schemata with a length $l_s < \epsilon(l - 1) + 1$ are considered.

A lower bound on the number of unique schemata processed by an initially random population can be estimated by first counting the number of schemata of length l_s or less. This is then multiplied by an appropriate population size such that, on average, no more than one of each schema of length $l_s / 2$.

As shown earlier, the number of schemata of size $l_s - 1$ in an initial population is given by $2^{(l_s - 1)}$. This calculation can be performed a total of $l - l_s + 1$ times and that the number of schemata of length l_s or less is $2^{(l_s - 1)} \cdot (l - l_s + 1)$. This is the number of schemata in a single string. In order to overestimate the number of schemata in the population, we just multiply by the number of strings, n . The count of the number of schemata in the population is then given by:

$$N = 2^{(l_s - 1)} \cdot (l - l_s + 1) \cdot n$$

This is certainly an overestimate of the number of schemata in the population as there will surely be duplicates of low-order schemata in large populations. A more refined estimate can be obtained by picking a population size $n = 2^{l_s/2}$. In this way we expect to have one or fewer of all schemata of order $l_s/2$ or more. As the number of schemata is

binomially distributed, half of the schemata are of higher order than $l_s/2$ and half are of smaller order. Counting only the higher order schemata, a lower bound on the number of schemata in the population is:

$$N \geq 2^{(l_s-2)} \cdot (l - l_s + 1) \cdot n$$

and that as $n = 2^{l_s/2}$, the number of schemata in the population can be written as:

$$N = (l - l_s + 1) \cdot n^3/4$$

i.e. the number of schemata is proportional to the cube of the population size. Hence, even though the crossover and mutation operators disrupt long, high-order schemata, genetic algorithms implicitly process a large quantity of schemata while processing a relatively small number of strings.

4.2 Schema Disruption and Combination

In a more general form, the schema theorem can be written as:

$$m(S, t+1) \geq m(S, t) \cdot F(S, t) / \bar{F}(t) [1 - \zeta]$$

where ζ is an error term that captures the damage caused by genetic operators such as crossover and mutation. The previous form of the reproductive schema growth equation applied in the case where single point crossover and mutation were applied. In the case where uniform crossover is applied, the survival rate is different.

Consider a schema k , composed of b_k bits and with a defining length $\delta(k)$. Let the probability of a bit in a given bit string location being the same in both parents be P_{ok} . Note that for a random population, $P_{ok} = 0.5$ but as the population converges, this probability will move away from 0.5 to both 0 and 1. If n_k bits are exchanged between a

parent containing schema k and an another parent containing essentially random bits, the schema k could survive in either of the offspring with probability:

$$P_1(n_k) = P_{ok}^{n_k}$$

$$P_2(n_k) = P_{ok}^{(b_k - n_k)}$$

and

$$P_S(n_k) = P_1(n_k) + [1 - P_1(n_k)] P_2(n_k)$$

which is independent of the defining length of a schema. If $M(m)$ is the number of ways to exchange m bits between two parents, $M(m)$ is given by $l-1$ for single point crossover and $\binom{l}{i}$ for the uniform crossover operator.

Schema k can have from zero to all of its bits exchanged during crossover. If m bits of the l bits of the string are exchanged, the number of possible ways to exchange i bits from the schema are:

$$\binom{m}{i} \binom{l-m}{b_k - i}$$

For each m , there are $M(m)$ ways to get there, and there are $l+1$ possible values of m . Given $P_S(n_k)$ and the above equation, it is possible to compute the average survival rate for both single-point and uniform crossover operators. [Syswerda, 1989, pg. 4] clearly shows that the average survival rate of schema for the uniform operator is inferior to that for the one and two-point crossover operators.

Given that at least some good schemata survive, they must be combined together in a single genome. For the first offspring to contain good schemata, say k and j , k must survive while j is constructed and for the second offspring, k must be constructed while j

survives. If $P_C(n_j, n_k)$ is the probability that schema j and k will combine, it is given by:

$$P_1(n_j, n_k) = P_{ok}^{n_j} P_{ok}^{(b_k - n_k)}$$

$$P_2(n_j, n_k) = P_{ok}^{(b_j - n_j)} P_{ok}^{n_k}$$

and:

$$P_C(n_j, n_k) = P_1(n_j, n_k) + [1 - P_1(n_j, n_k)] P_2(n_j, n_k)$$

As with schema survival, we must count how many times $P_C(n_j, n_k)$ occurs for all possible values of n_j and n_k . The number of ways that m bits of l are exchanged, and schema j exchanges n_j of its bits, while schema k exchanges n_k of its bits is given by:

$$\binom{m}{n_j} \binom{l-m}{b_j - n_j} \binom{m}{n_k} \binom{l-m}{b_k - n_k}$$

As, once again, there are $M(m)$ ways of to exchange m bits, the recombination rate can be calculated by counting the above for the possible values of m, b_j and b_k and using $P_C(n_j, n_k)$ to compute a weighted average. [Syswerda, 1989, pg. 5] shows that the uniform crossover operator has a slightly higher average combination rate than either one or two-point crossover and attributes the improved performance of the uniform crossover operator in the empirical studies undertaken to this factor.

Given the lack of *representational bias* of the uniform crossover operator, its *superior schema recombination* properties, and the studies that indicate *improved performance* when using it in function optimization problems, it was used as the basis for adaptive operator search. This is discussed in depth in Chapter 8.

5 Genetic Algorithms and other Optimization techniques

5.1 Overview

In this chapter genetic algorithms are compared with two optimization techniques. Firstly, the similarities and differences between evolutionary strategies and genetic algorithms are discussed. Secondly, genetic algorithms are compared to the family of annealing and reannealing function optimization techniques; concentrating on the most recent Very Fast Simulated Reannealing method.

5.2 Evolutionary Strategies

Evolutionary strategies (ES) emerged from Rechenberg's work in the late sixties and early seventies [Rechenberg, 1973] in the area of function optimization. In Rechenberg's work only one parent and one offspring was considered with a fixed step size and can crudely be characterized as being a hill climbing algorithm.

Schwefel extended the one parent, one offspring to a more general μ parents and λ offspring by invoking the biological metaphor of evolution. Schwefel proposed an ES capable of self adaptation [Schwefel, 1977, 1981]. An evolutionary strategy can be described using the 11 tuple:

$$(\mu, \lambda)\text{-ES} = (P^0, \mu, \lambda, \sigma, m, \lambda, \Delta\sigma, \lambda\sigma, f, g, t)$$

2

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where:

$$P^{(t)} = (a_1^{(t)}, \dots, a_{\mu}^{(t)}) \in I^{\mu}$$

$$\mu \in \mathbb{N}$$

$$\lambda \in \mathbb{N}; \lambda \geq \mu$$

$$r: (I^{\mu} \rightarrow I)$$

$$m: (I \rightarrow I)$$

$$s: (I^{\lambda} \rightarrow I^{\mu})$$

$$\Delta \sigma \in \mathbb{R}$$

$$\Delta \theta \in \mathbb{R}$$

$$f: (\mathbb{R}^n \rightarrow \mathbb{R})$$

$$g_j: (\mathbb{R}^n \rightarrow \mathbb{R}) \quad (j \in \{1, \dots, q\})$$

$$t: I^{\mu} \rightarrow \{0, 1\}$$

Population

Number of parents

Number of offspring

Recombination operator

Mutation operator

Selection operator

Step size meta control

Correlation meta control

Objective function

Constraint functions

Termination criterion

Every individual in the population $a_i = (x^i, \theta^i, \sigma^i) \in I^l$ consists of three vectors. These are $x^i \in \mathbb{R}^l$, the set of object variables, $\sigma^i \in \mathbb{R}^l$, the set of step sizes, and $\theta^i \in \mathbb{R}^l$, the set of inclination angles. The latter two parameters are internal strategy parameters that control the mutation of x^i .

A population P^l consists of μ parents which produce an intermediate population $P^{(t)}$ that comprises λ offspring by means of the recombination operator r and the mutation operator m .

$$P^{(t)} = (a_1^{(t)}, \dots, a_{\lambda}^{(t)}) \in I^{\mu}$$

Intermediate Population

$$a_i^{(t)} = m(r(P^l)) ; \forall i \in \{1, \dots, \lambda\}$$

New Population generation

From this point, evolutionary algorithms can take two forms. Firstly, in the $(\mu + \lambda)$ ES the intermediate population consists of the parents and the offspring - hence $\mu + \lambda$. A selection operator, s , is then applied such that the population in the next generation is reduced to μ .

$$P^{t+1} = S(P^{tt})$$

Culling the Intermediate Population

The selection operator uses the rule “survival of the fittest individuals” in order to remove less fit individuals from the population. The evolutionary strategy halts when the termination condition $t(P^t) = 1$. The individuals of the intermediate population are formed by the application of the recombination and mutation operators. If $v \in x^t, \theta^t, \sigma^t$ and the recombination operator takes two parents, a and b , it combines them according to one of five possibilities:

Table 10 Evolutionary strategy recombination operators

Result	Meaning
$v_{a,i}$	no recombination
$v_{a,i}$ or $v_{b,i}$	discrete
$1/2(v_{a,i} + v_{b,i})$	intermediate ^a
$v_{a,i}$	global, discrete
$1/2(v_{a,i} + v_{b,i})$	global, intermediate

a. This only has any meaning for alphabets of size greater than two.

In the case of discrete recombination, the vector components are chosen from either parent and r can be viewed as a type of crossover operator with a varying number of crossover points. In the case of global recombination, for each vector component the parents a_i and b_i are chosen for each position in the vector. This results in a considerably higher mixing of genetic information when compared to the discrete case.

Finally, an offspring is mutated before it is evaluated and subsequently placed in the intermediate population. Two types of mutation are defined. Firstly, simple mutations are possible:

$$m(a) = a''$$

$$\sigma = \sigma \bullet \exp(N_0(\Delta\sigma))$$

$$x'' = x' + N_0(\Delta\sigma)$$

where $N_0(\Delta\sigma)$ refers to a vector of independent normally distributed random numbers with zero mean. Here, the standard deviations σ are first mutated before the x vectors are themselves mutated.

Correlated mutations are also possible and were introduced in order to avoid a problem with the above mutation mechanism wherein search might be limited in particular directions as a result of premature convergence.

$$m(\dot{a}) = \ddot{a}$$

$$\sigma'' = \sigma' \bullet \exp(N_0(\Delta\sigma))$$

$$\theta'' = \theta' + N_0(\Delta\sigma)$$

$$x'' = x' + C_0(\sigma'', \theta'')$$

In the above equations C_0 refers to a normally distributed random vector with mean zero and probability density given by:

$$\Delta x = N_0(\sigma'')$$

$$p(C_0(\sigma'', \theta'')) = \sqrt{\frac{\det A}{(2\pi)^n}} e^{-\frac{1}{2} A^{-1} \Delta x^T A^{-1} \Delta x}$$

The diagonal elements of the matrix A^{-1} contain the independent variances of the mutation step sizes (σ^2) for the object variables x . The off-diagonal elements represent the covariances of the mutations.

The mutation parameter θ is encoded in the genetic representation of each member of the population and is modified in the same way. In this way, the evolutionary strategy may adapt to any preferred direction of search by means of self learning.

The strategy of self-adaptation works, as individuals with better parameter values are expected to perform better than the rest. Consequently, selection automatically favours these adapted settings and search speeds up.

Several of the differences between genetic algorithms and evolutionary strategies arise from the representation chosen and the quantity of genetic information which is included. Evolutionary strategies generally deal with real valued strings while genetic algorithms deal most often with bit strings. In short, genetic algorithms operate at the level of the genotype, whereas evolutionary strategies operate at the phenotypical level. This, however, may just be a consequence of the domain of their applications. Evolutionary strategies have been used primarily in function optimization, whereas genetic algorithms (as seen in the previous chapter) have been very widely used to solve very diverse problems.

Besides this, the additional vectors θ and σ allow for mutation control to occur individually for each object variable. In genetic algorithms, the mutation rate is usually a global value. Also, allowing θ and σ to be mutated during an algorithm run allows selection to favour better adapted search strategies. In a classical genetic algorithm, adaptation of the search parameters does not occur. It is just this kind of mechanism that precipitated this thesis.

