

Learning Linkage

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Abstract

The topic of linkage has, with a few notable exceptions, been largely ignored. Recent studies have shown this approach to be a profound mistake— that GAs ignoring linkage do so at their own computational peril. Inversion, the operator usually called upon to solve this problem, has proven too slow *vis a vis* the forces of selection. Inversion is a mutation like operator that acts on chromosomal structures. Where evolution by mutation is too slow and has failed, it remains possible that evolution by pairwise recombination or crossover can be successful. This paper shows that tight linkage can be evolved within the environment of a new crossover operator.

1 Introduction

Early studies focused on the concepts of building blocks and linkage as central to understanding the GA (Holland, 1975). Since then, the topic of building blocks has been heavily explored while the topic of linkage has, with a few notable exceptions, been largely ignored (Goldberg, Korb, & Deb, 1989). Recent studies (Thierens & Goldberg, 1993) have shown this approach to be a profound mistake— that GAs ignoring linkage do so at their own computational peril.

It has long been thought that having tight linkage should be evolutionarily advantageous (Holland, 1975). It has further been assumed that any operator working on the structural representation of chromosomes would eventually evolve tightly linked representations and allow for the solving of difficult problems. Unfortunately for inversion, the most commonly used of such operators, eventually doesn't come soon enough (Goldberg & Bridges, 1990).

The forces of selection are much too fast for inversion to accomplish its goals before the GA converges. Inversion is a mutation like operator that acts on chromosomal structures. Where evolution by mutation is too slow and has failed, it remains possible that evolution by pairwise recombination or crossover can be successful.

The purpose of this paper is to explore the theoretical basis for the assumption that tight linkage can be evolved within the environment of a new crossover operator.

We begin by defining and analyzing a measure of linkage. We proceed with the definition of a linkage-friendly crossover operator. We conclude with a theoretical and empirical investigation of this new operator and its interaction with our measure of linkage.

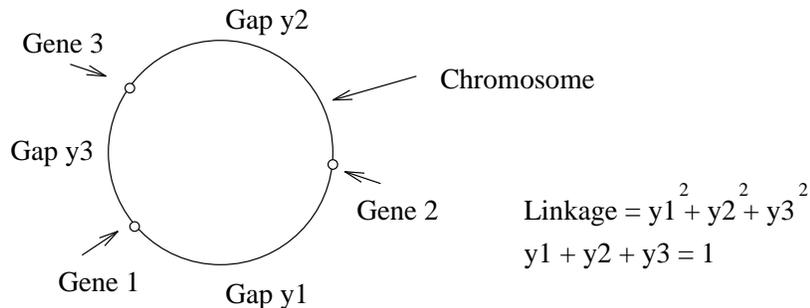


Figure 1: A three gene building block with its intergene gaps and linkage constraints.

2 A Measure Of Linkage

To rigorously show the evolution of “tight linkage”, we must be able to quantify a building block’s linkage within a chromosome. Previous studies have used the building block’s defining length as such a measure. This definition is appropriate under one-point crossover but irrelevant or imprecise under other crossover operators such as uniform and two-point crossover.

We take as a more general definition of a building block’s linkage the probability that that building block is conserved under whichever crossover operator is used. Our proposed crossover operator is similar to two-point crossover and so we use that crossover operator to define our measure of linkage.

We proceed now to a more concrete definition of linkage under our chosen crossover operator and to a calculation of the expected linkage of a randomly constructed order- k building block.

2.1 Calculating Linkage

We consider the case of a single building block embedded within an infinite sized chromosome. This both provides a limiting case for large problems as well as a model that is easily approachable in small problems with the addition of functionally neutral introns (Levenick, 1991).

This model has an elegant mathematical interpretation. Two-point crossover treats the chromosome as if it were connected end-to-end in a circle. When the number of genes defining a chromosome is small, the chromosome is akin to a necklace of beads or genes. As the amount of genetic material in the chromosome approaches infinity, the thickness of each of the above beads decreases to nothing. At the limit, a building block’s genes become equivalent to a set of points on the chromosomal circle.

This model allows a simple expression for the preceding definition of linkage. Consider the chromosomal circle in question to be of circumference 1. An order- k building block is then represented as k points on the circle. We label the successive distances between adjacent points on the circle y_1 through y_k . This building block is preserved under two-point crossover precisely when both crossover points lie within the same gap between adjacent genes. Given that the crossover points are distributed randomly and uniformly over the circle, the probability of both crossover points falling within the same gap equals $\sum y_i^2$. Figure 1 demonstrates this model and its interpretation of linkage.

