Determining the Impact of Spatial Networks and Elitism on Coevolutionary Genetic Algorithms

by

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ABSTRACT

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It has been demonstrated that spatial networks can improve the behaviour of coevolutionary genetic algorithms (GAs) when optimizing specific problems. We aim to determine whether this result generalizes for more basic problems by applying it to the one-max problem and some variations of that problem, on both cooperative and competitive coevolutionary systems. We confirm that spatial structures do help coevolutionary systems. Finally, we note that adding elitism to the spatial system, a simple but novel idea in the spatial GA world, increases the speed of convergence by an order of magnitude.
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# Table of Contents

List of Tables vii

List of Figures viii

1 Introduction 1
   1.1 Thesis Statement ........................................ 2
   1.2 Overview of Thesis ...................................... 4

2 Background 5
   2.1 The Genetic Algorithm ................................. 5
       2.1.1 Elitism ............................................. 8
   2.2 Coevolution .............................................. 9
       2.2.1 Coevolutionary Types .............................. 10
       2.2.2 Problems with Coevolution ......................... 13
   2.3 Spatial Genetic Algorithms ............................ 17
       2.3.1 Spatial Networks .................................. 20
   2.4 Spatial Coevolutionary Genetic Algorithms .......... 22
       2.4.1 Evaluative Networks ................................ 24
       2.4.2 Ties to Game Theory ............................... 26
   2.5 Evaluating Genetic Algorithms ......................... 27
       2.5.1 No Free Lunch ..................................... 29
   2.6 The Building Block Hypothesis ........................ 30
       2.6.1 Linear Separability ................................. 31
   2.7 Analytical Tools ........................................ 33
       2.7.1 Non-parametric Statistics .......................... 33
       2.7.2 Heat Map .......................................... 37

3 Methodology and Implementation 38
   3.1 Overview ................................................ 38
   3.2 GA Setup ............................................... 39
       3.2.1 Spatial Selection ................................... 40
List of Tables

<table>
<thead>
<tr>
<th>Table</th>
<th>Title</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>3.1</td>
<td>Experimental Factors</td>
<td>65</td>
</tr>
<tr>
<td>3.2</td>
<td>Problems Tested</td>
<td>66</td>
</tr>
<tr>
<td>3.3</td>
<td>List of Experiments Run</td>
<td>67</td>
</tr>
<tr>
<td>4.1</td>
<td>Summary of Experiments Run</td>
<td>92</td>
</tr>
<tr>
<td>4.2</td>
<td>The Importance of Each Mechanism on the Cooperative Coevolutionary GA</td>
<td>93</td>
</tr>
<tr>
<td>4.3</td>
<td>The Effect of Each Mechanism on the Competitive Coevolutionary GA</td>
<td>94</td>
</tr>
<tr>
<td>4.4</td>
<td>Results of Elitism Experiments</td>
<td>95</td>
</tr>
<tr>
<td>4.5</td>
<td>What is the main driving force leading to the performance boost seen</td>
<td>96</td>
</tr>
<tr>
<td></td>
<td>in cooperative coevolution?</td>
<td></td>
</tr>
</tbody>
</table>
**List of Figures**

2.1 Spatial Reproduction and Evaluation ........................................ 25

3.1 Grid 4 reproductive network .................................................... 45
3.2 Grid 8 reproductive network .................................................... 45
3.3 Ring 4 reproductive network .................................................... 45
3.4 Outer Matching Example ......................................................... 47
3.5 Inner Matching Example ......................................................... 48
3.6 Plateau at ‘1010’ on one-max matching ...................................... 49
3.7 Optimum at ‘1010’ on one-max extra matching ............................. 50

4.1 One-max ................................................................. 68
4.2 One-max Outer Matching ....................................................... 69
4.3 One-max Inner Matching ....................................................... 69
4.4 One-max Extra Outer Matching ............................................... 70
4.5 One-max Extra Inner Matching ............................................... 70
4.6 Royal Road ................................................................. 71
4.7 One-max Royal Road ........................................................... 71
4.8 One-to-One Host/Parasite Spatial Reproduction ............................ 72
4.9 Spatially Evaluated Host/Parasite Spatial Reproduction ................. 73
4.10 Purely Competitive Host/Parasite Spatial Reproduction ............... 74
4.11 Spatial structures on the coevolutionary GA .............................. 78
4.12 Spatial structures on the standard GA .................................... 79
4.13 Spatial structures on 1-to-1 Host/Parasite ................................ 80
4.14 Pure Outer Matching ......................................................... 81
4.15 Pure Inner Matching ......................................................... 81
4.16 One-max on non-spatial standard GA ....................................... 84
4.17 One-max on non-spatial coevolutionary GA ................................ 84
4.18 One-max with 10 Elite ....................................................... 85
4.19 One-max with Full Elite ..................................................... 85
4.20 Strict global elitism on non-spatial standard GA .......................... 87
4.21 Strict global elitism on 4 Graph standard GA ............................ 87
4.22 Strict global elitism on non-spatial coevolutionary GA ............... 88
4.23 Strict global elitism on 4 Graph coevolutionary GA ................. 88
4.24 Heat map of fitness values with varying levels of elitism on a spatial
coevolutionary GA ...................................................... 89
4.25 Heat map of fitness values with varying levels of elitism on a spatial
standard GA ............................................................. 89

A.1 One-max ............................................................. 108
A.2 One-max Outer Matching ............................................. 108
A.3 One-max Inner Matching .............................................. 109
A.4 One-max Extra Outer Matching ...................................... 109
A.5 One-max Extra Inner Matching ...................................... 110
A.6 Royal Road ......................................................... 110
A.7 One-max Royal Road .................................................. 111
A.8 One-to-One Host/Parasite Spatial Structures ......................... 112
A.9 Spatially Evaluated Host/Parasite Spatial Reproduction .......... 112
A.10 Purely Competitive Host/Parasite Spatial Reproduction .......... 113
A.11 Spatial structures on the coevolutionary GA ....................... 114
A.12 Spatial structures on the standard GA ............................... 115
A.13 Spatial structures on 1-to-1 Host/Parasite .......................... 116
A.14 Pure Outer Matching ................................................ 117
A.15 Pure Inner Matching ............................................... 117
A.16 One-max on Grid 4 standard GA ................................... 118
A.17 One-max on Grid 8 standard GA ................................... 118
A.18 One-max on non-spatial standard GA ............................... 119
A.19 One-max on Grid 4 coevolutionary GA ............................ 119
A.20 One-max on Grid 8 coevolutionary GA ............................ 120
A.21 One-max on non-spatial coevolutionary GA ....................... 120
A.22 One-max with no elite ............................................. 121
A.23 One-max with 1 elite ............................................ 121
A.24 One-max with 2 elite ............................................ 122
A.25 One-max with 5 elite ............................................ 122
A.26 One-max with 10 elite .......................................... 123
A.27 One-max with 50 elite .......................................... 123
A.28 One-max with full elitism ....................................... 124
A.29 Extra Inner Matching on non-spatial standard GA ............... 125
A.30 Extra Inner Matching on Grid 4 standard GA .................... 125
A.31 Extra Inner Matching on non-spatial coevolutionary GA ....... 126
Chapter 1

Introduction

The genetic algorithm (GA) is a search algorithm based on biological evolution that has proven to be a very powerful technique for solving optimization problems in computer science [14]. Using this biological phenomenon for inspiration, known as biomimicry, within computer science is one that has been around since the 1950s and 60s [26], but biomimicry in science and engineering goes back much later and has been around for millennia. Biological evolution is based on DNA which has often been described as being like nature’s computer code. This makes the idea of using computer code to simulate DNA an obvious one and is taken advantage of in the field of Natural Computing, of which the GA is a sub-field. In the natural world coevolution, defined as organism’s directly influencing one another’s fitness, is ubiquitous. A coevolutionary GA is a GA which has two or more populations evolving in parallel wherein their fitness’s are relative to organisms in the other population(s), but these systems are difficult to control and have proven to have wildly varying levels of success [20, 39, 47]. In order to help reconcile this problem researchers have experimented with added spatial reproductive structures to coevolutionary systems which suppress which organisms a single organism can reproduce with to nearby nodes in its neighbourhood [36, 54]. Space can also be used
to suppress fitness evaluations, only evaluating organisms with nearby coevolutionary partners. Inspiration for these mechanism again comes from nature where interaction is controlled by locality; organisms geographical distant from one another cannot reproduce or interact. After adding the spatial structure to their system they observed an immense increase in performance.

While researchers have noted increased performance on specific problems, little work has been done showing how general this solution is and to what extent it can improve performance. Additionally, it is unclear what about the spatial systems allow them to stabilize coevolution leading to its increased performance. Mitchell et al. [29] hypothesizes that spatial competitive coevolution allows the solution to focus on specific parts of a problem and eventually merge these solutions. While Weigand & Sarma [54] believe that spatial cooperative coevolution allows diversity to remain in the population allowing it to more freely explore a larger area of the problem space. This prevents the GA from focusing in too early in the coevolutionary process and getting trapped at local optima. Spatial networks can clearly have a powerful role in coevolutionary systems, however our lack of knowledge in what that role is needs to be addressed in order to fully take advantage of their benefits.

1.1 Thesis Statement

In this thesis we are using simple, easy to control problems to perform explorational experiments examining the previously observed impact of spatial reproductive and evaluative networks on competitive and cooperative coevolutionary GAs, to
show that both styles of coevolutionary GAs are impacted significantly by these networks. Through this process we will observe the applicability, and when applicable, the magnitude to which these networks effect the GA’s performance which should help us better understand their relationship. The effectiveness of local elitism on spatial coevolutionary systems is also considered using a modified version to match the mechanisms routinely used in the standard GA. This new mechanism is widely effective at improving the GA’s performance and provides deep insight into the relationship between the spatial and coevolutionary subsystems. These simple problems will also help highlight the role of linear separability on the effectiveness of using a coevolutionary GA. Using our generalized fitness problems, we find that the work of Weigand & Sarma, touting the advantage of spatial networks on cooperative coevolution, generalizes quite well, while the work of Mitchell et al. on competitive networks does not. Spatial structures do not benefit the performance for any of our competitive problems, they actually reduce performance in all cases!

This paper contributes to the study of the cooperative and competitive spatial coevolutionary GAs. It provides hypothesis for how spatial connectivity within the GA can effect its performance. This includes how spatial reproduction, spatial evaluation and how specific spatial attributes in these networks can effect overall performance. We define a number of new, simple, yet general problems, both cooperative and competitive in nature, to be run on our coevolutionary GA. We use these problems to gain a more general understanding of how these various parameters can effect the GA’s behaviour by reducing unintended noise other more specific problems can have. The role of elitism, and a new way of implementing it within the spatial
coevolutionary GA, is also explored and shown to provide a significant boost in the
GA’s performance. Three papers based on these topics, as presented in this thesis,
have been submitted for publication, though as of this writing they are still under
review [23, 24, 25].

1.2 Overview of Thesis

In Chapter 2, a review of past research in the areas of both spatial and coevolu-
tionary GAs, including work combining them, is provided. In Chapter 3, we explain
the methodology for how we will examine the effects of the various mechanisms being
added to the GA; the standard implementation of our GA is also provided. Then in
Chapter 4 we give the results of our experiments and analyze their ramifications. Fi-
nally, the thesis concludes in Chapter 5 with a summary of our results and directions
for future research.
Chapter 2

Background

2.1 The Genetic Algorithm

The GA is a search algorithm based on the natural process of evolution. It is one of the most prominent examples of evolutionary computation, which itself is a sub field of natural computing. Natural computing is a field concerned with using the natural world as inspiration for computer algorithms or techniques within computer science [11]. The GA is based on the general biological concepts which are responsible for passing genes to an organisms offspring. An organism passing genes to its offspring, or children, is known as reproduction. The usual way in which reproduction occurs is when two organisms come together and share their genes to create an offspring. These genes are in the form of deoxyribonucleic acid (DNA), formed by combinations of four amino acids. The way these four amino acids are combined within the DNA define the characteristics of the organism; this is known as the organisms phenotype. In this way these four amino acids can be considered as a type of biological code compromised of four symbols, generally written as A, C, G and T. We use a similar system in computer science using a binary code of two characters, 0 and 1. The standard GA uses binary characters for its genetic structure, though other symbolic
sets have been used to varying success.

In the natural world, DNA is passed from one generation to the next using many complex mechanisms. The GA was designed to be as true to the natural concept as possible, while maintaining simplicity. In nature, the organisms able to reproduce to form the next generation are those that survive the harshness of the world or out-compete their competition. This concept was termed *Survival of the Fittest* by Herbert Spencer [46] after reading Charles Darwin’s *On the Origin of Species* [7] to describe Darwin’s notion of natural selection\(^1\). In the GA, a fitness function is used to determine the fitness of each of the organisms based on its phenotype, a selection function is then used to determine which organisms will reproduce, with higher probability given to those with higher fitness. The distribution of fitness values across the possible genotypes from which the populations are drawn can be viewed as a fitness landscape; the population is attempting to navigate the landscape in order to find the highest ‘peak’, i.e. the global optimum. This concept was first introduced in evolutionary biology by Sewall Wright in 1932 [58]. When increased weight is given to organisms of higher fitness this is known as selection pressure. The higher the probability of reproduction given to the better fit organisms the greater the population’s selection pressure. This also applies to the natural world, severe selection pressure would correspond to a stressful existence due to something such as aggressive predation or a harsh climate. Therefore, an organism must be highly fit in order to survive and eventually reproduce, causing evolution to occur rapidly. In \(^1\)Darwin’s use of the phrase ‘Survival of the Fittest’ began after he’d read Spencer’s work, and subsequently, added it in a later edition of his book.
contrast, if the population exists in a mild climate with minimal predation they are
under a much lower selection pressure and evolution will occur much slower.

Once organisms have been selected to reproduce the two mating organisms’ DNA
strands are combined using crossover to create the offspring or children. Crossover is
simply splitting the two DNA strands at one or more points and swapping the split
sections between the two strands. Another process that occurs during reproduction
is point mutation which is the random ‘flipping’ of a bit of the genetic code. In the
GA this is simply known as mutation and is changing a 1 to a 0 or a 0 to a 1, while
in the natural world it corresponds to DNA having bits of amino acid changed to one
of the other amino acid types.

The GA’s ability as a search algorithm and determining what types of problems
it is best suited for has been a topic of much research and debate [28, 56]. In general,
it has been concluded that the GA is best suited for complex problems where little
domain knowledge is known. They must also be problems which are resistant to
hill-climbing (steepest decent) algorithms attempting to jump quickly to an answer.
These problems would contain things such as plateaus and local optima to confuse the
hill climber. A local optimum is a genetic location where changing any one single bit
will reduce the individuals fitness. A plateau is similar to a local optimum however it
allows for the individuals fitness to be reduced or remain the same with a single bit
flip. For more information on evaluating the genetic algorithm refer to section 2.5.
2.1.1 Elitism

A mechanism which most GA implementations use, but the natural world does not, is elitism. This mechanism has been around almost since the inception of the GA and has been shown to provide a significant improvement performance on the standard GA [9, 26]. Elitism prevents the GA from losing the most fit solution it has found while running through its search. In each generation, the GA will determine which organism has the highest fitness and push it through to the next generation without it having to go through reproduction. It is important to note that this organism can still be used to reproduce with and can create children, it merely cannot be lost.

Adding this mechanism to the GA is a symptom of the fact that natural evolution is considered a continuous process with no end point, the end of evolution in the natural world would correspond to the demise of the evolving organisms. In the GA however, the algorithm terminating means that it has found a solution, or has hit one of its other termination parameters and is being forced to stop. The GA is looking for an optimum, while the natural process is merely attempting to further its existence. While some authors have used effects similar to elitism in their coevolutionary GAs [39], little work has been done looking at its full effects on these systems.

A form of elitism, known as local elitism has been used in some non-coevolutionary spatial GA’s, most notably by De Jong & Sarma [10, 43]. This elitism method, instead of using a global elite, invokes a tournament between parents and children for inclusion in the next generation. The child, which has reproduced from the parent at that spatial location, must have a greater fitness than the parent in order for it to
take the parent’s place in the next generation. Therefore, the fitness of any individual organism is guaranteed to never get worse from generation to generation. However, this elitism style is far from a standard in spatial GAs, in fact, most researchers choose to not use any elite in their systems. A reason for this could be that this form of elitism may place too strong of a selection pressure on the population.

2.2 Coevolution

In nature, an organism’s fitness is not based on static fitness functions. They are affected not only by environment around them, but also by the other organisms they come into contact with. In natural terms, this would be saying that an organism’s fitness is not based on how fast it can run or how strong it is in the abstract, but instead is based on how fast or strong it is when compared with the other organisms it is in competition with. This, in effect, means that an organism’s fitness changes depending on the fitnesses of the organisms it is interacting with, i.e. its fitness is relative to the organism around it. The GA takes this effect into account when performing selection, the more highly fit nodes have a higher likelihood of being selected, however that organism’s absolute fitness would remain constant in future generations.

