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# A Genetic Algorithm Tutorial

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**Abstract**

This tutorial covers the canonical genetic algorithm as well as more experimental forms of genetic algorithms, including parallel island models and parallel cellular genetic algorithms. The tutorial also illustrates genetic search by hyperplane sampling. The theoretical foundations of genetic algorithms are reviewed, include the schema theorem as well as recently developed exact models of the canonical genetic algorithm.

*Keywords:* Genetic Algorithms, Search, Parallel Algorithms

## 1 Introduction

In its most general usage, *Genetic Algorithms* refer to a family of computational models inspired by evolution. These algorithms encode a potential solution to a specific problem on a simple chromosome-like data structure and apply recombination operators to these structures so as to preserve critical information. Genetic algorithms are often viewed as function optimizers, although the range of problems to which genetic algorithms have been applied is quite broad.

An implementation of a genetic algorithm begins with a population of (typically random) chromosomes. One then evaluates these structures and allocates reproductive opportunities in such a way that those chromosomes which represent a better solution to the target problem are given more chances to "reproduce" than those chromosomes which are poorer solutions. The "goodness" of a solution is typically defined with respect to the current population average, or the population median.

This particular description of a genetic algorithm is intentionally abstract because in some sense, the term *genetic algorithm* has two meanings. In a strict interpretation, *the genetic algorithm* refers to a model introduced and investigated by John Holland (1975) and by students of Holland (e.g., DeJong, 1975). It is still the case that most of the existing theory for genetic algorithms applies either solely or primarily to the model introduced by Holland, as well as variations on what will be referred to in this paper as *the canonical genetic algorithm*. Recent theoretical advances in modeling genetic algorithms also apply primarily to the canonical genetic algorithm (Vose, 1993).

In a broader usage of the term, a genetic algorithm is any population-based model that uses selection and recombination operators to generate new sample points in a search space. Many genetic algorithm models have been introduced by researchers largely working from an experimental perspective. Many of these researchers are application oriented and are typically interested in genetic algorithms as optimization tools.

The goal of this tutorial is to present genetic algorithms in such a way that students new to this field can grasp the basic concepts behind genetic algorithms as they work through the tutorial. It should allow the more sophisticated reader to absorb this material with relative ease. The tutorial also covers topics, such as inversion, which have sometimes been misunderstood and misused by researchers new to the field.

The tutorial begins with a very low level discussion of optimization to both introduce basic ideas in optimization as well as basic concepts that relate to genetic algorithms. In Section 2 variants of the canonical genetic algorithm are reviewed. In Section 3 the principle of hyperplane sampling is explored and some basic crossover operators are introduced. In Section 4 various versions of the schema theorem are developed in a step by step fashion and other crossover operators are discussed. In Section 5 binary alphabets and their effects on hyperplane sampling is considered. In Section 6 an exact model of the genetic algorithm is developed which assumes infinite population sizes. The last three sections of the tutorial covers alternative forms of genetic algorithms and evolutionary computational models, including specialized parallel implementations.

## 1.1 Encodings and Optimization Problems

Usually there are only two main components of most genetic algorithms that are problem dependent: the problem encoding and the evaluation function.

Consider a parameter optimization problem where we must optimize a set of variables to either maximize some target such as profit, or to minimize cost or some measure of error. We might view such a problem as a black box with a series of control dials representing different parameters; the only output of the black box is a value returned by an evaluation function indicating how well a particular combination of parameter settings solves the optimization problems. The goal is to set the various parameters so as to optimize some output. In more traditional terms, we wish to minimize (or maximize) some function $F(X_1, X_2, ...X_M)$.

Most users of genetic algorithms typically are concerned with problems that are nonlinear: in other words, it is not possible to treat each parameter as an independent variable which can be solved in isolation from the other variables. There are interactions such that the combined effects of the parameters must be considered in order to maximize or minimize the output of the black box. In the genetic algorithm community, the interaction between variables is sometimes referred to as epistasis.

The first assumption that is typically made is that the variables representing parameters can be represented by bit strings. This means that the variables are discretized in an a priori fashion, and that the range of the discretization corresponds to some power of 2. For example, with 10 bits per parameter, we obtain a range with 1024 discrete values. If the parameters are actually continuous then this discretization is not a particular problem. This

assumes, of course, that the discretization provides enough resolution to make it possible to adjust the output with the desired level of precision. It also assumes that the discretization is in some sense representative of the underlying function.

If some parameter can only take on an exact finite set of values then the coding issue becomes more difficult. For example, what if there are exactly 1200 discrete values which can be assigned to some variable $X_i$. We need at least 11 bits to cover this range, but this codes for a total of 2048 discrete values. The 848 unnecessary bits patterns may result in no evaluation (i.e., a default worst possible evaluation) or some parameter settings may be represented twice so that all binary strings result in a legal set of parameter values which can be evaluated. Solving such coding problems is usually considered to be part of the design of the evaluation function.

Aside from the coding issue, the evaluation function is usually given as part of the problem description. On the other hand, developing an evaluation function can sometimes involve developing a simulation. In other cases, the evaluation may be performance based and may represent only an approximate or partial evaluation. For example, consider a control application where the system can be in any one of an exponentially large number of possible states. Assume a genetic algorithm is is used to optimize some form of control strategy. In such cases, the state space must be sampled in a limited fashion and the resulting evaluation of control strategies is approximate and noisy (c.f., Fitzpatrick and Grefenstette, 1988).

The evaluation function must also be relatively fast. This is typically true for any optimization method, but it may particularly pose an issue for genetic algorithms. Since genetic algorithms work with a population of potential solutions, it incurs the cost of evaluating this population. Furthermore, the population is replaced (all or in part) on a generational basis. The members of the population reproduce, and their offspring must then be evaluated. If it takes 1 hour to do an evaluation, then it takes over 1 year to do 10,000 evaluations. This would be approximately 100 generations for a population of 100, but only 10 generations using a population of 1000 strings.

## 1.2 How Hard is Hard?

Assuming the interaction between parameters is nonlinear, the size of the search space is related to the number of bits used in the problem encoding. For a bit string encoding of length $L$, the size of the search space is $2^L$ and forms a hypercube. The genetic algorithm samples the corners of this $L$-dimensional hypercube.

Generally, most test functions are at least 30 bits in length and most researchers would probably agree that larger test functions are probably needed. Anything much smaller represents a space which can be enumerated. (Considering for a moment that the national debt of the United States in 1993 is approximately $2^{42}$ dollars, $2^{30}$ does not sound quite so large.) Of course, the expression $2^L$ grows exponentially with respect to $L$. Consider a problem with an encoding of 400 bits. How big is the associated search space? A classic introductory textbook on Artificial Intelligence gives one characterization of a space of this size. Winston (1992:102) points out that $2^{400}$ is a good approximation of the effective size of the search space of possible board configurations in chess. (This assumes the effective

branching factor at each possible move to be 16 and that a game is made up of 100 moves; $16^{100} = (2^4)^{100} = 2^{400}$). Winston states that this is "a ridiculously large number. In fact, if all the atoms in the universe had been computing chess moves at picosecond rates since the big bang (if any), the analysis would be just getting started."

The point is that as long as the number of "good solutions" to a problem are sparse with respect to the size of the search space, then random search or search by enumeration of a large search space is not a practical form of problem solving. On the other hand, any search other than random search imposes some bias in terms of how it looks for better solutions and where it looks in the search space. Genetic algorithms indeed introduce a particular bias in terms of what new points in the space will be sampled. Nevertheless, genetic algorithms belong to the class of methods known as "weak methods" in the Artificial Intelligence community because it makes relatively few assumptions about the problem that is being solved.

Of course, there are many optimization methods that have been developed in mathematics and operations research. What role do genetic algorithms play as an optimization tool? Genetic algorithms are often described as a global search method that does not use gradient information. Thus, nondifferentiable functions as well as functions with multiple local minima represent classes of problems to which genetic algorithms might be applied. Genetic algorithms, as a weak method, are robust but very general. If there exists a good specialized optimization method for a specific problem, then genetic algorithm may not be the best optimization tool for that application. On the other hand, some researchers work with hybrid algorithms that combine existing methods with genetic algorithms.

# 2 Variants of the Canonical Genetic Algorithm

The first step in the implementation of any genetic algorithm is to generate an initial population. In the canonical genetic algorithm each member of this population will be a binary string of length L which corresponds to the problem encoding. Each string is sometimes referred to as a "genotype" (Holland, 1975) or, alternatively, a "chromosome" (Schaffer, 1987). In most cases the initial population is generated randomly. After creating an initial population, each string is then evaluated and assigned a *fitness* value.

The notion of *evaluation* and *fitness* are sometimes used interchangeably. However, it is useful to distinguish between the *evaluation function* and the *fitness function* used by a genetic algorithm. In this tutorial, the *evaluation function,* or *objective function,* provides a measure of performance with respect to a particular set of parameters. The *fitness function* transforms that measure of performance into an allocation of reproductive opportunities. The evaluation of a string representing a set of parameters is independent of the evaluation of any other string. The fitness of that string, however, is always defined with respect to other members of the current population.

In the canonical genetic algorithm, fitness is defined by: $f_i/\bar{f}$ where $f_i$ is the evaluation associated with string $i$ and $\bar{f}$ is the average evaluation of all the strings in the population. Fitness can also be assigned based on a string's rank in the population (Baker, 1985; Whitley, 1989) or by sampling methods, such as tournament selection (Goldberg, 1990).

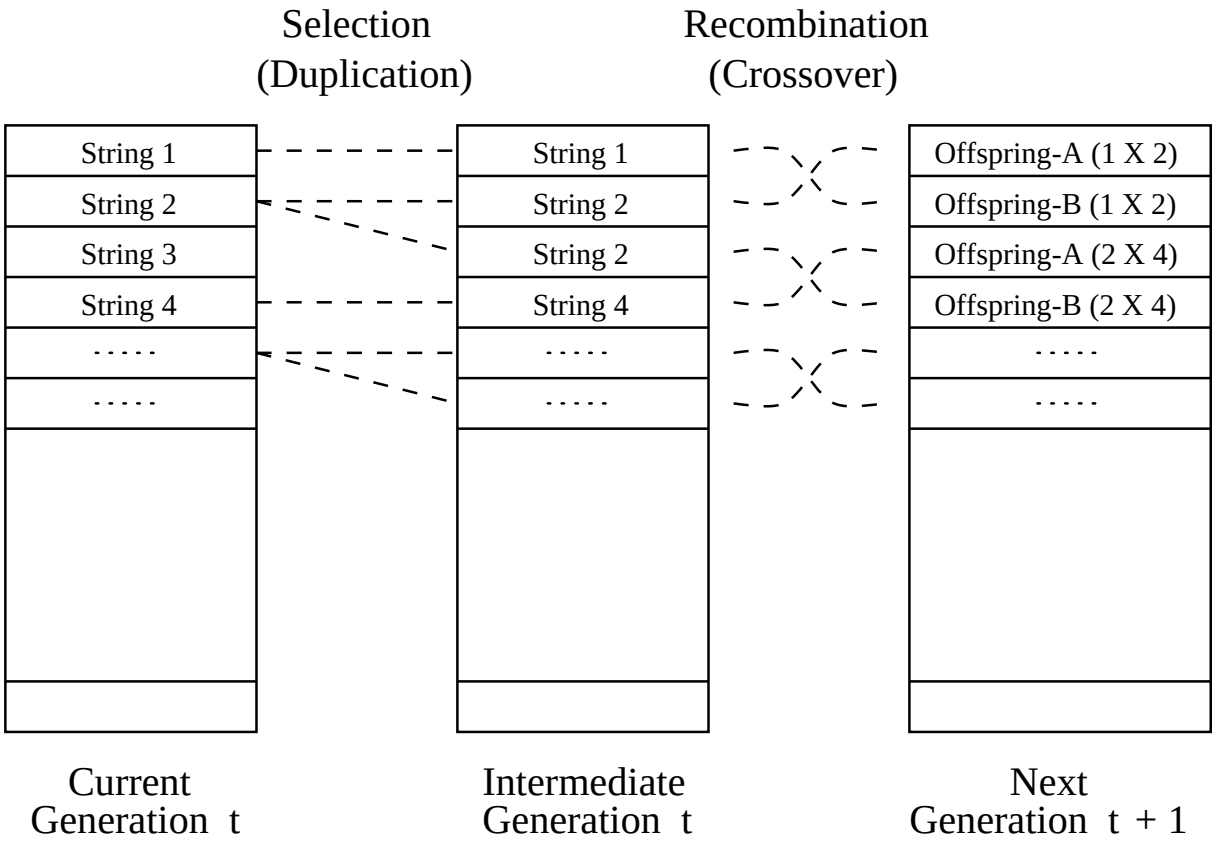



Figure 1: *One generation is broken down into a selection phase and recombination phase. This figure shows strings being assigned into adjacent slots during selection. In fact, they can be assigned slots randomly in order to shuffle the intermediate population. Mutation (not shown) can be applied after crossover.*

It is useful to view the execution of the genetic algorithm as a two stage process. It starts with the *current population*. Selection is applied to the current population to create an *intermediate population*. Then recombination and mutation are applied to the intermediate population to create the *next population*. The process of going from the current population to the next population constitutes one generation in the execution of a genetic algorithm. Goldberg (1989) refers to this basic implementation as a Simple Genetic Algorithm (SGA).