2.2 Random Linkage

We turn our attention now towards defining the ranges that bound our definition of linkage. We assume an order k building block. The maximum linkage attainable by this building block is 1. This case occurs when the points defining the building block are almost overlapping. Minimum linkage is attained when those points are maximally separated along the circle. In this case each of the successive gaps has length $1/k$ and the linkage equals $k(1/k^2) = 1/k$.

To calculate the starting point for any linkage learning algorithm, we calculate the expected linkage of a randomly created order k building block. Under two-point crossover, the fraction of the chromosome chosen for crossover is of random length and uniformly distributed over $[0, 1]$. If a fraction of the chromosome equal to p is chosen to be transferred during crossover, the probability that a random building block resides wholly in that portion or in the other portion of the chromosome (and thus is preserved) is $p^k + (1 - p)^k$. We calculate the expectation of this probability:

$$E(p^k + (1 - p)^k) = \int_0^1 p^k + (1 - p)^k dp = 2 \int_0^1 p^k dp = 2/(k + 1)$$

This value is termed the “random” linkage of an order- k building block and is the starting point for any linkage learning algorithm.

3 The Exchange Crossover Operator

The ability to evolve linkage requires a dynamic representation of gene positions. Genes and their alleles can be coded as (position,value) pairs, allowing them to reside anywhere in the chromosome. In this section, we propose and study a new crossover-like operator that manipulates such chromosomal structures. The defined operator is similar to two-point crossover.

The “Exchange” operator is defined on pairs of chromosomes with arbitrary structure. One chromosome is designated the donor and the other the recipient. The operator selects a random segment of genetic material from the donor and grafts it onto the recipient at a random location. The recipient chromosome then becomes overfull in that it could contain multiple copies of various genes. These duplicate are deleted leaving the resulting chromosome with at most one allele per gene. The structural form of the genes transferred from the donor remain intact in the recipient. The genes not deleted in the recipient are brought closer together.

The exchange operator considers both the donor and recipient to be connected circular chromosomes so as to avoid end effects. Both chromosomes are assumed to have an implicit orientation and genetic material is always chosen and grafted in the same orientation. This operator is directional in that it has different effects on the donor and recipient chromosomes. This asymmetry can be remedied by having the two chromosomes involved in an exchange alternately play both roles and produce two offspring.

Figure 2 shows the various steps involved in the exchange of the chromosome (4,0) (1,1) (2,1) (3,0) (5,1) onto the chromosome (2,1) (4,1) (1,0) (5,0) (3,1). First a random segment of genetic material, (2,1) (3,0), is chosen from the donor chromosome. Second, a grafting point, right after (4,1), is chosen in the recipient chromosome. Third, the donated material is injected at the grafting point forming the overfull chromosome (2,1) (3,0) (1,0) (5,0) (3,1) (2,1) (4,1). Last, the excess genes in the recipient are deleted forming the complete individual (2,1) (3,0) (1,0) (5,0) (4,1). In this way, two chromosomes with completely different structure are recombined to form a new individual with a full gene complement.

4 The Evolution Of Linkage

We now investigate the interaction between our defined model and the exchange operator. We focus on a single fully deceptive building block within a larger problem. We choose the class of deceptive building blocks because they are known to be problematic for GAs not using linkage information, and thus present a natural testbed for any linkage learning algorithm.

Since the exchange operator is directional, we separate our analysis into two distinct mechanisms. The first mechanism occurs when the optimal building block is the donor of genetic material; the