While both classes of search algorithm use principles from natural evolution, such as crossover (or recombination), mutation and selection, the operator design and subsequent dynamics differ considerably. Evolutionary strategies and genetic algorithms differ in their use of population. In evolutionary strategies, μ parents are used to generate λ offspring that are added together to form an intermediate population which is $\mu + \lambda$ in size. By means of selection the μ best are chosen and from these new parents a new generation is formed by selecting parents two at a time without bias and recombining genetic material. Finally, the offspring are mutated and become part of the next generation. In genetic algorithms the situation is quite different. Firstly, an intermediate population is generally not created¹. Parents are again selected two at a time, but the selection process is biased towards parents with high fitness. Also, genetic algorithms use crossover (or recombination) operators which allow for exchange of genetic material contained in the two parents being mated - not globally as in the case of the fourth and fifth operators as

1. Here, we speak of the classical roulette wheel selection process.

shown in Table 10. *Certainly the genetic algorithm provides a physically more reasonable recombination operator than these evolutionary strategy operators.*

It is possible to argue that the intermediate population formed in evolutionary strategies performs the same task as the roulette wheel selection process of genetic algorithms. However, it is deterministic, not stochastic. Being stochastic, it is possible for parents with low fitness values to be reproduced into the next generation. With static selection, it is possible to lose valuable genetic material early on with an evolutionary strategy and suffer premature convergence. The ratio μ/λ determines this. In genetic algorithms, premature convergence has also been acknowledged as a problem but is avoided by judicious choice of fitness scaling function [DeJong, 1975].

Mutation is used differently in evolutionary strategies and genetic algorithms. In genetic algorithms, mutation is used in order to maintain diversity - to recover lost alleles if you will. In evolutionary strategies, mutation is used in order to perform a hill climbing search procedure with the search control parameters being adapted simultaneously in order to speed up search. In genetic algorithms, mutation is considered to be a secondary operator - the principal search operator being the crossover operator. This is in complete contrast to evolutionary strategies where the mutation operator is considered to be the main search operator. The standard single (or n) point crossover operator found in genetic algorithms differs completely from the evolutionary strategy recombination operator. However, the uniform crossover operator [Syswerda, 1989] - the subject of this thesis¹ - is identical to the discrete recombination operator used in evolutionary strategies². It is interesting to note that the uniform crossover operator has seen increasing favour in genetic algorithm circles since its introduction by Syswerda.

Investigations comparing evolutionary strategies and genetic algorithms have been performed for a subset of the function test bed [Hoffmeister, Bäck, 1990]. The performance of evolutionary strategies and genetic algorithms were compared for functions f_6 and f_7 . While the solutions for evolutionary strategies were superior, it is

1. It is probably true that the discrete recombination operator found in evolutionary strategies provided that stimulus for this thesis.

2. Assuming that we ignore the cardinality of the alphabet.

unclear whether this statement can be generalized. The importance of parameter selection still appeared to be the deciding factor in algorithm performance.

The most important difference between genetic algorithms and evolutionary strategies *from the point of view of this thesis* is that the parameters controlling the search process are dynamic in evolutionary strategies but static in genetic algorithm search. It should be noted that evolutionary strategies only implement dynamic parameter setting for the mutation operator.

Chapter 8 provides details on the adaptive algorithm used for the crossover operator in genetic search.

5.3 Annealing Algorithms

Annealing algorithms are based upon ideas taken from the area of Statistical Mechanics in Physics. This class of algorithms rely on their ability to sample the solution space ergodically - concentrating trials in regions of high or increasing promise. Three approaches have been described in the literature and are outlined in the following three sections. Annealing algorithms have been applied in a wide range of application areas such as design [Kirkpatrick et al, 1983], finance [Ingber, 1990, 1991a] and neuroscience [Ingber, 1991b, 1992]. Firstly, the three approaches will be described; followed by a section which compares genetic algorithms to them.

Comprehensive coverage of simulated annealing algorithms can be found in [Davis, 1987]¹, [Collins et al, 1988], [Gelfand, 1987], [Johnson et al, 1987] and [Laarhoven and Aarts, 1987].

The idea of simulated annealing came from the observation that gradient descent methods frequently get trapped in local minima. The minimum that is found depends upon the starting conditions for the problem. This can easily be seen in Figure 22 where a solution

1. Also includes work on genetic algorithms.

found in valley A - a local minimum - can never be transformed to find the global minimum in valley B using gradient descent methods.

Figure 22 Fitness landscape of a typical function

The idea with simulated annealing is to allow occasional uphill steps¹. The metaphor is that of annealing in a foundry. In order to find a low energy state of a metal, the metal is heated and then its temperature is slowly reduced. The problem can best be described by imagining a ball bearing moving about on an energy landscape where the landscape is defined by the function to be minimized.

Referring to Figure 22, if all we can do is descend, we must find ourselves at the base of the valley labelled A and so the probability of finding the global minimum depends upon the search start point. In the above figure, as the valleys are of approximately equal width the probability of finding the global minimum is above 50%. However, if we consider a thermodynamic approach where a noise element is added to the solution, the higher the temperature of the ball bearing the more violent its thermal motion. Hence, a transition from valley A to valley B is possible and the potential for finding a global, rather than a local, minimum exists.

Solution points are generated randomly and their acceptance or rejection is based upon some distribution. In initial investigations, this was a Boltzmann distribution (see next section). The Boltzmann distribution has the functional form:

1. An excellent description of why simulated annealing works can be found in Chapter 6 of [Rumelhart et al. 1986]

$$P_k = \frac{1}{\left(1 + \exp^{-\Delta E_k/T}\right)}$$

where T is the “temperature” of the system and ΔE_k is the difference in values of the function being minimized (or the energies of the two states). It can easily be seen that at high temperature, p_k is approximately 1 and we have something which allows for almost random search. *Only states which have a very low energy when compared to the previous state will be accepted.* However, when T is small, the exponential term dominates and is approximately by:

$$P_k = \exp^{\Delta E_k/T}$$

In this case states with lower energy will be strongly favoured. It is assumed that when the temperature is low, and the exponential term dominates, that the solution is currently exploring the value containing the global minimum.

So, simulating annealing begins with a high temperature and via a temperature reduction schedule, reduces the volatility of the solution until a desired solution is reached. Simulating annealing can process cost functions of arbitrary degrees of non-linearity, discontinuities and noise and can statistically guarantee finding an optimal solution. The next sections formalize the above description.

5.3.1 Boltzmann Annealing

The technique of Boltzmann annealing (BA) was initially invented in order to assist in the solution of large dimensional integrals that arise in Statistical Physics but was subsequently generalized in order to apply to problems such as finding the optimal wiring for a densely wired computer chip [Kirkpatrick et al, 1983]. The BA process is essentially a Monte Carlo importance sampling technique.

Considering a problem with D defining parameters, or dimensions, Simulating annealing can then be characterized with three functional relationships:

1. $g(x)$: Probability density of state space of D parameters i.e. the way in which one solution is transformed to the next.
2. $p(x)$: Probability density for acceptance of new cost function value given the previous value.
3. $T(k)$: schedule of “annealing” the “temperature” T in annealing time steps k , i.e., of changing the volatility of the two previous probability densities.

The success of applying simulating annealing to physical problems depends upon the correct choice of the functions g and h . Using entropy and minimum free energy arguments [Ingber, 1993], many physical systems can be described using g of the form below.

$$g(x) = (2\pi T)^{-D/2} \exp \left[\frac{-\Delta x^2}{(2T)} \right] \quad (\text{Eq1})$$

where Δx is the difference between the current test point value and the previous test point value and where T is a measure of the fluctuations of the Boltzmann distribution g in the D dimensional x -space.

The acceptance probability, given a previous state E_k , is based upon the current state E_{k+1} . This is given by:

$$p(x) = \frac{1}{1 + \exp(\Delta E/T)} \quad (\text{Eq2})$$

where ΔE represents the “energy” difference between the present and previous values of the cost function. As [Ingber, 1993] shows, this is just the Boltzmann distribution contributing to the statistical mechanical partition function for the system. It can be shown [Geman and Geman, 1984] that a global maximum for $E(x)$ can be obtained if T is selected such that:

$$T(k) = \frac{T_0}{\ln(k)} \quad (\text{Eq3})$$

with T_0 being “large enough”. Although the above equations have been derived on the basis of having physical characteristics, [Kirkpatrick et al, 1983] demonstrates that the technique applies for problems with reasonable probability densities.

5.3.2 Fast Annealing

Fast annealing (FA) differs from Boltzmann annealing in the area of the generating function $g(x)$. In FA, a Cauchy distribution is used as it has a somewhat fatter tail than the Boltzmann distribution. This characteristic assists in allowing easier access to test local minima in the search for a desired global minimum. The Cauchy distribution is shown in the equation below:

$$g(x) = \frac{T}{(\Delta x^2 + T^2)^{(D+1)/2}} \quad (\text{Eq4})$$

The annealing schedule is also replaced by:

$$T(k) = \frac{T_0}{k} \quad (\text{Eq5})$$

5.3.3 Very Fast Annealing

In many physical problems we have a D-dimensional parameter space. Different parameters have different ranges and thus different annealing schedules which are determined by the curvature of the cost function at the local minima should be applied to them. The previous annealing algorithms use $g(x)$ distributions which apply across the range of real numbers and are insensitive to individual parameters. Furthermore, fast algorithms for the generation of a D-dimensional Cauchy random sequence do not exist.

Although the above sequence problem can be avoided by using a D-product of one dimensional Cauchy sequences, this leads to an annealing schedule given by:

$$T_i(k) = T_0/k^{1/D} \quad (\text{Eq6})$$

which is faster than the Boltzmann annealing schedule but still quite slow. Very fast simulated reannealing overcomes this problem by using the following:

$$x_k^i = x_k^i + y^i (B_i - A_i) \quad (\text{Eq7})$$

$$(y^i \in [-1,1]) : x_k^i = [A_i, B_i] \quad (\text{Eq8})$$

and defining the generating function:

$$g_T(y) = \prod_{i=1}^D \frac{1}{2(|y^i| + T_i) \ln(1 + T_i)} \quad (\text{Eq9})$$

The solution for y^i can be shown to be [Ingber, 1993]

$$y^i = \text{sgn}\left(u^i - \frac{1}{2}\right) T_i \left[(1 + 1/T_i)^{|2u^i - 1|} - 1 \right] \quad (\text{Eq10})$$

where u^i is a random number from [0,1]. The temperature annealing schedule is an exponential function given by:

$$T_i(k) = T_{0i} \exp(-c_i k^{1/D}) \quad (\text{Eq11})$$

where c_i is given by:

$$c_i = m_i \exp(-n_i D) \quad (\text{Eq12})$$

and m_i , n_i are VFSR tuning parameters. The acceptance function h_i is similarly defined, replacing the Boltzmann form used in the Boltzmann and Fast annealing algorithms. Equation 11 clearly shows that VFSR has an exponential temperature annealing schedule which is *considerably* faster than either Boltzmann or Fast annealing.

The term reannealing comes from the fact that periodically the annealing time is rescaled every 100 or so acceptance events - although this requires a knowledge of the derivative of the function to do this. Reannealing arises naturally out of the changing sensitivities of the x^i as the search progresses. If we define the sensitivity of the i th parameter as:

$$s_i = \frac{\partial F}{\partial x^i} \quad (\text{Eq13})$$

$$T_{ik} = T_{ik} (s_{max}/s_i) \quad (\text{Eq14})$$

Ingber has performed a number of experiments to contrast the performance of VFSR with genetic algorithm search for functions f_0 to f_5 and they are presented in [Ingber, Rosen, 1992]. To summarize the results presented there: VFSR results were marginally better for f_0 , f_1 , f_3 , and f_4 . However, as the paper points out, no attempts to optimize the parameters of the genetic algorithm were performed while presumably Ingber tuned the VFSR runs through a specification of the m_i and n_i parameters.

VFSR and genetic algorithms differ considerably in that VFSR works with a single solution, whereas genetic algorithms manipulate populations of solutions. VFSR, like all annealing algorithms is designed to sample the solution space ergodically; covering the space is a maximally efficient way.