We will first consider the construction of the intermediate population from the current population. In the first generation the current population is also the initial population. After calculating $f_i/\bar{f}$ for all the strings in the current population, selection is carried out. In the canonical genetic algorithm strings in the current population are copied (i.e., duplicated) in proportion to their fitness and placed in the intermediate generation.

There are a number of ways that the selection process can be carried out. For example, we might view the entire population as mapping onto a roulette wheel, where each individual is represented on the roulette wheel by a space that proportionally corresponds to its fitness. By repeatedly spinning the roulette wheel, individuals are chosen to fill the intermediate population. This amounts to "stochastic sampling with replacement."

A selection process that will more closely match the expected fitness values is "remainder stochastic sampling." For each string $i$ where $f_i/\bar{f}$ is greater than 1.0, the integer portion of this number indicates how many copies of that string are directly placed in the intermediate population. All strings (including those with $f_i/\bar{f}$ less than 1.0) then place additional copies in the intermediate population with a probability corresponding to the fractional portion of $f_i/\bar{f}$. For example, a string with $f_i/\bar{f} = 1.36$ places 1 copy in the intermediate population, and then receives a 0.36 chance of placing a second copy. A string with a fitness of $f_i/\bar{f} = 0.54$ has a 0.54 chance of placing one string in the intermediate population.

One can view "remainder stochastic sampling" as using a roulette wheel which represents the fractional parts of the fitness values in the correct proportions. In sampling with replacement, the same roulette wheel is used to pick copies of strings until the population is full. In sampling without replacement, the number of strings represented on the roulette wheel is reduced by one each time a string is chosen to be placed in the intermediate population.

After selection has been carried out the construction of the intermediate population is complete and recombination can occur. This can be viewed as creating the *next population* from the intermediate population. Crossover is applied to randomly paired strings with a probability denoted $p_c$. (The population should already be sufficiently shuffled by the random selection process.) Pick a pair of strings. With probability $p_c$ "recombine" these strings to form two new strings that are inserted into the next population.

Consider the following binary string: 1101001100101101. The string would represent a possible solution to some parameter optimization problem. New sample points in the space are generated by recombining two parent strings. Consider the string 1101001100101101 and another binary string, yxyyxyxxyyyyxyxxy, in which the values 0 and 1 are denoted by x and y. Using a single randomly chosen crossover point, recombination occurs as follows.

```
11010 \/ 01100101101
yxyyx /\ yxxyyyxyxxy
```

Swapping the fragments between the two parents produces the following offspring.

```
11010yxxyyyxyxxy          and          yxyyx01100101101
```

After recombination, we can apply a mutation operator. For each bit in the population, mutate with some low probability $m$. Typically the mutation rate is applied with less than 1% probability. In some cases, mutation is interpreted as randomly generating a new bit, in which case, only 50% of the time will the "mutation" actually change the bit value. In other cases, mutation is interpreted to mean actually flipping the bit. The difference is no more than an implementation detail as long as the user/reader is aware of the difference and understands that the first form of mutation produces a change in bit values only half as often as the second, and that one version of mutation is just a scaled version of the other.

After the process of selection, recombination and mutation are complete, the next population can be evaluated. The process of evaluation, selection, recombination and mutation forms one *generation* in the execution of a genetic algorithm.

The algorithm that has just been described is not precisely the genetic plan first described by Holland. All strings are selected according to fitness in the preceding version of the canonical genetic algorithm. However, Holland (1975) assumed that one string was picked according to fitness, and the second was picked randomly. These strings were then placed in the intermediate population as a pair. Holland's original algorithm can be summarized as follows. We will now characterize the process as one of directly constructing a new population from the old population.

1. Initialize Population.
2. Evaluate each member of the Population.
3. Select a chromosome from the Population based on fitness.
4. Perform crossover with probability $p_c$. If crossover is not performed, put chromosome into the New_Population and Goto Step 5. Otherwise:
   (a) Select mate from population with uniform probability.
   (b) Select crossover point between 1 and L-1 with uniform probability.
   (c) Recombine chromosomes and place both offspring in the New_Population.
5. If New_Population not full, Goto step 3.
6. New_Population full, Population = New_Population. Goto step 2.

One reason for considering both the simple genetic algorithm and Holland's original genetic plan is to understand the different theoretical constructs which can be found in the literature. Some literature is based on one form of the algorithm, while other works are based on the alternative form. See Schaffer (1987) for a nice discussion of these two forms.

## 2.1 Why does it work? Search Spaces as Hypercubes.

The question that most people who are new to the field of genetic algorithms ask at this point is why such a process should do anything useful. Why should one believe that this is going to result in an effective form of search or optimization?

The answer which is most widely given to explain the computational behavior of genetic algorithms came out of John Holland's work. In his classic 1975 book, *Adaptation in Natural and Artificial Systems*, Holland develops several arguments designed to explain how a "genetic plan" or "genetic algorithm" can result in complex and robust search by implicitly sampling hyperplane partitions of a search space.

Perhaps the best way to understand how a genetic algorithm can sample hyperplane partitions is to consider a simple 3-dimensional space (see Figure 2). Assume we have a problem encoded with just 3 bits; this can be represented as a simple cube with the string 000 at the origin. The corners in this cube are numbered by bit strings and all adjacent corners are labelled by bit strings that differ by exactly 1-bit. An example is given in the top of Figure 2. The front plane of the cube contains all the points that begin with 0. If "*" is used as a "don't care" or wild card match symbol, then this plane can also be represented by the special string 0**. Strings that contain * are referred to as schemata; each schema corresponds to a hyperplane in the search space. The "order" of a hyperplane

refers to the number of actual bit values that appear in its schema. Thus, 1** is order-1 while 1**1******0** would be of order-3.

The bottom of Figure 2 illustrates a 4-dimensional space represented by a cube "hanging" inside another cube. The points can be labeled as follows. Label the points in the inner cube and outer cube exactly as they are labeled in the top 3-dimensional space. Next, prefix each inner cube labeling with a 1 bit and each outer cube labeling with a 0 bit. This creates an assignment to the points in hyperspace that gives the proper adjacency in the space between strings that are 1 bit different. The inner cube now corresponds to the hyperplane 1*** while the outer cube corresponds to 0***. It is also rather easy to see that *0** corresponds to the subset of points that corresponds to the fronts of both cubes. The order-2 hyperplane 10** corresponds to the front of the inner cube.

A bit string matches a particular schemata if that bit string can be constructed from the schemata by replacing the "*" symbol with the appropriate bit value. In general, all bit strings that match a particular schemata are contained in the hyperplane partition represented by that particular schemata. Every binary encoding is a "chromosome" which corresponds to a corner in the hypercube and is a member of $2^l - 1$ different hyperplanes, where $l$ is the length of the binary encoding. (The string of all * symbols corresponds to the space itself and is not counted as a partition of the space (Holland 1975:72)). This can be shown by taking a bit string and looking at all the possible ways that any subset of bits can be replaced by "*" symbols. In other words, there are $l$ positions in the bit string and each position can be either the bit value contained in the string or the "*" symbol.

It is also relatively easy to see that $3^l - 1$ hyperplane partitions can be defined over the entire search space. For each of the $l$ positions in the bit string we can have either the value *, 1 or 0 which results in $3^l$ combinations.

Establishing that each string is a member of $2^l - 1$ hyperplane partitions doesn't provide very much information if each point in the search space is examined in isolation. This is why the notion of a population based search is so critical to genetic algorithms. A population of sample points provides information about numerous hyperplanes; furthermore, low order hyperplanes should be sampled by numerous points in the population. (This issue is reexamined in more detail in subsequent sections of this paper.) A key part of a genetic algorithm's *intrinsic* or *implicit parallelism* is derived from the fact that many hyperplanes are sampled when a population of strings is evaluated (Holland 1975); in fact, it can be argued that far more hyperplanes are sampled than the number of strings contained in the population. Many different hyperplanes are evaluated in an *implicitly parallel* fashion each time a single string is evaluated (Holland 1975:74); but, of course, it is the cumulative effects of evaluating a population of points that provides statistical information about any particular subset of hyperplanes.[1]

[1]Holland initially used the term *intrinsic parallelism* in his 1975 monograph, then decided to switch to *implicit parallelism* to avoid confusion with terminology in parallel computing. Unfortunately, the term *implicit parallelism* in the parallel computing community refers to parallelism which is extracted from code written in functional languages that have no explicit parallel constructs. *Implicit parallelism* does not refer to the potential for running genetic algorithms on parallel hardware, although genetic algorithms are generally viewed as highly parallelizable algorithms.

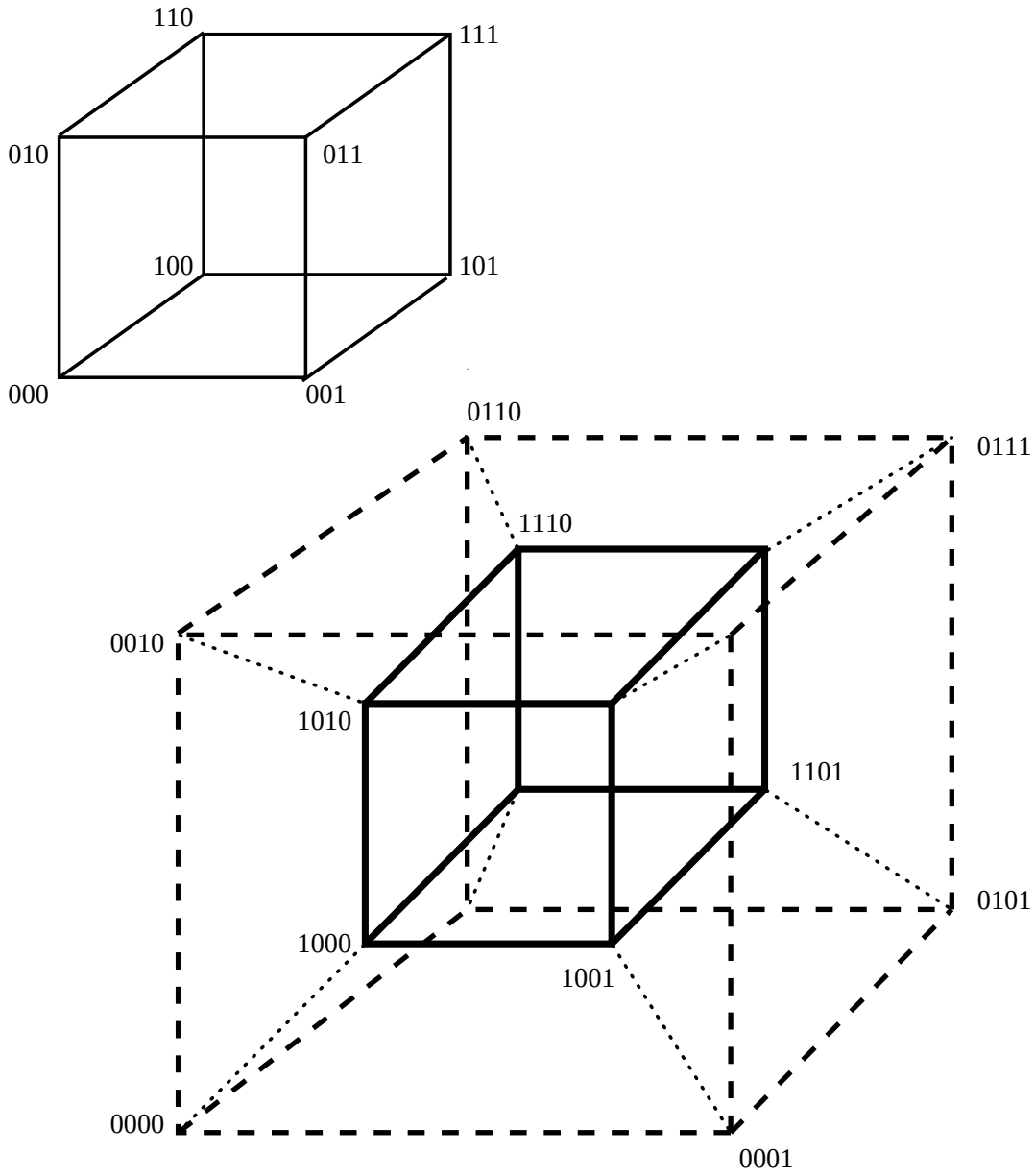



Figure 2: *A 3-dimensional cube and a 4-dimensional hypercube. The corners of the inner cube and outer cube in the bottom 4-D example are numbered in the same way as in the upper 3-D cube, except a 1 is added as a prefix to the labels of inner cube and a 0 is added as a prefix to the labels of the outer cube. Only select points are labeled in the 4-D hypercube.*

*Implicit parallelism* implies that many hyperplane competitions are simultaneously solved in parallel. The theory indicates that through the process of reproduction and recombination, the schemata of competing hyperplanes increase or decrease their representation in the population according to the relative fitness of the strings that lie in those hyperplane partitions. Because genetic algorithms operate on populations of strings one can track the proportional representation of a single schema representing a particular hyperplane in a population and indicate whether that hyperplane will increase or decrease its representation in the population over time when fitness based selection is combined with crossover to produce offspring from existing strings in the population.