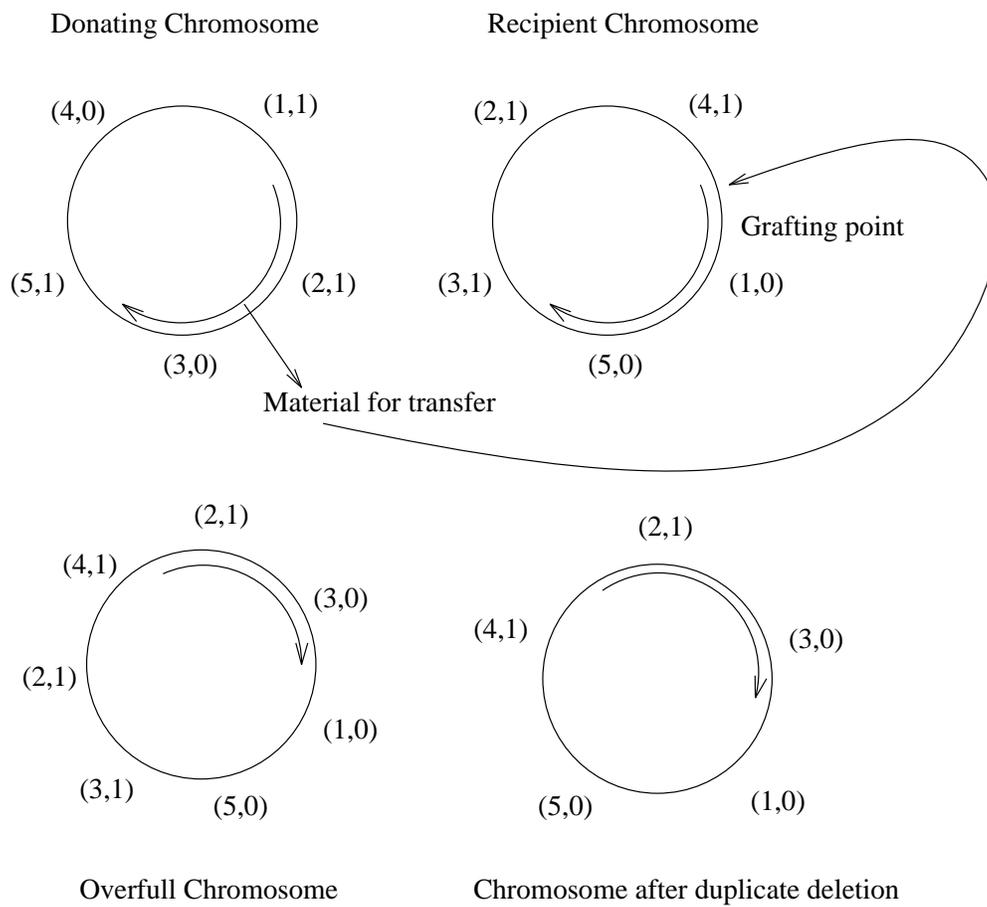


Figure 2: 5-gene chromosomes in the 4 steps of an exchange.

second occurs when it is the recipient of genetic material. In the following analysis, we consider the effect that both of these mechanisms have on the distribution of linkages of the optimal building block in the population. We find that the first mechanism introduces a linkage "skew" whereby the density function skews higher linkages in an effect identical to fitness-proportionate selection. We also find that the second mechanism introduces a linkage "shift" whereby the entire density function is shifted and compressed towards higher linkages.

Our analysis assumes that during the GA's operation, the population converges to a mix of only deceptive and optimal building blocks and that the optimal building block occupies only a small proportion of that population. We will revisit the validity of this assumption in a later section.

4.1 Linkage Skew

Let L_t be the density function of the optimal building block's linkages at generation t . We explore the evolution of L in one generation, considering only the first mechanism. Since by assumption the optimal building block occupies a small proportion of the population, we pay attention only to exchanges involving the optimal building block as a donor and the deceptive building block as a recipient.

The optimal building block either survives or is disrupted by the exchange operation. The survival rate of an optimal building block when exchanging onto a deceptive building block is $l/2$, where l is the building block's linkage. This is the chance that the building block is not interrupted by the crossover (l) and that it is copied whole instead of entirely ignored ($1/2$). Therefore, to a constant factor, at each point l inside the linkage domain, $L_{t+1}(l) = ClL_t(l)$. The constant factor is determined by $\int_0^1 L_{t+1}(l)dl = 1$. Since $\int_0^1 lL_t(l)dl = E(L_t)$, $C = 1/E(L_t)$. Therefore $L_{t+1}(l) = lL_t(l)/E(L_t)$.

In short, the building blocks in question have differential survival rates under crossover and these rates are based on the building blocks' linkages. The equations that describe this situation precisely mirror those of fitness-proportionate selection, with the linkage of a building block here playing the role of its fitness score.

4.2 Linkage Shift

Again, let L_t be the density function of the optimal building block's linkages at generation t . We explore the evolution of L during one generation, considering only the second mechanism. We thus pay attention only to exchanges involving the optimal building block as the recipient and the deceptive building block as the donor of genetic material.

