1. Introduction and Literature Review: So what the heck is a genetic algorithm, anyways?

A genetic algorithm is a process that uses the principles of evolution and natural selection to develop solutions to computational problems. Genetic algorithms, along with neural networks, swarm-based algorithms, and other biologically-inspired algorithms, have been found in recent years to be surprisingly adept at devising efficient solutions to computationally difficult problems with little human intervention. However, because the notion of a "genetic algorithm" is a very technical concept and is by no means common knowledge, the literature review is preceded by an overview of the theory and basic mechanisms behind genetic algorithms.

1.1. Evolutionary Underpinnings: Why we have fuzzy bunnies

Imagine a litter of baby rabbits living in a frigid tundra. During their development, they received DNA from each of their parents, but the DNA wasn't copied perfectly. Some random errors might have occurred, causing each child to be slightly different. If a few rabbits underwent a gene mutation causing them to be, say, slightly hairier than their siblings, those few will be better suited to survive in their chilly environment, making them more likely to survive, find mates of their own, and pass down their mutated genes to their babies. Their grandchildren will inherit this "hairiness gene" and be abnormally hairy like their parents, giving them an advantage over their less-hairy peers, and so on. It is statistically likely that after hundreds of generations, the hairiness gene will become predominant, filling the tundra with fuzzy bunnies.

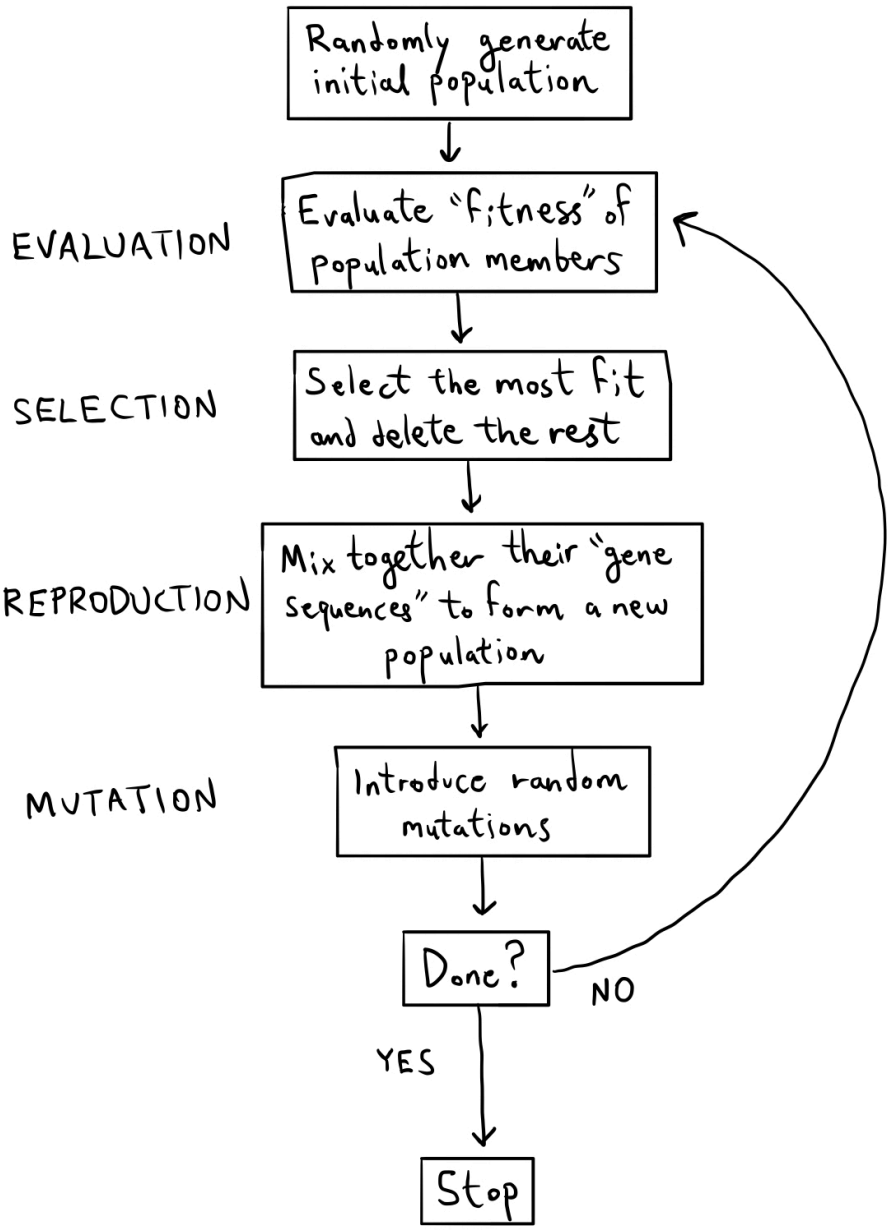
In *The Origin of Species*, Charles Darwin (1859) marvels over this process, which he calls "natural selection." Because of our more sophisticated modern understanding of genetics, biologists nowadays describe this process more precisely than Darwin did. Grant (1991), in an article published in *Scientific American*, defines natural selection as "differential success," or the process by which small, random adaptations increase the fitness of some organisms (p. 82). Gould, Keeton, and Gould (1996), two of whom were professors at Princeton University and Cornell University, define an organism's fitness as its "probable genetic contribution to succeeding generations," and define an adaptation as "a favorable characteristic that increases an organism's chances of perpetuating its genes, usually by leaving descendants" (p. 373). In nature, adaptations abound: Darwin (1859) lists diverse examples, like bird plumage used for courtship (p. 116), nectar used by plants to attract pollinators (p. 118), and the astoundingly complex human eye (p. 144).