# 3 Two Views of Hyperplane Sampling

Another way of looking at hyperspace partitions is presented in Figure 3. A function over a single variable is plotted as a one-dimensional space, with function maximization as a goal. The hyperplane 0****...** spans the first half of the space and 1****...** spans the second half of the space. Since the strings in the 0****...** partition are on average better than those in the 1****...** partition, the search will be proportionally biased toward this partition. In the second graph the portion of the space corresponding to **1**...** is shaded, which also highlights the intersection of 0****...** and **1**...**, namely, 0*1*...**. Finally, in the third graph, 0*10 is highlighted.

One of the points of Figure 3 is that the sampling of hyperplane partitions is not really effected by local minima. At the same time, increasing the sampling rate of partitions that are above average compared to other competing partitions does not guarantee convergence to a global optimum. The global optimum could be a relatively isolated peak, for example. Nevertheless, good solutions that are globally competitive should be found.

It is also a useful exercise to look at an example of a simple genetic algorithm in action. In Table 1, the first 3 bits of each string is given explicitly while the remainder of the bit positions are unspecified. The goal is to look at only those hyperplanes defined over the first 3 bit positions in order to see what actually happens during the selection phase where strings are duplicated according to fitness. The theory behind genetic algorithms suggest that the sampling rate of each hyperplane should change according to the average fitness of the strings in the population that are contained in the corresponding hyperplane partition. Thus, even though a genetic algorithm never explicitly evaluates any particular hyperplane partition, it should change the sampling rates of these hyperplanes as if it had.

The example population in Table 1 contains only 21 (partially specified) strings. Since we are not particularly concerned with the exact evaluation of these strings, the fitness values will be assigned according to rank. (The notion of assigning fitness by rank rather than by fitness proportional representation has not been discussed in detail, but the current example relates to change in representation due to fitness and not how that fitness is assigned.) The table includes information on the fitness of each string and the number of copies to be placed in the intermediate population. The number of copies produced during selection is determined by automatically assigning the integer part, then assigning the fractional part by generating a random value between 0.0 and 1.0 (a form of remainder stochastic sampling).

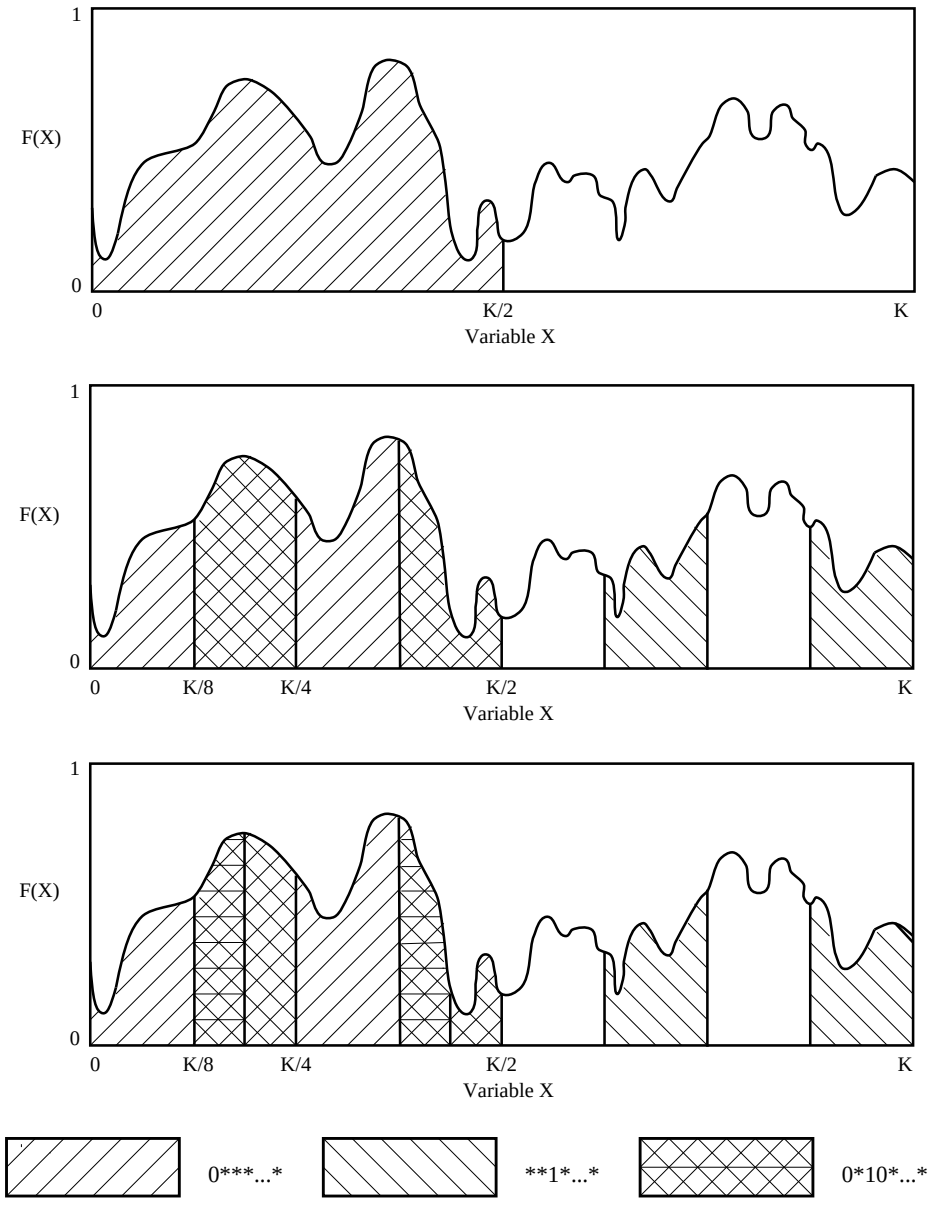



Figure 3: A function and various partitions of hyperspace. Fitness is scaled to a 0 to 1 range in this diagram.

| Strings and Fitness Values | | | |
|---|---|---|---|
| String | Fitness | Random | copies |
| $001b_{1,4}...b_{1,L}$ | 2.0 | – | 2 |
| $101b_{2,4}...b_{2,L}$ | 1.9 | 0.93 | 2 |
| $111b_{3,4}...b_{3,L}$ | 1.8 | 0.65 | 2 |
| $010b_{4,4}...b_{4,L}$ | 1.7 | 0.02 | 1 |
| $111b_{5,4}...b_{5,L}$ | 1.6 | 0.51 | 2 |
| $101b_{6,4}...b_{6,L}$ | 1.5 | 0.20 | 1 |
| $011b_{7,4}...b_{7,L}$ | 1.4 | 0.93 | 2 |
| $001b_{8,4}...b_{8,L}$ | 1.3 | 0.20 | 1 |
| $000b_{9,4}...b_{9,L}$ | 1.2 | 0.37 | 1 |
| $100b_{10,4}...b_{10,L}$ | 1.1 | 0.79 | 1 |
| $010b_{11,4}...b_{11,L}$ | 1.0 | – | 1 |
| $011b_{12,4}...b_{12,L}$ | 0.9 | 0.28 | 1 |
| $000b_{13,4}...b_{13,L}$ | 0.8 | 0.13 | 0 |
| $110b_{14,4}...b_{14,L}$ | 0.7 | 0.70 | 1 |
| $110b_{15,4}...b_{15,L}$ | 0.6 | 0.80 | 1 |
| $100b_{16,4}...b_{16,L}$ | 0.5 | 0.51 | 1 |
| $011b_{17,4}...b_{17,L}$ | 0.4 | 0.76 | 1 |
| $000b_{18,4}...b_{18,L}$ | 0.3 | 0.45 | 0 |
| $001b_{19,4}...b_{19,L}$ | 0.2 | 0.61 | 0 |
| $100b_{20,4}...b_{20,L}$ | 0.1 | 0.07 | 0 |
| $010b_{21,4}...b_{21,L}$ | 0 0 | – | 0 |

Table 1: A population with fitness assigned to strings according to rank. **Random** is used to determine whether or not to award a copy of a string for the fractional portion of the fitness measure.

If the random value is greater than the fractional remainder, then an additional copy is awarded to the corresponding individual.

Since the theory behind genetic algorithms suggests that many hyperplanes are processed implicitly in parallel when selection acts on the population of strings, Table 2 enumerates the 27 hyperplanes ($3^3$) that can be defined over the first three bits of the strings in the population and *explicitly* calculates the fitness of the sample of the corresponding hyperplane partition. The true value of the fitness associated with that hyperplane partition corresponds to the average fitness of all strings that lie in that hyperplane partition. The genetic algorithm uses the population as a sample for estimating the fitness of that hyperplane partition. Of course, the only time the sample is random is during the first generation. After this, the sampling is biased toward regions that have proven to contain strings that are above average with respect to previous populations.

| Schemata and Fitness Values | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| Schema | Avg | Exp | Obs | | Schema | Avg | Exp | Obs |
| 101*...* | 1.70 | 3.40 | 3 | | *0**...* | 0.99 | 10.9 | 10 |
| 111*...* | 1.70 | 3.40 | 4 | | 00**...* | 0.96 | 5.76 | 4 |
| 1*1*...* | 1.70 | 6.80 | 7 | | 0***...* | 0.93 | 9.30 | 10 |
| 01*...* | 1.38 | 6.90 | 6 | | 011*...* | 0.90 | 2.70 | 4 |
| *1*...* | 1.30 | 13.00 | 14 | | 010*...* | 0.90 | 2.70 | 2 |
| 11*...* | 1.22 | 6.10 | 8 | | 01**...* | 0.90 | 5.40 | 6 |
| 11**...* | 1.17 | 4.68 | 6 | | 0*0*...* | 0.83 | 4.98 | 3 |
| 001*...* | 1.16 | 3.48 | 3 | | *10*...* | 0.80 | 4.00 | 4 |
| 1***...* | 1.09 | 8.72 | 11 | | 000*...* | 0.76 | 2.28 | 1 |
| 0*1*...* | 1.03 | 6.18 | 7 | | **0*...* | 0.72 | 7.92 | 7 |
| 10**...* | 1.02 | 5.10 | 5 | | *00*...* | 0.66 | 3.96 | 4 |
| 1**...* | 1.01 | 10.1 | 12 | | 110*...* | 0.65 | 1.95 | 2 |
| ***...* | 1.00 | 21.0 | 21 | | 1*0*...* | 0.60 | 3.00 | 4 |
| | | | | | 100*...* | 0.50 | 1.00 | 1 |

Table 2: *The average fitnesses (Avg) associated with the samples from the 27 hyperplanes defined over the first three bit positions are explicitly calculated. The Expected representation (Exp) and Observed representation (Obs) are shown.*

If the genetic algorithm works as advertised, the number of copies of strings that actually fall in a particular hyperplane partition after selection should approximate the expected number of copies that should fall in that partition. The *expected* number of strings sampling a hyperplane partition after selection can be calculated by multiplying the number of copies in the current population before selection by the average fitness of the strings in the population that fall in that partition. Both the *expected* and *observed* number of copies in all 27 hyperplane partitions are given in Table 2. As can be seen, in most cases the match between expected and observed sampling rate is fairly good: the error is largely a result of sampling error due to the small population size.

At this point it is useful to begin formalizing the idea of tracking the sampling rate of a particular hyperplane, H. Let $M(H,t)$ be the number of strings sampling hyperplane H at the current generation $t$ in some population. Let $(t + intermediate)$ index the generation t after selection, and $f(H)$ be the average evaluation of the sample of strings in partition H in the current population. Formally, the notion that we are implicitly sampling a hyperplane $H$ according to hyperplane fitness is expressed as follows.

$$M(H, t + intermediate) = M(H,t)\frac{f(H)}{\bar{f}}.$$

## 3.1 Crossover Operators and Schemata

The *expected* representation of hyperplanes in Table 2 corresponds to the representation in the intermediate population after selection but before recombination. What does recombination do to the observed sampling rate of the hyperplane partitions? It is easy to see that the order-1 hyperplane samples are not affected by recombination, since the single critical bit is always inherited by one of the offspring. However, the observed sampling rate of hyperplane partitions of order-2 and higher can be affected by crossover. Furthermore, all hyperplanes of the same order are not necessarily affected with the same probability. Consider 1-point crossover. This recombination operator is nice because it is relatively easy to quantify its effects on different schemata representing hyperplanes. To keep things simple, assume we are are working with a string encoded with just 12 bits. Now consider the following two schemata.

`11**********` and `1**********1`

The probability that the bits in the first schema will be separated during 1-point crossover is only $1/L-1$, since in general there are $L-1$ crossover points in a string of length L. The probability that the bits in the second rightmost schema are disrupted by 1-point crossover however is $(L-1)/(L-1)$, or 1.0, since each of the L-1 crossover points separates the bits in the schema. This leads to a general observation: when using 1-point crossover the positions of the bits in the schema are important in determining the likelihood that those bits will remain together during crossover.

### 3.1.1 2-point Crossover

What happens if a 2-point crossover operator is used? A 2-point crossover operator uses two randomly chosen crossover points. Strings exchange the segment that falls between these two points. Ken DeJong first observed (1975) that two point crossover treats strings and schemata as if they form a ring, which can be illustrated as follows.