If any of the genes constituting the deceptive building block are copied onto the individual carrying the optimal building block, they will disrupt that building block. Even if an optimal building block is not disrupted, its linkage will be changed by the influx of new material and the corresponding deletion of this material from the original chromosome. We explore now the expected effect that the exchange operation has on an optimal building block with linkage value l given that it survives the exchange operation intact.

We assume that the gene distribution in the individual containing the deceptive building block is random. Let y_i be the gap lengths in the individual containing the optimal building blocks and let l be the building block's linkage. The optimal individual will receive genetic material from the deceptive individual at a random location. We begin by measuring the effect this crossover has on the linkage of this individual if that location falls within the gap of length y_1 and if the optimal building block survives the crossover intact.

Let ϵ be the length of genetic material transferred in the exchange again considering the chromosome to be a circle of circumference 1. Since we are only interested in the effects on building blocks that survive this transfer, this material will be assumed to contain none of the genes defining

the building block we are interested in. The transferred material must be deleted from the original individual for there to be no gene duplication. Therefore, the newly formed individual will have gap lengths y'_i that differ from the original gap lengths. The gap into which the genetic material is injected will expand while the remaining gaps all contract.

The expected change in the y'_i s is as follows:

$$\begin{aligned} y'_1 &= y_1 + (1 - y_1)\epsilon \\ y'_j &= y_j(1 - \epsilon), j \neq 1 \end{aligned}$$

We calculate the difference between the new linkage, $\sum y_i'^2$, and the old linkage, $\sum y_i^2$, by separately calculating the various coefficients of the powers of ϵ .

$$\begin{aligned} CF_{\epsilon^0}(\Delta l) &= y_1^2 + \sum_{j \neq 1} y_j^2 - \sum_i y_i^2 = 0 \\ CF_{\epsilon^1}(\Delta l) &= 2y_1(1 - y_1) - 2 \sum_{j \neq 1} y_j^2 = 2y_1 - 2l \\ CF_{\epsilon^2}(\Delta l) &= (1 - y_1)^2 + \sum_{j \neq 1} y_j^2 = 1 - 2y_1 + y_1^2 + \sum_{j \neq 1} y_j^2 = 1 - 2y_1 + l \\ \Rightarrow \Delta l &= 2(y_1 - l)\epsilon + (1 - 2y_1 + l)\epsilon^2 \end{aligned}$$

We now extend our calculation to a probabilistic choice of the gap into which genetic material is injected. The i^{th} gap is chosen as the recipient of a transfer with probability y_i . Multiplying the expected difference by the probability of choosing a particular gap and summing over all gaps, we get:

$$\begin{aligned} \Delta l &= \sum_i [y_i(2(y_i - l)\epsilon + (1 - 2y_i + l)\epsilon^2)] = \\ &= \sum_i [(2y_i^2 - 2ly_i)\epsilon + (y_i - 2y_i^2 + y_il)\epsilon^2] = \\ &= (2l - 2l)\epsilon + (1 - 2l + l)\epsilon^2 = (1 - l)\epsilon^2 \end{aligned}$$

We further extend our calculation to a probabilistic choice of the size of the material transferred, ϵ . The material chosen from the individual with the deceptive building block is assumed not to contain any of the building block's defining genes. The length of the segment originally chosen for exchange is uniform over $[0, 1]$. The segments that we consider in this analysis are those that do not contain any of the building block's genes in their material. A segment of length ϵ has a probability $(1 - \epsilon)^k$ of not containing any of the chosen building block's genes. Therefore, ϵ has a probability density at each point proportional to $(1 - \epsilon)^k$. The constant of proportionality is readily calculated as $(k + 1)$. We calculate the expected value of ϵ^2 and thus $(1 - l)\epsilon^2$:

$$\begin{aligned} E(\epsilon^2) &= \int_0^1 \epsilon^2 (1 - \epsilon)^k (k + 1) d\epsilon, \text{ by symmetry} = \\ &= (k + 1) \int_0^1 \epsilon^k (1 - \epsilon)^2 d\epsilon = (k + 1) \int_0^1 \epsilon^k - 2\epsilon^{k+1} + \epsilon^{k+2} d\epsilon = \\ &= (k + 1) (1/(k + 1) - 2/(k + 2) + 1/(k + 3)) = 2/(k + 2)(k + 3) \end{aligned}$$

Therefore $\Delta l = (1 - l)[2/(k + 2)(k + 3)]$ and thus $l(t + 1) = l(t) + (1 - l(t))[2/(k + 2)(k + 3)]$ is the simple recurrence describing the expectation of what happens to the linkage of any building block surviving an exchange under the second mechanism.