Through natural selection, biological mechanisms have developed that are far more complex than any manmade machine, yet "plainly bear the stamp of far higher workmanship" (Darwin, 1859, p.113). Humans benefit from natural selection not only through adaptations of our own (like our massive brains), but also by breeding domesticated animals and selecting for favorable characteristics like strength and speed in horses (Darwin, 1859, p. 124). However, as Darwin (1859) puts it, "natural selection will always act with extreme slowness" (p. 123) since it takes place over the course of generations, preventing us from fully harnessing its power of intricate design. That is, until the invention of the genetic algorithm.

1.2. The Genetic Algorithm (GA): Artificial animal husbandry

John Holland (1992), a pioneering researcher who helped develop genetic algorithms, describes how they work in an article for *Scientific American*. Given some difficult puzzle or task, different strategies can be encoded in strings of numbers (like a gene sequence) forming what is called the "solution space," or the set of all possible encoded solutions to the problem. A virtual "population" of solutions (most of which will be inept at first) are generated, then tested to see which, if only by chance, perform best at the task in question. The worst solutions are eliminated, while the strongest ones are preserved, mixed together in certain ways (emulating "reproduction"), and tweaked with random mutations, adding the element of chance that drives evolution. These children become the new population, and the process is repeated, often thousands of times. The result is, as Holland (1992) puts it, "programs that solve problems even when no person can fully understand their structure" (p. 66).

The general structure of a genetic algorithm has become very standardized, and many researchers presenting applications of genetic algorithms describe their structure using flow charts very similar to the following (see, for instance, Parvez & Dhar, Kim & de Weck, Kumar & Paneerselvam):



Melanie Mitchell, formerly a researcher at MIT and the author of the book *Complexity: A Guided Tour*, defines a few relevant terms in her book *An Introduction to Genetic Algorithms*. In a genetic algorithm, the "population" is defined at the set of possible solutions being tested, each of which is determined by a sequence of numbers called "genome." "Evaluation" is the phase of the algorithm during which each member of the population is tested to determine its "fitness," which is defined as the value of some numerical function depending on the problem being solved (in this paper, any mention of the "quality" of a solution refers to its fitness). "Selection" is the process of choosing the fittest members of

the population, “reproduction” or “recombination” is the process of combining the gene sequences of those selected to form a new population (which can be done in a number of different ways, as shall be discussed later), and “mutation” is the process of introducing random changes into the new gene sequences (Mitchell, 1996, p. 5-8).

Because this takes place on a computer, thousands of generations can go by in the blink of an eye, producing “clever” solutions to difficult problems without an ounce of human ingenuity required.