When viewed in this way, 1-point crossover is a special case of 2-point crossover where one of the crossover points always occurs at the wrap-around position between the first and last bit. Maximum disruptions for order-2 schemata now occur when the 2 bits are at complementary positions on this ring.

For 1-point and 2-point crossover it is clear that schemata which have bits that are close together on the string encoding are less likely to be disrupted by crossover. More precisely, hyperplanes represented by schemata with more compact representations should be sampled

at rates that are closer to those achieved under selection without crossover. To be even more precise, we need to define what is meant by a *compact representation* with respect to schemata. For current purposes a compact representation with respect to schemata is one that minimizes the probability of disruption during crossover. Note that this definition is operator dependent, since both of the 2 order-2 schemata examined in section 3.1 are equally and maximally compact with respect to 2-point crossover, but are maximally different with respect to 1-point crossover.

### 3.1.2 Linkage and Defining Length

Another concept that relates to this idea that different schemata are affected differently by crossover is *linkage.* Usually *linkage* refers to a set of bits that are physically adjacent (or at least close together) in the problem encoding. The idea behind linkage is that such bits act as "coadapted alleles" that tend to be inherited as a block. In this case an *allele* would correspond to a particular bit value in a specific position on the chromosome. Of course, linkage can be seen as a generalization of the notion of a *compact representation with respect to schema.* Equating linkage with physical adjacency in a string implicitly assumes that 1-point crossover is the operator being used; linkage for 2-point crossover is different and must be defined with respect to distance on the chromosome when treated as a ring. Nevertheless, linkage usually is equated with physical adjacency on a string, as measured by *defining length.*

The *defining length* of a schemata is based on the distance between the first and last bit in the schema with value either 0 or 1 (i.e., not a * symbol). Given that each position in a schema can be 0, 1 or *, then scanning left to right, if $I_x$ is the index of the position of the rightmost occurance of either a 0 or 1 and $I_y$ is the index of the leftmost occurance of either a 0 or 1, then the defining length is merely $I_y - I_x$. Thus, the defining length of $****1**0**10**$ is $12 - 5 = 7$. The defining length of a schema representing a hyperplane $H$ is denoted here by $\Delta(H)$. The defining length is a direct measure of how many crossover points fall within the significant portion of a schemata. If 1-point crossover is used, then $\Delta(H)/L - 1$ is also a direct measure of how likely crossover is to fall within the significant portion of a schemata during crossover.

### 3.1.3 Linkage and Inversion

Along with mutation and crossover, *inversion* is often considered to be a basic genetic operator. Inversion can potentially change the linkage of bits on the chromosome such that bits which have greater nonlinear interactions can potentially be moved closer together on the chromosome.

Typically, inversion is implemented by reversing a random segment of the chromosome. However, before one can start moving bits around on the chromosome to improve linkage, the bits must have a position independent decoding. A common error that some researchers make when first implementing inversion is too start reversing bit segments of a directly encoded chromosome. But just reversing some random segment of bits is nothing more than large scale mutation if the mapping from bits to parameters is position dependent.

A position independent encoding requires that each bit be tagged in some way. For example, consider the following encoding composed of pairs where the first number is a bit tag which indexes the bit and the second represents the bit value.

$$((6\ 0)\ (2\ 1)\ (7\ 1)\ (5\ 1)\ (3\ 0)\ (1\ 0)\ (4\ 0))$$

The linkage in this string can now be changed by moving around the tag-bit pairs, but the string remains the same when decoded: 010010110. One must now also consider how recombination is to be implemented. Goldberg and Bridges (1990), Whitley (1991) as well as Holland (1975) discuss the problems of exploiting linkage and the recombination of tagged representations.

# 4 The Schema Theorem

A foundation has been laid to now develop the fundamental theorem of genetic algorithms. The *schema theorem* (Holland, 1975) provides a lower bound on the change in the sampling rate for a single hyperplane from generation $t$ to generation $t+1$.

Consider again what happens to a particular hyperplane, $H$ when only selection occurs.

$$M(H, t + intermediate) = M(H, t)\frac{f(H)}{\bar{f}}.$$

To calculate M(H,t+1) we must consider the effects of crossover as the next generation is created from the intermediate generation. First we consider that crossover is applied probabilistically to a portion of the population. For that part of the population that does not undergo crossover, the representation due to selection is unchanged. When crossover does occur, then we must calculate losses due to its disruptive effects.

$$M(H, t+1) = (1 - p_c)M(H, t)\frac{f(H)}{\bar{f}} + p_c\left[M(H, t)\frac{f(H)}{\bar{f}}(1 - losses) + gains\right]$$

In the derivation of the schema theorem a conservative assumption is made at this point. It is assumed that crossover within the defining length of the schema is always disruptive to the schema representing H. In fact this is not true and an exact calculation of the effects of crossover is presented later in this paper. For example, assume we are interested in the schema 11*****. If a string such as 1110101 were recombined between the first two bits with a string such as 1000000 or 0100000, no disruption would occur in hyperplane 11***** since one of the offspring would still reside in this partition. Also, if 1000000 and 0100000 were recombined exactly between the first and second bit, a new independent offspring would sample 11*****; this is the sources of *gains* that is referred to in the above calculation. To simplify things, *gains* are ignored and the conservative assumption is made that crossover falling in the significant portion of a schema always leads to disruption. Thus,

$$M(H, t+1) \geq (1 - p_c)M(H, t)\frac{f(H)}{\bar{f}} + p_c\left[M(H, t)\frac{f(H)}{\bar{f}}(1 - disruptions)\right]$$

where *disruptions* overestimates losses by assuming crossover is always disruptive. We might wish to consider one exception: if two strings that both sample $H$ are recombined, then no disruption occurs. In Holland's original algorithm a mate is chosen uniformly without bias. Thus the probability of a mate sampling $H$ is just $M(H,t)$ divided by the population size which will be denoted by $P(H,t)$. Disruption is thus given by:

$$\frac{\Delta(H)}{L-1}(1-P(H,t)).$$

At this point, the inequality can be simplified. Both sides can be divided by the population size to convert this into an expression for $P(H,t+1)$, the proportional representation of $H$ at generation $t+1$. Furthermore the expression can be rearranged with respect to $p_c$.

$$P(H,t+1) \geq P(H,t)\,\frac{f(H)}{\bar{f}}\,\left[1-p_c\frac{\Delta(H)}{L-1}(1-P(H,t))\right]$$

We now have a useful version of the schema theorem (although it does not yet consider mutation); but it is not the only version in the literature. For example, this version is consistent with the fact that selection for the first parent string is fitness based and the second parent is chosen randomly. But we have also examined a form of the simple genetic algorithm where both parents are chosen based on fitness. This can be added to the schema theorem by merely indicating the alternative parent is chosen from the intermediate population after selection.

$$P(H,t+1) \geq P(H,t)\,\frac{f(H)}{\bar{f}}\,\left[1-p_c\frac{\Delta(H)}{L-1}(1-P(H,t)\,\frac{f(H)}{\bar{f}})\right]$$

Finally, mutation is included. Let $o(H)$ be a function that returns the order of the hyperplane H. The order of $H$ exactly corresponds to a count of the number of bits in the schema representing $H$ that have value 0 or 1. Let the mutation probability be $p_m$ where mutation always flips the bit. Thus the probability that mutation does affect the schema representing H is $(1-p_m)^{o(H)}$. This leads to the following expression of the schema theorem.

$$P(H,t+1) \geq P(H,t)\,\frac{f(H)}{\bar{f}}\,\left[1-p_c\frac{\Delta(H)}{L-1}(1-P(H,t)\,\frac{f(H)}{\bar{f}})\right]\,(1-p_m)^{o(H)}$$

## 4.1 Crossover, Mutation and Premature Convergence

Clearly the schema theorem places the greatest emphasis on the role of crossover and hyperplane sampling in genetic search. To maximize the preservation of hyperplane samples after selection, the disruptive effects of crossover and mutation should be minimized. This suggests that mutation should perhaps not be used at all, or at least used at very low levels.

The motivation for using mutation, then, is to prevent the permanent loss of any particular bit or allele. After several generations it is possible that selection will drive all the bits

in some position to a single value: either 0 or 1. If this happens without the genetic algorithm converging to a satisfactory solution, then the algorithm has *prematurely converged.* This may particularly be a problem if one is working with a small population. Without a mutation operator, there is no possibility for reintroducing the missing bit value. Also, if the target function is nonstationary and the fitness landscape changes over time (which is certainly the case in real biological systems), then there needs to be some source of continuing genetic diversity. Mutation, therefore acts as a background operator, occasionally changing bit values and allowing alternative alleles (and hyperplane partitions) to be retested.

This particular interpretation of mutation ignores its potential as a hill-climbing mechanism: from the strict hyperplane sampling point of view imposed by the schema theorem mutation is a necessary evil. But this is perhaps a limited point of view. There are several experimental researchers that point out that genetic search using mutation and no crossover often produces a fairly robust search. And there is little or no theory that has addressed the interactions of hyperplane sampling and hill-climbing in genetic search.

Another problem related to premature convergence is the need for *scaling* the population fitness. As the average evaluation of the strings in the population increases, the variance in fitness decreases in the population. There may be little difference between the best and worst individual in the population after several generations, and the selective pressure based on fitness is correspondingly reduced. This problem can partially be addressed by using some form of fitness scaling (Grefenstette, 1986; Goldberg 1989). In the simplest case, one can subtract the evaluation of the worst string in the population from the evaluations of all strings in the population. One can now compute the average string evaluation as well as fitness values using this adjusted evaluation, which will increase the resulting selective pressure. Alternatively, one can use some rank based form of selection.

## 4.2 How Recombination Moves Through a Hypercube

The nice thing about 1-point crossover is that it is easy to model analytically. But it is also easy to show analytically that if one is interested in minimizing schema disruption, then 2-point crossover is better. But operators that use many crossover points should be avoided because of extreme disruption to schemata. This is again a point of view imposed by a strict interpretation of the schema theorem. On the other hand, disruption may not be the only factor affecting the performance of a genetic algorithm.

### 4.2.1 Uniform Crossover

The operator that has received the most attention in recent years is *uniform crossover.* Uniform crossover was studied in some detail by Ackley (1987) and popularized by Syswerda (1989). Uniform crossover works as follows: for each bit position 1 to L, randomly pick each bit from either of the two parent strings. This means that each bit is inherited independently from any other bit and that there is, in fact, no linkage between bits. It also means that uniform crossover is unbiased with respect to defining length. In general the probability of disruption is $1 - (1/2)^{o(H)-1}$, where o(H) is the order of the schema we are interested in. (It doesn't matter which offspring inherits the first critical bit, but all other bits must be

inherited by that same offspring. This is also a worst case probability of disruption which assumes no alleles found in the schema of interest are shared by the parents.) Thus, for any order-3 schemata the probability of uniform crossover separating the 2 critical bits is always $1 - (1/2)^2 = 0.75$. Consider for a moment a string of 9 bits. The defining length of a schema must equal 6/8 before the disruptive probabilities of 1-point crossover match those associated with uniform crossover. We can define 84 different order-3 schemata over any particular string of 9 bits (i.e., 9 choose 3). Of these schemata, only 19 of the 84 order-2 schemata have a disruption rate higher than 0.75 under 1-point crossover. Another 15 have exactly the same disruption rate, and 50 of the 84 order-2 schemata have a lower disruption rate. It is relative easy to show that, while uniform crossover is unbiased with respect to defining length, it is also generally more disruptive than 1-point crossover. Spears and DeJong (1991) have shown that uniform crossover is in every case more disruptive than 2-point crossover for order-3 schemata for all defining lengths.

Despite these analytical results, several researchers have suggested that uniform crossover is sometimes a better recombination operator. One can of course point to its lack of representational bias with respect to schema disruption as a possible explanation, but this is unlikely since it is uniformly worse than 2-point crossover. However, Spears and DeJong (1991:314) speculated that, "With small populations, more disruptive crossover operators such as uniform or $n$-point ($n >> 2$) may yield better results because they help overcome the limited information capacity of smaller populations and the tendency for more homogeneity." Eshelman (1991) has made similar arguments outlining the advantages of disruptive operators.

There is another sense in which uniform crossover is unbiased. Assume we wish to recombine the bits string 0000 and 1111. We can conveniently lay out the 4-dimensional hypercube as shown in Figure 4. We can also view these strings as being connected by a set of minimal paths through the hypercube. To define a minimal path though the hypercube, pick one parent string as the origin and the other as the destination. Now change a single bit in the binary representation corresponding to the point of origin. Any such move will reach a point that is one move closer to the destination. In the following graph, which is arranged with respect to 0000 and 1111, it is easy to see that changing a single bit is a move up or down in this graph.