Unlike VFSR, genetic algorithms do not require any knowledge of function derivatives. VFSR also has a hidden tuning parameter, namely the choice of initial temperature. *Annealing algorithms have been shown to be extremely sensitive to the choice of*

annealing schedule. With a poor choice of annealing schedule, it is possible to converge to a value that is not the globally optimal value

A fundamental difference between simulated annealing and genetic algorithms is that simulated annealing deals with the problem parameters themselves - the phenotype - rather than an encoding - the genotype - usually a bit string as is the case for genetic algorithms.

Genetic algorithms also provide a superior ability for parallelization, as subpopulations can be evaluated independently on separate machines. While a certain degree of parallelization is possible for VFSR in cases where the cost function decomposes¹.

Interestingly, Ackley [Ackley, 1987] has integrated the approaches of simulated annealing, hill climbing and genetic algorithms in order to provide an optimization technique that improves on each. While Goldberg [Goldberg, 1990a] has used simulated annealing on populations and Boltzmann selection in order to improve the genetic algorithm.

Finally, evolutionary strategies and simulated annealing have been compared [Groot, Wuertz, 1990]. Their conclusion, for the travelling salesman and other problems, was that little difference between approaches could be seen. They noted that the difficulties of choosing optimal parameters for both approaches tended to be the most significant factor when determining which technique was better.

It can clearly be seen from the above comparisons that genetic algorithms do not modify their control parameters dynamically whereas evolutionary strategies do. It seems reasonable to expect that genetic algorithms might benefit from modification of their control parameters as the run progresses.

This is the subject of this thesis - the details of the adaptive process are found in Chapter 8

1. The function is of the form $\prod \phi_i(x_i)$ or $\sum \phi_i(x_i)$

6 Adaptive Genetic Algorithms

Chapter 5 described evolutionary strategies and simulated annealing where both classes of algorithm have been extended with an adaptive component. In the case of evolutionary strategies, the step size for the mutation operator is adaptive, while in the case of very fast simulated reannealing, problem variables and the temperature annealing schedule are dynamically rescaled in order to provide improved search. In [Hoffmeister, Bäck, 1990], they observe:

“Self adaptive strategy parameters remain a large blank area on the GA map.”

While this is not entirely true, little work has been done in this area. This chapter provides a review of the research that has been performed. It consists of 5 sections.

6.1 Convergence control

This section might well be re-titled “diversity maintenance” as this is the problem that convergence control attempts to solve. Premature convergence in genetic algorithms, where one (or possibly several) super individual(s) dominates the population causing premature allele loss, has long been considered a problem. While fitness scaling has been considered a partial solution [DeJong, 1975] to this problem, it provides for a static, rather than dynamic solution. Two of the adaptive approaches to convergence control are described below.

6.1.1 Ranking and Adaptive Population Size

The first due to Baker, [Baker, 1985] attempts to monitor rapid convergence due to domination of the population by one of more super individuals and its descendents. This is achieved using two modifications to the basic genetic algorithm. The first modification is to replace the standard roulette wheel selection with a ranking selection method.

In the ranking selection algorithm each individual receives an expected number of offspring based upon the rank of the bit string's performance and not on its absolute value. The allocation function is monotonic and linear, defined as in the table below:

Table 11 Ranking allocation function

Variable	Meaning	Formula
MIN	Lower bound	$2.0 - \text{MAX}$
INC	Difference between adjacent individuals	$2.0 * (\text{MAX} - 1.0) / \text{POP}$
LOW	Lowest individual's expected value	$\text{INC} / 2.0$
POP	Population size	input parameter
MAX	Upper bound for expected values	input parameter

Ranking just sorts the population based upon the fitness values of the individuals followed by calculation of the ranking allocation function. The allocation function is then used to compute the number of offspring of a given parent in the next generation. In Baker's function, the expected number of offspring for the fittest individual was determined by the setting of the MAX variable which, through experimentation was set at 1.1¹. Although not dynamic, this severely limits the contribution of any given individual and thereby reduces allele loss.

1. Interestingly, the average number of children per couple in western societies is approximately 2.2 – or 1.1 per individual.

Michalewicz [Michalewicz, 1992] proposes the use of a non-linear function:

$$prob(rank) = q(1 - q)^{rank - 1}$$

where $rank=1$ corresponds to the best individual, and $rank=$ population size represents the worst individual. The variable q is a user defined parameter.

The ranking selection method was coupled with a dynamic population size mechanism. Here, Baker defines a *percent involvement* measure as:

“We define percent involvement as the percentage of the current population which contributes offspring for the next generation.”

Individuals are added to the population until both the original population size and a user-defined percentage involvement value is reached. This ensures that during periods of slow convergence the population is constrained to be close to the original population size, as all individuals will be equally involved. However, during periods of rapid convergence - when the percentage involvement will tend to decrease - the population will grow. The population will subsequently shrink back towards the initial population size once convergence slows once more.

This mechanism thus allows for dynamic modification of a parameter (population size) through the monitoring of the percentage involvement measure. It is, however, still possible for a super individual to make up a large proportion of the population quickly even though allele loss is not seen.

The ranking and dynamic population strategy was used in the study of Shekel's foxholes function (f_5) and was shown to provide superior control of convergence - average bias values being considerably reduced.

6.1.2 Diversity Maintenance using Entropy

Population convergence can also be controlled by monitoring the degree of disorder (or entropy) in the population (or ensemble if we wish to use a term drawn from Thermodynamics.) The diversity of a population can be measured by considering the entropy of the system. This approach, due to [White, 1992], combines an elitist, selection strategy with a dynamic mutation operator probability in order to maintain population diversity¹.

The principal concern in this study was the premature convergence often observed in elitist strategy selection genetic algorithms. The elitist strategy ensures that the best solution will never be lost, while the adaptive mutation operator ensures that sufficient diversity will be maintained.

Considering only a binary alphabet here, and using the Shannon [Shannon, 1948] information-theoretic measure, the entropy of a population can be stated as:

$$E(\bar{p}) = - \left(\sum_{i=1}^l p_1^i \ln p_1^i + \sum_{i=1}^l p_0^i \ln p_0^i \right)$$

$$p_1^i = \left(\sum_{j=1}^{P_s} \text{bit}(i, j) \right) / P_s; p_0^i = 1 - p_1^i$$

where l is the length of the bit string, and P_s is the size of the population. It can easily be shown that this function is maximized with:

$$p_1^i = p_0^i = \frac{1}{2}; i = (1, \dots, l)$$

1. The entropy of a system has been monitored and used to control a classifier system [Wilson, 1987]. In Wilson's approach, if the change in classifier entropy is sufficiently positive or negative, the probability of crossover is decreased or increased respectively by a fixed percentage (in his experiments 10%). The results reported were good. However, further research has not been forthcoming and the generality of the technique is in question.

Defining E_{max} to be:

$$E_{max} = E(\overline{p_{max}}) = l \cdot \ln 2$$

the diversity of the population of bit strings can be defined:

$$D = \frac{E(\overline{p})}{E_{max}}$$

A plot of the diversity function in one dimension is shown in Figure 23.

Figure 23 Plot of the Diversity Function

The diversity function is a function that is convex, symmetric about 0.5, and lies in the range (0,1). The generational value of the mutation operator probability is generally defined to be:

$$p_m = g(D)$$

where $g(D)$ was defined to be:

$$g(D) = p_{max}^{-D} (p_{max} - p_{min})$$

p_{max} was constrained to be in (0, 0.1) and p_{min} to be less than p_{max} . The parameters p_{min} and p_{max} ¹ are algorithm parameters. With p_m approximately equal to 0.5 (i.e. when there is little diversity in the population) the genetic algorithm reduces to hill climbing search.

The dynamic mutation operator was applied to function f_1 and found to be extremely effective at preventing premature convergence, and allele loss. However, it was felt that the mutation rates were generally too high for reasonable diversity values and it was proposed that a non-linear $g(D)$ function be used. An alternative function proposed², but not investigated, was:

$$g(D) = p_{max} \exp(-Dk)$$

where k is constant such that:

$$k = -\ln\left(\frac{p_{min}}{p_{max}}\right)$$

By defining k in this way, the function $g(D)$ is constrained to lie in the range (p_{min}, p_{max}). It should be noted that the functional form of this equation draws its inspiration from the temperature annealing schedule used in simulated annealing. A plot of this Boltzmann-like form of $g(D)$, with (p_{min}, p_{max}) equals to (0.001, 0.5) is shown in Figure 24.

1. p_{max}, p_{min} values were 0.1, 0.0 in the study performed.
 2. This is similar to [Fogarty, 1989]

Figure 24 Mutation Probability as a Function of Diversity

From the form of this curve it can be seen that at high diversity - as in the initial randomly-generated population - the mutation probability is low.

Figure 25 Diversity as a function of trial for $f1$

However, as selection pressure gradually reduces the diversity of the overall population, the mutation probability rises slowly but with an ever increasing rate to its maximum value at $D=0$. A plot of the diversity seen in the population for function f1 as a function of trial can be seen in Figure 25.

The speed with which this function falls off is *strongly* influenced by the ratio $p_{\min}/p_{\max}$. A criticism that can be leveled against the above adaption mechanism is that it requires the calculation of a global measure - population diversity. Genetic algorithm purists¹ tend not to use mechanisms that require such calculations.

6.2 Punctuated Crossover

Traditional 1-point crossover is known to be biased in the sense that bits at the ends of the string are not manipulated with the same efficiency as those in other locations on the string and the success of the operator depends strongly on the representation chosen - the further apart "linked" genes are, the more likely they are to be split apart by the action of the crossover operator. In some sense, traditional 1-point crossover can be said to be "blind"; caring not for the allele at a particular location. This is in complete contrast to Nature's genetic crossover activity which strongly indicates that the location of crossover events depends upon the contents of the chromosomes at that location. Schaffer [Schaffer, 1987] identified this and it provided the motivation for the *punctuated crossover operator*. The idea of punctuation in strings was first documented in [Holland, 1975] but in Schaffer's work was used in quite a different way.

The punctuated crossover operator requires the doubling of the string length, where the first l bits are the conventional representation and the second l bits are interpreted as crossover punctuation. A one in a particular bit position means that crossover is allowed, whereas a zero in any given bit position implies that crossover at that location is

1. Purists in the sense of attempting to retain as much of the genetic metaphor as possible

prohibited. An alternative view of this representation is to think of it as a diploid structure. An example of this diploid view can be seen in Figure 26.

1	0	1	0	1	1	0	Conventional bit string
1	0	0	0	1	0	1	String augmentation for punctuated crossover

Figure 26 Punctuated crossover bit string representation

While the initial population conventional bit string components were generated randomly, the augmented parts were governed by P_{xo} , the probability that a crossover was allowed at a particular location. The punctuated crossover operator works by exchanging bits according to the punctuation in both parents. When a 1 bit is encountered in either parent, the bits begin going to the other offspring i.e. the bits are crossed over. When this occurs, the punctuation bits are also exchanged. The punctuation bits are considered to be linked to the conventional bit in the overall representation.

Thus, certain distributions of parental bits will result in all of the punctuation bits being passed to one of the offspring and none to its sibling, while others will tend to distribute groups of them. As a result of standard selection techniques, when an offspring fails to survive to the next generation, its punctuation bits die with it. Hence, the dynamics of punctuation bit distributions reflect an accumulating experience about where good locations for crossover are to be found.

As such, the mutation operator acts on both the conventional bit string and the punctuation bits. Schaffer indicates that this mechanism generates for superior results but provides no experimental evidence to support this view.

Schaffer provides results for the application of the punctuated crossover operator on functions f_1 to f_5 ; contrasting them with Grefenstette's results for the same

functions derived using a meta-GA [Grefenstette, 1986]. His results are significantly¹ better in the case of functions f_1, f_2, f_4, f_5 and no worse for f_3 .

These results, and the idea of an extended representation used to guide the crossover operator, are particularly important to the development of this thesis. Clearly, from Schaffer's work, adaptive crossover can play a significant part in the improvement of genetic search.

6.3 Meta-level Genetic Algorithms

Grefenstette's work [Grefenstette, 1986] on meta level genetic algorithms was first suggested by work done by Weinberg [Weinberg, 1970] where the results of a genetic algorithm run were passed to a higher level genetic algorithm (meta-GA) as shown in Figure 27.

Figure 27 Meta Genetic Algorithm Architecture

Grefenstette used the non-adaptive genetic algorithm in order to encode parameters for the adaptive genetic algorithm- such as probability of mutation, probability of crossover, and population size. The fitness of the bit strings in the meta-level genetic algorithm were computed by running a genetic algorithm with those parameters for a given function - one of functions f_1 to f_5 were used.