In the standard GA, an organism’s fitness is only relative to the population it exists in. The coevolutionary GA is one that has two or more populations of organisms which have the fitnesses of the organisms in each population based, to some extent, on the organisms in the other population(s). Each individual’s fitness is based on both
its own genetic make-up as well as the genetic make-up of one or more organisms in another population. These organism’s fitnesses are now relative, not only to the other organisms in their population, but also relative to the organisms they are coevolving with. Therefore, an organism’s ranking in a population will change depending on the organism(s) it is coevolving with, which will change each generation.

Some authors [38] have used the term coevolution to simply mean that the fitness of an individual is based on its own genotype/phenotype, as well as the genotype/phenotype from one or more other chromosomes, which can come from a different population, or even the same population. The definition we will be working with in this thesis specifies that the other chromosome(s) used to evaluate the individuals fitness must come from a different population. Much work has been done on coevolution since the early work by Hillis in 1990 [20]. Authors first focused on whether coevolution was a viable mechanism within the GA and were testing decidedly different systems who’s only real similarity was the fact that they all had multiple populations [20, 31, 39, 47]. We will continue to look at some of these alternatives throughout this background, focusing on the parameters we believe to be important and have put effort into testing.

2.2.1 Coevolutionary Types

Coevolution has many different subcategories in nature and each can provide its own spin-off to be used in the GA. Three primary categories include: predator/prey, host/parasite and cooperative. The predator/prey relationship is the most basic and easiest to understand, it is also the basis of much study within the field of Biology
most famously described by the Lotka-Volterra equation [21]. A classic example of
the predator/prey relationship could be the fox and the hare, the fox is the predator
attempting to eat its prey, the hare. Each evolves to attempt to best the other, if
the fox is weak or slow, it cannot catch any hares and will surely die from lack of
nutrition, while if the hare cannot adequately hide or run when necessary, it will
surely be eaten. The host/parasite relationship is similar to that of predator/prey,
where one organism is deriving its sustenance from the other, but different in that
while the parasite lives off of the host weakening it; it does not actually attempt to
kill it. A parasite will generally move to a new, healthier host than the one it was
exploiting when convenient as the death of its current host would also surely mean
the imminent demise of the parasite if it were not able to quickly find a new host.
An example of a parasite could be a flea living on your pet dog, the host. Both of
these coevolutionary types can be brought under the broader definition of competitive
coevolution.

Competitive coevolution is distinct from the other type of coevolutionary rela-
tionship known as mutualism. For simplicity, we will refer to this relationship as
cooperative coevolution as this is the term used by most other researchers in the
field. Mutualism is a relationship where both organisms benefit from each other. An
eexample could be a honey bee and flowers, where the bee gains nourishment from
the flowers nectar and the flower uses the bee to spread its pollen to other flowers in
order to reproduce.
2.2.1.1 Competitive Coevolution

The host/parasite model is the most popular coevolutionary form used by researchers [20, 29, 36, 40, 55]. This is a competitive approach where we would have two unique populations: the host and the parasite. The host is the population being optimized and the parasite is the population attempting to exploit the hosts. In essence, it is a problem in which individuals succeed at the expense of the other. A practical example is the genetic programming (GP) problem of creating a sorting network [20]; the host is a sorting network while the parasites are the sorting problems the host is attempting to solve. The hosts fitness is proportional to the number of parasitic problems it can correctly solve, while the parasites fitness is proportional to the number of host problems which cannot solve it.

The predator/prey relationship is one which has been referenced in some papers [18], but in general they dont seem to be any different than the host/parasite model, which a few authors have also noted [20, 26]. The GA does not have any form of ‘killing’ mechanism as an entire population is reproduced simultaneously at the beginning of each generation. It simply has a reduction is fitness as parasites exploit their hosts. This terminology is also easier to understand when used in the context of the GA: the ‘larger’ hosts are in the population we are interested in, while the parasites cause ‘problems’ for the hosts and are there to encourage the hosts to get better through evolution. When we use predator/prey it can be somewhat unclear as to which population is which. In this thesis we will stick to using the host/parasite convention, or simply use the term competitive, as these are the terms that appear
most commonly in the literature.

2.2.1.2 Cooperative Coevolution

The use of a cooperative coevolutionary GA is a simpler version of the coevolutionary GA and has also been studied a fair amount, though not nearly to the extent of the competitive coevolutionary case [39, 53, 54]. In this case, both organisms benefit from the other having a higher fitness as they work together to find the global optimum; the individuals interacting succeed together or they fail together. The cooperation could be a direct relationship where both organisms are found when both organisms are at their respective optimaums. In the simplest version, both organisms would be used to determine a single fitness and therefore are awarded the same fitness. However, more complicated relationships could be devised where each organism may be awarded a portion of the total; as long as the organisms’ fitnesses are a positive relation we would consider it cooperative coevolution.

2.2.2 Problems with Coevolution

There are a number of problems that can occur within a coevolutionary problem, which by design, cannot occur within the standard GA. We will go over some of more significant issues in the following sections. Many of these problems can be easily described using game theoretics, which many of the authors cited in this section do use. We will refrain from getting into too much detail here, but will briefly discuss the link between game theory and the coevolutionary GA in section 2.4.2.
2.2.2.1 Over-Specialization

While coevolution has been shown to improve performance in many studies, including the ones we’ve already discussed, this is not always the case. A host-parasite model attempted by Thompson [47] to help find ‘faults’ within a solution population was deemed a failure. Thompson found that a random selection of faults to test in each generation was more efficient than those found through coevolution. This means that coevolution was actually slowing down the rate at which he was able to find an acceptable solution. He claimed this was likely due to the solution population becoming preoccupied with optimizing for only a subset of the possible faults and never got around to attempting to solve the others. This problem has since become known as the over-specialization or focusing, defined as “focusing on a subset of the underlying objective” [8].

2.2.2.2 Loss of Gradient

A loss of gradient occurs when all solutions viewed have the same or extremely similar fitness [49]. This causes what is known as disengagement, which is when individuals can no longer be distinguished, rendering selection ineffective. Disengagement could mean that all solutions have converged to the same optimum, but that is more a problem with the GA’s termination mechanism. In general, it implies that chromosomes are significantly different, but returning the same fitness value. If fitnesses are merely similar, not exactly the same, an easy solution would be changing the selection technique to one of Rank Selection or Tournament Selection, as they can detect even
minute differences.

In the standard GA, disengaged fitness values could alternatively be caused from a ‘flat’ problem space where chromosomes are stuck on the same plateau; this would most likely imply a hard (or even impossible) problem, such as the ”needle in a haystack” problem [12]. This plateau effect can also occur based on the problem in the coevolutionary GA, but it can also be caused by ineffectual competition from the opposing population. If one population has become too ‘good’ for the other to compete then that population may have all of its individuals with ‘good’ fitness scores while none have reached the optimum. It has no way of detecting any difference due to the ineffectiveness of the opposition [34], and is unable to continue evolving effectively.

2.2.2.3 Cycling

*Cycling* is similar in concept to that of local optima, however instead of a single point, it is a set of points the GA gets stuck at. The competitive populations will cycle among a subset of points which are able to beat each other and solutions nearby, and thus, not allow the GA to continue progressing toward the global optimum as it has gotten stuck cycling through the same points [41]. This problem can be easily described with the game theoretic game of Rock-Paper-Scissors (RPS)[8]. This is a simple game wherein an individual is paired with another and each choose one of Rock, Paper, or Scissors. If the individual wins it receives a fitness of 2, if its ties a fitness of 1 and a loss a fitness of 0. Rock beats Scissors, Scissors beat Paper and Paper beats Rock. The individuals will then cycle among the 3 options as it can never find the optimal point, but continues to allow for change in the population.
Clearly this population has no optimal solution without using a game theoretic mixed strategy (selecting each option with probability 1/3), but one can imagine a larger more complicated problem with a similar game occupying a local optimum. In reality, this could even be part of a larger global maximum, but the GA may not know it as it continues to evolve through the cycle. This phenomenon could have also been at play in producing the problem Thompson [47] was having with his coevolutionary GA as it cycled through through solutions attempting to satisfy incompatible faults, though he does not give enough detail to do more than speculate.

2.2.2.4 The Red-Queen Effect

The Red-Queen effect is originally a term used in evolutionary biology to describe a similar effect to the one described here [48]. The Red-Queen Effect, as defined in the field of natural computing, is an phenomena found in a competitive GA where the quality of individuals could be improving, but its fitness does not [8, 37]. This occurs because rather than being compared against a static fitness function, like in the standard GA, individuals are compared against competing individuals who are also improving and an individual must improve just to maintain the same fitness. This concept of constant improvement through competition is sometimes refereed to as an arms race. What this means for the individual, is that it may have improved, but its probability of selection has not. The Red-Queen effect is not necessarily a negative thing, as an arms race forcing the individuals to get better is exactly what we would want to occur in the GA; each individual forces the other to excel or die. The Red-Queen becomes a problem when it masks phenomena that are problems,
such as disengagement and cycling. In order to distinguish the difference between these phenomena, one would have to define a static fitness function to compare the population against, thus removing the coevolutionary dynamic. It is clear that this option is not acceptable in most situations, it would remove the coevolutionary gains we have discussed previously, and additionally, it may be infeasible depending on the problem being tested. A consequence of the Red-Queen effect can also be seen when attempting to compare different coevolutionary systems; individuals are being compared against individuals in the same generation as themselves, therefore their fitnesses are relative to that generation. This makes it hard discern to what extent evolution is occurring and whether it is even happening at all, again, a most likely infeasible static fitness function would be required to fix this problem.

2.3 Spatial Genetic Algorithms

In continuing the theme at looking to nature for inspiration, we should consider the impact of geography on the evolutionary process. Organisms are not technically able to reproduce with every other organism which exists in the system, like in the standard GA; they are only able to reproduce and share their genetic code with the organisms which they can come into direct contact with. Sewall Wrights theory of isolation by distance within biology, discusses reasons for why superior genes do not take over an entire population [59], only organism near the organism which evolved those superior genes will be able to reproduce with them. These genes must flow either reproductively, or through physical movement, to flow through the entire population.
This has a great reduction on the speed at which they are able to take hold in the entire population. An important concept to note is that the greater the fitness boost a certain set of genes provides to the organism, the more rapidly those genes will flow through the population due to their greater increase in fitness. A positive feature of this effect, both in nature and the GA, is that some of the gains of such a gene could be short term. In nature, a gene could perhaps make an organism physically stronger but more susceptible to some predator or disease which the organisms has infrequent contact with. In this case, if all of the organisms had taken on that mutation they could be wiped out when reintroduced to that predator. Similarly, this can be an issue in the GA with respect to it getting stuck at local optima. The spatial structure allows the GA’s population to remain more diverse and allow it extra time to search a larger area before having too many of its organisms searching a single local optimum. However, that concept should make it clear that the spatial genetic algorithm will not work as well on a simple problem space with only a single optimum; the spatial structure will slow it from passing the best genetic information to all its organisms [3].

The idea of space as a mechanism in the GA is a concept researchers have been attempting to add to the GA with some success since the late 1980s. The GA is connected using a spatial structure which influences the organisms an individual organism can reproduce with. They are placed on a network structure and are only able to reproduce with organisms which are directly connected to them. The first researcher to begin looking at spatial GAs was Mühlenbein [30, 31]. He originally named it the parallel genetic algorithm (PGA), due to their implementation using parallel
computers. Many of these original PGAs were run using the Connection Machine [6, 19], a massive scale parallel super computing system connecting huge numbers of processors, as many as 65,536 (2^{16}), used to perform various computations. The GAs being used with the Connection Machine became known as fine-grained parallel GAs. Dan Hillis, the creator of the Connection Machine [19], is responsible for both creating the inspiration and technical tools used by many spatial GA researchers, but is also responsible for some of the early work in coevolutionary GAs [20].

One of the major reasons for success with the spatial GA was that it was shown to reduce the loss of diversity found in the standard GA [3]. The quality helped prevent the GA from getting stuck at local optima or plateaus, an advantage the standard GA already has over so-called classical hill-climber algorithms. This quality was shown to help it solve a Rosenbrock function run with 400 variables [31], a common math function tackled by many types of search functions. Despite these successes, work on the spatial GA began to decrease significantly in the late 1990s and has seen very little work in the past decade. This is probably, in part, due to the fact that while they theoretically promised a higher probability of finding the optimum, as well as a lower number of evaluations required to find it [16], they required a larger amount of memory and computing power than the classic GA. In addition, the spatial GA is somewhat more complicated to understand and code, due to the additional complication of handling networks using linked lists or adjacency matrices. This meant that while there had been significant success in theoretical terms, the real time performance and implementation of the spatial GA was lagging behind the standard GA, making it infeasible to apply. In addition, many of the early spatial GA’s were run using
Hillis’s Connection Machine, but his company which manufactured them, Thinking Machines, was defunct by 1994. With the primary method of experimenting with spatial GA’s now obsolete, their allure as a research area waned.

2.3.1 Spatial Networks

Graph theory has been a topic discussed in mathematics for centuries, however their impact on our daily have only been looked at in detail in the past 50 years or so. These spatial structures have been shown to have huge impacts on our daily lives and have become important topics in a wide variety of fields, including: economics - tracking market trends, including their collapse, engineering - designing power grids, geology - tracking earthquakes, and sociology - viewing social circles and their impact on our lives [50].

The famous mathematician Paul Erdős, along with Alfrédi Rényi, were some of the first researchers to look closely at these networks and defined the random graph model which now bares their names [13]. This model held as the status quo for describing how ‘real world’ networks formed for nearly four decades. This model assumed that networks were created at random, where new connections were created between any two nodes regardless of that node’s position or previous connections. In the late 1990s the work of both Watts & Strogatz [51], and Barabási & Albert [2] proved that real networks were much more complicated than what the Erdős and Rényi’s random model predicted. They discovered that when a node gained a connection it was much more likely to do so if it already had a connection to a node nearby in the network. Consequently, this implies that nodes with many connections
would be more likely to gain even more connections as they are closer to more nodes, these nodes with many connections are called hubs. These networks have become known as scale-free and this process in which scale-free networks are created is known as preferential attachment. These papers revolutionized the field, additionally both Duncan Watts [50] and Albert Barabási [1] wrote best-selling books on the topic popularizing it further and becoming a catalyst promoting network theory related research in numerous fields.

This research also influenced the work of GA researchers by convincing them to consider structures other than the standard grid used by most early spatial GA researchers [3]. They not only looked at different levels of connectedness, as others had done previously [42], but also how the spatial structure itself affected the performance of the GA. After using multiple test problems, Bryden et al. were unable to conclude that any one structure was better than the rest, in fact, they found that depending on the problem being tested, the best spatial structure varied greatly. A part of these results was that the complete graph, which simulates a standard GA, was best for some problems, mainly problems they termed as ‘simple’, such as the one-max problem. The more complex problems they tested, however, appeared to work better when put on their spatial structures with a lower number of connections. They proposed that the spatial structures with fewer connections were slowing down the loss of diversity within solutions, and helped prevent the GA from getting stuck at local optima. As part of this thesis, we will attempt to confirm these results and compare them with our new results comparing how these same spatial structures affect the behaviour of the spatial coevolutionary GA.
There are a few important definitions from network theory which will be useful in our discussion of the spatial GA [17]. A graph is made up of nodes which, in a spatial GA, will hold individuals/chromosomes which are connected to other nodes by some number of edges. The set of nodes an individual node is connected to through its edges is called its neighbourhood. In our structure the edges are undirected, meaning each connection implies that each node is aware of the other. The degree of a node is the number of connections connected to it, the degree of the graph is the number of connections per node in the graph. A path length between two nodes is the minimal number of connections necessary to travel from one node to the other. The largest minimal path length among every set of two nodes in the entire population, i.e. the longest ‘shortest path’, is called its diameter.

2.4 Spatial Coevolutionary Genetic Algorithms

The spatial coevolutionary genetic algorithm is a merger of the coevolutionary and spatial variants of the GA. One of the earliest spatial coevolutionary GAs is also one of the first Coevolutionary GAs. Dan Hillis, cited by many as the founder of coevolutionary GAs, initially created his GA to use a spatial reproductive grid [20]. He does not give a specific reason as to why he chose to use spatial reproduction other than saying that his experience suggests that it is better to use a mating program with some type of spatial locality. Whether his intuition was correct or not, many coevolutionary researchers coming directly after him chose to drop the spatial reproduction component of his GA in favour of simpler systems, instead choosing to focus
purely on the coevolutionary aspect of it.