1.3. Applications: What do bunnies and jet engines have in common?

Genetic algorithms have been applied to various difficult mathematical problems and even produced solutions surpassing those designed by humans. Al-Sultan, Hussain and Nizami (1996) use a GA to quickly obtain approximate solutions to the “set-covering problem”, which is computationally difficult and time-consuming to solve in exact form. Mitchell, Crutchfield, and Das (1996) show how GAs develop a counterintuitive method of globally sharing local information in cellular automata. Simpson (1997) finds that a GA’s solution to the “bridge club scheduling problem” outperforms the four other dominant solution algorithms to which he compares it, in terms of solution quality and efficiency. These findings together confirm that the mindless genetic algorithm can often display more mathematical “ingenuity” than humans.

The genetic algorithm is not simply an esoteric artifact whose power is limited to solving math puzzles, and it has been applied to diverse real-world problems. Metawa, Hassan, and Elhosney (2017) show how GAs can be used to efficiently automate bank lending decisions by accepting data about the loan applicant as input and generating an optimal loan decision. Xiao (n.d.) designs a GA to solve spatial partitioning problems and postulates an application to political redistricting. Genetic algorithms have even proven useful when it comes to designing new technologies. Holland (1992) explains how GAs were combined with physics simulators to design optimal jet engine turbines. Various researchers have applied GAs to develop movement and path planning in mobile robots, like Achour and Chaalal (1996) and, more recently, Bezák (2012) and Sedreh and Zadeh (2018). Genetic algorithms’ plentiful applications need not even be restricted to the private sector: Beligiannis, Moschopoulos and Likothanassis (2009) applied GAs to the scheduling of Greek schools and found that the method they developed was a great improvement on the standard method due to its customizability.

Genetic algorithms are clearly a powerful tool driving mathematical discovery, private profit, public benefit, and technological innovation. In the next section, we shall see how changing certain parameters of a GA can alter its efficiency or the quality of its final solution. Because GAs have such wide-ranging applications, any improvement made to the structure of a genetic algorithm has the potential to enhance any of its implementations listed above.

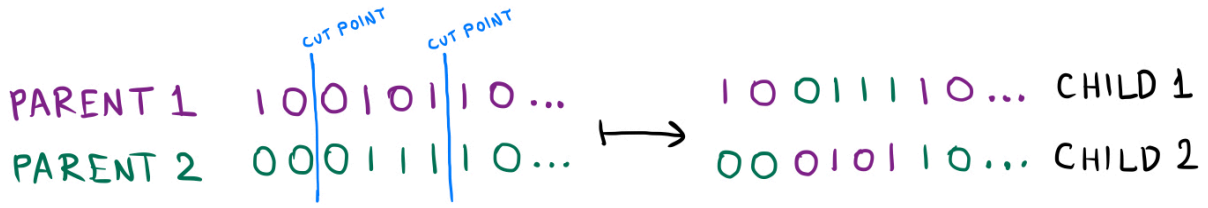
1.4. Area of Inquiry and Research Question: When two arrays love each other very much...

In an earlier section, “reproduction” was defined as the process through which the selected genomes of a population are combined to form a new population. However, there are many different ways of “combining” strings of digits. Two parents could be chosen from among the selected and their genomes spliced at a randomly chosen point, as shown in Figure 1:

FIGURE 1

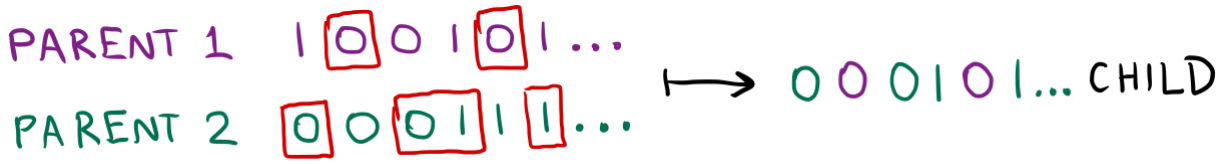
...or their genomes could be spliced using two randomly chosen cut points, as in Figure 2:

FIGURE 2



...or a child genome could even be formed by randomly choosing a character from either of its parents at each position in the sequences, as seen in Figure 3:

FIGURE 3



Each of these different methods is called a "crossover operator" (abbreviated CO). Umbarkar and Sheth (2015) and Kora and Yadlapalli (2017), in identically titled papers, list various crossover operators. It happens that the crossover operator showcased in Figure 1 is called "single-point crossover," the CO in Figure 2 is "two-point crossover," and that in Figure 3 is called "single point crossover" (although Umbarkar and Sheth call it "discrete crossover" when only one child is formed). Their papers include many different and more elaborate crossover operators, some of which even involve more than two parents.