This was an extremely expensive process, requiring a single genetic algorithm run in order to compute the fitness of a string at the meta-level. While infeasible

1. statistically significant.

as a technique for general function optimization, the experiment did yield results for functions f_1 to f_5 which were better than those previously reported.

Grefenstette's new settings have become a default standard for researchers using binary representation, thus saving researchers considerable time in deriving parameter setting appropriate to their domains.

Schaffer [Schaffer et al, 1989] subsequently extended Grefenstette's work to include functions f_6 , f_7 and three problems drawn from the areas of filter design, a 30 city travelling salesman problem and a graph partitioning problem.

6.4 Adaptive Operator Selection

In the traditional genetic algorithm, the number of operators that can manipulate the bit string is fixed, and the probability with which they can be applied is constant. Further, it is also the case that the operators are applied in a given sequence. It was Davis' [Davis, 1989] observation that different operators are generally required at different stages of the search process and that the genetic algorithm should adapt and be able to select which operators amongst those available to apply and in what order¹. Davis worked with a set of five operators, in a non-binary string representation. The operators used are briefly described in the next five paragraphs.

The **GUARANTEED-UNIFORM-CROSSOVER** operator creates a child from two parents by deciding on a field-by-field basis which child receives the corresponding value from which parent².

The **GUARANTEED-AVERAGE** operator creates a child by averaging the fields of the two parents. Randomly rounding up or down in the case of an intermediate value³.

1. That is from generation to generation.

2. Largely equivalent to the uniform crossover operator [Syswerda, 1989].

3. This is functionally equivalent to the intermediate recombination operator described in [Hoffmeister, Back, 1990].

The **GUARANTEED-MUTATION** operator creates a child from one parent by passing down the parent's fields and, with 10% probability, replace each value by a random value between 0 and the maximum allowed for the variable.

The **GUARANTEED-BIG-CREEP** operator creates one child from one parent by passing down the parent's fields and, with 20% probability, altering a field by replacing it with a value that is 1.2 or 3 units above or below the parent's value.

The **GUARANTEED-LITTLE-CREEP** operator creates one child from one parent by passing down the parent's fields and, with 10% probability, altering a field by replacing it with a value that is 1 unit above or below the parent's field value.

In all of the above operators, a child was retained only if it differed from its parents.

The idea is that adaptation of operator probabilities takes place based upon the performance of the operator's offspring. In short, if the operator produces offspring with a fitness which is superior to that of the parents, then the fitness of the operator should increase. However, if the operator produces offspring with a fitness which is inferior to that of the parents, then the fitness of that operator should decrease. Davis further believed that:

“...an adaptive mechanism should alter the probability of applying an operator in proportion to the observed performance of the individuals created by that operator in the course of the run.”

and that:

“.. purely local measures are not sufficient. One must reward an operator that sets the stage for this production.”

This is often referred to as a credit assignment problem and is common in Machine Learning problems. To paraphrase the above quote, a window must be maintained over which reward-penalty actions are to be performed. An operator bids to be the one selected and at the end of the window, these bids are allocated

to the operators that have caused increasingly fit offspring is proportion to their fitness increase.

The adaptive algorithm used by Davis was:

When a child is generated, record its parent(s) and operator

When the new child is best, give it credit equal to the extent to which its fitness exceeds the current highest fitness value.

A portion of the child's credit is paid to the credits of its parents, and grandparents and so on, for W generations.

The performance of the operator during a given interval I is:

$$perf_{operator} = \frac{\sum credit_{children}}{numberOfChildren}$$

The adaptation of operator fitness at the end of the update period is calculated using the following algorithm:

Let x be the probability mass to adapt ($0 < x < 1$).

If the $perf_{i,j}$ values are all zero, operator probabilities values remain unchanged.

Otherwise, multiply all operator probability values by (1-x). This is the base probability, $p_{base}(i,j)$, for each operator.

The adaptive probability, $p_{adaptive}(i,j)$, component is computed using:

$$p_{adaptive}^i = \frac{perf_i \cdot x}{\sum_i perf_i}$$

and that:

$$p_{newFitness}^i = p_{baseFitness}^i + p_{adaptive}^i$$

The $p_{newFitness}$ values are then used as operator probabilities for the next genetic algorithm interval (I). In Davis' work, the window of adaptation, W, was set to be 100 and the algorithm's adaptation interval to be 50. The value of α was set to be 0.15 i.e. 15% of the probability mass was reallocated during a single adaptation.

Davis' method provides a general method for having a genetic algorithm choose which operators to apply for itself. Theoretically, it should be possible to seed the problem with a set of candidate operators and have the algorithm decide which to apply as the algorithm progresses - some operators eventually being discarded.

Although Davis' approach provides a very general approach for adaptive operator probabilities based upon the quality of the offspring that they produce, the technique has the significant drawback of having to resolve the **credit assignment problem** i.e. the apportionment of credit to an operator that set the stage for the production of a high calibre offspring. This is a common problem in Machine Learning.

6.5 Adaptive Mutation

Globally manipulated mutation operator probabilities have been proposed. In [Hesser, Männer, 1991], an exponentially decaying mutation operator probability is used to control search. The form of the operator probability draws its inspiration from concepts found in simulated annealing and evolutionary strategies and is given by the equation below:

$$p_m(t) = \sqrt{\frac{\alpha}{\beta}} \cdot \frac{\exp\left(-\gamma \frac{t}{\lambda \sqrt{l}}\right)}{\lambda \sqrt{l}}$$

Here, α, β and γ are search dependent parameters, λ is the population size and l the length of the bit string. Fogarty [Fogarty, 1989] documents various adaptive mutation operator

strategies applied to the problem of optimization of parameters used in the control of industrial burner valves. The most promising strategy is that of an initial mutation probability which decays exponentially with each succeeding generation - again hinting at the annealing schedule for temperature found in simulated annealing search algorithms.

Bäck in [Bäck, 1991] introduces an adaptive mutation operator which encodes mutation operator probabilities directly into the genetic representation of the individuals. Further, mutation rates are also subject to mutation and selection in that they undergo evolution as well as the object variables. Unlike Hesser and Männer, no global control of mutation rate adaption is required. Initial mutation rates are set randomly.

As a consequence of this approach, the mutation operator probability is no longer an external parameter of the genetic algorithm. Each bit position now has an associated mutation probability, initially set randomly. The bits encoding the mutation probability represent a number between 0 and 0.5. The mutation mechanism works by first mutating the mutation rates p_i with mutation probabilities p_i and then using the mutated probabilities p_i' to mutate the object variables themselves.

In this way, the mutation rates private to particular variables are subject to mutation and therefore change probabilistically over time. This process is directed by the selection process, which selects good object variable information as appropriate strategy parameter settings.

Bäck used this mechanism in order to study the functions f_1, f_7 and f_{15} and obtained remarkably good results - considerably better than through non-adaptive means. A schematic of the adaptive mechanism is shown in Figure 28.

Figure 28 :Schematic of mechanism used for adaptive mutation

Bäck maintains that the self-adaptation mechanism works by an interaction of sufficient genetic diversity within the strategy parameters and an implicit link between advantageous settings of strategy parameters and good function values, thereby providing selective pressure towards optimal operator parameter values.

This adaptive operator is relevant to this thesis for two reasons. Firstly, the representation is extended in order to encode mutation operator probability on a per-bit basis. Secondly, the representation acts on itself in order to change the values of the operator probabilities themselves.

7 Automata Theory

Learning automata have been used in the literature to model biological learning systems and also to determine the optimal action an environment offers. The learning is achieved by the automaton interacting with the environment and processing its responses to the actions that are chosen. Automata have seen use in applications such as parameter optimization, statistical decision making and telephone routing [Lakshmivarahan, 1981], [Narendra and Thathachar, 1974], [Narendra and Thathachar, 1980], [Narendra et al., 1977]. The latter paper provides an excellent survey of automata, as does the book by Lakshmivarahan.

Figure 29 Automaton interaction with its environment

The automaton learning process can be described as follows. The automaton is offered a set of actions by the environment with which it interacts and must choose one of those actions. When an action is chosen, the automaton is either rewarded or penalized by the environment with a certain probability. A learning automaton is one which learns the optimal action i.e. the action which has the minimum penalty probability, and eventually

chooses this action more frequently than other actions. The cycle of action-environmental feedback is shown in Figure 29.

Stochastic learning automata can be classified into two main classes. These are fixed structure stochastic automata (FSSA) and automata whose structures evolve with time. Examples of the former type are the Tsetlin [Tsetlin, 1961, 1973], Krinsky and Krylov automata. Examples of the latter type are called variable structure stochastic automata (VSSA) as a result of the time-varying nature of their transition and output matrices. In practice they are defined in terms of action-probability updating¹ rules which are either of a continuous or discrete nature. Examples of applications using discrete action-probability updating rules can be found in [Oommen, Hansen, 1984] and [Oommen, 1988].

$$FSSA = (\alpha, \Phi, \beta, F, G)$$

$\alpha = \{\alpha_1, \dots, \alpha_R\}$	is the set of actions from which automaton chooses
Φ	is the set of automaton states
$\beta = \{0, 1\}$	is its set of inputs - 1 representing a penalty, 0 a reward
F	is a matrix defining the state transition of the automation on receiving an input. F may be stochastic.
G	is a matrix which determines the action taken by the automaton if it is in a given state.

The selected action serves as an input to the environment which gives a response $\beta(n)$ at time n , where $\beta(n)$ is either 0 or 1. This response is fed back to the automaton. Thus the environment penalizes the automaton with the penalty c_i , where:

$$c_i = Pr[\beta(n) = 1 | \alpha(n) = \alpha_i] \quad i = (1, \dots, R)$$

Initially, the c_i are unknown and the purpose of the automaton is to compute them as a result of its interaction with the environment. The $\min(c_i)$ is the best action, i. If c_i is equal to the minimum penalty probability, and $P_i(n) = Pr[\alpha(n) = \alpha_i]$ then the

1. Due to Varsharski and Vorontsova. Proof is by construction.

aim is to have $P_L(n) = 1$; $P_i(n) = 0 \quad \forall i \neq L$. i.e. the automaton learns to choose the optimal action.

A variable structure stochastic automaton learns by employing a probability updating rule such that the action probability vector at the $(n+1)$ st time instant is computed using the probability vector at the n th time instant in conjunction with the automaton environment interaction at the n th time instant. Hence, if $\mathbf{P}(n)$ is the action probability vector at time n , the VSSA is fully defined by specifying a function $\mathbf{H}$ such that:

$$\mathbf{P}(n+1) = \mathbf{H}(\mathbf{P}(n), \alpha(n), \beta(n))$$

Studies have centered around two classes of function $\mathbf{H}$, both being linear. In the first class, $\mathbf{H}$ is a continuous function allowing $\mathbf{P}(n)$ to take any value between 0 and 1. In the second class, $\mathbf{H}$ allows $\mathbf{P}(n)$ to take a discrete number of values in the range 0 to 1. In the discrete case, linearity is taken to mean that the increments in probability are all equal. This latter class of automata, due to Oommen, are significantly easier to analyze¹, have an expected convergence time which is finite, and appear to have superior accuracy when compared to their continuous counterparts [Oommen, Hansen, 1984].

Automata can also be broadly classified in terms of their Markovian representations. Learning automata are either ergodic or possess absorbing barriers. Automata of the former class converge with a distribution that is independent of the initial distribution of the action probabilities. This is not the case for automata that are absorbing. While absorbing automata are well suited for stationary environments, ergodic automata are ideal for nonstationary environments because they do not get locked into any particular action [Lashmivarahan, 1981]. As such, this class of automata are well suited for use with genetic algorithms, as the feedback from the environment, is noisy. This point will be discussed in the next chapter.

1. These automata can be analyzed using finite state Markov chains.

In automata theory, an automaton is said to be ϵ -optimal if the mean error (or penalty) associated with it after an infinite number of interactions with the environment can be made as close to the minimum possible value by suitable choice of automaton parameters. This is defined by:

$$M(n) = \sum_{i=1}^R c_i p_i$$

where R is the number of actions available to the automaton, and c_i are the penalty probabilities. So, a learning automaton is ϵ -optimal if:

$$\lim_{n \rightarrow \infty} M(n) \rightarrow c_{\min} + \epsilon$$

An automaton is said to be expedient if:

$$\lim_{n \rightarrow \infty} M(n) < M_0$$

where M_0 is the initial expected penalty.