All of the points between 0000 and 1111 are reachable by some single application of uniform crossover. However, 1-point crossover only generates strings that lie along two complementary paths (in the figure, the leftmost and rightmost paths) through this 4-dimensional hypercube. In general, uniform crossover will draw a complementary pair of sample points with equal probability from all points that lie along *any* complementary minimal paths in the hypercube between the two parents, while 1-point crossover samples points from only two specific complementary minimal paths between the two parent strings. It is also easy to see that 2-point crossover is less restrictive than 1-point crossover, since it can sample pairs of points where the bits inherited from each parent appears as a continuous substring–in this case all strings except 0101 and 1010. But, of course, this coverage does not hold for spaces of higher dimensions. The number of bits that are different between two strings is just the Hamming distance, $\mathcal{H}$. Not including the original parent strings, uniform crossover can generate $2^{\mathcal{H}-1}$ different strings, while 1-point crossover can generate $2(\mathcal{H} - 1)$ different

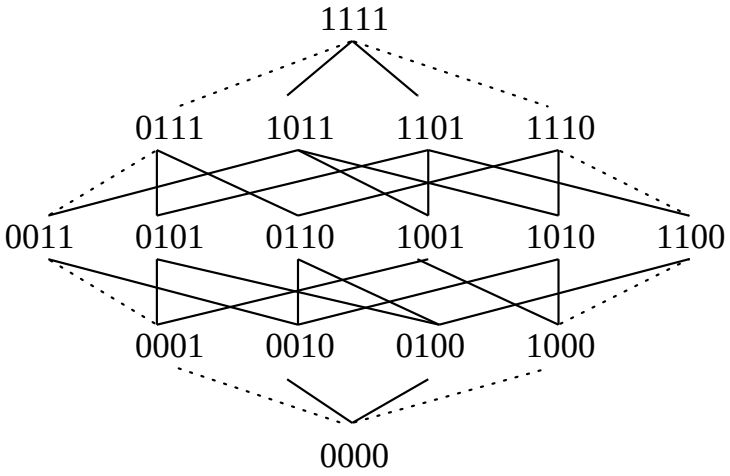



Figure 4: *This graph illustrates paths though 4-D space. A 1-point crossover of 1111 and 0000 can only generate offspring that reside along the dashed paths at the edges of this graph.*

strings since there are $\mathcal{H}$ crossover points that produce unique offspring (see the discussion in the next section) and each crossover produces 2 offspring. The 2-point crossover operator can generate $2\binom{\mathcal{H}}{2} = \mathcal{H}^2 - \mathcal{H}$ different offspring since there are $\mathcal{H}$ choose 2 different crossover points that will result in offspring that are not copies of the parents and each pair of crossover points generates 2 strings.

## 4.3 Reduced Surrogates

Consider crossing the following two strings and a "reduced" version of the same strings, where the bits the strings share in common have been removed.

```
0001111011010011          ----11---1-----1
0001001010010010          ----00---0-----0
```

Both strings lie in the hyperplane 0001**101*01001*. The flip side of this observation is that crossover is really restricted to a subcube defined over the bit positions that are different. We can isolate this subcube by removing all of the bits that are equivalent in the two parent structures. Booker (1987) refers to strings such as `----11---1-----1` and `----00---0-----0` as the "reduced surrogates" of the original parent chromosomes.

When viewed in this way, it is clear that recombination of these particular strings occurs in a 4-dimensional subcube, more or less identical to the one examined in the previous example. Uniform crossover is unbiased with respect to this subcube in the sense that uniform crossover will still sample in an unbiased, uniform fashion from all of the pairs of points that lie along complementary minimal paths in the subcube defined between the two original parent strings. On the other hand, simple 1-point or 2-point crossover will not. To help illustrate this idea, *we recombine the original strings*, but examine the offspring in their "reduced" forms. For example, simple 1-point crossover will generate offspring `----11---1-----0` and `----00---0-----1` with a probability of 6/15 since there are 6 crossover points in the

original parent strings between the third and fourth bits in the reduced subcube and L-1 = 15. On the other hand, `----10---0-----0` and `----01---1-----1` are sampled with a probability of only 1/15 since there is only a single crossover point in the original parent structures that falls between the first and second bits that define the subcube.

One can remove this particular bias, however. We apply crossover on the reduced surrogates. Crossover can now exploit the fact that there is really only 1 crossover point between any significant bits that appear in the reduced surrogate forms. There is also another benefit. If at least 1 crossover point falls between the first and last significant bits in the reduced surrogates, the offspring are guaranteed not to be duplicates of the parents. (This assumes the parents differ by at least two bits). Thus, new sample points in hyperspace are generated. Note that recombining the *original* parent strings between any of the first four bits results in offspring that are duplicates of the parents.

The debate on the merits of uniform crossover and operators such as 2-point reduced surrogate crossover is not a closed issue. To fully understand the interaction between hyperplane sampling, population size, premature convergence, crossover operators, genetic diversity and the role of hill-climbing by mutation requires better analytical methods.

# 5 The Case for Binary Alphabets

The motivation behind the use of a minimal binary alphabet is based on relatively simple counting arguments. A minimal alphabet maximizes the number of hyperplane partitions directly available in the encoding for schema processing. These low order hyperplane partitions are also sampled at a higher rate than would occur with an alphabet of higher cardinality.

Any set of order-1 schemata such as $1^{***}$ and $0^{***}$ cuts the search space in half. Clearly, there are L pairs of order-1 schemata. For order-2 schemata, there are $\binom{L}{2}$ ways to pick locations in which to place the 2 critical bits positions, and there are $2^2$ possible ways to assign values to those bits. This can be illustrated as follows:

| Order 1 Schemata | | | |
|---|---|---|---|
| 0*** | *0** | **0* | ***0 |
| 1*** | *1** | **1* | ***1 |

| Order 2 Schemata | | | | | |
|---|---|---|---|---|---|
| 00** | 0*0* | 0**0 | *00* | *0*0 | **00 |
| 01** | 0*1* | 0**1 | *01* | *0*1 | **01 |
| 10** | 1*0* | 1**0 | *10* | *1*0 | **10 |
| 11** | 1*1* | 1**1 | *11* | *1*1 | **11 |

In general, if we wish to count how many schemata representing hyperplanes exist at some order $i$, this value is given by $2^i\binom{L}{i}$ where $\binom{L}{i}$ counts the number of ways to pick $i$ positions that will have significant bit values in a string of length $L$ and $2^i$ is the number of ways to assign values to those positions.

These counting arguments naturally lead to questions about the relationship between population size and the number of hyperplanes that are sampled by a genetic algorithm. One can take a very simple view of this question and ask how many schemata of order-1 are processed and how well are they represented in a population of size N. These numbers

are based on the assumption that we are interested in hyperplane representations associated with the initial random population, since selection changes the distributions over time. In a population of size N there should be N/2 samples of each of the 2L order-1 hyperplane partitions. Therefore 50% of the population falls in any particular order-1 partition. Each order-2 partition is sampled by 25% of the population. In general then, each hyperplane of order $i$ is sampled by $1/2^i$ of the population.

## 5.1 The $N^3$ Argument

These counting arguments set the stage for the claim that a genetic algorithm processes on the order of $N^3$ hyperplanes when the population size is N. The derivation used here is based on the proof found in the appendix of Fitzpatrick and Grefenstette (1988).

First, pick a minimal level of representation. We wish to have at least $\phi$ samples before claiming that we are statistically sampling hyperplanes of order $\theta$. Let $\theta$ be the highest order of hyperplane which is represented in a population of size $N$ by at least $\phi$ copies; $\theta$ is given by $log(N/\phi)$.

Recall that the number of different hyperplane partitions of order-$\theta$ is given by $2^\theta \binom{L}{\theta}$ which is just the number of different ways to pick $\theta$ different positions and to assign all possible binary values to each subset of the $\theta$ positions. Thus, we now only need to show

$$2^\theta \left( \begin{array}{c} L \\ \theta \end{array} \right) \geq N^3 \qquad \text{which implies} \qquad 2^\theta \left( \begin{array}{c} L \\ \theta \end{array} \right) \geq (2^\theta \phi)^3$$

since $\theta = log(N/\phi)$, $2^\theta = N/\phi$ and $N = 2^\theta \phi$. Fitzpatrick and Grefenstette now make the following arguments. Assume $L \geq 64$ and $2^6 \leq N \leq 2^{20}$. Pick $\phi = 8$, which implies $3 \leq \theta \leq 17$. By inspection the number of schemata processed is greater than $N^3$.

Notice that this counts only those schemata that are exactly of order-$\theta$. While it is true that the number of schemata of order-$\theta$ is the dominating factor when counting the total number of schemata processed, the sum of all schemata from order-1 to order-$\theta$ that are processed is given by: $\sum_{x=1}^{\theta} 2^x \binom{L}{x}$.

## 5.2 The Case for Nonbinary Alphabets

There are two basic arguments against using higher cardinality alphabets. First, there will be fewer explicit hyperplane partitions. Second, the alphabetic characters (and the corresponding hyperplane partitions) associated with a higher cardinality alphabet will not be as well represented in a finite population. This either forces the use of larger population sizes or the effectiveness of statistical sampling is diminished.

The arguments for using binary alphabets assume that the schemata representing hyperplanes must be explicitly and directly manipulated by recombination. Antonisse (1989) has argued that this need not be the case and that higher order alphabets offer as much richness in terms of hyperplane samples as lower order alphabets. For example, using an alphabet of the four characters A, B, C, D one can define all the same hyperplane partitions in a binary

alphabet by defining partitions such as (A and B), (C and D), etc. In general, Antonisse argues that one can look at the all subsets of the power set of value assignments over the a "don't care" positions in a schema as defining hyperplanes. Viewed in this way, higher cardinality alphabets yield *more* hyperplane partitions that binary alphabets. Antonisse's arguments fail to show however, that the hyperplanes that corresponds to the subsets defined in this scheme are actually *processed* in a meaningful and useful way by a genetic algorithm.

There are other arguments for nonbinary encodings. Davis (1991) typically argues that the disadvantages of nonbinary encodings can be offset by the larger range of operators that can be applied to problems, and that more natural or problem dependent aspects of the coding can be exploited. Schaffer and Eshelman (1992) as well as Wright (1991) have made interesting arguments for real-valued encodings. Goldberg (1991) has suggested that virtual minimal alphabets can emerge from higher cardinality alphabets, thus facilitating hyperplane sampling.

# 6 An Executable Model of the Genetic Algorithm

Consider the complete version of the schema theorem before dropping the gains term and simplifying the calculation of losses.

$$P(Z,t+1) = P(Z,t)\frac{f(Z)}{\bar{f}}(1 - \{p_c \text{ losses}\}) + \{p_c \text{ gains.}\}$$

This is also part of an idealized model of a simple genetic algorithm (Goldberg, 1987). In the current formulation, Z might refer to either a string or a schema representing a hyperplane. Since modeling strings models the highest order schemata, the model implicitly includes all lower schemata. In the remainder of this paper, the equations are developed only for strings. Given a specification of Z, one can calculate string losses and gains. Losses occur when a string crosses with another string and the resulting offspring fails to preserve the original string. Gains occur when two different strings cross and independently create a new copy of some string. For example, if Z = 000 then recombining 100 and 001 will always produce a new copy of 000. Assuming 1-point crossover is used as an operator, the probability of "losses" and "gains" for the string Z = 000 are calculated as follows:

$$\text{losses} = P_{I0}\frac{f(111)}{\bar{f}}P(111,t) + P_{I0}\frac{f(101)}{\bar{f}}P(101,t)$$
$$+P_{I1}\frac{f(110)}{\bar{f}}P(110,t) + P_{I2}\frac{f(011,t)}{\bar{f}}P(011,t).$$

$$\text{gains} = P_{I0}\frac{f(001)}{\bar{f}}P(001,t)\frac{f(100)}{\bar{f}}P(100,t) + P_{I1}\frac{f(010)}{\bar{f}}P(010,t)\frac{f(100)}{\bar{f}}P(100,t)$$
$$+P_{I1}\frac{f(011)}{\bar{f}}P(011,t)\frac{f(100)}{\bar{f}}P(100,t) + P_{I2}\frac{f(001)}{\bar{f}}P(001,t)\frac{f(110)}{\bar{f}}P(110,t)$$
$$+P_{I2}\frac{f(001)}{\bar{f}}P(001,t)\frac{f(010)}{\bar{f}}P(010,t).$$

When Z is a string $P_{I0} = 1$ and represents the probably of crossover somewhere on the string. For Z = 000 there are two other order-2 schemata that are of interest. The first order-2 schema of interest, $h_1$, spans from the first to the second bit and the second order-2 schema of interest, $h_2$, spans from the second to the third bit. These are of interest because the defining lengths of these order-2 schemata provide probability information about the disruption of the order-3 schema. The probability that one-point crossover will fall between the first and second bit is merely $\Delta(h_1)/(L-1)$, which will be referred to as $P_{I1}$. Likewise, $P_{I2}$ will denote the probability that one-point crossover will fall between the second and third bit which is given by $\Delta(h_2)/(L-1)$.

The equations can be generalized to cover the remaining 7 strings in the space. This translation is accomplished using bitwise addition modulo 2 (i.e., a bitwise exclusive-or denoted by $\oplus$. See Figure 4 and Section 6.4). The function $(S_i \oplus Z)$ is applied to each bit string, $S_i$, contained in the equation presented in this section to produce the appropriate corresponding strings for generating an expression for computing all terms of the form P(Z,t+1).