The idea of a spatial reproduction network in coevolutionary GAs did not get completely lost; Pagie & Hogeweg [35, 36] attempted to prove Hillis intuition using another GP style problem and found that adding spatial reproduction to it had merit. They showed that a spatial coevolutionary system using a host/parasite model was more effective than a non-spatial coevolutionary GA at modelling a specific numerical function: \( \frac{1}{1+x} + \frac{1}{1+y} \). In this problem the host population is made up of proposed math functions and the parasites are specific points used to test the problem. Mitchell et al. [29, 55] used the same problem to prove in more detail that, for this function, spatial coevolution was more efficient at finding a solution than either the classic GA or a non-spatial coevolutionary GA. Mitchell et al. proposed that the success of the spatial coevolutionary GA was due to its ability to maintain diversity while the coevolved parasite population targeted weaknesses in the host population, forcing it to solve these problems.

Very little work has been done on the spatial coevolutionary GA using problems more general than the GP problems discussed previously. Wiegand & Sarma did look at the spatial coevolutionary GA trying to optimize a simple two variable (x, y) mathematical function, using a GA rather than GP style system in a cooperative coevolutionary setup, where one population holds the x values and the other the y values [54]. They also found that spatial coevolution was beneficial to their cooperative coevolutionary setup, but admit that the area still requires further work; we look to extend much of what they did in their paper in this thesis. The general mechanisms found in all of the papers in this section were used as a starting point for much of the
work done in here, the details of which will be discussed in the methodology section.

2.4.1 Evaluative Networks

In this document when we have discussed networks on the GA we have so far been referring to its reproductive network, however there is another network of interest in the coevolutionary GA. This is the evaluative network which specifies the other individuals an individual is being evaluated with/against. The reproductive network is realistically the only network related concept to consider when looking at the standard GA, as the organisms are only evaluated by a static fitness function. The work of Pagie & Hogeweg and Mitchell et al. both generally ignore the evaluative network topic, and instead just focus on their GA’s reproductive networks [29, 36]. The evaluative networks they use are either non-existent, with evaluative pairings either being against the entire population or selected randomly from the population. Otherwise, the evaluative network is simply the same as the reproductive network, i.e. any organism that an individual could potentially reproduce with are in the same spatial location as the organisms in the coevolving population that organism is to be evaluated with. The concept of varying the evaluative network from the reproductive network was briefly discussed by Weigand & Sarma [54] but, while they consider it an important concept, they don’t go into much detail on its effects. Another, simpler method of comparison is a one-to-one mapping returning a single fitness value, as shown in Figure 2.1, versus comparing against a larger number of the nodes and needing to decide how to define fitness among the set of nodes. Most authors have used an averaging system, using the mean of the fitness comparisons [36, 29], while others
have used the maximum (elite) values from the set being compared [39]. Hillis [20] originally used the simple one-to-one mapping with each individual in his parasite population representing 10-20 different sorting problems and setting the host’s fitness proportional to the percentage of problems in that chromosome it could solve. There are a variety of other methods which could be used, but appear to have not been, such as using the median or minimum fitnesses. The minimum fitness may sound odd when we are attempting to maximize our fitness, but it could be useful to attempt to find general solutions, rather than ones specializing in solving one subset of problems.

For most of this thesis we will be using a simple one-to-one mapping, with reasoning being described in more detail in Chapter 3.

Figure 2.1: Spatial reproduction on a grid with a one-to-one evaluative network
2.4.2 Ties to Game Theory

Another field which has embraced spatial networks is game theory. Game theory is the study of strategic decision making, wherein individual players choose a strategy and are awarded a payoff. We can begin to see parallels between the fields when we consider equivalent terms: player → organism, strategy → chromosome and payoff → fitness. The parallels continue when we consider that game theory is most extensively used in the biological sciences, though it originated in economics. Prominent evolutionary biologists Martin Nowak and Robert May, originally added a spatial component to game theory in their 1992 paper published in Nature [32]. Their reasoning for adding spatial networks to game theory was to view the evolution of game theoretic strategies, specifically Prisoner’s Dilemma, over many generations. Viewing the evolution of strategies can, in many ways, be considered a sub-field of GAs, as noted by Nowak [33]. The idea of evolving strategies is clearly comparable with evolving an optimal solution, as we see in GAs. We would also consider this field to be coevolutionary as the payoff, and therefore the relative ranking within the population, is based on the strategy of the other players. As game theory is already a coevolutionary discipline by definition, the success of adding a spatial component to it is an inspiration for adding a spatial component to coevolutionary GAs.

In general, the GA field is mostly interested in the final outcome of the operation, the optimum of the search space, while game theory is more interested in the mechanisms which got them there. A GA researcher would use simple mechanisms to explore a complicated space, such as the Rosenbrock function or various other
classic search problems. In general, the game theory community would consider more complicated mechanisms, or interactions, to explore a simple space, ex: Prisoners Dilemma. Using game theoretic techniques to study phenomena within coevolutionary and spatial GAs has been put into practise by many notable GA researchers hoping to better understand them [53].

2.5 Evaluating Genetic Algorithms

Evaluating a genetic algorithm is not a simple task; there are numerous variables and mechanisms to consider when designing a new GA. While this paper has alluded to a classic GA, there is really no single officially recognized set of GA mechanism. In general, when people refer to a classic GA, they are generally referring to the GA mechanisms described by David Goldbergs book [14]. However, that book still does not specify many exact parameters to be used in the GA, only a general guideline to what the basic mechanisms should be. With that in mind, it is still somewhat difficult to really determine what type of GA we are testing with, or against when attempting to improve upon it. It is simply left up to each researcher to determine which mechanisms, and settings of those mechanisms, they wish to use. Generally, when the researcher is choosing mechanisms they aren’t directly testing, their only reasoning is that another researcher they were citing did it that way, or they arbitrarily chose something because it sounded good without really knowing the true effects. This has lead to many GAs in the literature using many different parameters and can make it difficult to directly compare one researcher’s work to another. It can also
become difficult to determine if the resulting effects are indeed from the mechanism being tested and not based on some interplay from the other mechanism choices they arbitrarily made. This effect leads to the desire to start from the beginning by testing each mechanism we believe could be important and, within reason, is the approach taken for this thesis.

Another obstacle when attempting to evaluate a GA is determining which problems to test your GA against. For many years, the so-called De Jong Test Suite was considered the de facto way to test a GA [52]. This is a set of 5 problems Kenneth De Jong originally used in his PhD thesis to test his own GA in 1975 [9]. While the test suite has a number of useful test problems, including the Rosenbrock function, which is used as a standard test problem for many search algorithms, it is by no means an exhaustive list of problem features which should be tested. Whitley et al. [52] discuss the De Jong test suite, as well as an additional 5 problems they consider commonly used in the GA field, and explain where they feel the test suite falls short. A few of the attributes they claim that a good test suite should have include the problem being: resistant to hill climbing, i.e. containing local minima, or at least plateaus to confuse the hill climber; have a canonical form, i.e. a specific way of representing the problem so that anyone implementing it will do so in the same manner; and be scalable, i.e. having the ability to be made easier/harder by decreasing/increasing their size. These attributes were considered as the problems were selected for the experiments in this thesis.

After the test problems have been selected, we will still need to determine what criteria we wish to use when defining when we can declare a problem solved. A
few common ways are: setting a maximum number of generations and checking how
often we have found the solution by that generation; setting a standard error, \( \epsilon \), and
recording the number of generations it took to get to that point; or possibly, recording
the amount of real time it took to find the solution. When comparing GAs with
significantly different mechanisms, it is also fairly common to measure the number of
fitness function evaluations taken before finding the solution. In general, when using
a fairly simple problem where finding a solution (or at least getting within \( \epsilon \)) is trivial
we would use the standard error option, while for more complex problems we would
set a maximum generation to ensure experiments could finish in a reasonable amount
of time.

### 2.5.1 No Free Lunch

A significant contribution to the discussion of acceptable test suites is the now
infamous No Free Lunch (NFL) papers by Wolpert and Macready [57, 56]. They
argued that no single algorithm can outperform random search when viewed over
the infinite space of possible problems. This, at first, led many to claim the end of
GAs, while others noted (correctly) that it was more a commentary on all black-box
search techniques, and did not hamper the GA more than any other search technique,
including basic hill climbers [5, 12]. However, NFL does not even truly hamper any
testing technique; it was merely a commentary attempting to bring some common
sense to a trap some researchers were falling into: claiming that their mechanisms
were best because their system worked better on a specific problem (or subset of
problems).
Christensen & Oppacher argue that NFL assumes that we know nothing about the search space and as long as we can make a general assumption about the searchability of a problem, then researchers can still make the same claims they were making previously [5]. A searchable problem, according to Christensen & Oppacher, is a problem in which data gained from points observed previously have some correlation to the overall structure of the problem allowing an algorithm to predict future performance. They argue that problems we are more likely to encounter and want to solve, in general, are much more likely to be searchable than the random search spaces NFL relies on to make its case. While the impact of NFL has lessened from what many observers first believed it to be, it still teaches a valuable lesson that choosing a set of test problems is not a trivial task. We must be sure to select test problems which can allow us to accurately test the types of problems we are interested in. To summarize, no single search algorithm will be the best for every problem, especially when the algorithm has no specific knowledge about the problem’s space, it can only be better for solving a specific problem or set of problems.

2.6 The Building Block Hypothesis

The building block hypothesis is an explanation as to why the GA is able to work so well when solving some problems. It is the idea held by many and most notably described by Goldberg and Holland [15]. The hypothesis is that the GA worked from taking short, highly fit sections of a solution string, a building block, and recombining them with other highly fit sections of string. Eventually, by recombining better and
better sections of strings, we are able to find a solution. This was a hypothesis which many researchers believed to be true, but it was just a generally accepted fact, not something which had actually been tested or proven.

Mitchell et al. attempted to prove this hypothesis using what they called the Royal Road function, a function which rewarded the GA for the creation of these building blocks [27, 28]. What they found surprised them, instead of helping the GA, this function actually hurt it when compared with more standard functions that did not reward the creation of building blocks. While this did not disprove the building block hypothesis, it did call into question what many researchers had considered fact. Mitchell et al. tried to explain the failure of the Royal Road function as being due to what they termed hitchhikers. Hitchhikers are sections of strings which become attached to the good building block, making them hard to remove due to the lack of a significant difference in fitnesses between the strings with good and bad hitchhikers. This is a theory that remains in the literature without having any clear attempts to prove or disprove it.

2.6.1 Linear Separability

The concept of linear separability in a GA is related to the Royal Road function, as this function rewards the GA for connecting ‘blocks’ of good genes making different slots in the GA depends on one another. In general, linear separability is the concept that a bit at one, or many, location(s) of a chromosome do not affect what the optimal bit is at another location, i.e. the bit which would produce the best available fitness. This is important when considering the building block hypothesis, as good blocks
may only remain good when considering the full chromosome it is a part of. If any of the genes part of that block are ‘wrong’, then the chromosome does not gain or lose fitness based on any of the other genes that would be in that block. This effect is part of what makes a non-separable problem harder than a separable one, the solver cannot independently solve for an individual bit and is forced to consider a much larger section of the system to gain any information. A completely linear separable problem is one in which each bit could be viewed independently in order to find the solution. For example, the one-max problem is a completely linear separable problem, to find the fitness you simply count up the number of bits, their location in the string is irrelevant. Problems such as one-max are ones which hill-climbers perform much better than the GA as they have the natural ability to look at each bit independently.

Linear separability is also important when working with cooperative coevolutionary GAs. When organisms are evaluated with chromosomes coming from another population and are not linear separable their fitnesses can fluctuate wildly. Therefore, we must consider the fact that an organisms fitness partner could change dramatically, not only affecting the overall fitness, but also its relative fitness when compared with its peers. For example, in a host-parasite model we could have a host with a very good absolute fitness when compared with a complete population of parasites, but if it is paired with parasites which happens to exploit its only remaining weaknesses, it could end up with a very low relative fitness score. Alternatively, we could have another host with a low overall fitness which is paired with parasites all attempting to exploit the only strength that host has and it can end up with a very high overall fitness. This would lead to a ‘worse’ host having a greater relative fitness. This
concept is well known to researchers working with host/parasite models [29], and is in some ways encouraged, as it can promote a greater diversity of solutions, but it is something to keep in mind when studying their behaviour. In this thesis, many of our problems have organisms genes being split between multiple populations, which we will discuss more in section 3.4, but this can lead to lower levels of linear separability. We will look at the effect linear separability has on coevolutionary GA performance in section 3.5.5.

2.7 Analytical Tools

We will be using a number of statistical tools throughout this thesis to both accurately prove statements being made as well as providing tools for visualizing concepts.

2.7.1 Non-parametric Statistics

Most standard statistical tests used in research literature, such as the Student’s t-test or ANOVA, require an assumption of normality for the data they are testing. In many cases, even if the data being tested is not normally distributed, as long as it is nearly so, these tests will still be fairly accurate. If the distribution of the data is far from normal there are generally two approaches for statistically testing it: either finding the source of non-normality and removing/fixing it to normalize the data, or using other statistical techniques which do not require an assumption of normality, i.e. non-parametric statistics.
Most of the experiments we will be running are based on the number of generations a GA takes before it has found the optimal solution. We will be changing parameters for each set of GA runs and comparing their time until completion. This setup implies that our data will not be normally distributed, the GA’s generations until completion will have a fixed minimum of 1, and an infinite maximum that may have a non-zero probability. Furthermore, in practice we do have a maximum generation meaning, if the solution cannot be found by that time, the number of generations to the solution for that run is effectively infinite. This could be caused be a variety of reasons, such as, an impossible problem, an ill defined termination function, or the GA falling into something like the ‘cycling trap’, discussed in Section 2.2.2.3. After a constant number of runs, the data could appear fairly normal, especially if it is a problem setup which has its average number of generations far enough from the start point without any possible ‘traps’ it could fall into. Given that, while using standard statistical tests could be fairly accurate for much of our data, that would be on a case by case basis, and preliminary results have shown that at least some our data is definitely not normal. Therefore, we have chosen to use non-parametric statistical tests for all of our data to stay consistent.

2.7.1.1 Wilcoxon Rank-Sum

As we have decided to use non-parametric statistical tests, we will use the Wilcoxon rank-sum test (also known as the Mann-Whitley U test) when looking for statistical significance in our results. For non-normal data sets, this test is significantly more efficient than the Student’s t-test, allowing for greater accuracy, when
comparing the similarity of two sets of data [22]. The Wilcoxon rank-sum test is slightly less efficient on normally distributed data than the t-test, but this loss is well worth the gains when compared with the gains on the non-normal data.

2.7.1.2 Holmes-Bonferroni

Where appropriate, we will also be using the *Holmes-Bonferroni post-hoc correction* [22]. This is a method for accounting for the problem of multiple comparisons. This is a phenomena in statistics which occurs when attempting to consider multiple hypothesis using multiple data set comparisons. When we make numerous comparisons, we are more likely to draw the wrong conclusion from one of our conclusions. In general, it is a rare occurrence to make the wrong conclusion on a single comparison, but when we are making many comparisons, it is actually fairly likely that at least one will be incorrect. For example, if we are using a t-test (or in our case the Wilcoxon rank-sum) with a statistical significance level of 0.05, we are 95% sure we are seeing a significant result. However, if we were to test, say, 10 separate variables and compare them to our control experiment we are now 95% sure in 10 different results, but this would mean that we are \((1 - 0.05)^{10} \approx 0.6\), or 60%, sure that all of our results are accurate i.e. a 40% chance that one of our results are incorrect. In order to account for this problem we add a correction value to each of our \(p\)-values and confirm that each of these values are in the 0.05 threshold. A Bonferroni correction is if all of the values are still within this threshold, then we can say that we have a 95% confidence in our overall experiment. The Holmes-Bonferroni is a more powerful test, as instead of using a simple threshold, it sequentially sums how close each result is to the given
confidence level and uses those values as its less conservative, and therefore more powerful, threshold.

2.7.1.3 ANOVA

We have chosen not to use ANOVA because of the problem with the non-parametric ranked ANOVA on multi-factorial problems [44]. Our data is both non-parametric and there are multiple factors involved, making ANOVA a poor choice. In general this problem with ANOVA is related to our need to use the Holmes-Bonferroni post-hoc correction, with multiple factors ANOVA is much more likely to give us a false positive. The Kruskal-Wallis and Friedman tests could also be applied for some of our problems involving multiple levels of a single parameter, however in general we find that the factor levels they are strong enough that it becomes clear that there are differences among factor levels and simple pair-wise testing is powerful enough to make these distinctions [22].