A number of discretized linear automata have been studied. The discretized linear reward-inaction (DL_{RI}) automaton is absorbing and ϵ -optimal in all random environments. The discretized linear inaction-penalty automaton (DL_{IP}) is ergodic and expedient in all random environments. If artificially absorbing barriers are added to the DL_{IP} automaton, the automaton is ϵ -optimal in all random environments. Finally, the discretized nonlinear reward-inaction (DN_{IP}) is ϵ -optimal in all random environments. These results are proven in [Oommen, 1986].

The automaton of most interest in this thesis is the two action, discretized linear reward penalty (DL_{RP}) automaton. This automaton can be shown to be ergodic and ϵ -optimal in all random environments where $c_{\min} < 0.5$ [Oommen, Christensen, 1988]. The DL_{RP}

automaton has $N+1$ states where N is an even integer. The automaton has a set of states $S = \{s_0, s_1, \dots, s_N\}$. Associated with the state s_i is the probability i/N that represents the probability of choosing action a_1 . Hence the probability of choosing action a_2 is given by $(1-i/N)$. As any one of the action probabilities completely defines the vector of action probabilities, it is possible to consider just $p_1(n)$ with no loss of generality. The transition map for the DL_{RP} automaton can be specified, given $s(n) = s_k$ as:

$$\begin{aligned}
 s(n+1) &= s_{k+1} && \text{if } a(n) = a_1 \text{ and } b(n) = 0 \\
 &&& \text{or } a(n) = a_2 \text{ and } b(n) = 1 \\
 &= s_{k-1} && \text{if } a(n) = a_1 \text{ and } b(n) = 1 \\
 &&& \text{or } a(n) = a_2 \text{ and } b(n) = 0 \\
 s(n+1) &= s(n) && \text{if } s(n) = s_0 \text{ or } s_N \text{ and } b(n) = 0 \\
 &= s_1 && \text{if } s(n) = s_0 \text{ and } b(n) = 1 \\
 &= s_{N-1} && \text{if } s(n) = s_N \text{ and } b(n) = 1
 \end{aligned}$$

It can be seen from the above that an automaton in state s_0 has to choose action a_2 , and similarly if it is in s_N it must choose action a_1 . The change in action probabilities can be written for $0 < p_1(n) < 1$ as:

$$\begin{aligned}
 p_1(n+1) &= p_1(n) + 1/N && \text{if } a_1 \text{ is chosen and } b(n) = 0 \\
 &&& \text{or } a_2 \text{ is chosen and } b(n) = 1 \\
 &= p_1(n) - 1/N && \text{if } a_1 \text{ is chosen and } b(n) = 1 \\
 &&& \text{or } a_2 \text{ is chosen and } b(n) = 0
 \end{aligned}$$

$$\begin{aligned}
p_1(n+1) &= p_1(n) && \text{if } p_1(n) = 0 \text{ or } 1 \text{ and } b(n) = 0 \\
&= 1/N && \text{if } p_1(n) = 0 \text{ and } b(n) = 1 \\
&= 1 - 1/N && \text{if } p_1(n) = 1 \text{ and } b(n) = 1
\end{aligned}$$

The increments between probability states are thus $1/N$ - all increments being equal. Furthermore, if $c_1 < c_2$, the automaton has no absorbing barriers except in the degenerate cases when $c_1 = 0$ or $c_2 = 1$. With the observation of these limitations, the Markov chain is ergodic and that the limiting distribution of being in any state is independent of the corresponding initial distribution. Thus the $p_1(n)$ behave as a homogeneous Markov chain.

The DL_{RP} automaton is the only known ergodic symmetric linear reward penalty VSSA that is ϵ -optimal in any random environment¹ where the minimum penalty is less than 0.5. It is considerably better than the L_{RP} which is at best expedient [Lakshmivarahan, 1981].

In the context of this thesis, the $p_1(n)$ correspond to the probability of performing a crossover as a specific bit location and $p_2(n)$ is the probability of not performing a crossover at that same bit position. The environmental response is determined by the evaluation of the fitness function for a given offspring - a reward being given for a fitter individual, a penalty for an inferior offspring. While introduced here, the integration of automata and the crossover operator is the subject of the next chapter and is dealt with in depth there.

1. With the degenerate cases previously observed. Two other schemes, the Modified Discretized Linear Reward-Penalty (MDL_{RP}) scheme and the Absorbing Discretized Linear Reward Penalty (ADL_{RP}) scheme are also described in [Oommen, Christensen, 1988]. Both of these schemes are also ϵ -optimal in any random environment - without the limitations on c_{min} previously described.

8 Adaptive Crossover Using Automata

As has been shown in previous chapters, the genetic algorithm and other search strategies have benefitted from modifying the search parameters themselves dynamically. This has been achieved by extending the problem representation in order to encode the search parameter and by providing feedback from the environment in order to reward successful operator action.

In this chapter we build upon the ideas drawn from previous work in adaptive operator probabilities by associating a linear reward-penalty automaton with each object variable¹ in the representation and by providing input to the automaton based upon the fitness of the offspring produced by the action of the adaptive crossover operator.

The adaptive uniform crossover operator is an extension of the uniform crossover operator [Syswerda, 1989]. In the uniform crossover operator, decisions as to whether bits are exchanged between parents are made on a bit-by-bit basis. The uniform crossover operator has been shown to be superior to one and two-point crossover in a large number of environments through extensive empirical studies. The uniform crossover operator has been chosen here because of its lack of representational bias i.e. defining length has no meaning for this operator and that adaption can occur at the bit level. Chapters 2 and 4 describe the mechanics and theory of the uniform crossover operator.

1. In this implementation, every bit.

This chapter consists of four sections. The first section describes the representation necessary for genetic algorithms using the adaptive uniform crossover operator, and the modifications required in the algorithm needed to employ it. The second section describes the adaptive multi-point crossover operator. The third section presents the results obtained by using adaptive uniform crossover operator on all functions in the function test bed. Finally, the fourth section discusses the results obtained in the experimental study.

8.1 The adaptive uniform crossover operator

The basic idea of the adaptive uniform crossover operator is to identify groups of bits within the bit string that should be kept together when crossover occurs. Stated another way, we wish to learn from previous crossover operations in order to minimize schema disruption in future crossovers. This is shown schematically in Figure 30.

Figure 30 Schematic of adaptive uniform crossover operator

In Figure 30 the basic bit string representation is augmented at each bit position with an automaton, shown as a vertical set of states. The ● associated with each automaton indicates the current state of that automaton. Each state of the automaton maps to a probability of crossover value for that bit string location. State changes occur as a result of feedback from the environment; in this case the environment is provided by the change in value of the fitness of the offspring when compared to the parents.

The principle used here is that bits which were kept together during crossover, and generated superior offspring, should be kept together in future crossover operations¹.

Similarly, bits which were kept together during crossover, and generated inferior offspring, should not be kept together in future crossover operations¹.

Finally, bits which were kept together during crossover, and generated offspring with no discernible fitness change, may or may not be kept together in future crossover operations¹.

The algorithm used for updating automaton state can be described as:

```

If offspring fitness > Father's fitness then reward bits which
came from Father with probability  $p_{\text{sameReward}}$ ;
If offspring fitness > Mother's fitness then reward bits which
came from Mother with probability  $p_{\text{sameReward}}$ ;
If offspring fitness < Father's fitness then penalize bits
which came from Father with probability  $p_{\text{samePenalty}}$ ;
If offspring fitness < Mother's fitness then penalize bits
which came from Mother with probability  $p_{\text{samePenalty}}$ ;
If offspring fitness = Father's fitness then reward bits which
came from Father with probability  $p_{\text{sameReward}}$  or penalize bits
which came from Father with probability  $p_{\text{samePenalty}}$ ;
If offspring fitness = Mother's fitness then reward bits which
came from Mother with probability  $p_{\text{sameReward}}$  or penalize bits
which came from Mother with probability  $p_{\text{samePenalty}}$ .

```

Subject to the limitation $p_{\text{sameReward}} + p_{\text{samePenalty}} \leq 1$.

-
1. statistically speaking.
 2. Do nothing with probability $1 - p_{\text{sameReward}} - p_{\text{samePenalty}}$.

A reward is given to an automaton if its fitness exceeds that of a parent by the floating point tolerance value, $f_{\text{tolerance}}$. Similarly, an automaton is penalized if its fitness is less than that of a parent by the floating point tolerance, $f_{\text{tolerance}}$. Actually, with a non-zero $f_{\text{tolerance}}$ value, a dead-band controller has been included in the system. A reward implies that the automaton moves from state i to state $i+1$. Similarly, a penalty implies that the automaton moves from state i to state $i-1$. If the automaton is in state n prior to a reward, nothing happens. If the automaton is in state zero prior to a penalty being applied, nothing happens. This is implied in Figure 30 and more explicitly demonstrated in Figure 31.

Figure 31 Automaton reward-penalty scheme

From the above algorithm it can be seen that all bits will be rewarded if the fitness of an offspring exceeds the fitness of both of its parents. If the fitness exceeds that of one parent, but is inferior to that of the other, certain bits will be rewarded while others will be penalized. The rewarding and penalizing of an offspring in the situation where its fitness is equal to that of one or both parents is useful in preventing stagnation of the crossover probability at a non-optimal value. The environment gives us incomplete information, in

that in certain situations bits will be rewarded which were not the direct cause of improvement. Similarly, for the same reason, bits may be penalized in error. However, over many trials the tendency is for more correct information to be imparted by the environment than incorrect information. If this were not so, the basic genetic algorithm would not work and the Schema theorem would be in error.

The adaptive uniform crossover operator is also modified from that used in the case of the Syswerda uniform operator. In the case of the uniform crossover operator, a random integer from the set $\{0,1\}$ is chosen. If the result is 1, the bits are exchanged; otherwise nothing happens. With the adaptive uniform crossover operator, the probability of crossover for the two parents is first obtained using:

$$p_{xovr}^i = P^i(s_i)$$

where P^i is the function mapping automaton state to a probability value and s_i is the state of the automaton associated with the i th bit. The function P^i , being a probability, is constrained to lie in $(0,1)$ and is monotonic increasing¹. It is a discrete function, but could be represented by a noisy function if a degree of uncertainty needs to be added to the automaton.

The crossover at a particular bit occurs if the following condition prevails:

$$\sqrt{p_{xovr_{father}}^i \cdot p_{xovr_{mother}}^i} \geq rnd(0, 1)$$

Namely, if the geometric mean of the adaptive crossover probability values exceeds a randomly generated probability value from the uniform distribution, crossover occurs. Otherwise, bits are copied directly to the offspring. An

¹ This is a desirable characteristic of the function. It would not make sense to reduce the probability of crossover after the environment has indicated a reward and subsequently moved the automaton from state i to $i+1$.

alternative formulation of the crossover operator was to use the arithmetic mean as shown below:

$$\frac{p_{xovr_father}^i + p_{xovr_mother}^i}{2} \geq rnd(0, 1)$$

It can easily be shown that the geometric mean of two numbers is less than the arithmetic mean which, in the context of the above, means that the adaptive crossover operator is more conservative - exchanging fewer bits - when using the geometric mean.

With the extended representation chosen, the action of mutation now has an effect upon not only the object variable bit but also the associated automaton. If we take mutation of a bit to be the flipping of that bit, then when toggled, the automaton is affected because the automaton state is a function of the value of the bit at that location. If the bit is flipped, logically we lose all information on the state of the automaton and it should therefore be reset. Being essentially unknown, the state is set to a random value.

The initial states of all automata were set to be the same such that the probability of crossover equalled 0.5 - identical to the uniform operator¹. One extension proposed is to initialize the automata randomly, thereby injecting further diversity into the population as suggested by Bäck [Bäck, 1991].

8.2 The adaptive multi-point crossover operator

The adaptive multi-point crossover operator is similar in concept to the adaptive uniform crossover operator and the same extended representation as shown in Figure 30 and Figure 31 is used for the encoding.