The effect of the CO used on the the efficiency of a GA and the quality of its solutions is not fully understood. Several researchers have applied multiple different COs to the same problem and compared the results, but there exists no clear consensus. Picek and Golub (2010a) compared the performance of many COs and remarked (despite not finding any conclusive results) that the GAs with uniform or two-point crossover typically performed best, while those with single-point crossover or no crossover at all typically performed worst. However, Magalhaes-Mendes (2013) compared four different COs and found that uniform crossover performed second-best, supporting the results of Picek and Golub (2010a), but they ranked single-point crossover highest, contradicting them. These results are not necessarily incompatible, but rather suggest that there is no unique "best" CO, and that different COs may be better suited for different problems depending on the topology of their "solution spaces." Pujlic and Manger (2013) confirmed this by applying each of eight different COs that performed well on the "travelling salesman problem" (TSP) to the "vehicle routing problem" (VRP), discovering that "the obtained relative ranking of operators is quite different" (p.374).

This does not mean that the CO should be ignored, as various researchers have shown that is can have a considerable effect on the GA's outcome. Both Emmanouilidis and Hunter (2000) and Ortiz-Boyer, Hervás-Martinez, and García-Padrajas (2005) specifically designed COs for problems involving neural networks, with promising results: the former noted that their GA found more viable solutions than the

typical GA with n-point crossover, and the latter showed that their GA actually outperformed the traditional GA. Eiben and Raué (1994) also insightfully noticed that COs that recombined the genomes of three or more parents for each child often outperformed GAs with standard two-parent crossover.

This suggests the following question: how does the crossover operator used in a genetic algorithm affect the quality of the solutions obtained? Of course, it is impossible to answer this question in general, since the optimal CO depends on the problem to which the GA is applied, as explained above. However, the purpose of this paper is to shed some light on the issue by applying GAs with a variety of different COs to a two-dimensional spatial navegation problem, and analyzing the results using both statistical methods and evolutionary reasoning.

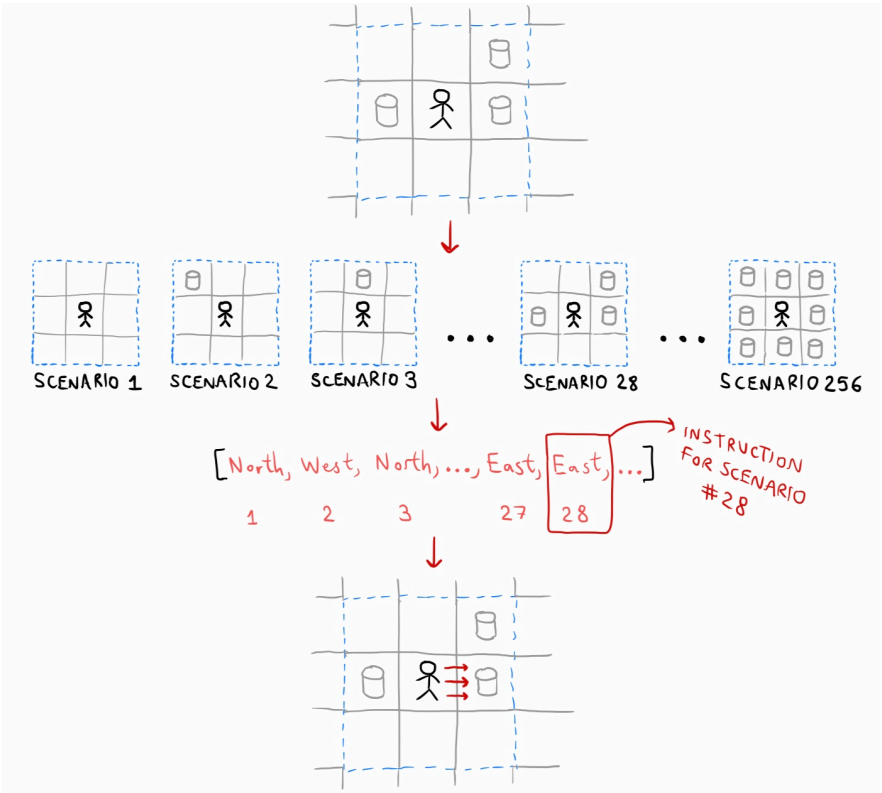
2. Methods:

2.1. The Problem: Robby, the Soda-Can-Collecting Robot

In her 2009 book *Complexity: A Guided Tour*, Melanie Mitchell constructs a simple and illustrative example of a genetic algorithm. Mitchell describes a game to be played on a 10 by 10 grid by a member of her virtual population (who she affectionately names Robby the Soda-Can-Collecting Robot) in which "soda-cans" are strewn randomly about the grid and the player is awarded points for collecting as many as possible in a limited number of turns.