2.7.1.4 Non-parametric Boxplot

As much of the data presented in this thesis is non-parametric, the best way to present it is through the use of a boxplot. We will be using the default non-parametric boxplot found in R. This box plot contains a box representing the upper and lower quartiles (25-75%) and a bar in the box representing the median (50%) value. Whiskers are drawn from the box up/down to the most extreme data point found within 1.5 times the interquartile range. All ‘extreme’ data point outside of the range of the box and whiskers are marked as dots on the graph.
2.7.2 Heat Map

A heat map is used to track the fitness of individuals within the population. The data points are drawn on a grid with highest fit individual in the pictured generation drawn with the lightest colour (white) and the least fit individual in the pictured generation drawn in a dark colour (red). The other individuals are drawn with colours between white and red based on their fitness relative to the most and least fit individuals; individuals with lower fitness closest to red and higher fitness closer to white. It is important to note that the colours in each heat map are based on the max/min fitnesses among individuals in the pictured generation not the max/min possible fitnesses. Due to this, it is not helpful to consider the colours of nodes in different generations, only the distribution of fitnesses within each generation. Finally, the heat map should be thought of as a toroidal structure with the edges of each graph are connected to the opposite side (i.e. top to bottom, left to right).
Chapter 3

Methodology and Implementation

3.1 Overview

This thesis will explore the impact of adding coevolutionary and spatial components to the standard GA using specific, scalable test problems designed to contain a variety of features in order to see a range of behaviours from the tested mechanisms. We will then increase the complexity of our problems until we, hopefully, find when and why each GA type handles a certain problem better or worse. To this end, our GA and the problems we run on it will be designed to fluidly go between the spatial and non-spatial system as well as the standard and coevolutionary systems.

In addition to our general exploration, we are attempting to confirm, or disprove, the hypotheses presented by Mitchell et al. [29] and Weigand & Sarma [54] for why they believe spatial system helped their coevolutionary GAs. Another sub-goal of this thesis is looking at the attributes of different spatial structures being used on the GA and viewing how they impact the performance of a standard spatial GA versus a coevolutionary standard GA; thus expanding the work of Bryden et al. [3] to coevolutionary GAs. We will also explore the notion of elitism within each GA type; preliminary research has shown that elitism had significant and varying effects
based on the type of the GA. We will view elitism simultaneously with the effects of spatial structure and we believe this may allow us to gain a deeper understanding to the impact of spatial reproduction on our coevolutionary systems.

3.2 GA Setup

The standard GA setup for all problems being tested in this paper used a number of consistent features and mechanisms. Any of the parameters which we are not explicitly testing remained constant through all tests. We are aware that there may be some interaction effects between these parameters, but the combinatorial explosion of parameter settings necessitates the focussing on factors that we consider relevant for our initial exploration. Whether crossover or mutation has any interaction effects, which at this time we believe to be highly likely, should be explored in future studies.

We are attempting to emulate the framework and parameters most commonly used in the GA community, which are generally based on the recommendations of Goldberg’s 1989 book [14]. Our GA is using both mutation and crossover. The mutation rate is $2/L$, where $L$ is the organism’s chromosome length. The probability of crossover is 0.8, using uniform crossover with a parameter of 0.3, as recommended by Spears & De Jong [45]. The chromosome length used is either 32 or 60 depending on the problem being solved, see section 3.4 for details. The population size will be 100, which is somewhat larger than Goldberg’s recommended default of 50 as we needed a population large enough to allow the embedding of non-trivial spatial structures. The population did not need to be any larger than 100 as the problems
we are solving are not complicated enough to warrant it, and rapid experimentation was desired. The termination parameter is set for finding the exact optimum ($\epsilon = 0$) as the problems being tested have discrete genomes and are simple enough that, in most cases, the GA should have no problem solving them. In addition, we will use a maximum generation of 5000 in order to prevent extreme outliers from slowing down our experimentation, and as a precautionary measure, in case we are mistaken about the ease of solving some problems. Any GA run that does not find the solution by the 5000th generation will be recorded as 5000. This comes with the understanding that any generations recorded as 5000 are considered ‘failures’; they were unable to find our solution in the given number of generations. While an elite size of 1 is what is generally used by most researchers the size used does vary. Our preliminary results have indicated that higher levels of elitism were significantly more effective than lower values for our coevolutionary systems. Therefore, wherever it has not been explicitly stated, we chose a value of 2 in order to both: keep our elite value close to the norm in the field, and at a value where coevolutionary systems begin to perform significantly better. Elitism will be discussed in more detail in section 3.2.3. Finally, we run 50 repetitions of each experiment presented in order to collect enough data to draw statistically relevant conclusions.

3.2.1 Spatial Selection

The selection mechanism used for reproduction, while keeping close to a standard spatial GA, will have a few slight differences in order to create a seamless transition between the spatial and non-spatial GA using a complete graph to simulate the non-
spatial GA. The spatial reproduction used is similar to what was used by Mitchell et al. [29]. However, instead of their system of exponential rank selection to determine parents from among the neighbourhood, we will use binary tournament selection. The neighbourhood is defined by the spatial structure being used for that GA, the location being selected is included in its own neighbourhood. With 0.8 probability another individual is selected, with replacement, to cross with the first individual. Therefore, if a second individual is not selected it will not undergo crossover. Once crossover has occurred one of the children is selected at random to inhabit that location. This is the same mechanism used for the standard GA, the spatial structure being used is just a complete graph, i.e. every individual is in every other individual’s neighbourhood, so there is no restrictions on reproduction.

3.2.2 Coevolution

The coevolution mechanism we are using for these experiments is modelled after the work of Weigand & Sarma [54] which has been discussed in section 2.2. We will have both cooperative and competitive coevolutionary problems, the specifics of these problems will be discussed in section 3.4. The cooperative coevolutionary problems we will be using will be discussed in terms of the standard GA, when they are implemented on the coevolutionary system their genetic sequence will simply be split in the middle with half of each sequence in the other population. The competitive problems will attempt to emulate the work of Mitchell et al’s GP style system [29], but using a GA framework; i.e. a linear homologous representation instead of a tree based representation.
3.2.3 Elitism

In a standard GA elitism is important, it prevents the best solution found so far from being accidentally lost through the randomness involved in selection. This allows important genetic information to remain within the population, continually disseminating important genetic information throughout the population. The effect of the elite is not so clear when dealing with spatial GAs; the genetic material from the elite member can only be of immediate use to its local neighbourhood. If we use the ‘global’ elite as seen in a standard GA, pushing it through to the next generation unchanged, this limits the amount of spatial variation the elite is able to induce. In fact, when you consider the elite is already limited by spatial reproduction, this standard elite mechanism could easily stall evolutionary process in the very area that has the most promising solution. Some spatial reproductive systems, instead of using a global elite, invoke a tournament between parents and children for inclusion in the next generation as a form of local elitism, as discussed in section 2.1.1. However, this style of elitism is far from being a standard practise, and could easily place too strong a selection pressure on the population.

In order to facilitate direct comparison between our standard and spatial GAs we introduce an ‘intermediate’ elitism mechanism between local and global. Instead of implementing local elitism on all nodes, we choose $k$ unique elite and for each of those ‘global’ elite we apply local elitism. In other words, we globally select elites and implement it locally. This system allows us to smoothly transition between the spatial and standard GA without having to change our elitism procedure, for the
standard GA the elite value will simply have to ‘win’ its slot into the next generation. We are relatively unconcerned about the rare occasion in which the elite loses its spot, which could not occur in the ‘true’ standard implementation; that gene would no longer by the elite value in successive generations anyway. For our experiments we will use elitism levels of $k = 0, 1, 2, 5, 10, 50$ and $100$.

We should make special note of the elite size of 100 as this implies full elitism for the entire population. On the spatial GA this would be the same as local elitism as all nodes are being selected. However, this makes things slightly more complicated when we consider the non-spatial GA, in this case a child is essentially chosen at random to fill a location and must undergo local elitism with whatever individual happened to occupy that space in the previous generation. With full elitism, elites are no longer really function as true elites, as even the ‘poor’ nodes operate with the same mechanism. In this case elites will lose their spots in the population regularly due to that being the only way fitnesses can improve. The GA should still be able to function under these conditions, at least for some problems, it will just have a very high selection pressure. If we used the classic elitism style with full elitism, by definition, the GA could not evolve as the children would have no available nodes to occupy in each generation. These impacts will be considered as part of our elitism discussion in section 3.5.6.
We will be using a number of spatial structures in order to view the different structure’s effects on our GA’s performance; the same structures are used on both the standard and coevolutionary GA. There are 8 different spatial structures we will be using, with varying levels of degree and diameter. The first is the simple grid structure which could be consider the ‘default’ spatial structure as it is used by many other authors [20, 54]. This simple grid connects each node to the node above, below and to each side on the toroidal grid as shown in figure 3.1; we refer to this structure as Grid 4 due to its degree of 4. Another fairly common structure is a larger grid structure connecting each node with the 8 nodes surrounding it on the toroidal grid [29, 36], making it a more connected version of Grid 4. We refer to this larger grid as Grid 8, it is pictured in figure 3.2. Ring 2 is a standard ring structure in which each node is only connected to 2 neighbours. Ring 4 consists of Ring 2’s connections as well as its neighbours’ neighbour to attain a degree of 4, the same as Grid 4. Ring 8 is the same as Ring 4, except is connected to 4 nodes on each side giving it a degree of 8. Rand 4 and Rand 8 are random graphs reconstructed for each GA run with an average degree of 4 and 8 respectively. These graphs are created using a simple algorithm where we add connections one at a time between two nodes, selected at random, until we’ve added degree \times \text{popsize} connections; duplicate and self connections are prevented. Our 9th and final structure, is the complete graph which is used to simulate the standard GA, as every node is in every other node’s neighbourhood.
The degree of each structure provides the minimum time genetic information can travel between individuals, while the diameter measures the minimum time genetic information can travel across the population. Each structure has a degree equal to its name and the following diameters: 9 for Grid 4, 4 for Grid 8, 50 for Ring 2, 25 for Ring 4, 13 for Ring 8, and 1 for Complete. For Rand 4 & 8 the diameter will vary based on each run and can even be infinite if the graph is disjoint.
3.4 Problem Test Suite

3.4.1 One-max

One-max, also called Max-Ones by some researchers, is one of the simplest problem a GA can solve and is one that has been used by numerous researchers in the field [26, 14]. In addition, it is a problem which is easily scaled and modified to change its structure in simple, predictable ways. The methods in which we are able to modify this simple problem will be discussed further on in this section.

In the one-max problem the GA is using a binary bit string where the fitness of an individual is equal to the number of 1s its chromosome contains. This problem is scalable to any chromosome length. For these experiments we have chosen to use a chromosome length of 60. Therefore the maximum, or optimum, fitness is 60 represented by a chromosome containing all 1s.

3.4.2 Matching

The previous one-max problems being discussed are all problems which are completely linearly separable, meaning that each bit is completely independent of any other bit. A good test suite should contain both separable and non-separable problems [52]. In order to provide a simple non-separable problem, we will directly link the fitness of our chromosome based on how genes at one location compare with genes in another. If the gene at one location matches a gene at the other location it is considered to be ‘matched’ and the individual’s fitness will be increased. This is a pure non-separable problem as the fitness of the chromosome is completely linked with the
rest of the chromosome. We will be using chromosomes of length 32 for all matching problems.

This problem is similar to the \textit{coordination game} in game theory. The coordination game is where two actors (organisms) get the maximum payoff (fitness) when they have a matching strategy (chromosome) \cite{4}, so they must attempt to ‘coordinate’ their choices. As mentioned in section 2.4.2, we are using this simple game theoretic problem to examine the GA’s behaviour. In this problem there is no single optimum, as any completely matched chromosome is considered an equivalent optimum. In fact, for the chromosomes of length 32 we are using there are $2^{32} \approx 4 \times 10^9$ possible solutions, $2^{16} \approx 6.5 \times 10^4$ of which are optimums. Using various methods for choosing matches, as discussed below, we will be able to examine the GA’s performance through different types of linear separability.

\subsection*{3.4.2.1 Pure Outer Matching}

\begin{center}
\textbf{Outer Matching}
\end{center}

\begin{figure}[h]
\centering
\includegraphics[width=0.5\textwidth]{outer_matching.png}
\caption{Here we see an example of outer matching on a chromosome of length 8. The nodes at positions 1-4 are matched with 5-8.}
\end{figure}

Pure outer matching has the fitness of the individual based purely on its matching score. The genes of the first half of the chromosome will be matched with the second
half. For our chromosome of length 32 genes 1-16 are matched with genes 17-32. An example of pure outer matching on a chromosome of length 8 is shown in figure 3.5.

### 3.4.2.2 Pure Inner Matching

For pure inner matching, the fitness of the individual is again based purely on matching, but the way the genes are matched is different. The genes in the first quarter of the chromosome are matched with the second quarter, and the genes of the 3rd quarter are matched with the 4th i.e. genes 1-8 are matched with genes 9-16 and genes 17-24 are matched with genes 25-32. An example of pure inner matching on a chromosome of length 8 is shown in figure 3.5.

![Inner Matching](image)

Figure 3.5: Here we see an example of inner matching on a chromosome of length 8. The nodes at positions 1-2 are matched with 3-4, and 5-6 are matched with 7-8.

### 3.4.3 One-max Matching

In one-max matching we are combining the standard one-max problem with the pure matching problems. An individual’s fitness score will be the sum of the two fitness functions. For both the matching problems there is a synchronized local optima with one-max’s optimum of all 1’s. This is the global optimum as it is the only
chromosome which would give the individual a maximum score on both matching and one-max. In this problem, one-max is technically worth twice that of the matching problem; a one-max fitness point is awarded for each 1 bit, while a matching fitness point is awarded for every two matched bits. For the chromosomes of length 32 we are using this means a maximum fitness of 48: 32 for one-max and 16 for matching. It is worth noting that each of the previous optima locations in the matching problem are now plateaus in the one-max matching problem, making it somewhat harder to solve. Figure 3.6 shows an example of the fitness plateau at chromosome ‘1010’ for one-max outer matching.

Figure 3.6: Plateau at ‘1010’ on one-max matching. All chromosomes with a single bit flipped from ‘1010’ are displayed; none cause the fitness to increase. Note that the maximum fitness for this problem would be 6 at ‘1111’, this can be reached with two bit flips from ‘1010’.
3.4.4 One-max Extra Matching

The extra matching problem uses the same mechanism as one-max matching problem, except we will change the weighting. Instead of using the default weightings, where matching is worth half as much as the one-max problem, we will multiply the matching value by 2 so that matching is now worth as much as the one-max problem. The standard matching problems will still have the same optimal value of all 1’s, however the search space is more interesting as it contains a large number of local optima, albeit small ones. Figure 3.7 shows an example of the local fitness optimum at chromosome ’1010’ for one-max outer matching.

![Local Max at ‘1010’ on One-Max Extra Outer Matching](image)

Figure 3.7: Optimum at ‘1010’ on one-max extra matching. All chromosomes with a single bit flipped from ‘1010’ are displayed; all cause the fitness to decrease. Note that the maximum fitness for this problem would be 8 at ‘1111’.

To show that this problem indeed contains many local optima, we use a simplified example of an 8 bit chromosome with two 4 bit matching segments at a local optimum.
We separate them by a space for easy comparison: 1001 1001 produces a one-max value of 4 and contains 4 matches producing a fitness of: $4 + 4 \times 2 = 12$. To prove that this is a local optimum, consider changing either of the 0 bits to a 1, this adds 1 to the one-max fitness, but subtracts 2 from the matching fitness due to loss of the single match (remember that matches are now doubled). If, on the other hand, you change a 1 bit to a 0 bit, the function will lose both the one-max point and the matching double point. In either case, the fitness will drop leading us to conclude that we are at a local maximum. A chromosome length of 32 will result in $2^{32}$ possible solutions, $2^{30}$ of which are local maxima, with the global maximum being one of them.

### 3.4.5 Royal Road

The royal road problem, developed by Mitchell et al. [27], is discussed in section 2.6. It was designed to be a simple problem which the GA should be well suited to solving. While its goal was not really achieved, with the standard GA not performing as well as they theorized, they were able to formulate an interesting, yet simple, test problem. We decided we could use this problem as part of our test suite and attempt to find out if the performance would change after adding spatial and coevolutionary components.

There are a few variations of the Royal Road problem discussed in [27] and [28], but we have chosen just to test with what we consider the simplest version. In our implementation, we will use a chromosome length of 32, creating 4 ‘blocks’ of 8 genes and reward a fitness score of 8 for each block a chromosome has correct. This problem is fundamentally the same problem as one-max, as we attempt to find the chromosome
of all 1’s. However, its fitness landscape is significantly different, there are 15 massive plateaus below the global optimum as there are only 5 levels of fitness\(^1\).

### 3.4.5.1 One-max Royal Road

Similar to what we did with the matching problem in section 3.4.3, we will create a variation on the Royal Road problem by combining it with the one-max problem. As before, the fitness score will be a combination of the two on a 32 bit chromosome creating a maximum fitness of 64 for the all 1’s chromosome. This problem does not have the plateaus of the previous problem, but it is also not as smooth as the one max problem. The fitness landscape is fairly smooth with sudden jumps in fitness as the chromosomes connect building blocks.