We now note that the probability of survival under this mechanism does not depend on the actual linkage of the optimal building block itself but only on whether the individual gets lucky and survives a crossover from a randomly ordered individual. Therefore, no "skew" occurs as in the first mechanism. What does happen however, is that the linkage density and correspondingly the average linkage for optimal building blocks surviving crossover "shifts" over to a higher linkage according to the above difference equation in each generation.

4.3 Experiments

We have dissected the proposed crossover into two mechanisms. We now experimentally verify the pair of theories proposed above. We design two sets of experiments that induce the assumptions made in the above analysis and attempt to verify our conclusions.

4.3.1 Linkage Skew

For a fully deceptive building block we use a 4 bit trap function with a deceptive to optimal fitness ratio of 0.6. In order to approach the infinite chromosome model, we embed this building block within a chromosome of 150 genes, the other 146 of which are nonfunctional. We initialize the population with 6400 chromosomes all containing the optimal building block but with random orderings.

One generation of our simulation involves crossing this population with artificially generated individuals containing randomly ordered deceptive building blocks. We consider only one of the two children of the exchange - where the donor contains the optimal building block - as we are investigating the first mechanism only. Finally, only the optimal building blocks surviving the crossover are used to repopulate the next generation of 6400 chromosomes. This is because we are interested solely in the density function of the linkages of the optimal building block. Conceptually, our population here would in an actual GA represent the subpopulation consisting only of representatives of the optimal building block.

We run this simulation 50 generations and repeat it 30 times measuring at each step the population linkage's average and standard deviation.

We made the claim that the density of the linkages of the optimal building block under this mechanism operated identically to fitness-proportionate selection with the building block's linkage playing the role of its fitness. Fitness-proportionate selection abides by a simple recurrence from generation to generation. The expected increase in the average fitness in one generation equals the ratio of the variance to the average fitness at that generation.

To evaluate our hypothesis, we compare a plot of the average linkages of our experiments over the 50 generations versus a constructed variable l . This constructed variable begins at the random linkage of $2/(k+1)$ (0.4 here) and follows by $l(t+1) = l(t) + \sigma^2(t)/l(t)$ as is dictated by the equations of fitness-proportionate selection. As we see in Figure 3, these two plots are identical and our hypothesis is reflected in this experiment.

4.3.2 Linkage Shift

We repeat the above set of experiments for the second mechanism. This time, we restrict ourselves to using the deceptive building block as the donor and the optimal building block as the recipient. Based on our calculations above, our constructed variable in this case begins at 0.4 and follows the recurrence $l(t+1) = l(t) + (1-l(t))/21$.

Figure 4 shows that the original model is approximately correct. Any discrepancy between theory and experiment probably arises from the discretization of a continuous model. We adjust the model for the fact that a building block's linkage in our experiment has an approximate maximum linkage of $(146/150)^2 = 0.947$. We formulate an adjusted recurrence relation $l(t+1) = l(t) + (0.947 - l(t)) * 1/21$. This adjusted model agrees quite well with our experiments and we are given good reason to believe that the model is accurate.

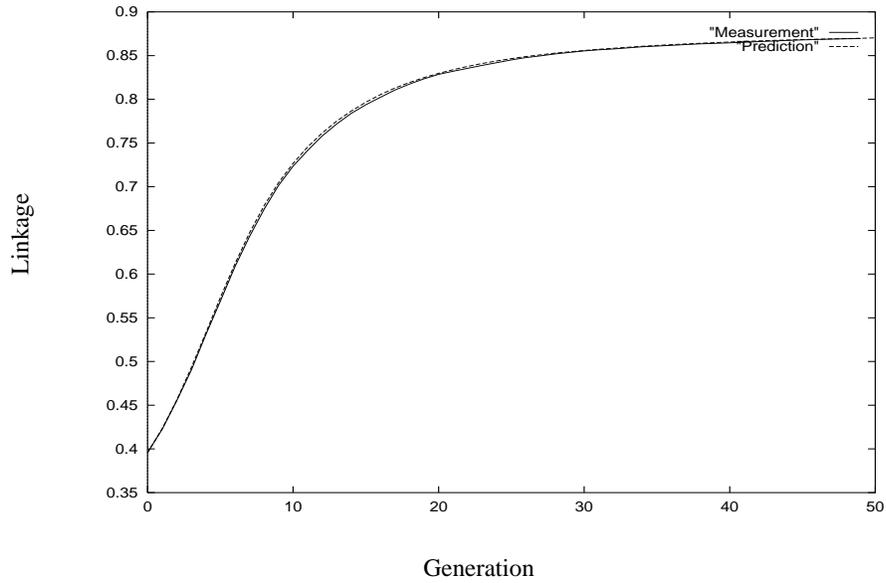


Figure 3: Predicted versus measured linkage averages under mechanism 1.