1. Again, it is useful to observe that 0.5 is far from optimal in the case of certain functions.

However, the meaning of the state of the automaton now changes. The state of the automaton now maps to a weight as shown in the equation below:

$$h^i = H^i(s_i)$$

where h^i is the weight associated with bit i , and H^i the mapping of automaton state to bit weight. The probability of crossover at any given bit is then given by:

$$p_{c\text{ovr}}^i = \frac{h^i}{\sum_{i=1} h^i}$$

For single point crossover, the crossover point is chosen probabilistically from the distribution defined by the $p_{c\text{ovr}}^i$ values. For n-point crossover, the n crossover points are chosen probabilistically from the same distribution without replacement. That is, if point one is chosen for the first crossover point, it is unavailable for selection for the second or subsequent crossover points.

The algorithm for rewarding or penalizing automata remains unchanged from that used for the adaptive uniform crossover operator.

8.3 Experimental setup and results overview

The adaptive uniform crossover operator was tested against all functions in the function test bed - f_1 to f_{24} . The results were compared using equivalent genetic algorithm search parameters to the uniform crossover operator. A modified version of Grefenstette's genetic algorithm experimental tool GENFSIS¹ was used for all

1. The version GENFSYS, was obtained from Dr. Back (baeck@ls11.informatik.uni-dortmund.de).

experimental runs. In all genetic algorithm runs, the same basic parameters were chosen. These are shown in Table 12:

Table 12 Common experimental parameters

Variable	Meaning	Value
P_s	Population size	50
P_m	Probability of mutation (per bit)	0.001
N_e	Number of experiments	100
N_t	Number of trials per experiment	10,000
S	Selection mechanism	Roulette wheel
Coding	How object variable is encoded in the bit string	Gray coding
l	Length of the object variable encoding part of an individual.	$l = 32n$ (n being the number of objective function variables)

The crossover probability for the uniform crossover operator was set to 0.5. The geometric form of the crossover exchange operator was used to decide whether bit wise crossover was to take place and P^i had the functional form:

$$P^i(s) = s/n; s = 0, \dots, n$$

By choosing this particular functional form, the automata become examples of the DI_{RP} automaton; with the properties described in the previous chapter. Restating the above equation in the form of probability updating rules, we see that the probability increases by $1/n$ if we exchanged bits and the offspring containing the bit was more successful than the parent. Similarly, if we did not exchange bits and the offspring containing the bit was less successful than the parents, the probability of crossover increases by $1/n$.

If an exchange of bits took place and the offspring containing the bit was less successful than the parent, the probability of crossover decreases by $1/n$. Finally, if the bits are not

exchanged, and the offspring containing the bit was less successful than the parents, the probability decreases by $1/n$.

Hence the function spans the probability range (0,1) and is linear. The values of the various automata probabilities are shown in Table 13:

Table 13 Adaptive crossover operator parameters

Variable	Meaning	Value
$P_{\text{superiorReward}}$	Probability with which an automaton will be rewarded if the offspring is fitter than the parent.	1.0
$P_{\text{inferiorPenalty}}$	Probability with which an automaton will be penalized if the offspring is less fit than the parent.	1.0
$P_{\text{samePenalty}}$	Probability with which an automaton will be penalized if the offspring is as fit but no fitter than the parent.	0.0
$P_{\text{sameReward}}$	Probability with which an automaton will be rewarded if the offspring is as fit but no fitter than the parent.	0.0
$f_{\text{tolerance}}$	Floating point tolerance used to decide whether an offspring is more or less fit than its parent(s).	0.0

In the three charts which follow in the next section, the best-at-trial¹ fitness is plotted. Other interesting statistics which were reviewed, but not included due to space constraints, were online and offline performance, and population diversity. The y axis is the difference in fitness values of the best solution in the population between the non-adaptive and adaptive runs. The x axis is the trial number. *Therefore, if the curve falls below the x axis, the adaptive run is superior to the non-adaptive run².*

8.4 Discussion

In this study, naive parameter settings for the various automaton probabilities were chosen in order to test the robustness of the adaptive approach with the purpose of the study being

1. The best-at-trial fitness is the fitness of the member of the population which has the minimum value.

2. As the function optimization problems are minimization problems.

to achieve better¹ solutions in a given number of trials. Similarly, a simple, linear probability mapping function was chosen. The results presented in Appendix B clearly demonstrate the utility of the adaptive uniform crossover operator to assist in genetic search. Setting aside f_{10} for the moment, of the remaining 23 functions, 13 show improvement, 6 show no discernible improvement and 4 are actually worse. While the improvements seen in certain functions are small, in others, such as f_3 , f_{11} and f_{17} , they are considerable. Certainly, the belief that more "good" than "bad" information is provided by the environment seems to be supported by the empirical results that the adaptive uniform crossover operator is able to produce better solutions than by using the uniform operator alone.

Figure 32 f_3 difference between non-adaptive and adaptive runs

As can be seen from the above chart, the adaptive run is initially worse than the non-adaptive run. This is due to the fact that the information being fed back from the environment is actually very poor - we are exchanging too many bits in the crossover operation and schema are not being correctly identified. However, as the run progresses,

1. Here, better means that the best-at-trial fitness is lower in the adaptive run. Actually this measure can easily be shown to be equivalent to faster convergence in that the best-at-trial fitness in the adaptive run reaches a given fitness threshold earlier in the run (assuming that we wait until 5000 trials or later).

the value of information being fed back from the environment improves and the DL_{RP} automata begin to converge. *That is, subsets of bits which should be exchanged during crossover begin to emerge.* The value of the feedback from the environment evidently increases rapidly as the adaptive run is superior to the non-adaptive run beyond 2500 trials.

Figure 33 f_6 difference between non-adaptive and adaptive runs

The above chart again clearly shows the same pattern as seen in Figure 32. Initially, the value of feedback from the environment is quite small leading to sizeable differences between the non-adaptive and adaptive runs. Sometimes the adaptive run is better, and at other moments the non-adaptive run is superior. However, as we converge, the value of feedback from the environment increases considerably and the automaton at each bit position begins to stabilize the correct bit patterns to keep together during the crossover operation. In the above chart, the adaptive run is clearly superior to the non-adaptive run after approximately 6000 trials. Stated another way, although the feedback from the environment has initially been quite poor, the automata have recovered in order to increase the joint access probabilities for bits responsible for improved fitness.

What is happening here is that we are initially *too* optimistic in our reward/penalty scheme. We should probably have a relatively low value for the $P_{\text{superiorReward}}$ and $P_{\text{inferiorPenalty}}$ probabilities initially and have them increase as the population converges.

A contrary indicator to the previous statement can be seen in function f_{10} . Function f_{10} is interesting because it exhibits behaviour which, during the early part of the run, strongly supports the view that the automata are identifying schema which are part of better and better sub-tours. However, after approximately 3000 trials, the improvement between adaptive and non-adaptive runs starts to degrade until at 6000 trials the two runs have identical best-at-trial fitness values. Thereafter, the non-adaptive run exhibits superior

Figure 34 f_{10} difference between non-adaptive and adaptive runs

performance. This is due to a combination of two effects. Firstly, the Travelling Salesman Problem encoded in f_{10} is a permutation or cycle problem.

Consider, for a moment, a 5 city tour. Then the tour 1-2-3-4-5-1 has an identical length to the tour 2-3-4-5-1-2. However, the bit string representations of these two tours is quite different. *What is important in these two tours is the relative positions of the cities in the tour remains constant.* The bit string encodes - in a left to right manner - the tour itself

However, the automata associated with the bits in the bit string encoding the tour are designed such that the *absolute values* of the bits are important. The constant shuffling of bits to make a valid tour ensures that the feedback from the environment will not be correct and therefore the automata state changes based upon erroneous information.

Secondly, a problem of *stagnation* can occur. While this is not restricted to the Travelling Salesman Problem, it is probable that this caused the steady decay in relative fitness when compared to the non-adaptive case. The stagnation problem occurs when the automata are in states which map to very high or very low probability values. If, in these situations, fitness improvements are not seen in the offspring, no changes to the automata will be observed and the tendency will be for the same bits to be exchanged in subsequent trials.

Obviously, the model described earlier in the chapter can deal with this problem by setting the $P_{\text{sameReward}}$ and $P_{\text{samePenalty}}$ probabilities to be non-zero. Similarly, setting $P_{\text{superiorReward}}$ or $P_{\text{inferiorPenalty}}$ to be values other than one would ensure that the stagnation problem could be monitored by not always rewarding superior or penalizing inferior offspring. By making the various automata transition probabilities non-deterministic we are making the statement that the environment is providing noisy information, which we should treat accordingly.

Using the naive probability settings described earlier, we can see that the feedback from the environment can deceive the automata early in a genetic algorithm run. This tends to indicate that gradually increasing the reward/penalty probabilities might improve algorithm performance. It should also be noted that in the random initial population, approximately one half of the bits are exchanged during crossover. This is an extremely large number of bits, containing potentially many schema. We would expect that the automata would perform better when fewer bits are exchanged. This implies that initializing the automata such that significantly fewer bits are exchanged early in the run might improve performance as the schema being identified would be smaller.

9 Conclusions

Genetic algorithms have been proven to be a powerful search procedure capable of solving problems in a diverse range of application areas. Although powerful, the setting of parameters to control the search procedure - the size of the population, the values of probabilities controlling crossover and mutation - remains a time consuming process with little but heuristics to aid in their choice. No comprehensive theory exists in order to predict optimal settings for search control parameters.

Control of population diversity, or convergence control, has also been identified as a problem in genetic algorithms where the selection procedure causes excessive loss of genetic material early in the genetic experiment. Research has identified fitness scaling as a means by which allele loss can be controlled, but this makes the choice of fitness function more difficult than it already is. Automated control of population diversity is considered to be highly desirable. This thesis has proposed a mutation operator whose probability is a function of the diversity of the population and provided empirical evidence to support the claims for the utility of this operator in a genetic algorithm environment.

In a classical genetic algorithm, learning occurs at one level. Namely, object variables change under the influence of the mutation and crossover operators and are guided by selection. Neither the operators, nor the probabilities with which they are applied, change as the algorithm searches for an optimal solution. However, it has been shown that other search mechanisms, such as evolutionary strategies, benefit considerably by being able to adapt control parameters as the search proceeds.

This thesis has reinforced the desirability of having the genetic algorithm evolve optimal parameters for search. At the very least, the genetic algorithm should be able to start with "poor" parameter values and improve upon them as further trials take place.

The focus of adaption has been the identification of highly fit schema and the minimization of schema disruption when applying the crossover operator. While research has shown that the uniform crossover operator does not disrupt "long" schema as much as does multi-point crossover, the operator is unable to pick out fit schema as they emerge during the search process. As such, the uniform crossover operator is unable to assist in the "growth" of schema which the Schema Theorem tells us is the basis of success for all genetic algorithms.

This thesis proposes extensions to the uniform crossover operator in order to have the crossover probability adapt as genetic search proceeds: identifying bit patterns which should be kept together i.e. schema identification. The basic principle is to increase the probability with which the bits remain together when mated with another string in some future trial. An adaptive crossover operator has been proposed, requiring extensions to the basic representation for any problem wherein an automaton encodes the probability that a given bit will be exchanged with the other parent under the action of the modified uniform crossover operator.

A comprehensive set of experiments has been performed in order to verify that improvements to the basic genetic algorithm can be made. From these experiments it has been concluded that the basic adaptive crossover operator works well for problems where the bits have absolute value - such as is the case in function optimization - but in problems such as the Travelling Salesman Problem - where the relative bit positions are important - the automata are misled by the environment, causing inferior performance to be observed.

Integrating automata with genetic algorithms has shown promise, as this thesis has demonstrated. However, like all research, with new knowledge comes new

questions. As such, the new adaptive uniform crossover operator has introduced new dimensions of complexity into an already complex system.

Further work is obviously warranted in order to answer the questions which this thesis has raised.

9.1 Direction Of Future Work

The scope for further work is considerable. Future work can be classified in the following way:

- automata investigations
- parameter investigations
- theoretical study
- operator investigations
- integration with other adaptive operators
- application to genetic programming

These points are briefly discussed in the next six sections.

9.1.1 Automata Investigations

In this thesis, only a single type of automaton has been used in experiments and it has shown promise in assisting in adaptive parameter specification. Other automata, such as reward only, or penalty only, should be investigated in order to determine their effectiveness in improving genetic search.