### 3.4.6 Cooperative Problems (Mutalism)

The problems discussed above have all been based on the standard single population GA. Each of these problem can be easily be modified to be solved using a two population cooperative coevolutionary GA. We will simply separate the chromosome at its midpoint and have two populations with chromosomes of equal size. There will be a one-to-one evaluation used, shown in Figure 2.1, so the fitness of the individual in each population will be the same as its partner in the other population. The standard one-max problem will have a chromosome length of 60 on the standard GA, and will therefore use a chromosome size of 30 for each of the two populations, the

\(^1\)There are 5 fitness levels, as we count the number of blocks: 0 to 4. There is one plateau at 0 blocks, four different plateaus at 1 block, six at 2 blocks and four at 3 blocks. There is only one solution at 4 blocks, the global optimum.
other problems with a chromosome length of 32 on the standard GA will have two populations using a chromosome length of 16.

This concept is partially on display in figures 3.4 & 3.5. The chromosomes are split at their midpoint and we can see matching taking place between the populations in the outer matching problem, and within populations in the inner matching problem. The consequences of this will be considered in section 3.5.5.

3.4.6.1 Spatially Evaluated One-max

This is a spin on the coevolutionary one-max problem, where instead of connecting two chromosomes in each population, we evaluate each individual by a spatially determined set of individuals from the other population. As seen in other spatially evaluated systems, we setup the system to use the average fitness from among its partners [29].

This was a problem we wanted to include for completeness, but we don’t believe it is actually that interesting and will not be providing in-depth results. This problem is not that interesting because it will take significantly longer to find a solution than our one-to-one one-max problem, because it would not be declared ‘solved’ until all of its spatially determined partners were correct rather than just one partner. Preliminary results agreed with this assertion, so we chose not to pursue it further. However, it would be interesting to look into the extent of these effects and if adding further mechanisms could improve the performance. For instance, we could see a significant increase in performance if we used the maximum from each comparison set instead of the mean, this mechanism is similar to the one used by Potter & De Jong where
comparisons are only with best chromosomes from each population [39].

3.4.7 Competitive (Host/Parasite)

The problems described here are unique from the rest; we cannot directly port a problem from the standard GA space to work as a competitive problem. These problems are meant to be used to help confirm the work of Pagie & Hogeweg, and Mitchell et al. [29, 36]. Their work used the competitive GP style problem as described in section 2.4. We wish to emulate the somewhat complex GP problem using a simple GA problem in order to see how the spatial framework effects its behaviour. We offer 3 superficially similar, but fundamentally different host/parasite problems attempting to emulate that behaviour.

Each of the three presented problems use the same general structure as the GP problem; there is a population of hosts and another population of parasites. The host is attempting to solve the problem, in this case one-max, while the parasite is attempting to find weakness in the host and gain fitness for any weakness found. The differences between them are in the details of how each fitness function is defined.

3.4.7.1 One-to-One Host/Parasite

This is the most basic version of the three problems. We are simply comparing each host with the parasite at the same location in the other population. The host will receive a fitness equal to the number of 1’s it contains plus the number of 0’s where the parasite has a 0 in the same location. In effect, it will only lose fitness where the parasite ‘attacks’ it by having a 1 where it has a 0. The parasite has fitness
equal to the number of 1’s it contains where the host has a 0, or in more general terms every spot it successfully ‘attacks’. This implies that while the parasite population is not attempting to solve the one-max problem, it will still generally achieve greater fitness scores by being closer to the chromosome of all 1’s. Both the host and parasite will have a chromosome length of 30.

It is important to consider that just because a host has reached a perfect fitness of 30 does not mean it has solved the one-max problem; the GA will only terminate when a host has successively found the all 1’s chromosome. This effect, where hosts have reached the maximum fitness but have not found the solution, is disengagement. The parasites must improve in order to distinguish between hosts and prevent a loss of gradient, as discussed in section 2.2.2.2.

### 3.4.7.2 Spatially Evaluated Host/Parasite

Spatially evaluating the host by a set of parasites is the same problem as the one-to-one host/parasite described above, except the results will be averaged over an evaluative network. The average fitness for all individuals compared against will be the fitness awarded to the individual. We will be using 3 separate evaluative networks to compare their performance: Grid 4, Grid 8 and Complete. In the complete case this just means that the individuals are being compared against the entire population; each individual's fitness is just an average of that comparison.

This problem is similar to the cooperative spatially evaluated one-max, but unlike that problem, a competitive system does not have to ‘wait’ for the nodes it is connecting to find the optimum solution. It should be clear that spatial evaluation on
cooperative and competitive system have fairly different properties and behaviour.

3.4.7.3 Purely Competitive Host/Parasite

In this problem the fitness of the host no longer has a direct link to the problem being solved. The host is still simply trying to solve the one-max problem, however its fitness is based purely on the parasites it is compared against. Each host will be connected to a number of parasites corresponding to its evaluative network, we will use the Grid 8 for all of these problems since we are trying to recreate a simplified version of Mitchell et al.’s work [29]. This problem will again be tested on a reproductive network of Grid 4, Grid 8 and Complete.

The parasite will be made up of a chromosome of length 16. It will have 4 numbers encoded in 4 bit binary referencing a specific position in the genetic sequence of the host. The fitness of the parasite will be equal to the sum of genetic locations in all hosts it is compared against that contain a 0. We are simulating the parasite finding a location to ‘attack’ and being successful whenever the host does not have a 1 there. Therefore, the fitness of the host will be coming directly from the parasites, it cannot gain fitness independent of the parasites as in the above problems.

3.5 Experiments

3.5.1 Spatial Effects on Standard and Coevolutionary GAs

The first experiment we will perform is confirming previous working claiming the performance improvement provided by spatial reproduction on coevolutionary
systems. We will also consider the same problems on the standard and spatial standard GAs in order to compare these general results to our coevolutionary GA and isolate the spatial and coevolutionary mechanisms. We will test the performance on each of the available problems in our simple test suite, our coevolutionary problems will all be cooperative for this section. This includes: One-max, One-max Outer Matching, One-max Inner Matching, One-max Extra Outer Matching, One-max Extra Inner Matching, Royal Road and One-max Royal Road. Based on the hypothesis of Wiegand & Sarma [54] in which they believe that spatial structures help the coevolutionary system based on slowing down the flow of genetic information, we believe that they should in fact hurt a problem such as One-max due to its simple structure. It is unnecessary to slow genetic flow while solving One-max, as any positive information can only serve to help the chromosome. The same should also be true for our standard matching problems and Royal Road, though these problems are somewhat more complicated and their plateaus could cause some interaction effects that have no been considered. Nevertheless, the simplicity of One-max is the most important for confirming this hypothesis. We also include the One-max Extra Matching problems, as these problems contain local optima which could lead to them being positively influenced by the cooperative spatial structure and seeing an increase in performance for the spatial coevolutionary GA on this problem could help confirm Wiegand & Sarma’s hypothesis.

We will be looking at both spatial and non-spatial, standard and coevolutionary GAs, the spatial GA will be run with Grid 4 while the non-spatial will simply use the Complete network. The one-max problem will also be run on the Grid 8 structure for
both the standard and coevolutionary GAs to provide additional detail. An elite value of 2 will be used for all problems. Many of the experiments presented in this section have also been submitted as part of the paper submitted to the PPSN conference [25] and is currently under review.

3.5.2 Spatial Effects on Competitive Coevolutionary GAs

This experiment is an extension of section 3.5.1, we will consider spatial structures on the competitive coevolutionary GA. We will attempt to confirm the work of Mitchell et al. [29], they claimed that spatial structures helped their competitive coevolutionary GA. They hypothesized that the spatial network helped their problem as it allowed their ‘host solvers’ to focus on individuals parts of the problem and eventually combine those parts to solve the problem. We will be using the problems described in section 3.4.7, each being a separate attempt at simulating a GP style problem with a simpler competitive one-max solver. Each of these problems will be run on the coevolutionary GA with Grid 4, Grid 8 and Complete (non-spatial) reproductive networks using an elite size of two.

The first problem we are using, one-to-one host/parasite, is the simplest, and if spatial reproduction helps this problem we will know that Mitchell et al.’s focussing hypothesis is correct, as it forces the hosts to focus on specific parts of the problem. The second problem, spatially evaluated host/parasite, includes a spatially evaluated framework which is closer to Mitchell et al.’s model as spatial evaluation is used there. If this second problem shows an improvement while the first does not, we will know that the spatial evaluation is important to competitive coevolution. The final problem
is a purely competitive problem, where its fitness is based purely on its performance against the parasites, rather than a more complex fitness function as seen in the other two problems. If this problem is successful with spatial reproduction while the others are not, we will know that pure competition is important to the success of the competitive GA, allowing success to be purely driven by the parasites.

### 3.5.3 Spatial Evaluative Effects

We will also be viewing the impact of spatial evaluative networks on our coevolutionary GAs, as opposed to the spatial reproductive networks investigated in the previous experiments. This is an area which is only of interest within a spatial coevolutionary GA as it does not exist in any other GA type, therefore, it has not been discussed in much depth. Wiegand & Sarma [54] briefly mention that they believe it is an important concept in the coevolutionary GA, but do not get into much detail. We will present a few general results on this topic in this section, and confirm its importance on the coevolutionary GA.

We will use problems from the previous section, the one-to-one and spatially evaluated host/parasite problems. They are each evaluated on different spatial evaluative networks and their performance will be compared to consider the impact of these spatial evaluative networks. We will also consider a cooperative coevolutionary one-max problem being spatially evaluated on a Grid 8 structure and compare its performance to the one-to-one cooperative one-max problem.
3.5.4 The Effect of Distinct Spatial Structures

We have tested whether spatial structures have any effect on the GA’s performance in sections 3.5.1 & 3.5.2. Here we will test different attributes of the spatial structures to see what attributes affect the performance. While work has been done testing different spatial structures on the standard GA, where Bryden et al. [3] found that the complete spatial structure provided the best performance for one-max, little has been done on the coevolutionary GA. We attempt to confirm the result of Bryden et al. and begin exploring different spatial structures on the coevolutionary GA. Experiments will be run using all 9 of the graphs discussed in section 3.3. These experiments will be run solving the one-max problem on the standard, cooperative coevolutionary, and the one-to-one competitive coevolutionary GA. All of the problems will again use two elites. This work has been submitted to the ALife conference and is currently under review [24].

3.5.5 Linear Separability Across Coevolutionary Populations

We hypothesize that the coevolutionary GA is negatively effected by linear separability over populations. In order to test the impact of linear separability over the coevolutionary populations we use the simplest problems available: pure inner and outer matching. Outer matching matches across our coevolutionary population, while inner matching will simply match within each population. Based on our hypothesis, we predict that inner matching should have better performance on the coevolutionary systems than outer matching, and outer matching should be much worse on the
coevolutionary problem than on the standard GA.

As we want this to be treated as a standard optimization problem we will maintain the same parameters as we have used for the other experiments. Therefore we will use a chromosome length of 16 for each population and an elite size of 2.

We will also consider the one-max extra outer and inner matching problems shown in section 3.5.1. These problems contain a more realistic optimization problem, with the same linear separability split as the pure matching problems mentioned above. If the same performance difference is observed in these problems our hypothesis will be strengthened further.

3.5.6 Exploring the Effects of Elitism

For the problems tested so far we have used an elite size of 2; in this section we will observe the impact of changing the elite size. Elitism on coevolutionary systems has so far been an ignored topic, and our preliminary results have shown a massive effects in performance, so we present a formal study on its effects. These effects will be examined by comparing elitism’s impact on the standard, spatial standard, coevolutionary and spatial coevolutionary GA’s. We will use elitism levels of 0, 1, 2, 5, 10, 50 and 100. The problems tested will included: one-max, extra inner matching and one-to-one one-max host/parasite\(^2\). One-max is used as our simplest available problem, extra inner matching as a coevolutionary problem with local optima, and the one-to-one host/parasite problem as our simplest competitive problem. The spatial

\(^2\)One-to-one host/parasite will only be run on the coevolutionary GA’s as it does not have a direct mapping to the standard GA in order to make a fair comparison.
structure being used for these problems will be the Grid 4 structure, though the
straight one-max and one-max host/parasite experiments will also contain the Grid
8 structure. These experiments have been submitted to the ALife conference and is
currently under review [23].

For this section we anticipate that the results will show that, while elitism im-
proves the performance of all GA types, it will have an increased impact on the
standard and coevolutionary spatial GAs. We believe this because of Mitchell et
al.’s hypotheses that spatial coevolutionary GA’s improved performance comes from
slowing down genetic flow [29], elitism on the spatial coevolutionary GAs will allow
genetic flow to be slowed further in the best genetic regions. It will also allow genetic
information to flow more quickly into worse regions due to the absence of elites. In
the non-spatial GA, as genetic information can come from anywhere, while we expect
the elites to provide a positive performance boost, we expect that boost to be weaker
than on the spatial GAs.

3.5.6.1 Globally Selected Local Versus Strict Global

In the previous section we have studied the impact of our ‘new’ elitism method,
globally selected local elitism, on our various GA systems. We will compare our
elitism method with the classic strict global elitism, where elites are pushed directly
through to the next population without having to partake in a tournament with its
children, as discussed in section 2.1.1. Strict global elitism is the elitism style used
on the standard GA, so we wish to compare its effects on both the standard GA
as a control and the coevolutionary GA to view the importance (or lack thereof) of
globally selected local elitism. Our hypothesis is that globally selected local elitism will be of most importance to the spatial GAs as the strict elitism prevents evolution at the very spot in the spatial GA that provides the most promise. The non-spatial GAs, however, have no concept of space, and should therefore, not be worried about which specific node is occupied by the elite.

To run this experiment we will be using the one-max problem on all 4 GA types, using elite levels of 1, 2, 5 and 10. We do not use an elite level of 0 as that is just the absence of elitism. We also do not use an elite level of 100 as this would not allow for any change within the system for strict global elitism, all of the organisms would just be pushed through to the next population without undergoing any reproduction.

3.5.6.2 Fitness Heat Maps

We will use heat maps to view the effects of elitism on the spatial standard and spatial coevolutionary GAs by tracking fitness levels through a typical run\(^3\). This will allow us to view the movement and behaviour of the elites while examining their impact on the organisms’ fitnesses within the GA from generation to generation. We believe this experiment is useful and important as we have noticed an extreme improvement from 1 to 2 elites in the previous experiments and wish to see why they are interacting in this manner. For higher levels of elitism we expect highly fit regions to emerge around our elites; encouraging the elites to gather together. We have this expectation as the improvement we are seeing should only occur if the elites

\(^3\)We do not bother running this on the non-spatial GA’s as the location of any of the nodes would be completely random.
are directly interacting in some manner.

These heat maps will be created using the one-max problem, on a the Grid 4 reproductive structure, displaying elite levels of 0, 2, 5, 10 and 100. We believe that only testing a single problem is necessary as the performance gains from elitism are fairly consistent across all problems, so we simply use one-max. We will display a single sample run for each GA type at each elite level. Five graphs will be displayed for each run, with the first showing the 10th generation and the last showing the final generation. The generations the other three graphs display will be variable on the length of the GA, as each run will have a different number of generations. The three ‘middle’ graphs will be approximately evenly spaced through the GA’s generations, showing roughly the 0.25, 0.50 and 0.75 percentile generations.
3.6 Experimental Factors Summary

There are a large number of factors and levels within each factor, so in this section we include a summary of the factors, levels and which ones were experimented with. Table 3.1 is a summary of the various experimental factors used and Table 3.2 is the set of problems used to test the various experimental factors. In Table 3.3 we display a list of all of the experiments run in this thesis.