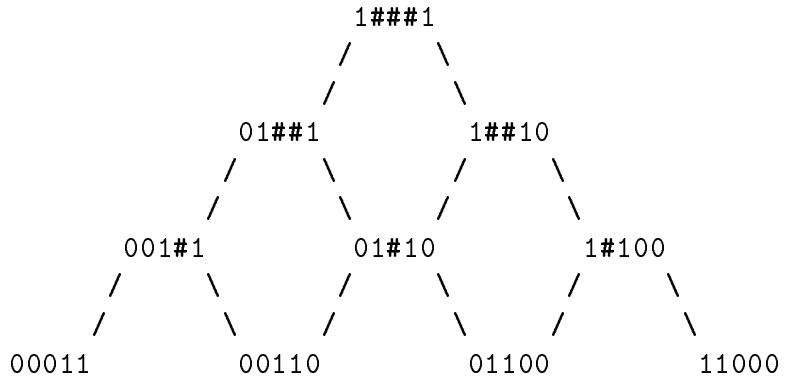
## 6.1 A Generalized Form Based on Equation Generators

The 3 bit equations were generated by hand; however, a general pattern exists which allows the automatic generation of equations for arbitrary problems (Whitley, Das and Crabb, 1992). The number of terms in the equations is greater than the number of strings in the search space. Therefore it is only practical to develop exact equations for problems with approximately 15 bits in the encoding.

The development of a general form for these equations is illustrated by generating the loss and gain terms in a systematic fashion. Note that the equations need only be defined once for one string in the space; the *standard form* of the equation is always defined for the string composed of all zero bits. Let $S$ represent the set of binary strings of length $L$, indexed by $i$. In general, the string composed of all zero bits is denoted $S_0$.

## 6.2 Generating String Losses for 1-point crossover

Consider two strings 00000000000 and 00010000100. Using 1-point crossover, if the crossover occurs before the first "1" bit or after the last "1" bit, no disruption will occur. Any crossover between the 1 bits, however, will produce disruption: neither parent will survive crossover. Also note that recombining 00000000000 with any string of the form 0001####100 will produce the same pattern of disruption. We will refer to this string as a generator: it is like a schema, but # is used here instead of * to better distinguish between a generator and the corresponding hyperplane. Bridges and Goldberg (1987) formalize the notion of a generator in the following way. Consider strings B and B′ where the first $x$ bits are equal, the middle $(\delta + 1)$ bits have the pattern $b\#\#...\#b$ for B and $\bar{b}\#\#...\#\bar{b}$ for B′. Given that the strings are of length $L$, the last $(L - \delta - x - 1)$ bits are equivalent. The $\bar{b}$ bits are referred to as "sentry bits" and they are used to define the probability of disruption. In standard form, $B = S_0$ and the sentry bits must be 1. The following directed acyclic graph illustrates all generators for "string losses" for the standard form of a 5 bit equation for $S_0$.




The graph structure allows one to visualize the set of all generators for string losses. In general, the root of this graph is defined by a string with a sentry bit in the first and last bit positions, and the generator token "#" in all other intermediate positions. A move down and to the left in the graph causes the leftmost sentry bit to be shifted right; a move down and to the right causes the rightmost sentry bit to be shifted left. All bits outside the sentry positions are "0" bits. Summing over the graph, one can see that there are $\sum_{j=1}^{L-1} \; j \cdot 2^{L-j-1}$ or $(2^L - L - 1)$ strings generated as potential sources of string loss.

For each string $S_i$ produced by one of the "middle" generators in the above graph structure, a term of the following form is added to the *losses* equations:

$$\delta(S_i)\frac{f(S_i)}{\bar{f}}\; P(S_i, t)$$

where $\delta(S_i)$ is a function that calculates the number of crossover points between sentry bits in string $S_i$, thus defining the critical crossover region for this particular string.

## 6.3 Generating String Gains for 1-point crossover

Bridges and Goldberg (1987) note that string gains for a string B are produced from two strings Q and R which have the following relationship to B.

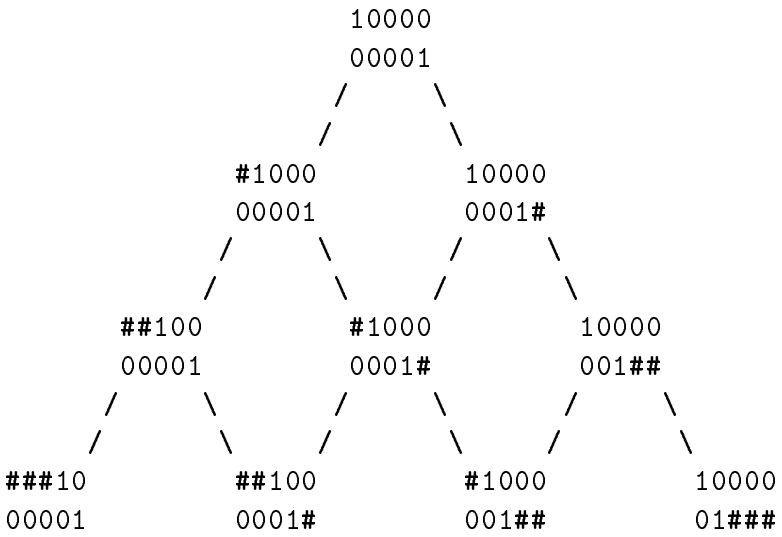
| Region -> | beginning | middle | end |
|---|---|---|---|
| Length -> | a | r | w |
| Q Characteristics | $\#\#...\#\bar{b}$ | = | = |
| R Characteristics | = | = | $\bar{b}\#...\#$ |

The "=" symbol denotes regions where the bits in Q and R match those in B; again B = $S_0$ for the *standard form* of the equations. Sentry bits are located such that 1-point crossover between sentry bits produces a new copy of B, while crossover of Q and R outside the sentry bits will not produce a new copy of B.

Bridges and Goldberg define a beginning function A[B,$\alpha$] and ending function $\Omega\,[B, \omega]$, assuming $L - \omega > \alpha - 1$, where for the standard form of the equations:

$$A\,[S_0, \alpha] = \#\#...\#\#1_{\alpha-1}0_{\alpha}...0_{l-1} \qquad \text{and} \qquad \Omega\,[S_0, \omega] = 0_0...0_{L-\omega-1}1_{L-\omega}\#\#...\#\#.$$

These generators can again be presented as a directed acyclic graph structure composed of paired templates which will be referred to as the upper A-generator and lower Ω-generator. The following are the generators in a 5 bit problem.




In this case, the root of the directed acyclic graph is defined by starting with the most specific generator pair. The A-generator of the root has a "1" bit as the sentry bit in the first position, and all other bits are "0." The Ω-generator of the root has a "1" bit as the sentry bit in the last position, and all other bits are "0." A move down and left in the graph is produced by shifting the left sentry bit of the current upper A-generator to the right. A move down and right is produced by shifting the right sentry bit of the current lower Ω-generator to the left. Each vacant bit position outside of the sentry bits which results from a shift operation is filled using the # symbol.

This graph structure allows one to observe that the number of generator pairs at each level of the tree is equal to the depth of the level at which the pair is located (where the root is level 1). Also, for any level $k$, the number of string pairs generated at that level is $2^{k-1}$ for each pair of generators. Therefore, the total number of string pairs that must be included in the equations to calculate string gains for $S_0$ of length $L$ is $\sum_{k=1}^{L-1} k \cdot 2^{k-1}$.

Let $S_{\alpha+x}$ and $S_{\omega+y}$ be two strings produced by a generator pair, such that $S_{\alpha+x}$ was produced by the A-generator and has a sentry bit at location $\alpha - 1$ and $S_{\omega+y}$ was produced by the Ω-generator with a sentry bit at $L-\omega$. (The x and y terms are simply correction factors added to $\alpha$ and $\omega$ in order to uniquely index a string in $S$.) Let the critical crossover region associated with $S_{\alpha+x}$ and $S_{\omega+y}$ be computed by a corresponding function $\sigma(S_{\alpha+x}, S_{\omega+y}) = L - \omega - \alpha$. For each string pair $S_{\alpha+x}$ and $S_{\omega+y}$ a term of the following form is added to the *gains* equations:

$$\frac{\sigma(S_{\alpha+x}, S_{\omega+y}) + 1}{L-1} \; \frac{f(S_{\alpha+x})}{\bar{f}} \; P(S_{\alpha+x}, t) \; \frac{f(S_{\omega+y})}{\bar{f}} \; P(S_{\omega+y}, t)$$

where $(\sigma(S_{\alpha+x}, S_{\omega+y}) + 1)/(L-1)$ is the probability that 1-point crossover will fall within the critical region defined by the sentry bits located at $\alpha - 1$ and $L - \omega$.

The generators are used as part of a two stage computation where the generators are first used to create an exact equation in standard form. This allows the resulting equations to be implemented in an executable form with a simple transformation function for all other strings in the space.

## 6.4 The Vose and Liepins Models

The executable equations developed by Whitley (1993a) represent a special case of the model of a simple genetic algorithm introduced by Vose and Liepins (1991). In the Vose and Liepins model, the vector $s^t \epsilon \Re$ represents the $t$ th generation of the genetic algorithm and the $i$ th component of $s^t$ is the probability that the string $i$ is selected for the gene pool. Using $i$ to refer to a string in $s$ can sometimes be confusing. The symbol $S$ has already been used to denote the set of binary strings, also indexed by $i$. This notation will be used where appropriate to avoid confusion. Note that $s^t$ corresponds to the expected distribution of strings in the *intermediate population* in the generational reproduction process (after selection has occurred, but before recombination).

In the Vose and Liepins formulation,

$$s_i^t \sim P(S_i, t) f(S_i)$$

where $\sim$ is the equivalence relation such that $x \sim y$ if and only if $\exists \gamma > 0 \mid x = \gamma y$. In this formulation, the term $1/\bar{f}$, which would represent the average population fitness normally associated with fitness proportional reproduction, can be absorbed by the $\gamma$ term.

The expected number of strings is also represented as a vector $p^t \epsilon \Re$ where the $k$ th component of the vector is equal to the proportional representation of $k$ at generation $t$ **before** selection occurs. This would be the same as $P(S_k, t)$ in the notation more commonly associated with the schema theorem. Finally let $r_{i,j}(k)$ be the probability that string $k$ results from the recombination of strings $i$ and $j$. Now, using $\mathcal{E}$ to denote expectation,

$$\mathcal{E}\ p_k^{t+1} = \sum_{i,j}\ \ s_i^t\ s_j^t\ r_{i,k}(k).$$

To further generalize this model, the function $r_{i,j}(k)$ is used to construct a mixing matrix $M$ where the $i,j$th entry $m_{i,j} = r_{i,j}(0)$. Note that this matrix gives the probabilities that crossing strings $i$ and $j$ will produce the string $S_0$. For current purposes, assume *no mutation* is used and 1-point crossover is used as the recombination operator. Then matrix $M$ is obviously symmetric and is zero everywhere on the diagonal except for entry $m_{0,0}$ which is 1.0. Note that $M$ is expressed entirely in terms of string gain information. Therefore, the first row/column of the matrix is the *inverse* of that portion of the string *losses* probabilities that corresponds to $\delta(S_i)$, where each string in the set $S$ is crossed with $S_0$. For completeness, the $\delta(S_i)$ for strings not produced by the string generators is 0.0 and, thus, the probability of obtaining $S_0$ during reproduction is 1.0. The remainder of the matrix can be calculated using string gain generators and $\frac{\sigma(S_{\alpha+x}, S_{\omega+y})+1}{L-1}$. For each pair of strings produced by the

| A Transform Function to Redefine Equations | |
|---|---|
| $000 \oplus 010 \Rightarrow 010$ | $100 \oplus 010 \Rightarrow 110$ |
| $001 \oplus 010 \Rightarrow 011$ | $101 \oplus 010 \Rightarrow 111$ |
| $010 \oplus 010 \Rightarrow 000$ | $110 \oplus 010 \Rightarrow 100$ |
| $011 \oplus 010 \Rightarrow 001$ | $111 \oplus 010 \Rightarrow 101$ |

Figure 5: *The operator $\oplus$ is bit-wise exclusive-or. Let $r_{i,j}(k)$ be the probability that $k$ results from the recombination of strings $i$ and $j$. If recombination is a combination of crossover and mutation then $r_{i,j}(k \oplus 0) = r_{i\oplus k, j\oplus k}(0)$. The strings shown here are reordered with respect to 010.*

*string gains generators* determine their index and enter the value returned by the function into the corresponding location in M. For completeness, $\sigma(S_j, S_k) = -1$ for all arbitrary pairs of strings not generated by the string gains generators, which implies entry $m_{j,k} = 0$.

Once defined $M$ does not change since it is not affected by variations in fitness or proportional representation in the population. Thus, given the assumption of no mutations, that $\gamma$ is updated each generation to correct for changes in the population average, and that 1-point crossover is used, then the standard form of the executable equations corresponds to the following portion of the Liepins and Vose model:

$$s^T M s$$

where $T$ denotes transpose.