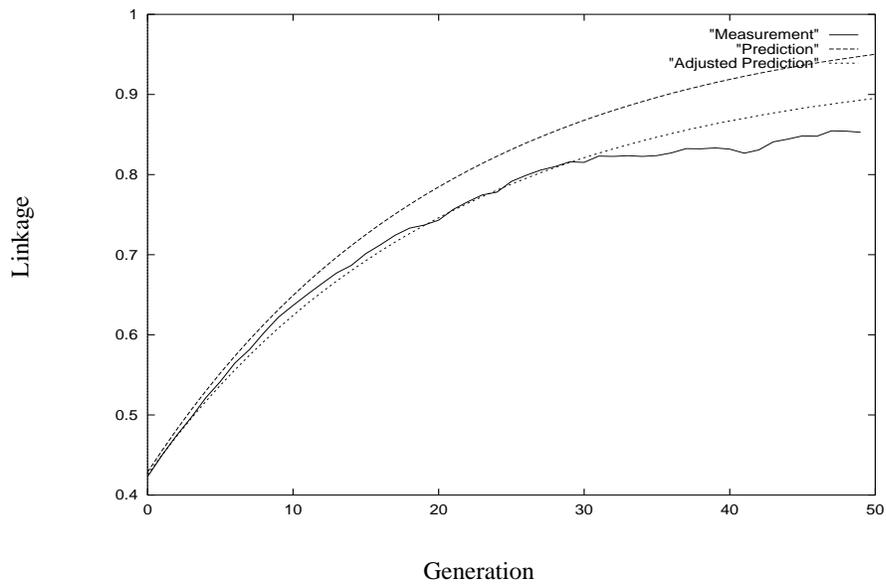


Figure 4: Predicted versus measured linkage averages under mechanism 2.

5 The Role Of Selection

So far, we have discussed the evolution of linkage in terms of the actions of the exchange operator's effects. Our discussion thusfar involves no role for the mechanism of selection in this evolution. When all is said and done, evolution is driven by the survival of the fittest and in GAs this means selection. It turns out that the effect of selection is necessary for the satisfaction of the first of our assumptions as well as the preservation of the optimal building block within a finite population.

Our first assumption was that the population converges to a mix of individuals containing only optimal and deceptive building blocks at some point during its evolution. It is unlikely that an initial distribution of chromosomes will consist solely of these two types of individuals. However, in a deceptive problem, and under the action of selection, the population does eventually migrate to a mix largely composed of deceptive and optimal building blocks and our assumption is satisfied.

Additionally, our distributional analysis does not consider overall rates of building block survival under the proposed crossover operator. Each generation of exchange eliminates a sizable fraction of the optimal building blocks in the population. In finite populations, selection is needed to counter-balance this loss of optimal individuals.

We now explore how far the predicted linkage-learning can take us in a real and uncontrolled setting including the effects of selection.

6 Uncontrolled Testing Of Linkage Learning

We remove all artificial constructs from our experiments and instead focus on running the GA the way a practitioner might. We look for traces of the proposed linkage-learning and make some conclusions as to the usefulness of the algorithm suggested by the exchange operator.

We focus on learning the linkage of a 3-bit deceptive subproblem embedded within a larger coding string of 100 bits the remainder of which are nonfunctional. We use a trap function with a deceptive to optimal fitness ratio of 0.6. In contrast with the previous experiments, we now have to choose a level of selection for this experiment.

The survival rate for optimal building blocks at an average linkage of l when crossing with deceptive building blocks is $l/2 + 1/(k + 1)$. The first and second terms here originate respectively from the first and second mechanisms. With a k of 3 the minimum attainable linkage is $1/4$ and the survival rate thus has a minimum of $1/2$. We therefore theorize that a selection rate of 2 should be enough to guarantee convergence to the optimal building block in this case. On the other hand, when a building block has tight linkage, its survival rate into the next population is $1/2 + 1/4 = 3/4$. Therefore we theorize that a selection rate of $4/3$ is near the minimum level of selection that can be used while still expecting convergence to the global optimum.