<table>
<thead>
<tr>
<th>GA Types</th>
<th>Spatial Types</th>
<th>Elitism Type</th>
<th>Elitism</th>
</tr>
</thead>
<tbody>
<tr>
<td>Standard</td>
<td>Ring 2</td>
<td>Globally Selected Local Elitism</td>
<td>0 (None)</td>
</tr>
<tr>
<td>Spatial</td>
<td>Ring 4</td>
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</tr>
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<td>2</td>
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<tr>
<td>Spatial Coevo</td>
<td>Grid 4</td>
<td></td>
<td>5</td>
</tr>
<tr>
<td></td>
<td>Grid 8</td>
<td></td>
<td>10</td>
</tr>
<tr>
<td></td>
<td>Rand 4</td>
<td></td>
<td>50</td>
</tr>
<tr>
<td></td>
<td>Rand 8</td>
<td></td>
<td>100 (Full)</td>
</tr>
<tr>
<td></td>
<td>Complete</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cooperative</td>
<td>Competitive</td>
<td></td>
<td></td>
</tr>
<tr>
<td>---------------------------------</td>
<td>---------------------------------</td>
<td></td>
<td></td>
</tr>
<tr>
<td>One-max</td>
<td>One-to-One</td>
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<tr>
<td>Inner Matching</td>
<td>Spatially Evaluated</td>
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<td>Outer Matching</td>
<td>Purely Competitive</td>
<td></td>
<td></td>
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<tr>
<td>One-max Inner Matching</td>
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<tr>
<td>One-max Outer Matching</td>
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<td></td>
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</tr>
<tr>
<td>One-max Extra Inner Matching</td>
<td></td>
<td></td>
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</tr>
<tr>
<td>One-max Extra Outer Matching</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Royal Road</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>One-max Royal Road</td>
<td></td>
<td></td>
<td></td>
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Table 3.3: List of Experiments Run

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<thead>
<tr>
<th>Problem</th>
<th>GA Types</th>
<th>Spatial Type</th>
<th>Elite Amount</th>
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<tbody>
<tr>
<td>One-max</td>
<td>All</td>
<td>All</td>
<td>2</td>
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<tr>
<td>One-max</td>
<td>All</td>
<td>Grid 4, Grid 8 &amp; Complete</td>
<td>All</td>
</tr>
<tr>
<td>One-max Extra Inner Matching</td>
<td>All</td>
<td>Grid 4, Grid 8 &amp; Complete</td>
<td>All</td>
</tr>
<tr>
<td>One-max Outer Matching</td>
<td>All</td>
<td>Grid 4 &amp; Complete</td>
<td>2</td>
</tr>
<tr>
<td>One-max Inner Matching</td>
<td>All</td>
<td>Grid 4 &amp; Complete</td>
<td>2</td>
</tr>
<tr>
<td>One-max Extra Outer Matching</td>
<td>All</td>
<td>Grid 4 &amp; Complete</td>
<td>2</td>
</tr>
<tr>
<td>One-max Extra Inner Matching</td>
<td>All</td>
<td>Grid 4 &amp; Complete</td>
<td>2</td>
</tr>
<tr>
<td>Royal Road</td>
<td>All</td>
<td>Grid 4 &amp; Complete</td>
<td>2</td>
</tr>
<tr>
<td>One-max Royal Road</td>
<td>All</td>
<td>Grid 4 &amp; Complete</td>
<td>2</td>
</tr>
<tr>
<td>Pure Outer Matching</td>
<td>All</td>
<td>Grid 4 &amp; Complete</td>
<td>2</td>
</tr>
<tr>
<td>Pure Inner Matching</td>
<td>All</td>
<td>Grid 4 &amp; Complete</td>
<td>2</td>
</tr>
<tr>
<td>One-to-One Host/Parasite</td>
<td>Coevolution</td>
<td>Grid 4 &amp; Complete</td>
<td>2</td>
</tr>
<tr>
<td>One-to-One Host/Parasite</td>
<td>Coevolution</td>
<td>Grid 4, Grid 8 &amp; Complete</td>
<td>All</td>
</tr>
<tr>
<td>Spatially Evaluated Host/Parasite</td>
<td>Coevolution</td>
<td>Grid 4, Grid 8 &amp; Complete</td>
<td>2</td>
</tr>
<tr>
<td>Purely Competitive Host/Parasite</td>
<td>Coevolution</td>
<td>Grid 4, Grid 8 &amp; Complete</td>
<td>2</td>
</tr>
<tr>
<td>One-Max with Strict Global Elitism</td>
<td>All</td>
<td>Grid 4 &amp; Complete</td>
<td>All</td>
</tr>
</tbody>
</table>
Chapter 4

Results and Analysis

This results section will contain a full discussion of the results found in our experiments, as well as a few choice graphs displaying some of the results found. The full set of results and p-values can be found in appendix A.

4.1 Spatial Effects on Standard and Coevolutionary GAs

![Image](One-Max.png)

Figure 4.1: One-max

The goal of this set of results was to determine if previous research finding increased performance from adding a spatial network to a coevolutionary GA would
extend to the problem in our simple test suite. We start by viewing the performance of a variety of problems looking at both the spatial (Grid 4) and non-spatial (complete) coevolutionary GA. We will also continue to look at the same problems on the spatial and non-spatial standard GA to view their comparative performances. The first, and perhaps most powerful result, is the one-max problem. This problem very clearly shows a massive difference in performance between the non-spatial and spatial coevolutionary GAs on the one-max problem, the spatial coevolutionary GA provides an extreme increase in performance, so much so that statistical tests are not even necessary to see this (though the full set of \( p \)-values are provided in appendix A.1). In fact, the spatial coevolutionary GA has performance which is statistically indistinguishable from the standard GA, and despite the spatial network’s massive effect on the coevolutionary GA it has almost no effect whatsoever on the standard GA. This result on its own brings Wiegand & Sarma’s hypotheses into question [54].

![One-Max Outer Matching](image1)

![One-Max Inner Matching](image2)

Figure 4.2: One-max Outer Matching  
Figure 4.3: One-max Inner Matching

The four matching problems, shown in figures 4.3-4.5, again all show that the
non-spatial coevolutionary GA has the worst performance. We also see a significant
decrease in performance between the matching and extra matching problems on all
GA types, this makes sense when you consider the extra noise from the increased
matching. As we will discuss in section 4.5, we also see that the outer matching
problems are significantly worse on the coevolutionary GAs than the inner matching
problems. On both inner matching problems we actually see that the coevolution-
ary spatial GA is the best GA type. Not only is the spatial component improving
coevolutionary performance, but it is improving it so much so that it allows the
coevolutionary GA to out preform standard GA.

Finally we have the Royal Road and One-max Royal Road functions, figures 4.6 & 4.7. In both cases we again see the coevolutionary spatial GA has the best per-
formance. The most impressive result is the incredible improvement found on the
standard Royal Road function for both coevolutionary GAs. This problem was used
by Mitchell et al. [27] to attempt to prove the building block hypothesis, and while
that experiment was generally considered to be a failure, its possible that research should be reopened using a coevolutionary GA. We hypothesize that the coevolutionary GA may be more adept at combining good building blocks, assuming they are linearly separable across the populations, which in this case they are.

We have very clearly shown here that the improvements provided by spatial networks on coevolutionary GAs have not been exaggerated, however the hypothesis for why we are seeing this improvements appear to be lacking. The hypothesis that slowing genetic flow is a positive effect, is reasonable for problems with complex landscapes, but we have now shown its extreme improvement on much simpler problems. We have also shown that for many problems the spatial coevolutionary GAs outperforms the standard GA. Therefore, the spatial component is not only improving coevolutionary performance, but it is improving it so much so that it is outperforming the standard GA, even while the non-spatial coevolutionary GA is significantly worse than the standard GA. This effect is extremely powerful and should not be ig-
nored, most importantly we should keep in mind that just because the standard GA severely out-competes a coevolutionary GA on a specific problem, it does not mean that the standard GA will continue to out-compete the coevolutionary GA once a spatial component has been added.

4.2 Spatial Effects on Competitive Coevolutionary GAs

Figure 4.8: Spatial reproductive structures on coevolutionary GA with one-to-one host/parasite

The results seen in this section are significantly different than what we’ve seen so far in our cooperative coevolutionary problems. In the previous sections we found that spatial structures almost unanimously improved the GA’s performance, or provided inconclusive results as to its effect. In this section we find that all of our competitive problems are hampered by the introduction of a spatial reproductive framework,
and they have the best performance using complete reproduction. We have experimented with a variety of spatial evaluative techniques to explore whether changing this mechanism would affect the effectiveness of spatial reproduction.

![Competitive One-Max Spatially Evaluated Host/Parasite](image)

Figure 4.9: Spatial reproductive structures on coevolutionary with spatially evaluated host/parasite

The goal of this set of experiments was confirming the work of Mitchell et al.’s [29] hypothesis that combination of the spatial reproductive and evaluative networks improved performance as it allowed the host to focus on specific part of a problems. We were using much simpler problems than Mitchell et al.’s GP style modelling problem, but we believe that our problem should still contains all of the features necessary for their hypothesis to hold. In particular, we attempted to model our ‘purely competitive’ problem to match as closely as possible to Mitchell et al.’s using a simple structure, however even this problem was unable to confirm their work.
These experiments were unable to confirm Mitchell et al.’s hypothesis, and in fact provided fairly significant evidence that it may be incorrect. It is possible that the effect they were seeing was based on the more complex nature of the GP style problem they were studying than we were able to emulate with our simple test suite problems. However, if that is the case, then their focusing hypothesis will need to be updated. We provide a possible explanation for what they were seeing in the next section. In any case, it is interesting to note the cooperative GA’s consistent benefit from spatial structures compared to how they hamper the competitive GA’s.

Figure 4.10: Spatial reproductive structures on coevolutionary with purely competitive host/parasite
4.3 Spatial Evaluative Effects

Here we consider the impact of separating the spatial evaluative and reproductive networks. In the previous section we can see an extreme improvement in performance when we are using the spatially evaluated host/parasite in figure 4.9, compared with the one-to-one comparison seen in figure 4.8. The one-to-one host/parasite problem has significantly lower performance than the spatially evaluated problem. Even when we compare the one-to-one evaluation on a complete reproductive network, where it has the best results, and the spatially evaluated problem one a 4 Grid reproductive network, where it has its worst results, we obtain a $p$-value of $1.609e-07$, confirming, with very strong statistical significance, that the spatially evaluated host/parasite mechanism provides better performance. Therefore, spatial evaluation is improving the performance of the GA more than the spatial reproduction is hurting it. As Mitchell et al. was combining these effects, it is possible that their improvements came more from the spatial evaluation than reproduction, and they may have seen an even greater improvement in performance had they removed the spatial reproduction and stuck strictly with spatial evaluation.

We hypothesize that our 1-to-1 host/parasite problem is having poor performance compared with the spatially evaluated problem as it is running into a Red-Queen type effect. The Red-Queen effect is generally based generation to generation where the GA is unable to determine if its organisms’ performance is improving in each generation due to the current generation being unable to be adequately compared with previous generations. The generations are incomparable due to relative fitness measures, if
both of the hosts and parasites improve equally then there will be no increase in performance. In this case, we are looking within a single generation as we believe that our hosts cannot adequately be compared with each other, which is important for reproductive selection. We believe this is due to each host being evaluated by separate parasites of varying quality. In a classic non-spatial coevolutionary GA, organisms in the host population are generally evaluated by the same set of chromosomes, so this has not been an issue for past researchers. If a single, fairly average, host is being compared with a disengaged, poorly fit parasite, it may have a very high fitness score. Meanwhile, a strong host compared against a strong parasite will have a lower fitness score and the average host will be given higher reproductive priority without actually having better genetics. We see a reduction to this effect in the spatial evaluated host/parasite problem, the host’s fitness is being averaged over multiple parasites, making its fitness less dependant on a single parasite. This gives the GA more information to distinguish between hosts, thereby reducing the Red-Queen effect.

We also tested the spatially evaluated cooperative one-max presented in section 3.4.6.1, but we found that its performance was so greatly hampered that it was never able to find a solution in 5000 generations in the 50 repetitions we tested. This complete failure makes it clearly worse than the non-spatially evaluated cooperative one-to-one one-max, it has a success rate of 0% compared to the one-to-one system’s 100% success rate. We believe that spatially evaluated cooperative coevolution could work significantly better if alternative evaluation methods were used, in particular using the max result instead of the mean. This is similar to the work done by Potter
& De Jong [39] in which they reported success with their method, and therefore, should be looked into in more detail in future work. The results of this section and the previous one have shown that competitive coevolution appears to benefit more from spatial evaluation than reproduction, while cooperative coevolution benefits more from spatial reproduction than evaluation. Clearly these two coevolutionary types need to be considered as completely separate mechanisms due to their significantly different behaviours.

4.4 Distinct Spatial Structures

The results of this experiment is shown in figures 4.11-4.13, p-values are given in appendix A.3. We can easily see the extreme difference in performance on the cooperative coevolutionary GA based on the number of connections, figure 4.12. In fact, the non-spatial coevolutionary GA has the worst performance and is the only system to report any failures to find a solution in under 5000 generations. The standard GA shows a very different story, figure 4.12, we see almost no change in performance on the various spatial structures. The competitive coevolutionary host/parasite GA again shows different results, figure 4.13. As we’ve noted in the previous section, we see exactly the opposite behaviour as we saw in the cooperative coevolutionary GA, the best results come from the complete structure with the worst from the graphs with the least connections.

On the coevolutionary GA we have found that the spatial structures are important, in particular, it is the degree of these structures that appears to be the main
Figure 4.11: Spatial structures on the coevolutionary GA

driver of performance, not the structure itself. Using a Kruskal-Wallis test among each degree level cannot identify any difference between the ring, random and grid network structures. The competitive coevolutionary system has obvious effects based on the structure’s differences in degree as well, but again, minimal effects based on structure. The Ring 4 appears to be significantly different from the other structures with a degree of 4, which does provide some evidence that the structure may have some role, but the structures of degree 8 are again indistinguishable. On the standard GA using a Kruskal-Wallis test, we cannot find any difference between the
spatial structures based on degree. We must resort to testing all spatial structures at once before we can even say for sure if the spatial structures are having any effect on performance at all. This test returned a $p$-value of 0.007812, therefore, the structures are having some effect, but it is so weak that we are unable to even say for sure which structure is best.

With the results varying so dramatically between the cooperative and competitive coevolutionary GAs it is unclear which spatial structure is best. What is clear is that while the spatial structures have nearly a non-existent role on the performance of
the standard GA, they have a huge role on coevolutionary systems. We can say with certainty that the complete graph is best for the competitive coevolutionary GA and that the Ring 2 is best for our cooperative GA, but this difference in the results does not allow us to make much of a general conclusion. The cooperative coevolutionary GA is best with graphs of lower connectivity and worst with the complete graph. The competitive coevolutionary is best with higher connectivity and worst on the tightly connected structures. In both cases the structures with intermediate connectivity perform at a level in between that of the tighter structures and the complete

Figure 4.13: Spatial structures on 1-to-1 Host/Parasite
graph. This suggests that there is a smooth transition in performance from spatial to non-spatial correlating to how connected/unconnected reproduction is.

4.5 Linear Separability

![Pure Outer Matching](image1)

![Pure Inner Matching](image2)

Our linear separability experiments have returned results roughly equivalent to what we predicted. The performance on all GA types for inner matching, shown in figure 4.15 are all statistically the same, $p$-values are shown in A.4. However, once we’ve added a cross population component to the matching in outer matching, the coevolutionary GAs get much worse, as shown in figure 4.14. Both coevolutionary GAs are significantly worse than both standard GAs. The standard spatial and non-spatial GA’s have a no statistical difference in performance between them, while the spatial coevolutionary GA is significantly better than its non-spatial counterpart. This is quite interesting when we consider that the inner matching problem had
roughly the same performance on both the coevolutionary systems. If we consider both the one-max outer matching and extra matching problems, seen in figures 4.2-4.5, we can see the same change in performance as we do in this pure matching problem. We can confidently say that coevolutionary spatial reproduction cause a significant increase in performance for problems that are not linear separable across populations. The extreme decrease in performance between in Outer Matching and Extra Outer Matching problems also show us that as we increase the weight of the non-separable components of our problem the performance suffers immensely.

We see that when a chromosome is non-separable, yet split between 2 populations, its performance is much worse than when it is contained in a single non-spatial coevolutionary GA. This makes sense when we consider that the multi-population GAs will have their chromosomes crossing over and mutating separately from each other, meaning they will be getting paired against whatever partner happens to end up at that location next. On the standard GA, the genes each individual gene is matched against is kept contained in the same chromosome. One way to think of this is that matching is attempting to synchronize with a partner to get the same combination, regardless of what that combination is. On the standard GA you are attempting to coordinate with same partner every generation, but on the coevolutionary GA you get a new partner every round. At least when we have spatial coevolution, there is the reproductive network keeping similar genetic material in the same place to helping keep similar partners together. The non-spatial coevolutionary GA, however, is really just waiting to ‘get lucky’ by linking up two coordinating by chromosomes by chance.

It is important to note that this matching isn’t completely ‘luck’, even on the
coevolutionary GA, it is still significantly more efficient than a random walk through various chromosomes. A random walk would imply that for our chromosome of length 16 we have $2^{16}$ possible combinations making the probability of finding a match at random: $1/2^{16} \approx 0.0000153$. Since we make 100 comparisons per population the probability of finding a match in any one generation increases to 0.00153, 0.153% or 1 in every $\approx 653.6$ populations. However over 50 trials our median value for matching is 210 making the coevolutionary GA over 3x better than the random walk. There is clearly something going on here other than pure randomness. It is possible that the overall GA starts converging to certain values making all of the chromosomes converge to the same match, otherwise it could just be based on the 2 elites we have in our population. If the performance gain rests purely on the elites we would be seeing a performance increase of over 300% just from the 2 elites, this type of performance increase again holds to what we saw in section 4.6, though we would need to rerun this matching problem with no elites to know for sure.

### 4.6 Elitism

Viewing the impact of elitism on each of these three problems, on both the standard and coevolutionary GA, makes it very clear that the greater the number of elites, the better the performance. The full set of graphs and their associated $p$-values can be found in appendix A.5-A.7. We see an extreme trend for all problems where performance increases exponentially from having no elites all the way up to full (100) elitism. The impact of increasing elitism appears fairly uniform on all problems.
tested. This effect, which may be obvious on the one-max problem, was not so clear for the extra matching problem, with its numerous, albeit small, local optima.