The researcher will apply genetic algorithms to a variation of Mitchell's "soda-can collection problem," which is an appropriate choice for a few different reasons. The purpose of this research is not only to observe how various reproduction methods affect a genetic algorithm, but also to propose intuitive explanations for any effects observed. The simplicity of this problem makes it perfect, since the focus of this research is the structure of a genetic algorithm, not the problem that it is being used to solve. Further, this problem is easy to visualize and display graphically, facilitating qualitative (in addition to quantitative) analysis.

The modified version of Mitchell's problem proceeds as follows. The game takes place in 10 by 10 square grid that wraps around at the edges (that is, a 10 x 10 toroidal grid). For each of the 100 squares, a "soda can" is placed in that square with probability *p*, resulting in a random scattering of cans across the grid. The player starts in the top-left corner of the board and then moves about the board according to rules determined by its genome.



During each turn, the player "observes" the 8 squares to which it is horizontally, vertically, and diagonally adjacent. Each of these squares either contains a soda can or does not, meaning that there are $2^8 = 256$ possible observations. These possible scenarios are enumerated, and each one is assigned an instruction (go north, go south, go east, or go west) in the player's gene sequence. See the figure above.

The player follows the instructions in its genome for 50 turns, at which point the player's score is set equal to the total number of cans collected and the game ends.

2.2. Implementation and Data Collection: Getting down to business

A single trial of the genetic algorithm consists of the following steps:

(1) An **initial population** of 50 individuals is generated.

(2) 40 10 x 10 grids are randomly generated and stored in an array.

(3) Each player plays the game on each of these grids and is assigned a fitness value equal its average score. This is the **evaluation** step.

(4) The players are sorted by fitness value, and the players with the lowest 50% of scores are discarded. This is the **selection** step.

(5) Depending on the reproduction method being used, one or more parents are randomly chosen with equal probability from among the selected players, and their gene sequences are recombined to form one member of the new population.

(6) Each of the 256 entries in the child's gene sequence may randomly be changed with probability *p*, which varies depending on the trial. This is the **mutation** step.

(7) Steps 5 and 6 are repeated until the new population reaches the same size as the previous population. This is the **reproduction** step.

(8) The old population is erased entirely and replaced with the new population.

(9) Steps 2 through 8 are repeated 100 times in total before the algorithm ends.

This process conforms to the structure of a genetic algorithm outlined earlier using a flowchart, which was derived from the process used previously by other researchers. A copy of the researcher's code, written in Python, can be found in Appendix A. The decision to run the algorithm for 100 generations is based on preliminary observations (while testing the program) that population fitness usually plateaus by the hundredth generation.

The following statistics will be collected from the genetic algorithm as it runs:

- The average fitness value of players from each generation
- The fitness value of the "most fit" player from each generation
- The variance of the fitness values of players from each generation
- The average hamming distance between genomes (defined as the number of discrepancies between them) of players from each generation

The first and second sets of statistics will help assess the solution quality and convergence speed of the genetic algorithm, which the third and fourth will help assess the effect of the reproduction method on genetic diversity.

The following is a list of all COs that will be employed, along with abbreviations that will be used later for brevity's sake and descriptions of each CO. For visual explanations of each operator, see Appendix B.