We run the GA through alternating stages of selection and exchange. We observe the population for 75 generations, which turns out to be long enough for all our runs to reach convergence. We vary the selection rate from 2.0 down to 1.2 by increments of 0.1. Fractional selection rates are implemented by a probabilistic choice of tournament size. That is, a selection rate of 1.3 implies a 30% of a tournament size of 2 and a 70% chance of a tournament size of 1. At each level of selection, we repeat our experiment 20 times. We gather averages at each generation for both the number of optimal building blocks and the average linkage for those building blocks. The population sizes are chosen large enough to avoid stochastic effects.

Figure 5 shows the various convergence plots as the selection ranges from 2.0 to 1.2. As theorized, the selection rates from 1.3 on up all show a convergence to the global optimum. With a selection rate of 1.2, we see the opposite, the population converges to the deceptive attractor. As we had predicted, the main indicator of the way the population would swing is the struggle between the

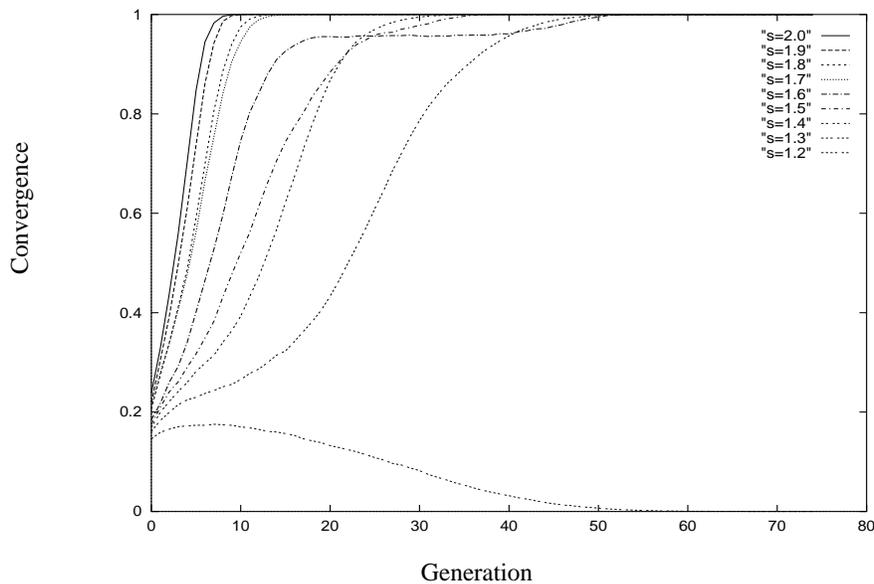


Figure 5: Uncontrolled convergence under various rates of selection.

conservative forces of selection and the destructive forces of crossover.

Figure 6 shows the average values for the linkages of the optimal building blocks at the various generations and levels of selection. We observe that the linkage-learning becomes more pronounced as the rate of selection decreases and is only really significant at a selection rate of 1.2. Unfortunately, at this level of selection, the population converges to the wrong building block.

This observation makes sense if we take a second to consider the framework in which linkage-learning occurs. Our theory becomes applicable only when a large fraction of the population has converged to the deceptive attractor and then remains applicable at the most until the population converges. The faster the selection rate, the less time the linkage evolution has to work under. Unfortunately, we can only slow down the selection rate so much before violating the schema theorem and leading convergence to an incorrect conclusion. Theoretically, investigating selection rates between 1.2 and 1.3 we might be able to precariously balance this process so as to lead to higher levels of linkage-learning. However, this method does not present us with a practical alternative because such a fine search for a selection rate then becomes its own intractable problem.

The level of linkage learned in these problems still seems quite a bit shy of what we would have expected from our initial experimentation. This is most likely because our assumption of negligible optimal building block representation is violated in the real setting. We term this violation the "homogeneity effect" and in the next section, we study the destructive effects of this violation on our theory of the two linkage-learning mechanisms.

7 The Homogeneity Effect

In this section, we take a brief look at how the homogeneity effect changes the theory we had developed early on in this chapter. We will see that it has detrimental effects on both the first and second mechanisms of linkage learning. Because the homogeneity effect results in practice from a having a non-negligible proportion of optimal individuals, it acts much like a negative feedback effect preventing linkage learning as convergence is taking place.