While the fitness terms are defined explicitly in the executable equation, so far it has been assumed that $s$ includes fitness information without explicitly indicating how this is calculated. Fitness information is later added to the Vose and Liepins model. For now, however, this expression is first generalized to cover all strings in the search space. Vose and Liepins formalize the notion that bitwise exclusive-or can be used to remap all the strings in the search space, in this case represented by the vector $s$. They show that if recombination is a combination of crossover and mutation then

$$r_{i,j}(k \oplus q) = r_{i\oplus k, j\oplus k}(q) \quad \text{and specifically} \quad r_{i,j}(k) = r_{i,j}(k \oplus 0) = r_{i\oplus k, j\oplus k}(0).$$

This allows one to reorder the elements in $s$ with respect to any particular point in the space. This reordering is equivalent to remapping the variables in the executable equations (See Figure 4). A permutation function, $\rho$, is defined as follows:

$$\rho_j < s_0, ..., s_{V-1} >^T = < s_{j\oplus 0}, ..., s_{j\oplus(V-1)} >^T$$

where the vectors are treated as columns and V is the size of the search space. A general operator $\mathcal{M}$ can now be defined over s which remaps $s^T M s$ to cover all strings in the search space.

$$\mathcal{M}(s) = < (\rho_0\ s)^T M \rho_0\ s, ..., (\rho_{N-1}\ s)^T M \rho_{N-1}\ s >^T$$

Recall that $s$ carries fitness information such that it corresponds to the intermediate phase of the population (after selection, but before recombination) as the genetic algorithm goes from generation $t$ to $t+1$. Thus, to complete the cycle and reach a point at which the Vose and Liepins models can be executed in an iterative fashion, fitness information is now explicitly introduced to transform the population at the beginning of iteration $t+1$ to the next intermediate population. A fitness matrix $F$ is defined such that fitness information is stored along the diagonal; the $i,i$ th element is given by $f(i)$ where $f$ is the fitness function.

The transformation from the vector $p^{t+1}$ to the next intermediate population represented by $s^{t+1}$ is given as follows:

$$s^{t+1} \sim F\mathcal{M}(s^t).$$

Vose and Liepins give equations for calculating the mixing matrix M which not only includes probabilities for 1-point crossover, but also mutation. More complex extension of the Vose and Liepins model include finite population models using Markov Models (Nix and Vose, 1992). Vose (1993) surveys the current state of this research.

# 7 Other Models of Evolutionary Computation

Up to this point, the discussion has focused on the canonical genetic algorithm introduced by Holland (1975) and on related forms, such as the Simple Genetic Algorithm described by Goldberg (1989). But there are also several other population based algorithms that are either spin-offs of Holland's genetic algorithm, or which were developed independently. *Evolution Strategies* and *Evolutionary Programming* refers to two computational paradigms that use a population based search and largely rely on mutation rather than crossover.

Evolutionary Programming is based on the early work by Fogel, Owens and Walsh (1966), *Artificial Intelligence Through Simulated Evolution.* The individuals, or "organisms," in this study were finite state machines. Organisms that best solved some target function obtained the opportunity to reproduce. Parents were mutated to create offspring.

There has been renewed interest in Evolution Programming as reflected by the 1992 *First Annual Conference on Evolutionary Programming* (Fogel and Atmar 1992). Fogel and Atmar (1990) also compare genetic operators against Gaussian mutation and report that a population based search using only mutation found the best solution slightly more often search using crossover (6 out of 10 experiments), thus raising the issue as to the relative merits of mutation versus crossover.

*Evolution Strategies* are based on the work of Rechenberg (1973) and Schwefel (1975; 1981) and are discussed in a survey by Bäck, Hoffmeister and Schwefel (1991). Two examples of Evolution Strategies (ES) are the $(\mu+\lambda)$-ES and $(\mu,\lambda)$-ES. In $(\mu+\lambda)$-ES $\mu$ parents produce $\lambda$ offspring; the population is then reduced again to $\mu$ parents by selecting the best solutions from among both the parents and offspring. Thus, parents survive until they are replaced by better solutions. The $(\mu,\lambda)$-ES is closer to the generational model used in canonical genetic algorithms; offspring replace parents and then undergo selection. Recombination operators

have been defined for evolutionary strategies, but they tend to look different from Holland-style crossover, allowing operations such as averaging parameters, for example, to create an offspring. There is also generally a much greater emphasis on mutation.

## 7.1 Genitor

Genitor (Whitley 1988; 1989) was the first of what Syswerda (1989) has termed "steady state" genetic algorithms. The name "steady state" is somewhat of a misnomer, since Syswerda (1991) has shown that such genetic algorithms show more variance that canonical genetic algorithms in the terms of hyperplane sampling behavior. Such algorithms are therefore more susceptible to sample error and genetic drift. These algorithms would not closely conform to the kind of "idea sampling behavior" seem in the executable models of canonical genetic algorithms. The advantage, on the other hand, is that the best points found in the search are maintained in the population. This often results in a more aggressive form of search that in practice is often quite effective.

On the surface, there are three main differences between Genitor-style algorithms and canonical genetic algorithms. First, reproduction occurs one individual at a time. Two parents are selected for reproduction and produce an offspring that is immediately placed back into the population. The second major difference is in how that offspring is placed back in the population. In Genitor, the worst individual in the population is replaced. The important thing is that offspring do not replace parents, but rather some the least fit (or some relatively less fit) member of the population.

The third major difference between Genitor and other forms of genetic algorithms is that fitness is assigned according to rank rather than by fitness proportionate reproduction. Ranking helps to maintain a more constant selective pressure over the course of search.

As pointed out in a recent paper by DeJong and Sarma (1993) Holland examined both generational reproductive plans such as the canonical genetic algorithm and plans where a single individual was produced and inserted into the population; replacement was done by deleting one individual using a random uniform distribution. Holland also showed that generational reproduction and one-at-a-time selection and reproduction were theoretically equivalent, but that one-at-a-time selection was more subject to genetic drift.

One real difference between algorithms such as Genitor and the canonical genetic algorithm lies in the replacement scheme. Goldberg and Deb (1991) have shown that by replacing the worst member of the population Genitor generates much higher selective pressure that the canonical genetic algorithm. But higher selective pressure is not the only difference between Genitor and the canonical genetic algorithm. To borrow from the terminology used by the Evolution Strategy community (as suggested by Larry Eshelman), Genitor is a $(\mu + \lambda)$ strategy while the canonical genetic algorithm is a $(\mu, \lambda)$ strategy. This implies that the accumulation of improved strings in the population is monotonic in Genitor.

## 7.2 CHC

Another genetic algorithm that monotonically collects the best strings found so far is the CHC algorithm developed by Larry Eshelman (1991). CHC stands for *Crossover* using generational elitist selection, *Heterogeneous* recombination (by incest prevention) and *Cataclysmic* mutation, which is used to restart the search when the population starts to converge.

CHC explicitly borrows from the $(\mu + \lambda)$ strategy of Evolution Strategies. After recombination, the N best unique individuals are drawn from the parent population and offspring population to create the next generation. This also implies that duplicates are removed from the population. As Goldberg has shown with respect to Genitor, this kind of "survival of the fittest" replacement method already imposes considerable selective pressure, so that there is no real need to use other selection mechanism. Thus CHC used random selection, except restrictions are imposed on which strings are allowed to mate. Strings with binary encodings must be a certain Hamming distance away from one another before they are allowed to reproduce. This form of "incest prevention" is designed to promote diversity. Eshelman also uses a form of uniform crossover called HUX where exactly half of the differing bits are swapped during crossover. CHC is typically run using small population sizes (e.g. 50); thus using uniform crossover in this context is consistent with DeJong and Spears (1991) conjecture that uniform crossover can provide better sampling coverage in the context of small populations.

The rationale behind CHC is to have a very aggressive search (by using monotonic selection through survive of the best strings) and to offset the aggressiveness of the search by using high disruptive operators such as uniform crossover. With such small population sizes, however, the population convergences to the point that the population begins to more or less reproduce many of the same strings. At this point the CHC algorithm uses cataclysmic mutation; this is the only time mutation is used in the CHC algorithm. All strings undergo heavy mutation, except that the best string is preserved intact. After mutation, the search is restarted using only crossover. Eshelman and Schaffer have reported quite good results using CHC on a wide variety of test problems (Eshelman 1991; Eshelman and Schaffer 1991).

## 7.3 Hybrid Algorithms

L. "Dave" Davis states in the *Handbook of Genetic Algorithms,* "Traditional genetic algorithms, although robust, are generally not the most successful optimization algorithm on any particular domain" (1991:59). Davis argues that hybridizing genetic algorithms with the most successful optimization methods for particular problems gives one the best of both worlds: correctly implemented, these algorithms should do no worst than the (usually more traditional) method with which the hybridizing is done. And in many case the hybridization can result in a superior method since the genetic algorithm introduces the advantages of a broader, population based search. Of course, it also introduces the additional computational overhead of a population based search.

In general, Davis' approach to genetic algorithms is to customize the genetic algorithm to fit the problem rather than forcing the problem to fit into the constraints imposed by

the canonical genetic algorithm. Thus, Davis often uses real valued encodings instead of binary encodings, and employs "recombination operators" that may be domain specific. Other researchers, such as Michalewicz (1992) also use nonbinary encoding and specialized operations in combination with genetic based model of search.

Mühlenbein takes a similar opportunistic view of hybridization. In a description of a parallel genetic algorithm Mühlenbein (1991) states, after the initial population is created, "Each individual does local hill-climbing." Furthermore, after each offspring is create, "The offspring does local hill-climbing."

Researchers interested in theory and those interested in practical results tend to have very different view toward problem encodings. But the experimental researchers and theoreticians are particularly divided on the issue of hybridization.

By adding hill-climbing or hybridizing with some other optimization methods, learning is being added to the evolution process. Coding the learned information back onto the chromosome means that the search utilizes a form of Lamarckian evolution. The chromosomes improved by local hill-climbing or other methods are placed in the genetic population and allowed to compete for reproductive opportunities.

The main criticism is that *if* we wish to preserve the schema processing capabilities of the genetic algorithm, then Lamarckian learning should not be used. Changing information in the offspring inherited from the parents results in a loss of inherited schemata. This alters the statistical information about hyperplane partitions that is implicitly contained in the population. Therefore using local optimization to improve each offspring undermines the genetic algorithm's ability to search via hyperplane sampling. Hybrid algorithms that incorporate local optimizations should result in greater reliance on hill-climbing and less emphasis on hyperplane sampling. It follows that the resulting search should be less global, since it is hyperplane sampling that gives the genetic algorithm its global search ability.

Despite the theoretical objections, hybrid genetic algorithms typically do well at optimization tasks. There may be several reasons for this. First, the hybrid genetic algorithm is hill-climbing from multiple points in the search space. Unless the objective function is severely multimodal it may be likely that some strings (offspring) will be in the basin of attraction of the global solution, in which case hill-climbing is a fast and effective form of search. Second, a hybrid strategy impairs hyperplane sampling, but does not disrupt it entirely. For example, using learning or local optimization to improve the initial population of strings only biases the initial hyperplane samples, but does not interfere with subsequent hyperplane sampling. Third, in general hill-climbing may find a small number of significant improvements, but may not dramatically change the offspring. In this case, the effects on schemata and hyperplane sampling may be minimal.

# 8 Hill-climbers or Hyperplane Samplers?

In a recent paper entitled, "How genetic algorithms really work: I. Mutation and Hillclimbing," Mühlenbein shows that an Evolution Strategy algorithm using only mutation work quite well on a relatively simple test suite. Mühlenbein implies that for many problems

"many *nonstandard* genetic algorithms work well and the *standard* genetic algorithm performs poorly." (1992:24).

Whitley et al. (1991) analyzed the behavior of a Genitor-style genetic algorithm to investigate its hill-climbing behavior. The test problem was a small neural network optimization problem. Each parameter (i.e., weight) was represented a single real-valued number instead of a bit encoding. Relatively high mutation rates were also used. The experiments showed that as the population size was decreased down to a population of 1 individual, search became faster but that the probability of converging to a satisfactory solution decreased. Convergence was 90% for a population of 50 strings, 80% for a population of 5 strings and 72% for a population of 1 string that used only mutation. But the population of 1 string converged (when it converged) a order of magnitude faster than the population of 50 strings.

This raised a very interesting issue. When is a genetic algorithm a hyperplane sampler and when it is a hill-climber? This is a nontrivial question since it is the hyperplane sampling abilities of genetic algorithms that are usually touted as the source of global sampling. On the other hand, researchers in the evolutionary programming community tend to argue that crossover is unnecessary and that mutation is sufficient for robust and effective search. It should be emphasized that all of the theory concerning hyperplane sampling has been developed with respect to the canonical genetic algorithm. And the alternative forms of genetic algorithms often use mechanisms, such as monotonic selection of the best strings, which could easily lead to increased hill-climbing. This is a question which the genetic algorithm community needs to consider in more detail. Of course, the answer may often be that many genetic algorithms exploit a bit of both. In practice, however, there may some clues as to when hill-climbing is a dominant factor in a search.

First, hyperplane sampling requires larger population. Small populations are much more likely to rely on hill-climbing. A population of 20 individuals just doesn't provide very much information about hyperplane partitions, except perhaps the very low order hyperplanes (note that there are only 5 samples of each order-2 hyperplane in a population of 20). Second, very high selective pressure suggests hill-climbing may a dominant role in a search. Some researchers use an exponential bias toward the best individuals. But if one has a population of 100 strings and the 5 best individuals reproduce 95% of the time, then the effect population size is probably not large enough to support hyperplane sampling.