Another interesting behaviour to note is the more dramatic increase in performance on the coevolutionary problems with increased elitism, as seen in figures 4.16 & 4.17. We see in both of the cooperative and competitive problems that the coevolutionary GA is much worse at 0 elites, with a near 0% success rate completing problems within the 5000 generation. However, by the time we have reached 10 elites, the spatial coevolutionary method has the best performance on both problems; one-max at 10 elite is shown in figure 4.18. We predicted that our intermediate elitism would result in an increase in performance on the spatial GAs, but this is not the case. For the standard GA, elitism increases its performance on both the spatial and non-spatial GAs, however it does so fairly uniformly and does not offer any extra improvement to the spatial GA. On both one-max and one-max inner matching, we see that the spatial coevolutionary GA is significantly better than the non-spatial co-
evolutionary GA at lower elitism levels, but by the time we have reached full elitism the coevolutionary GA with complete reproduction is best for both problems, shown in figure 4.19. On the host/parasite problem, the complete spatial structure is simply best at all levels of elitism, each spatial structure type has a consistent improvement in performance with increased elitism.

Figure 4.18: One-max with 10 Elite  Figure 4.19: One-max with Full Elite

Another point to note is that the larger Grid 8 structure has a performance between that of the Grid 4 and the complete graph for all problems. This makes it clear that performance is either strictly increasing or decreasing based on the connectivity of the structure. Graphs containing a more direct comparison of each elite type, using the same data can be seen in appendix A.5-A.7. We will also discuss this more in section 4.4.

We had anticipated that the results would show an increase in performance on the two spatial GAs compared to the non-spatial ones as elitism increased. Instead, we find that there is no change on the standard GA, and the non-spatial cooperative
coevolutionary GA shows a greater improvement as elitism is increased. We also see the competitive coevolutionary GA’s results show a consistent increase in performance on all spatial types. It is clear that elitism has a significant effect on the GA’s performance and that its effects vary based on the problem type being studied. It is also clear, at least for these simple problems, that higher levels of elitism improve performance.

4.6.1 Globally Selected Local Versus Strict Global

Looking at the effect of our globally selected local elitism versus the classic hard elitism displays some interesting results. The globally selected local elitism is used on all of the other problems throughout this thesis, one-max in particular is shown in figures 4.16 & 4.17 (as well as in appendix A.5), classic elitism is shown in figures 4.20-4.23 with p-values reported in appendix A.8.

As we predicted, classic elitism is still able to strongly influence GA performance on all GA types. We see a steady trend of performance improvements on all GA types up to 50 elites, however we do note a diminishing returns effect as the performance increases begins to trail off at higher levels. As mentioned previously, when strict global elitism reaches full elite the GA will completely stop functioning as organisms can no longer evolve. We also predicted that globally selected local elitism would be important for the spatially connected problems, however these results show that this change in elitism mechanism has a much more significant impact for the coevolutionary systems than the spatial ones. For the standard GA, as we predicted, we see no statistical difference between the elite mechanisms until we have a large number
of elites (more than 10), while on the standard spatial GA we can see these results sooner, with a $p$-value of 0.000141 at 5 elites. This result shows that our prediction was correct in that it globally selected local elitism helps our spatial structure, however the coevolutionary problems are affected significantly more showing a statistical difference at every elite level on both the spatial and non-spatial GAs\textsuperscript{1}.

Figure 4.20: Strict global elitism on non-spatial standard GA  
Figure 4.21: Strict global elitism on 4 Graph standard GA

We hypothesize that the local elitism’s increased importance to the coevolutionary GAs is based on a type of ‘synergy’ between the the two connected organisms in each population. The elites in the two populations will end up in the same location as connected organisms share the same fitness, so the elites in both populations will be in the same location. This allows the population to keep two strong individuals (the elites) ‘linked up’, allowing them to work together (coevolve) and eventually find the optimum. When we are using strict elitism, the linked up individuals are unable

\textsuperscript{1}With the exception of the non-spatial coevolutionary at 1 elite, due to numerous failures to find a solution with both mechanisms
to continue evolving as they are ‘locked’ into their current set of chromosomes. Instead of the current elites eventually getting more highly fit (or possibly chromosomes nearby), the GA must instead wait until the other individuals in the two populations find their respective optimums at the same reproductive location in the same generation. If one of the chromosomes in either population is only close to the optimum, and not at it, the pair will be given elite status and prevented from changing further to find the optimum itself. The GA is being slowed at the position that has the most promising solution.

Figure 4.22: Strict global elitism on non-spatial coevolutionary GA

Figure 4.23: Strict global elitism on 4 Graph coevolutionary GA

4.6.2 Fitness Heat Maps

The heat maps are shown in figure 4.24 & 4.25 for the coevolutionary and standard GA respectively. As expected, the heat maps produce results with interesting consequences. The first thing to mention is that we see very little difference when looking at the heat maps of the standard GA versus those of the coevolutionary GA.
Figure 4.24: Heat map of fitness values with varying levels of elitism on a spatial coevolutionary GA

Figure 4.25: Heat map of fitness values with varying levels of elitism on a spatial standard GA
This implies that the movement of fitness, and therefore elites, have similar behaviour in both GA types. This is interesting, considering the fact that we have shown in our earlier experiments that elites are much more important to the success of the coevolutionary GA than the standard one. This increased success clearly has nothing to do the elites movement within the population.

Another point of interest is that we see a significant difference in the fitness structure of the GA as we increase the number of elites. We can see that our elites are grouped near each other to form clusters of highly fit nodes. We see evidence of this in all graphs shown, but it is most readily apparent looking at the 3rd and 4th graphs of the 10 elite coevolutionary GA. We can also see this effect looking at the standard GAs graph with 5 elites, though they are focused around the bottom left corner which involves them wrapping around our toroidal structure and can be somewhat hard to visualize on our 2D grid.

The final point to note is the difference between the 0 elite heat maps versus 100 elites (full elitism), one might think that these graphs would be the same as we have no elite clustering, however this is not quite true. While the early generations show little to differentiate them, in the later generations the nodes in the full elitism heat maps have a much more average set of data than the in the non-elite heat maps. Full elitism appears to not only help the GA find the optimum faster, but also increases the average fitness of the population as well.
4.7 Results Summary Tables

This section contains a number of tables summarizing the results of the experiments run in this thesis. There are many different experiments run throughout the thesis attempting to help understand why we are seeing these various effects. Previously proposed explanations have not been well tested using a full experimental framework looking at alternative hypothesis. This thesis is a first attempt at filling this gap in knowledge.

A brief summary of the primary experiments run in this thesis can be found in Table 4.1. Tables 4.2 & 4.3 provide the basic results on the necessity of spatial reproduction and coevolution to cooperative and competitive problems. The results of elitism’s role is found in Table 4.4, and finally, Table 4.5 provides a more in-depth on the hypotheses regarding spatial coevolution’s role in improving performance in cooperative coevolutionary systems.
<table>
<thead>
<tr>
<th>Experiment</th>
<th>Result</th>
</tr>
</thead>
<tbody>
<tr>
<td>Run a number of problems on a cooperative coevolutionary GA with and without spatial reproduction.</td>
<td>The cooperative coevolutionary GA has improved performance with spatial reproduction.</td>
</tr>
<tr>
<td>Run a number of problems on a competitive coevolutionary GA with and without spatial reproduction.</td>
<td>The competitive coevolutionary GA has reduced performance with spatial reproduction.</td>
</tr>
<tr>
<td>Run a number of problems on a cooperative coevolutionary GA with and without spatial evaluation.</td>
<td>The cooperative coevolutionary GA has reduced performance with spatial evaluation.</td>
</tr>
<tr>
<td>Run a number of problems on a competitive coevolutionary GA with and without spatial evaluation.</td>
<td>The competitive coevolutionary GA has reduced performance with spatial evaluation.</td>
</tr>
<tr>
<td>Run the coevolutionary GA with a number of spatial structures and compare performance</td>
<td>The degree of the structures is the most significant attribute; overall structure has a minimal effect</td>
</tr>
<tr>
<td>Display fitness across various GA runs using a Heat Map</td>
<td>Elites are shown to generally occur very close to each other at all elite levels</td>
</tr>
<tr>
<td>Run a GA with a linearly separable matching problem and compare its performance against a non-linearly separable matching problem.</td>
<td>The problem linearly separable across populations has significantly increased performance over the non-linearly separable problem.</td>
</tr>
</tbody>
</table>
Table 4.2: The Importance of Each Mechanism on the Cooperative Coevolutionary GA

<table>
<thead>
<tr>
<th>Alternatives</th>
<th>Experiment</th>
<th>Result</th>
</tr>
</thead>
<tbody>
<tr>
<td>Only Spatial Reproduction</td>
<td>Run the spatial non-coevolutionary GA and compare the performance with the standard GA.</td>
<td>Performance shows no significant change; spatial reproduction has no effect in this experiment.</td>
</tr>
<tr>
<td>Only Coevolution</td>
<td>Run the cooperative coevolutionary GA and compare performance with the standard GA.</td>
<td>Performance is significantly lower than the standard GA; coevolution hurts performance.</td>
</tr>
<tr>
<td>Coevolution and Spatial Reproduction</td>
<td>Run the cooperative coevolutionary GA with spatial reproduction and compare performance with both the standard and coevolutionary GAs.</td>
<td>Performance is on par, or better than the standard GA and significantly better than the cooperative coevolutionary GA.</td>
</tr>
</tbody>
</table>

**Conclusion:** We need the coevolution and spatial mechanisms in order to provide the best performance when dealing with cooperative coevolutionary problems.
Table 4.3: The Effect of Each Mechanism on the Competitive Coevolutionary GA

<table>
<thead>
<tr>
<th>Alternatives</th>
<th>Experiment</th>
<th>Result</th>
</tr>
</thead>
<tbody>
<tr>
<td>Only Spatial Reproduc-</td>
<td>Run the spatial non-coevolutionary GA and compare performance with the</td>
<td>Performance shows no significant change; spatial reproduction has no effect in this experiment.</td>
</tr>
<tr>
<td>tion</td>
<td>standard GA.</td>
<td></td>
</tr>
<tr>
<td>Only Coevolution</td>
<td>Run the competitive coevolutionary GA and compare performance with the</td>
<td>Performance shows a significant reduction in performance on the coevolutionary GA.</td>
</tr>
<tr>
<td></td>
<td>standard GA.</td>
<td></td>
</tr>
<tr>
<td>Coevolution and Spatial</td>
<td>Run the competitive coevolutionary GA and compare performance with the</td>
<td>Performance shows a significant reduction when spatial reproduction is added.</td>
</tr>
<tr>
<td>Reproduction</td>
<td>standard GA.</td>
<td></td>
</tr>
</tbody>
</table>

**Conclusion:** Competitive coevolution is hindered by spatial reproduction when tested using our test suite. This is in opposition of results by Mitchell et al, however due to the nature of our simple experiments we cannot say much more. However, this does provide evidence that there is a more fundamental reason for the performance increase seen by Mitchell et al than their ‘focusing’ hypothesis.
Table 4.4: Results of Elitism Experiments

<table>
<thead>
<tr>
<th>Question</th>
<th>Experiment</th>
<th>Result</th>
</tr>
</thead>
<tbody>
<tr>
<td>What is the optimal number of elites?</td>
<td>Run a variety of problems while increasing the number of elites.</td>
<td>The more elites added to the problem the more performance is improved.</td>
</tr>
<tr>
<td>Is globally determined local elitism necessary?</td>
<td>Compare the performance between globally determined local elitism and strict global elitism on the standard GA.</td>
<td>Minimal improvement seen when using globally determined local elitism.</td>
</tr>
<tr>
<td></td>
<td>Compare the performance between globally determined local elitism and strict global elitism on the cooperative coevolutionary GA.</td>
<td>There is a significant increase in performance.</td>
</tr>
</tbody>
</table>

**Conclusion:** Globally determined local elitism has a minimal effect on the standard GA, while it provides large gains in improvement on the cooperative coevolutionary GA. In general, elitism provides significant gains to the GA and should be used for most problems.
Table 4.5: What is the main driving force leading to the performance boost seen in cooperative coevolution?

<table>
<thead>
<tr>
<th>Hypothesis</th>
<th>Experiment</th>
<th>Result</th>
<th>Analysis</th>
</tr>
</thead>
<tbody>
<tr>
<td>Spatial reproduction improves performance by slowing down reproduction and maintaining diversity. This prevents premature convergence, which is generally a significant problem for coevolutionary systems.</td>
<td>Compare the performance of a standard coevolutionary system and a spatial coevolutionary system solving one-max.</td>
<td>The performance of one-max is improved when using the spatial system.</td>
<td>Diversity should not matter within the one-max problem, therefore another effect must causing the improvement.</td>
</tr>
<tr>
<td></td>
<td>Compare the performance of a standard coevolutionary system and a spatial coevolutionary system solving one-max matching. This problem has many local optima where increased diversity should show an improvement in performance.</td>
<td>The performance of one-max matching is improved using the spatial system. Its performance is improved by roughly the same amount as in the one-max problem.</td>
<td>As both problems are improved by roughly the same amount, the added need for diversity in this problem did not lead to increased performance.</td>
</tr>
<tr>
<td></td>
<td>Previously observed result from elitism experiments.</td>
<td>Increasing the number elites has been observed to improve performance for various problems.</td>
<td>This conflicts with maintaining diversity as elites will actually reduce diversity.</td>
</tr>
</tbody>
</table>
Spatial reproduction improves diversity by slowing down reproduction allowing both populations to remain in sync and not decouple.

<table>
<thead>
<tr>
<th>Compare the performance of a standard coevolutionary system and a spatial coevolutionary system solving one-max.</th>
<th>The performance of one-max is improved when using spatial reproduction.</th>
<th>Keeping two good one-max solutions together allows each population to use that good solution to work toward the optimum.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Compare the performance of a standard coevolutionary system and a spatial coevolutionary system solving one-max matching.</td>
<td>The performance of one-max is improved by using spatial reproduction.</td>
<td>As in one-max, keeping two good one-max solutions together allows each population to use that good solution to work toward the optimum.</td>
</tr>
<tr>
<td>Previously observed result from elitism experiments.</td>
<td>Increasing the number elites has been observed to improve performance for various problems.</td>
<td>Having an elite forces the GA to keep its best organism(s) in both populations, which of course are in the same place, keeping these solutions ‘linked’ together.</td>
</tr>
<tr>
<td>View heat maps of fitness distribution from a variety of sources.</td>
<td>Heat maps show that high fitness individuals tend to occur near each other.</td>
<td>Highly fit organisms occurring near each other show that highly fit individuals need to be ‘linked’ for best performance.</td>
</tr>
</tbody>
</table>

**Conclusion:** While we cannot say that diversity is never the driving force, it is not a major force in the problems tested. Meanwhile, linkage between populations appears to be a significant factor to the performance of the systems.
Chapter 5

Summary and Future Work

It has been proposed that spatial structures can stabilize coevolutionary algorithms [29, 54]; through simple easy to understand functions we have explored this proposal, verified it with some caveats, and in the process have come to a much deeper understanding of spatial coevolutionary systems. We have shown that elitism, spatial reproduction, and spatial evaluation all have a significant impact on the performance of competitive and cooperative coevolutionary GAs. Specifically, we found that spatial reproduction improves the performance of cooperative coevolutionary systems, hinders competitive coevolutionary systems, and has a minimal effect, if any at all, on the standard GA. We have also shown that spatial evaluation can have a significant impact on the performance of coevolutionary systems, improving competitive performance and hindering cooperative performance. Next, we showed that elitism can provide significant gains on all GA types for a variety of problems, which while it was known that this was true for the standard GA, we have confirmed that this is also true for spatial and coevolutionary GAs. Finally, we have shown the importance of encouraging linear separability between the coevolving populations; the coevolutionary system was able to provide the best performance increases when the problem was separable between the populations.
While many of the mechanisms discussed are fairly independent of each other, the most interesting effect is seen between spatial reproduction and elitism. Both effects improve performance on the cooperative coevolutionary GA, combining these features does as well, up until we have reached very high levels of elitism. In particular, our new globally selected local elitism mechanism is responsible for the greatest gain in performance. It is clear that this type of elitism is important to the success of the coevolutionary GA. Based on the fact that we found a decreasing effectiveness from spatial reproduction as we increased the level of elitism, we believe that the two mechanisms are improving the GA in a similar manner. This fact allows us to hypothesize that the improvement in performance comes from keeping good solutions connected close together. This is also supported by looking at the heat maps in section 4.6.2. Once the GA has found a good match, spatial reproduction slows the flow of genetic material around the match to keep it good, while the local elitism prevent the solution from undergoing large changes which would harm their synergistic relationship. In both cases, these mechanisms keep the positive synergy of these problems intact over many generations, hopefully allowing those individuals to eventually find the optimum. We begin to see a degradation in the benefit provided each mechanisms as both are increased, they start to prevent full exploration of a space due to the flow of genetic information being slowed throughout the GA, rather than just areas of high fitness. Elitism helps promote good genes to congregate and grow in specific areas of the GA, but with higher levels of elitism, poor genes are ultimately labelled as elites, and are then contained with the same mechanisms promoting slow gene flow around the good genes. When we have the high levels of
elitism and remove the spatial reproductive framework the inferior genes are now able to reproduce more easily with good genes, and at the same time, are only able to improve thanks to their local elitism. This hypothesis also explains why the strict global elitism does not improve performance as much as our globally selected local elitism; strict elitism does not allow either individual to change, thus preventing them from working towards the optimum.