Also, this thesis has considered automata whose probability updating rules are of a discrete nature. However, the probability updating rules might be modified in such a way as to make them continuous - perhaps depending upon the degree to which the child is inferior or superior to the parent. Another alternative might be to replace the DL_{RP} automaton with the MDL_{RP} ¹ automaton as the latter exhibits superior properties in "noiser" environments.

1. See [Oommen, Christensen, 1988] page 454.

9.1.2 Parameter Investigations

During the course of experimental investigation of the adaptive uniform crossover operator, a single set of parameters were selected. This was done in order to assess the robustness of the algorithm - given that the selection of parameter values was particularly naive and did not use the full power of the automaton¹. This sometimes led to stagnation of the adaption and degraded the efficiency of the crossover operator. By enabling the component of the operator which rewards or penalizes the operator in the situation where offspring have the same fitness as their parents, it is strongly believed that such stagnation would be reduced.

Similarly, the simple linear function chosen to represent the adaptive uniform crossover probability as a function of state is probably *too* simple. That is, the rate of change of probability² is the same across all states. A non-linear function such as are used in annealing algorithms should be investigated.

Finally, the utility of the noise function - where the state probability has a degree of uncertainty associated with it - should be investigated.

9.1.3 Theoretical Study

This thesis has undertaken to propose and evaluate empirically - through experimentation - the value of integrating automata with a genetic operator in order to provide adaptive operators. A theoretical investigation of the properties and dynamics of this class of operator needs to be performed.

9.1.4 Operator Investigations

Although the uniform crossover operator has been selected for consideration in this thesis, the idea of augmenting the representation with automata at each bit position and subsequently using the automata in order to determine the probability of crossover can be applied elsewhere. For example, the one or two

1. Rewarding or penalizing in the case of no parent to child improvement was not modelled.

2. The rate of change for the linear model is just $1/n$, where n is the number of automaton states.

point crossover operators could be controlled by these automata as described in section 8.2. Obviously, experiments need to be performed in order to verify the utility of this and other such adaptive operators.

Also, an adaptive operator which is able to deal with the Travelling Salesman Problem should be designed.

9.1.5 Integration with other Adaptive Operators

This thesis has concentrated on enhancing the crossover operator alone. Previous studies [Bäck,1991] have indicated that an adaptive mutation operator can significantly improve genetic search. Studies should be performed in order to determine whether the integration of these two classes of adaptive operator provide still further improvements in genetic search.

9.1.6 Application to Genetic Programming

Genetic programming is a recent invention and has shown considerable promise in solving problems where an ill-defined or unbounded¹ representation is required. However, as with most genetic algorithms, control parameters are static and are chosen on an ad hoc basis.

Associating an automaton with each node in the tree would allow for two possibilities. Firstly, the probability of crossover at any site becomes adaptive and that promising sub-trees, or sub-programs can emerge. Secondly, automatic function definition is possible in that when a node accumulates a given fraction of the probability mass, it means that the sub-program should become a function in its own right and the probability mass redistributed amongst all nodes in the tree.

1. Here we refer to size. Bit string algorithms usually manipulate fixed strings all of equal length

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Appendix A Test Functions

This appendix contains the set of test functions used for the experiments performed in this thesis. The functions have been designed in order to display the following properties:

1. continuous/discontinuous
2. convex/nonconvex
3. unimodal/multimodal
4. quadratic/nonquadratic
5. low dimensionality/high dimensionality
6. deterministic/stochastic (or noisy)

These properties were first set out in DeJong's thesis [DeJong, 1975].

A.1 Sphere Model

$$f_1(\vec{x}) = \sum_{i=1}^n x_i^2$$

$$-5.12 \leq x_i \leq 5.12$$

$$\min(f_1) = f_1(0, \dots, 0) = 0$$

A.2 Generalized Rosenbrock's Function

$$f_2(\vec{x}) = \sum_{i=1}^{n-1} (100 - (x_{i+1} - x_i^2))^2 + (x_i - 1)^2$$

$$-5.12 \leq x_i \leq 5.12$$

$$\min(f_2) = f_2(1, \dots, 1) = 0$$

A.3 Step Function

$$f_3(\vec{x}) = 0.1 + \sum_{i=1}^n \left\lfloor x_i \right\rfloor$$

$$-5.12 \leq x_i \leq 5.12$$

$$\min(f_3) = f_3([-5.12, 5], \dots, [-5.12, 5]) = 0$$

A.4 Quartic Function with Noise

$$f_4(\vec{x}) = \sum_{i=1}^n x_i^4 + \text{gauss}(0, 1)$$

$$-1.28 \leq x_i \leq 1.28$$

$$\min(f_4) = f_4(0, \dots, 0) = 0$$

A.5 Shekel's Foxholes

$$f_s(x) = \frac{1}{K} + \sum_{i=1}^N \frac{1}{c_i + \sum_{j=1}^n (x_j - a_{ij})^2}$$

$$(a_{ij}) = \begin{bmatrix} 32 & 16 & 0 & 16 & 32 & 32 & \dots & 0 & 16 & 32 \\ 32 & 32 & 32 & 32 & 32 & 16 & \dots & 32 & 32 & 32 \end{bmatrix}$$

$$65,536 \leq x \leq 65,536$$

$$f_s(a_{ij}, a_{ij}) = c_{ij}, K = 500$$

$$\min(f_s) = f_s(-32, -32) = 1$$

A.6 Schwefel's Function 1.2

$$f_n(x) = \sum_{i=1}^n \left(\sum_{j=1}^i x_j \right)^2$$

$$65,536 \leq x \leq 65,536$$

$$\min(f_n) = f_n(0, \dots, 0) = 0$$

A.7 Generalized Rastrigin's Function

$$f(x) = nA + \sum_{i=1}^n x_i^2 - A \cos(\omega x_i)$$

$$A = 10; \omega = 2\pi$$

$$5.12 \leq x_i \leq 5.12$$

$$\min(f) = f(0, \dots, 0) = 0$$

A.8 Sphere Model, Changing Environment

$$f_8(\vec{x}(t)) = \begin{cases} \sum_{i=1}^n x_i^2 & t \bmod a \text{ even} \\ \sum_{i=1}^n (x_i - b)^2 & t \bmod a \text{ odd} \end{cases}$$

$$a = 250 \text{ generations}; b = 4$$

$$\min(f_8) = \begin{cases} f_8(0, \dots, 0) & t \bmod a \text{ even} \\ f_8(b, \dots, b) & t \bmod a \text{ odd} \end{cases} = 0$$

$$5.12 \leq x_i \leq 5.12$$

A.9 Ackley's Function

$$f_9(\vec{x}) = -a \exp \left(-b \sqrt{\frac{1}{n} \sum_{i=1}^n x_i^2} \right) - \exp \left(\frac{1}{n} \sum_{i=1}^n \cos(2\pi x_i) \right) + a + e$$

$$a = 20; b = 0.2; e = 2\pi$$

$$-32,768 \leq x_i \leq 32,768$$

$$\min(f_9) = f_9(0, \dots, 0) = 0$$

A.10 Krolak's 100 City TSP

$$f_{10}(\vec{x}) = \sum_{i=1}^n d(c_{\pi(i), m(i)}, c_{\pi(i+1), m(i+1)})$$

$$5.12 \leq x_i \leq 5.12$$

$$\min(f_{10}) = 21285$$

A.11 Low Autocorrelation Binary Sequences

$$f_{11}(x) = \sum_{k=1}^{L-1} \left(\sum_{i=0}^{L-k} \beta_i \beta_{i+k} \right); \beta_i = \begin{cases} -1, \alpha_i=0 \\ 1, \alpha_i=1 \end{cases}$$

A.12 Hamming Distance to 0^l

$$f_{12}(a) = \sum_{i=1}^l \alpha_i$$

$$\min(f_{12}) = f_{12}(0, \dots, 0) = 0$$

A.13 Weierstrass-Mandelbrot Fractal Function

$$f_{13}(x) = \sum_{i=0}^n \left(\frac{C(x_i)}{C(1) + |x_i|^{2-D}} + x_i^2 + 1 \right)$$

$$C(x) = \sum_{j=0}^{\infty} \frac{1 - \cos(b^j x)}{b^{j(2-D)}}$$

$$1 \leq D \leq 2; b > 1$$

$$\dots 5.12 \leq x_i \leq 5.12$$

A.14 Fully Deceptive Function

$$f_{14}(a) = \begin{cases} 2^{-l} f_{14}(a) \approx 0 \\ (1 + o(a))^{-1/l}, 0 < f_{14}(a) < l \\ 0, f_{14}(a) \approx 1 \end{cases}$$

A.15 Weighted Sphere Model

$$f_{15}(x) = \sum_{i=1}^n x_i^2$$

$$5.12 \leq x_i \leq 5.12$$

$$\min(f_{15}) = f_{15}(0, \dots, 0) = 0$$

A.16 Fletcher and Powell (fixed A,B matrices)

$$f_{\text{Fletcher}}(\mathbf{x}) = \sum_{i=1}^n (\mathbf{x}_i - B_i)^2$$

$$A_i = \sum_{j=1}^n (a_{ij} \sin \alpha_j + b_{ij} \cos \alpha_j)$$

$$B_i = \sum_{j=1}^n (a_{ij} \sin \alpha_j + b_{ij} \cos \alpha_j)$$

$$a_{ij}, b_{ij} \in [-100, 100]$$

$$\alpha_j \in [-\pi, \pi]$$

$$(a_{ij}) = \begin{bmatrix} -25.5668 & 96.1559 & 15.2661 & 23.2340 & 1.15129 \\ -97.5908 & -82.9516 & 50.3364 & 96.5520 & 29.4616 \\ 36.3096 & 54.3934 & 76.9586 & 64.3481 & 0.66188 \\ -58.7916 & 30.4881 & 22.9354 & 36.1643 & 62.2798 \\ 66.5820 & 18.2818 & 2.30184 & 8.6698 & 80.3784 \end{bmatrix}$$

$$(b_{ij}) = \begin{bmatrix} -38.9994 & -49.1546 & 52.2403 & 66.4195 & 36.6538 \\ -6.49429 & -97.6865 & 39.6743 & 91.4542 & 17.2329 \\ -67.1681 & -42.8325 & 42.9307 & 36.9705 & 8.3463 \\ -53.1271 & 2.74637 & 27.6244 & 72.7537 & 46.1198 \\ -1.47036 & -95.2547 & 78.6214 & 54.3113 & 84.6737 \end{bmatrix}$$

$$(\alpha_j) = [1.98961 \quad 1.39376 \quad 2.03048 \quad 0.621016 \quad 3.12736]$$

A.17 Fletcher and Powell (with random A,B matrices)

$$f_{17}(x) = \sum_{i=1}^n (A_i - B_i)^2$$

$$A_i = \sum_{j=1}^n (a_{ij} \sin \alpha_j + b_{ij} \cos \alpha_j)$$

$$B_i = \sum_{j=1}^n (a_{ij} \sin x_j + b_{ij} \cos x_j)$$

$$a_{ij}, b_{ij} \in [-100, 100]$$

$$\alpha_j \in [-\pi, \pi]$$

In this function, the a_{ij} and b_{ij} matrices are allowed to vary randomly.