# 9 Parallel Genetic Algorithms

Part of the biological metaphor used to motivate genetic algorithms is that it is inherently a parallel form of search. In nature populations of thousands or even millions of individuals exist in parallel. This suggests a degree of parallelism that is directly proportional to the population size used in genetic search. It also suggests a way of using larger population sizes without increasing the amount of time that it takes to evaluate a single generation. Gordon, Whitley and Bohm (1992) have shown that when genetic algorithms are executed on a dataflow simulator which exploits all sources of parallelism, the time required to execute a single generation is indeed independent of population size. Of course, large populations also typically display slower convergence, which means that while the time to execute a

single generation may not change with larger population sizes, the number of generations to convergence may increase.

In this paper, three different ways of exploiting parallelism in genetic algorithms will be reviewed. First, a parallel genetic algorithm similar to the canonical genetic algorithm will be reviewed; next an *Island Model* using distinct subpopulations will be presented. Finally, a fine grain massively parallel implementation that assumes one individual resides at each processor will be explored. It can be shown that such algorithms are in fact a subclass of cellular automata (Whitley 1993b). Therefore, while these algorithms have been referred to by a number of somewhat awkward names (e.g., fine grain genetic algorithms, or massively parallel genetic algorithms) the name *cellular genetic algorithm* is used in this tutorial.

In each of the following models, strings are mapped to processors in a particular way. Usually this is done in a way that maximizes parallelism while avoiding unnecessary processor communication. However, any of these models could be implemented in massively parallel, fine grain fashion; similarly, any of these models could be implemented using a more course grain implementation. What does tend to be different is the role of local versus global communication.

## 9.1 Global Populations with Parallelism

The most direct way to implement a parallel genetic algorithm is to implement something close to a canonical genetic algorithm. The only change that will be made is that selection will be done by *Tournament Selection* (Goldberg 1990).

Tournament selection implements an approximate form of ranking. Recall that the implementation of one generation in a canonical genetic algorithm can be seen as a two step process. First, selection is used to create an intermediate population of duplicate strings selected according to fitness. Second, crossover and mutation is applied to produce the next generation. Instead of using fitness proportionate reproduction or directly using ranking, tournaments are held to fill the intermediate population. Assume two strings are selected out of the current population after evaluation. The best of the two strings is then placed in the intermediate population. This process of randomly selecting two strings from the current population and placing the best in the intermediate population is repeated until the intermediate population is full. A simple argument can be used to illustrate how this procedure will approximate a linear ranking with a bias of 2.0. A linear bias of 2.0 implies the best individual should be assigned a fitness of 2.0, the individual at the 75th percentile in the population should be assigned a fitness of 1.5, the median individual should be assigned a fitness of 1.0, the individual at the 25th percentile should be assigned a fitness of 0.5 and the worst individual in the population should have a fitness of 0.0. Now consider a tournament size of two, where the best of the two is selected. On average, each individual in the population is involved in two tournaments. Of course, the best individual will win both and in expectation will place 2 copies in the intermediate population. The median individual should have a 50% chance of winning any tournament, and thus, in expectation, places 1 copy in the intermediate population. The worst individual cannot win a tournament and has an effective fitness of 0.0.

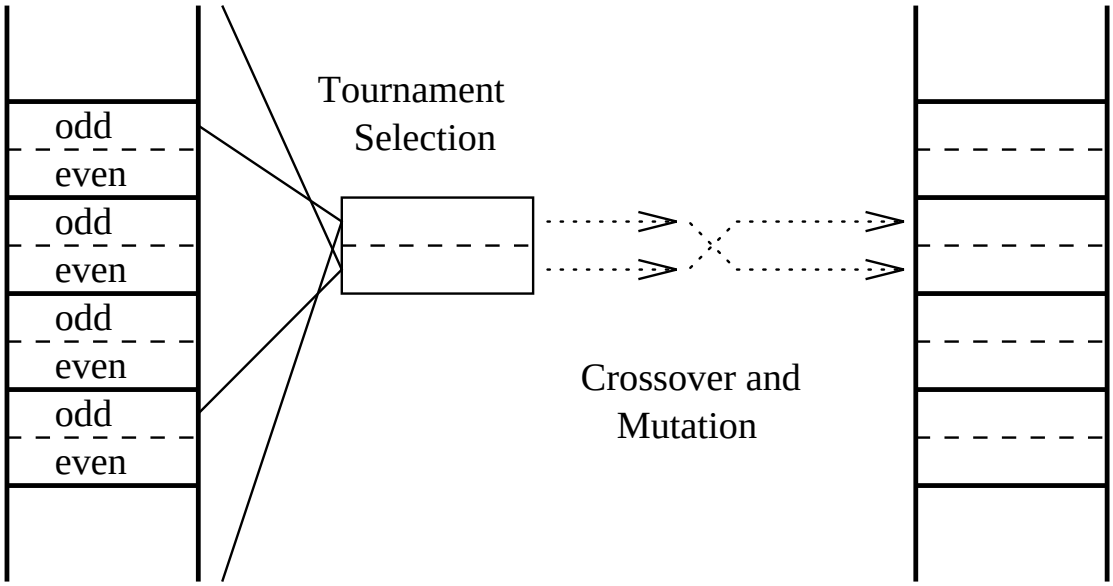


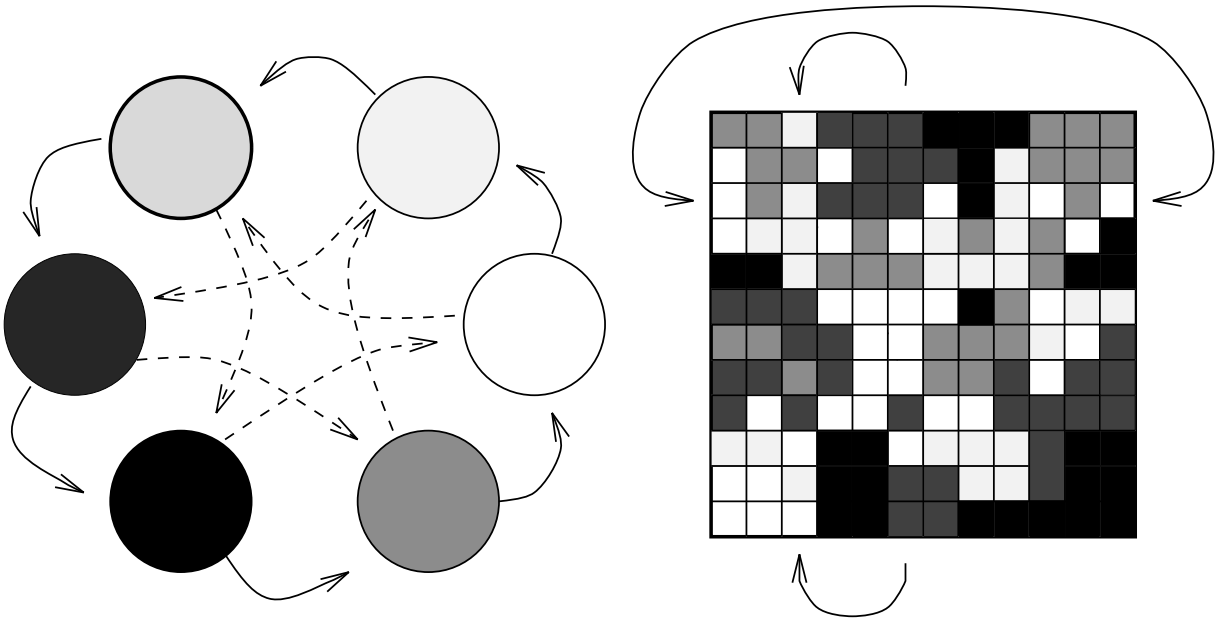

Figure 6: *An example of exploiting fine-grain parallelism in a simple genetic algorithm using Tournament Selection.*

With the addition of tournament selection, a parallel form of the canonical genetic algorithm can now be implemented in a fairly direct fashion. A simple genetic algorithm can be executed in parallel on N/2 processors, where N is the population size. Assume the processors are numbered 1 to N/2 and the population size is even. At each processor X resides two strings labeled 2X and 2X-1. First, the strings are evaluated. Next each processor holds two independent tournaments by randomly sampling strings in the population and each processor then keeps the winners of the two tournaments. The new strings that now reside in the processors represent the intermediate generation. Tournament selection also has the side of effect of randomly shuffling the intermediate population. Probabilistic crossover can be implemented by instructing those processors numbered less than $p_c * N/2$ to execute crossover on the strings in residence. All processors can carry out mutation on both strings, thus completing a single generation.

Note that this model is relatively fine grained, but preserves the global (i.e., *panmictic*) mating scheme characteristic of canonical genetic algorithms. This same basic approach also be implemented in parallel with 4, 6 or any even number of strings per processor.

## 9.2 Island Models

One motivation for using *Island Models* is to exploit a more course grain parallel model. Assume we wish to use 16 processors and have a population of 1,600 strings; or we might wish to use 64 processors and 6,400 strings. One way to do this is to break the total population down into subpopulations of 100 strings each. Each one of these subpopulations could then execute as a normal genetic algorithm. It could be a canonical genetic algorithm, or Genitor, or CHC. But occasionally, perhaps every five generation or so, the subpopulation would swap a few strings. This *migration* would allow the subpopulation to share genetic material.



An Island Model Genetic Algorithm

A Cellular Genetic Algorithm

Figure 7: *An example of both an island models and a cellular genetic algorithm. The coloring of the cells in the cellular genetic algorithm represents genetically similar material that forms virtual islands isolated by distance.*

(Whitley and Starkweather, 1990; Gorges-Schleuter, 1991; Tanese 1989; Starkweather et al., 1991.)

Assume for a moment that one executes 16 separate genetic algorithms, each using a population of 100 string *without migration.* In this case, 16 independent searches occurs. Each search will be somewhat different since the initial populations will impose a certain sampling bias; also, genetic drift will tend to drive these populations in different directions. Sampling error and genetic drift are particularly significant factors in small populations and, as previous noted, are even more pronounced in genetic algorithms such as Genitor and CHC when compared to the canonical genetic algorithm.

By introducing migration, the Island Model is able to exploit differences in the various subpopulation, which in fact represent a source of genetic diversity. Each subpopulation is an island, and there is some designated way in which genetic material is moved from one island to another. If a large number of strings migrate each generation, then global mixing occurs and local differences between islands will be driven out. If migration is too infrequent, it may not be enough to prevent each small population from prematurely converging.

## 9.3 Cellular Genetic Algorithms

Perhaps the easiest way to understand this model is to work from the architecture to the algorithm. Assume we have 2,500 simple processors laid out on a 50x50 2-dimensional grid. Processors only communicate with their immediate neighbors (e.g. north, south, east and

west: NSEW). But, the processors on the left edge of the grid wrap around so that they are directly connected to the processors in the same row on the right edge. Likewise, the processors on the bottom row are connect to the processors in the same column in the top row, thus forming a torus. How should one implement a genetic algorithm on such an architecture?

One can of course assign one string per processor or cell. But global random mating would now seen inappropriate given the communication restrictions. Instead, it is much more practical to have each string (i.e., processor) seek a mate close to home. One way to do this would be to have each processor check the location to the north, south, east and west, make a copy of the best string that it finds, then recombine the resident string with the selected string. Alternatively, some form of local probabilistic selection could be used. In either case, only one offspring would be produced. (Either one of the two possible offspring could be randomly selected, or they both could be evaluated and the best retained.) The offspring would become the new resident at that processor.

There are no explicit islands in the model, but there is the potential for similar effects. Assuming that mating is restricted to adjacent processors (i.e., NSEW), if one neighborhood of strings is 20 or 25 moves away from another neighbor of strings, these neighborhoods are just as isolated as two subpopulations on separate islands. This kind of separation is referred to as *isolation by distance.* (Wright, 1932; Collins and Jefferson, 1991; Muhlenbien, 1991; Gorges-Schleuter, 1991). Of course, neighbors that are only 4 or 5 moves away have a greater potential for interaction.

After the first random population is evaluated, the pattern of string over the set of processors tends to be itself rather random. After a few generations, however, there are many small local pockets of similar strings with similar fitness values. This is because local mating and selection creates local evolutionary trends, again due to sampling effects in the initial population and genetic drift. After several more generations, competition between these local groups means that now there are fewer different kinds of neighborhoods and of course the remaining neighborhoods are larger.

The mating scheme outlined for the cellular genetic algorithm is one of many possible schemes. The common theme is that selection and mating is typically restricted to a local neighborhood. Manderick (personal communication) reports that the population must be composed of at least 1000 individuals before local trends can emerge. Search proceeds by one neighborhood taking over another, although interesting new genetic mixes often appear at the boundaries between neighborhoods and may give rise to the emergence of a whole new local neighborhood.

# 10 Conclusions

One thing that is striking after reviewing the various genetic algorithms and the various parallel models is the richness of this form of computation. What may seem like simple changes in the algorithm often result in surprising kinds of emergent behavior. Recent theoretical advances have also improved out understanding of genetic algorithms and have

opened to the door to using more advanced analytical methods. We now need to use these tools in combination with empirical experiments to decide to which classes of problems genetic algorithms are best suited, as well as what kinds of problems are best solved using other algorithms.

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