We have shown great success in understanding the behaviours in our cooperative systems, and have confirmed the work of Weigand & Sarma [54] in which they found that spatial reproduction is important for improving the performance in cooperative coevolutionary GAs. However, we have found flaws with their provided explanation for why this was occurring and have presented a new hypothesis for why we believe we are seeing this improvement. They had also found that spatial evaluation was important to their problem, but we found that this did not help for the simple one-max problem. Lastly, when viewing our results for competitive coevolution, our results were opposite of Mitchell et al.’s [29]. They found that spatial reproduction was improving the performance of the GA for their problem, but we found that it actually hurt the GA when solving our simple problems. We did, however, find that spatial evaluation provided a significant boost to performance, and it is possible that this is the true mechanism responsible for the performance increases found in their work. More research is required to determine why performance on certain problems is improved by spatial reproduction, and diminished on others.

All of the effects shown in this thesis have a massive effect on the performance of the coevolutionary GA and none should be overlooked when choosing the mechanisms
to use in the design of a new GA. It is clear that spatial reproduction and elitism both
have profound effects on cooperative GAs, however their interaction effects need to
be examined in more detail, in order to find an optimal amount of each. In addition,
more work needs to be undertaken with spatial structures on competitive GA’s, as
from previous work they clearly have a significance affect on performance, but with
difficulty reproducing this effect on the simple problems used here, it is obviously a
significantly different and more complicated effect than on the cooperative GA.
Bibliography


Appendix A

Full Results With Accompanying $p$-Values

This section of the appendix contains a complete set of graphs, displaying all of the data presented in section 4 of this document. All $p$-values displayed in this section have been found using the Wilcoxon rank-sum test and a Holmes-Bonferroni post-hoc correction where appropriate.

Throughout this appendix we will be using the following short-forms in order to conserve space in some of our tables and graphs:

- Coevolution $\rightarrow$ Coev
- Standard $\rightarrow$ Std
- Spatial $\rightarrow$ Spt
- Complete $\rightarrow$ Comp
A.1 Spatial Effects on Standard and Coevolutionary GAs

<table>
<thead>
<tr>
<th>GA Type</th>
<th>$p$-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Coev Comp</td>
<td>Coev Spt</td>
</tr>
<tr>
<td>Coev Comp</td>
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</tr>
<tr>
<td>Coev Comp</td>
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<td>Std Spt</td>
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<tr>
<td>Coev Spt</td>
<td>Std Comp</td>
</tr>
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<td>Std Spt</td>
<td>Std Comp</td>
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</table>

Figure A.1: One-max

<table>
<thead>
<tr>
<th>GA Type</th>
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<tbody>
<tr>
<td>Coev Comp</td>
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<tr>
<td>Coev Comp</td>
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</tr>
<tr>
<td>Coev Comp</td>
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<td>Std Spt</td>
<td>Std Comp</td>
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</table>

Figure A.2: One-max Outer Matching
### Figure A.3: One-max Inner Matching

![Box plot for One-Max Inner Matching](image1)

<table>
<thead>
<tr>
<th>GA Type</th>
<th>p-value</th>
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<tbody>
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<td>Coev Comp</td>
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<td>Std Spt</td>
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<td>Coev Spt</td>
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### Figure A.4: One-max Extra Outer Matching

![Box plot for One-Max Extra Outer Matching](image2)

<table>
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<tr>
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<td>Coev Comp</td>
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<td>Coev Comp</td>
<td>Std Comp</td>
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<tr>
<td>Coev Spt</td>
<td>Std Spt</td>
</tr>
<tr>
<td>Coev Spt</td>
<td>Std Comp</td>
</tr>
<tr>
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<td>Std Comp</td>
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\begin{table}[h]
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\begin{tabular}{|c|c|c|}
\hline
GA Type & $p$-value & Coev Spt, Std Spt, Std Comp, Coev Comp
\hline
Coev Comp & 1.91e-04 &
\hline
Coev Comp & 1.00 &
\hline
Coev Comp & 1.00 &
\hline
Coev Spt & 2.64e-04 &
\hline
Coev Spt & 0.0101 &
\hline
Std Spt & 1.00 &
\hline
\end{tabular}
\caption{One-max Extra Inner Matching}
\end{table}

Figure A.5: One-max Extra Inner Matching

\begin{table}[h]
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\begin{tabular}{|c|c|c|}
\hline
GA Type & $p$-value & Coev Spt, Std Spt, Std Comp, Coev Comp
\hline
Coev Comp & 0.0326 &
\hline
Coev Comp & 9.35e-09 &
\hline
Coev Comp & 2.88e-10 &
\hline
Coev Spt & 7.98e-12 &
\hline
Coev Spt & 7.98e-12 &
\hline
Std Spt & 0.442 &
\hline
\end{tabular}
\caption{Royal Road}
\end{table}

Figure A.6: Royal Road
Figure A.7: One-max Royal Road
A.2 Coevolutionary Spatial Evaluative Effects

**Figure A.8:** Spatial reproductive structures on coevolutionary GA with one-to-one host/parasite

**Table A.1**

<table>
<thead>
<tr>
<th>Spatial Type</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Grid 4</td>
<td>Grid 8</td>
</tr>
<tr>
<td>Grid 4 Complete</td>
<td>Grid 8 Complete</td>
</tr>
<tr>
<td>Grid 8 Complete</td>
<td></td>
</tr>
</tbody>
</table>

**Figure A.9:** Spatial reproductive structures on coevolutionary with spatially evaluated host/parasite

**Table A.2**

<table>
<thead>
<tr>
<th>Spatial Type</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Grid 4</td>
<td>Grid 8</td>
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<td>Grid 4 Complete</td>
<td>Grid 8 Complete</td>
</tr>
<tr>
<td>Grid 8 Complete</td>
<td></td>
</tr>
</tbody>
</table>
Figure A.10: Spatial reproductive structures on coevolutionary with purely competitive host/parasite

<table>
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<tr>
<td>Grid 4</td>
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<td>Grid 8</td>
<td>0.0439</td>
</tr>
<tr>
<td>Grid 8 Complete</td>
<td>0.0767</td>
</tr>
</tbody>
</table>
A.3 Distinct Spatial Structures

Wilcoxon rank-sum test

<table>
<thead>
<tr>
<th>Structures of Degree</th>
<th>$p$-value</th>
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<tbody>
<tr>
<td>2</td>
<td>1.77e-06</td>
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<tr>
<td>4</td>
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</tr>
<tr>
<td>8 Complete</td>
<td>2.2e-16</td>
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Kruskal-Wallis rank-sum test

<table>
<thead>
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<th>Structures Tested</th>
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<tbody>
<tr>
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<td>All Structures</td>
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</table>

Figure A.11: Spatial structures on the coevolutionary GA
Wilcoxon rank-sum test

<table>
<thead>
<tr>
<th>Structures of Degree</th>
<th>p-value</th>
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</thead>
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<tr>
<td>2 4</td>
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<td>4 8</td>
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Kruskal-Wallis rank-sum test

<table>
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Figure A.12: Spatial structures on the standard GA
Wilcoxon rank-sum test

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</table>

Kruskal-Wallis rank-sum test

<table>
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</thead>
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</table>

Figure A.13: Spatial structures on 1-to-1 Host/Parasite
A.4 Linear Separability

<table>
<thead>
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</tr>
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<td>Coev Comp Std Spt</td>
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<tr>
<td>Coev Comp Std Comp</td>
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</tr>
<tr>
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<tr>
<td>Coev Spt Std Comp</td>
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<td>Std Spt Std Comp</td>
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</table>

Figure A.14: Pure Outer Matching

<table>
<thead>
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</tbody>
</table>

Figure A.15: Pure Inner Matching
A.5 One-max Elitism

![Elitism on Standard GA Grid 4 - One-Max](image1)

<table>
<thead>
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<td>2</td>
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<td>10</td>
</tr>
<tr>
<td>10</td>
<td>50</td>
</tr>
<tr>
<td>50</td>
<td>100</td>
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</table>

Figure A.16: One-max on Grid 4 standard GA

![Elitism on Standard GA Grid 8 - One-Max](image2)

<table>
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</tr>
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<td>10</td>
<td>50</td>
</tr>
<tr>
<td>50</td>
<td>100</td>
</tr>
</tbody>
</table>

Figure A.17: One-max on Grid 8 standard GA
Figure A.18: One-max on non-spatial standard GA

Figure A.19: One-max on Grid 4 coevolutionary GA
Figure A.20: One-max on Grid 8 coevolutionary GA

Figure A.21: One-max on non-spatial coevolutionary GA
Figure A.22: One-max with no elite

Figure A.23: One-max with 1 elite
### Figure A.24: One-max with 2 elite

### Figure A.25: One-max with 5 elite
Figure A.26: One-max with 10 elite

Figure A.27: One-max with 50 elite
Figure A.28: One-max with full elitism
A.6 One-max Extra Inner Matching Elitism

<table>
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</thead>
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</tr>
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<td>2.03e-05</td>
</tr>
<tr>
<td>2</td>
<td>6.3e-09</td>
</tr>
<tr>
<td>5</td>
<td>1.32e-05</td>
</tr>
<tr>
<td>10</td>
<td>4.53e-09</td>
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<td>0.0736</td>
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Figure A.29: Extra Inner Matching on non-spatial standard GA

<table>
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<td>1.04e-05</td>
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<tr>
<td>2</td>
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</table>

Figure A.30: Extra Inner Matching on Grid 4 standard GA
Figure A.31: Extra Inner Matching on non-spatial coevolutionary GA

Figure A.32: Extra Inner Matching on Grid 4 coevolutionary GA
**Figure A.33:** Extra Inner Matching with no elite

**Figure A.34:** Extra Inner Matching with 1 elite
### Table A.35: Extra Inner Matching with 2 elite

<table>
<thead>
<tr>
<th>GA Type</th>
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</tr>
</thead>
<tbody>
<tr>
<td>Coev Comp</td>
<td>1.91e-04</td>
</tr>
<tr>
<td>Coev Comp</td>
<td>1.00</td>
</tr>
<tr>
<td>Coev Comp</td>
<td>1.00</td>
</tr>
<tr>
<td>Coev Spt</td>
<td>2.63e-04</td>
</tr>
<tr>
<td>Coev Spt</td>
<td>0.0101</td>
</tr>
<tr>
<td>Std Spt</td>
<td>1.00</td>
</tr>
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</table>

### Table A.36: Extra Inner Matching with 5 elite

<table>
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<tbody>
<tr>
<td>Coev Comp</td>
<td>0.0256</td>
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<tr>
<td>Coev Comp</td>
<td>0.0184</td>
</tr>
<tr>
<td>Coev Comp</td>
<td>0.232</td>
</tr>
<tr>
<td>Coev Spt</td>
<td>8.02e-07</td>
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<tr>
<td>Coev Spt</td>
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<tr>
<td>Std Spt</td>
<td>0.232</td>
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</table>

Figure A.35: Extra Inner Matching with 2 elite

Figure A.36: Extra Inner Matching with 5 elite
<table>
<thead>
<tr>
<th>GA Type</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Coev Comp Coev Spt</td>
<td>0.754</td>
</tr>
<tr>
<td>Coev Comp Std Spt</td>
<td>2.73e-05</td>
</tr>
<tr>
<td>Coev Comp Std Comp</td>
<td>0.0443</td>
</tr>
<tr>
<td>Coev Spt Std Spt</td>
<td>2.73e-05</td>
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<tr>
<td>Coev Spt Std Comp</td>
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<tr>
<td>Std Spt Std Comp</td>
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</table>

Figure A.37: Extra Inner Matching with 10 elite

<table>
<thead>
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<tbody>
<tr>
<td>Coev Comp Coev Spt</td>
<td>0.173</td>
</tr>
<tr>
<td>Coev Comp Std Spt</td>
<td>1.18e-10</td>
</tr>
<tr>
<td>Coev Comp Std Comp</td>
<td>1.19e-05</td>
</tr>
<tr>
<td>Coev Spt Std Spt</td>
<td>5.05e-08</td>
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<tr>
<td>Coev Spt Std Comp</td>
<td>6.93e-03</td>
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<tr>
<td>Std Spt Std Comp</td>
<td>1.12e-06</td>
</tr>
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</table>

Figure A.38: Extra Inner Matching with 50 elite
Figure A.39: Extra Inner Matching with 100 elite
A.7 One-to-One Host/Parasite Elitism

Figure A.40: One-to-One Host/Parasite on Grid 4 coevolutionary GA

<table>
<thead>
<tr>
<th># of Elites</th>
<th>p-value</th>
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</thead>
<tbody>
<tr>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>1</td>
<td>6.64e-03</td>
</tr>
<tr>
<td>2</td>
<td>1.28e-07</td>
</tr>
<tr>
<td>5</td>
<td>5.24e-08</td>
</tr>
<tr>
<td>10</td>
<td>3.25e-09</td>
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<tr>
<td>50</td>
<td>5.62e-12</td>
</tr>
<tr>
<td>100</td>
<td>0.735</td>
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</tbody>
</table>

Figure A.41: One-to-One Host/Parasite on Grid 8 coevolutionary GA

<table>
<thead>
<tr>
<th># of Elites</th>
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<tbody>
<tr>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>1</td>
<td>3.00e-03</td>
</tr>
<tr>
<td>2</td>
<td>6.65e-11</td>
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<tr>
<td>5</td>
<td>5.29e-07</td>
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<tr>
<td>10</td>
<td>4.22e-08</td>
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<tr>
<td>50</td>
<td>1.04e-11</td>
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<tr>
<td>100</td>
<td>0.0224</td>
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Figure A.42: One-to-One Host/Parasite on non-spatial coevolutionary GA

Figure A.43: One-to-One Host/Parasite with no elite
Figure A.44: One-to-One Host/Parasite with 1 elite

<table>
<thead>
<tr>
<th>GA Type</th>
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<tbody>
<tr>
<td>Grid 4</td>
<td>1.18e-03</td>
</tr>
<tr>
<td>Grid 4 Complete</td>
<td>1.71e-08</td>
</tr>
<tr>
<td>Grid 8</td>
<td>1.18e-03</td>
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<tr>
<td>Grid 8 Complete</td>
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</table>

Figure A.45: One-to-One Host/Parasite with 2 elite

<table>
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<tbody>
<tr>
<td>Grid 4</td>
<td>1.18e-03</td>
</tr>
<tr>
<td>Grid 4 Complete</td>
<td>1.18e-03</td>
</tr>
<tr>
<td>Grid 8</td>
<td>1.18e-03</td>
</tr>
<tr>
<td>Grid 8 Complete</td>
<td>1.18e-03</td>
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</table>
### Figure A.46: One-to-One Host/Parasite with 5 elite

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<tr>
<td>Grid 4</td>
<td>Grid 8</td>
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<tr>
<td>Grid 4</td>
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<td>Grid 8</td>
<td>Complete</td>
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</table>

### Figure A.47: One-to-One Host/Parasite with 10 elite

<table>
<thead>
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<th>GA Type</th>
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<tbody>
<tr>
<td>Grid 4</td>
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<td>Grid 4</td>
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<td>Grid 8</td>
<td>Complete</td>
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</table>
### Figure A.48: One-to-One Host/Parasite with 50 elite

<table>
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<tr>
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<td>Grid 4 Complete</td>
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<td>Grid 8 Complete</td>
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### Figure A.49: One-to-One Host/Parasite with full elitism

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<tbody>
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<tr>
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<td>Grid 8 Complete</td>
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A.8 Strict Global Elitism

<table>
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<tr>
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<th>Strict Global</th>
<th>Globally Selected</th>
<th>Received</th>
<th>p-value</th>
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</thead>
<tbody>
<tr>
<td>1</td>
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<td>1047</td>
<td>1.00</td>
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<tr>
<td>2</td>
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<td>669.5</td>
<td>1.00</td>
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<td>5</td>
<td>318.5</td>
<td>331</td>
<td>1.00</td>
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<tr>
<td>10</td>
<td>217.5</td>
<td>167</td>
<td>0.0777</td>
<td></td>
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<tr>
<td>50</td>
<td>165.5</td>
<td>91</td>
<td>1.08e-14</td>
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</table>

Figure A.50: Global elitism on non-spatial standard GA
Figure A.51: Global elitism on Grid 4 standard GA
Figure A.52: Global elitism on non-spatial coevolutionary GA
Strict Global Elitism
Coevolution GA - Grid 4 - One-Max

Figure A.53: Global elitism on Grid 4 coevolutionary GA