A.18 Shekel-5

$$f_{18}(x) = - \sum_{i=1}^m \frac{1}{(x - A(i)) (x - A(i))^T + c_i}$$

$$n = 4; m = 5$$

$$0 \leq x_i \leq 10$$

Table 14 Coefficients for f_{18}

i	A(i)				c_i
1	4	4	4	4	0.1
2	1	1	1	1	0.2
3	8	8	8	8	0.2
4	6	6	6	6	0.4
5	3	7	3	7	0.4

$$\min(f_{18}) = f_{18}(0, \dots, 0) = 0$$

A.19 Shekel-7

$$f_{19}(x) = - \sum_{i=1}^m \frac{1}{(x - A(i)) (x - A(i))^2 + c_i}$$

$$n = 4; m = 7$$

$$0 < x_i < 10$$

Table 15 Coefficients for f_{19}

i	A(i)				c_i
1	4	4	4	4	0.1
2	1	1	1	1	0.2
3	8	8	8	8	0.2
4	6	6	6	6	0.4
5	3	7	3	7	0.4
6	2	9	2	9	0.6
7	5	5	3	3	0.3

$$min(f_{19}) = f_{19}(0, \dots, 0) = 0$$

A.20 Shekel-10

$$f_{20}(x) = \sum_{i=1}^m \frac{1}{(x - A(i)) (x - A(i))^T + c_i}$$

$$n = 4; m = 10$$

$$0 \leq x_i \leq 10$$

Table 16 Coefficients for f_{20}

i	A(i)				c_i
1	4	4	4	4	0.1
2	1	1	1	1	0.2
3	8	8	8	8	0.2
4	6	6	6	6	0.4
5	3	7	3	7	0.4
6	2	9	2	9	0.6
7	5	5	3	3	0.3
8	8	1	8	1	0.7
9	6	2	6	2	0.5
10	7	3.6	7	3.6	0.5

$$\min(f_{20}) = f_{20}(0, \dots, 0) = 0$$

A.21 Griewank-2

$$f_{21}(\vec{x}) = \sum_{i=1}^n \frac{x_i^2}{d} - \prod_{i=1}^n \cos\left(\frac{x_i}{\sqrt{i}}\right) + 1$$

$$d = 200; n = 2$$

$$\min(f_{21}) = f_{21}(0, \dots, 0) = 0$$

$$-100, 0 \leq x_i \leq 100, 0$$

A.22 Griewank-10

$$f_{22}(\vec{x}) = \sum_{i=1}^n \frac{x_i^2}{d} - \prod_{i=1}^n \cos\left(\frac{x_i}{\sqrt{i}}\right) + 1$$

$$d = 4000; n = 10$$

$$\min(f_{22}) = f_{22}(0, \dots, 0) = 0$$

$$-600, 0 \leq x_i \leq 600, 0$$

A.23 Galar

$$f_{23}(\vec{x}) = (\exp(-5x_1^2) + 2\exp(-5(1-x_1)^2)) \cdot \exp\left(-5\sum_{i=1}^n x_i^2\right)$$

$$-5, 0 \leq x_i \leq 5, 0$$

A.24 Kowalik

$$f_{24}(x) = \sum_{i=1}^{11} \left(a_i \frac{x_i (b_i^2 + b_i x_2)}{b_i^2 + b_i x_1 + x_2} \right)^2$$

$$n = 4$$

$$-5.0 \leq x_i \leq 5.0$$

$$\min(f_{24}) = f_{24}(0.1928, 0.1908, 0.1231, 0.1358) \approx 0.0003075$$

Table 17 Coefficients for f_{24}

i	a_i	$1/b_i$
1	0.1957	0.25
2	0.1947	0.5
3	0.1735	1
4	0.1600	2
5	0.0844	4
6	0.0627	6
7	0.0456	8
8	0.0342	10
9	0.0323	12
10	0.0235	14
11	0.0246	16

Appendix B Results

This appendix contains the results of using the adaptive uniform crossover operator in the domain of function minimization. The definitions of the functions in the test bed used in this study can be found in Appendix A. Three graphs for each function are included. Each chart is a plot of the fitness of the best solution in the population after a given number of trials plotted against the number of trials. The first graph shows the results of the best at trial¹ fitness for the standard uniform crossover operator. The second graph shows the results of the best-at-trial fitness for the adaptive uniform crossover operator. The final graph shows the difference between the best-at-trial fitness for the standard uniform crossover operator and the adaptive uniform crossover operator. *Therefore, in the third graph, when the difference values fall below zero, the adaptive run is superior to the non-adaptive run.*

1. Best-at-trial means the fitness of the best solution in the population after a given number of trials.

B.1 Results

The adaptive uniform crossover operator was tested against all functions in the function test bed - f_1 to f_{24} . The results were compared using equivalent genetic algorithm search parameters to the uniform crossover operator. A modified version of Grefenstette's genetic algorithm experimental tool GENESIS¹ was used for all experimental runs. In all genetic algorithm runs, the same basic parameters were chosen. These are shown in Table 18:

Table 18 Common experimental parameters

Variable	Meaning	Value
p_c	Population size	50
p_m	Probability of mutation (per bit)	0.001
N_p	Number of experiments	100
N_t	Number of trials per experiment	10,000
S	Selection mechanism	Roulette wheel
Coding	How object variable is encoded in the bit string	Gray coding
l	Length of the object variable encoding part of an individual.	$l = 32n$ (n being the number of objective function variables)

The crossover probability for the uniform crossover operator was set to 0.5. The geometric form of the crossover exchange operator was used to decide whether bit-wise crossover was to take place and P' had the functional form: $P'(s) = s/n; s = 0, \dots, n$, making the automata examples of the DL_{RP} class of automata.

1. The version GENESYS, was obtained from Dr. Back (baeck@ls11.informatik.uni-dortmund.de).

The values of the various automata probabilities are shown in Table 19:

Table 19 Adaptive crossover operator parameters

Variable	Meaning	Value
$P_{\text{superiorReward}}$	Probability with which an automaton will be rewarded if the offspring is fitter than the parent.	1.0
$P_{\text{inferiorPenalty}}$	Probability with which an automaton will be penalized if the offspring is less fit than the parent.	1.0
$P_{\text{samePenalty}}$	Probability with which an automaton will be penalized if the offspring is as fit but no fitter than the parent.	0.0
$P_{\text{sameReward}}$	Probability with which an automaton will be rewarded if the offspring is as fit but no fitter than the parent.	0.0
$f_{\text{tolerance}}$	Floating point tolerance used to decide whether an offspring is more or less fit than its parent(s).	0.0

In all of the charts which follow in sections B.1.1 to B.1.24, the best-at-trial fitness is plotted. Other interesting statistics which were reviewed, but not included due to space constraints, were online and offline performance and population diversity. The y axis represents the best-at-trial fitness and the x axis the trial number. Being function minimization problems, we expect the best-at-trial fitness to decrease with increasing trial number. The occasional increase in best-at-trial fitness for some functions is due to the stochastic nature of the roulette wheel reproduction strategy which can destroy the best solution in the population at any time. Generally, the best-at-trial measure for the function test bed is monotone, decreasing in nature.

B.1.1 Sphere Model **Figure 35** $f1$ non-adaptive fitness **Figure 36** $f1$ adaptive fitness

Figure 37 f_1 adaptive - non-adaptive comparison

B.1.2 Generalized Rosenbrock's Function

Figure 38 f_2 adaptive fitness

Figure 39 f_2 non-adaptive fitness

Figure 40 f_2 adaptive - non-adaptive comparison

B.1.3 Step FunctionPlot of f_3 versus Trial for adaptive run **Figure 41** f_3 adaptive fitnessPlot of f_3 versus Trial for non-adaptive run **Figure 42** f_3 non-adaptive fitness

Figure 43 f3 adaptive - non-adaptive comparison

B.1.4 Quartic Function with Noise

Figure 44 f4 non-adaptive fitness

Appendix B: Results

Plot of f4 versus Trial for adaptive run

Figure 45 f4 adaptive fitness

Plot of f4 versus Trial difference between adaptive and non-adaptive runs

Figure 46 f4 adaptive-non-adaptive comparison

B.1.5 Shekel's FoxholesPlot of f_5 versus Trial for adaptive run **Figure 47 f_5 adaptive fitness**Plot of f_5 versus Trial for non-adaptive run **Figure 48 f_5 non-adaptive fitness**

Figure 49 $f5$ adaptive - non-adaptive comparison

B.1.6 Schefel's Function 1.2

Figure 50 $f6$ adaptive fitness

Figure 51 f_6 non-adaptive fitness **Figure 52** f_6 adaptive - non-adaptive comparison

B.1.7 Generalized Rastrigin's Function**Plot of f_7 versus Trial for non-adaptive run** **Figure 53 f_7 non-adaptive fitness****Plot of f_7 versus Trial for adaptive run** **Figure 54 f_7 adaptive fitness**

Figure 55 f_7 adaptive - non-adaptive comparison

B.1.8 Sphere Model, Changing Environment

Figure 56 f_8 non-adaptive fitness

Plot of f8 versus Trial for adaptive run

Figure 57 f8 adaptive fitness

Plot of f8 versus Trial difference between adaptive and non-adaptive runs

Figure 58 f8 adaptive - non-adaptive comparison

B.1.9 Ackley's FunctionPlot of f_9 versus Trial for non-adaptive run **Figure 59** f_9 non-adaptive fitnessPlot of f_9 versus Trial for adaptive run **Figure 60** f_9 adaptive fitness

Figure 61 f_9 adaptive - non-adaptive comparison

B.1.10 Krolak's 100 City TSP

Figure 62 f_{10} non-adaptive fitness

Figure 63 f10 adaptive fitness **Figure 64 f10 adaptive - non-adaptive comparison**

B.1.11 Low Autocorrelation Binary Sequences **Figure 65 f11 non-adaptive fitness** **Figure 66 f11 adaptive fitness**

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**PM-1 3½"x4" PHOTOGRAPHIC MICROCOPY TARGET
NBS 1010a ANSI/ISO #2 EQUIVALENT**

Figure 67 f11 adaptive - non-adaptive comparison

B.1.12 Hamming distance to 0^l (origin) **Figure 68 f12 non-adaptive fitness** **Figure 69 f12 adaptive fitness**

Figure 70 f_{12} adaptive - non-adaptive comparison

B.1.13 Weierstrass-Mandelbrot Fractal Function

Figure 71 f_{13} non-adaptive fitness

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Plot of f13 versus Trial for adaptive run

Figure 72 f13 adaptive fitness

Plot of f13 versus Trial difference between adaptive and non-adaptive runs

Figure 73 f13 adaptive - non-adaptive comparison

B.1.14 Fully Deceptive Function **Figure 74 f14 non-adaptive fitness** **Figure 75 f14 adaptive fitness**

Figure 76 f14 adaptive - non-adaptive comparison

B.1.15 Weighted Sphere Model

Figure 77 f15 non-adaptive fitness

Figure 78 f_{15} adaptive fitness **Figure 79** f_{15} adaptive - non-adaptive comparison

B.1.16 Fletcher and Powell (fixed A,B matrices)**Plot of f16 versus Trial for non-adaptive run** **Figure 80 f16 non-adaptive fitness****Plot of f16 versus Trial for adaptive run** **Figure 81 f16 adaptive fitness**

Figure 82 $f16$ adaptive - non-adaptive comparison**B.1.17 Fletcher and Powell (with random A,B matrices)** **Figure 83** $f17$ non-adaptive fitness

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Figure 84 f_{17} adaptive fitness **Figure 85 f_{17} adaptive - non-adaptive comparison**

B.1.18 Shekel-5**Plot of f18 versus Trial for non-adaptive run** **Figure 86 f18 non-adaptive fitness****Plot of f18 versus Trial for adaptive run** **Figure 87 f18 adaptive fitness**

Figure 88 f18 adaptive - non-adaptive comparison

B.1.19 Shekel-7

Figure 89 f19 non-adaptive fitness

Appendix B: Results

Plot of f19 versus Trial for adaptive run

Figure 90 f19 adaptive fitness

Plot of f19 versus Trial difference between adaptive and non-adaptive runs

Figure 91 f19 adaptive - non-adaptive comparison

Appendix B: Results

B.1.20 Shekel-10

Plot of $f20$ versus Trial for non-adaptive run Figure 92 $f20$ non-adaptive fitnessPlot of $f20$ versus Trial for adaptive run Figure 93 $f20$ adaptive fitness

Figure 94 $f20$ adaptive - non-adaptive comparison

B.1.21 Griewank-2

Figure 95 $f21$ non-adaptive fitness

Figure 96 f21 adaptive fitness **Figure 97 f21 adaptive - non-adaptive comparison**

B.1.22 Griewank-10

Plot of f22 versus Trial for non-adaptive run

Figure 98 f22 non-adaptive fitness

Plot of f22 versus Trial for adaptive run

Figure 99 f22 adaptive fitness

Figure 100 f22 adaptive - non-adaptive comparison

B.1.23 Galar

Figure 101 f23 non-adaptive fitness

Figure 102 f_{23} adaptive fitness

Figure 103 f_{23} adaptive - non-adaptive comparison

B.1.24 Kowalik

Figure 104 f_{24} non-adaptive fitness

Figure 105 f_{24} adaptive fitness

Figure 106 f24 adaptive - non-adaptive comparison

END

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FIN