1. Asexual (**AS**) - a parent creates an exact duplicate of itself.
2. 2-parent single-point crossover (**2P1PX**) - a cut point is randomly selected, and the child's genes before the cut point are taken from one parent, while the genes after the cut point are taken from another parent.
3. 2-parent double-point crossover (**2P2PX**) - two cut points are randomly selected, and the child's genes before the first cut point and after the second cut point are taken from one parent, while the genes between the cut points are taken from another parent.
4. 3-parent double-point crossover (**3P2PX**) - two cut points are randomly selected, and the child's genes before the first cut point are taken from one parent, the genes between the two cut points are taken from another parent, and the genes after the second cut point are taken from a third parent.
5. 2-parent segmented crossover (**2PSX**) - each character in the genome has probability p=0.2 of becoming a cut point. The child's genes are taken from one parent until a cut point is reached, at which point the child begins to take genes from a second parent, switching back to the first parent when another cut point is reached, and so on.
6. 3-parent segmented crossover (**3PSX**) - cut points are chosen the same way as in 2PSX. The child's genes are taken from the first parent until a cut point is reached, and then they are taken from the second parent until another cut point is reached, and then genes are taken from the third parent until another cut point is reached, and finally genes are taken from the first parent again, and this process repeats until the gene sequence is filled.
7. 2-parent uniform crossover (**2PUX**) - each character in the child's gene sequence is either equated to the corresponding character in the first parent's or the second parent's gene sequence, with equal probability p=0.5.
8. 3-parent uniform crossover (**3PUX**) - each character in the child's gene sequence is either equated to the corresponding character in the first parent's, the second parent's, or the third parent's gene sequence with equal probability p=0.33.
9. Wright's Heuristic 2-parent uniform crossover (**W2PUX**) - each character in the child's gene sequence is either equated to the corresponding character in the first parent's or the second parent's gene sequence, with a bias towards the parent with the higher fitness value. More specifically, the probability that a character is taken from one parent is proportional to that parent's fitness value.
10. Wright's Heuristic 3-parent uniform crossover (**W3PUX**) - analogous to W2PUX, but with three parents.
11. Universal uniform crossover (**UUX**) - all players surviving selection become parents, and the elements of the child's gene sequence are chosen from among them with equal probability.

All of the above COs were obtained from or inspired by the literature, with some modification by the researcher needed to adapt them to the problem at hand. Deslauriers (2006) compared asexual and sexual COs with very complex and nuanced results, justifying the inclusion of **AS**. Umbarkar and Sheth (2015) and Kora and Yadlapalli (2017) list **2P1PX**, **2P2PX**, and **2PUX** as common COs, Picek and Golub (2010b) describe **2PSX**, and Lim et. al. (2017) describe Wright's Heuristic crossover, which the researcher combined with uniform crossover to create **W2PUX**. The findings of Eiben and Raué (1994), suggesting that COs involving many parents often perform better, inspired the researcher to develop **3P2PX**, **3PSX**, **3PUX**, **W3PUX**, and **UUX**, which are many-parent adaptations of these more common COs.

The entirety of data collection will consist of [44*k] trials. The trials are partitioned into 44 groups of [k, INSERT NUMBER HERE] trials each, and the trials in a particular group are determined by a specific CO and one of four mutation probabilities p=0.1,0.3,0.5, or 0.7. Grouping the trials this way should allow the researcher to observe the isolated effects of each CO, as well as the relative compatibility of each CO with higher or lower mutation probabilities.

2.3. Data Analysis and Limitations: What could possibly go wrong?

The data analysis phase of research will be divided into two sections: quantitative and qualitative analysis. The goal of quantitative analysis will be to statistically establish, with high confidence, a ranking of the 11 COs with respect to their effects on solution quality, convergence speed, and population diversity. This will be accomplished by formulating objective measurements of each of these three qualities and manipulating the data collected according to accepted statistical methods. The purpose of qualitative analysis will be to explain *why* and *how* the COs effect these aspects of the GA. This portion of the analysis will necessarily be less rigorous, because it will involve the (admittedly error-prone) researcher using mathematical and evolutionary intuition to postulate tentative explanations for the phenomena observed.

It may seem strange and inappropriate to apply qualitative analysis to a problem so seemingly quantitative in nature. However, recall that the findings of Manger (2013) suggested that the effect of a CO on a GA may vary from problem to problem, meaning that any quantitative results obtained will be specific to the "soda can collection problem" and not generalizable to GAs as a whole. Although qualitative analysis involves some speculation, it may shed some light on the nature of GAs in general, making qualitative results less reliable but more generalizable.

That said, the generalizability of results will still be limited. The 11 COs chosen for examination are by no means exhaustive, and there are so many conceivable COs that the researcher clearly cannot examine all of them. Further, there is a whole class of GAs in which genomes contain continuous decimal values rather than discrete integer values, which makes them so different from the GAs considered here that they are nearly untouchable by any generalization.