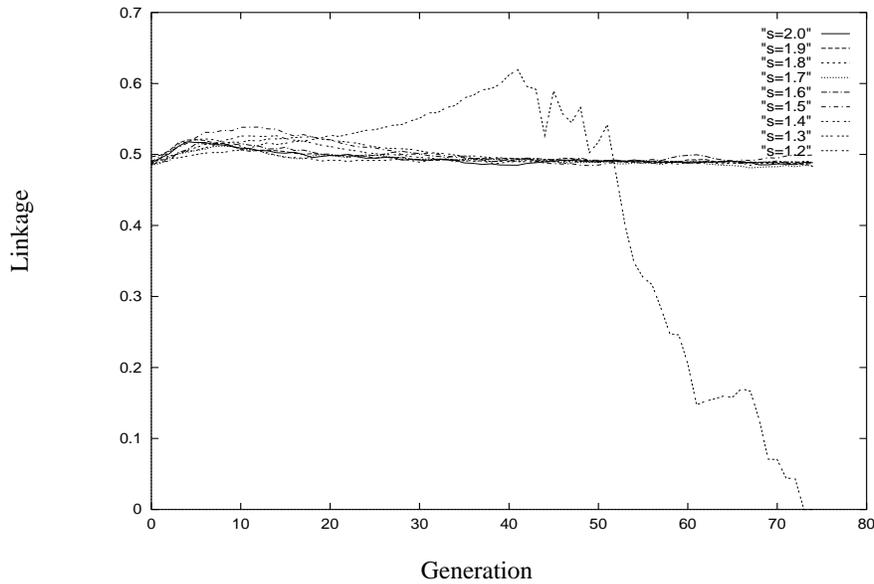


Figure 6: Uncontrolled linkage-learning under various rates of selection.

7.1 Linkage Skew

In the first mechanism, we showed a direct correlation under exchange between the survival probability under crossover of a building block and its linkage. We assumed that to survive, a building block must be copied whole from an optimal individual to a deceptive individual. This is not necessary if the receiving individual has a certain number of alleles that agree with the optimal building block. In that case, only the remaining genes need be copied over. In addition, the resulting building block's linkage need not be the same as that of the parent optimal building block since the positioning of the genes in the recipient parent is assumedly random. We now derive a more general expression for a building block's survival probability under the first mechanism.

Picture the optimal individual in Figure 7. As usual, let the y_i be the lengths of the intergene gaps and $l = \sum y_i^2$ be the optimal building block's linkage. Let p be the proportion of genes in the

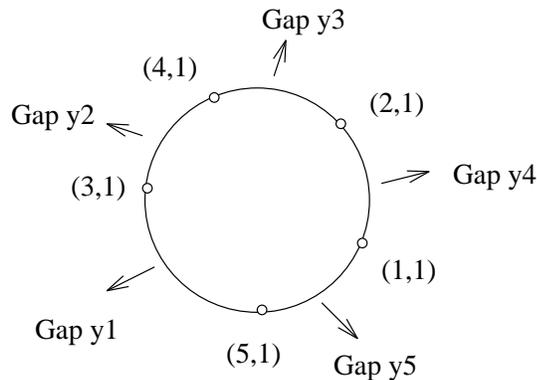


Figure 7: A sample 5-gene optimal building block

recipient individual that agree with the optimal building block. In our original calculations, $p = 0$ and the probability of survival equaled $l/2$. However, with a nonzero p , the two crossover points in the exchange can occur outside the same gap and still lead to a child with the optimal building block if the missing genes are picked up from the recipient individual.

Two crossover points, one in the gap of length y_1 and one in the gap or length y_2 (picking the outside segment for transfer) yield an optimal individual with probability p . This is the probability that the missing gene, (3,1), is present in the recipient individual. Similarly, two crossover points in the gaps of length y_0 and y_2 (again picking the outside segment for transfer) yield an optimal individual with probability p^2 —the probability that two genes are picked up from the recipient individual. Considering all indexes *mod* 5, the adjusted survival probability becomes:

$$l/2 + p \sum y_i y_{i+1} + p^2 \sum y_i y_{i+2} + p^3 \sum y_i y_{i+3} + p^4 \sum y_i y_{i+4} + p^5 l/2$$

We verify that when $p = 1$ the above formula equals $(\sum(y_i))^2 = 1$ as expected. We note that the above formula is not completely determined by a building block's linkage and is dependent on other functions of the intergene spacing. Calculations of the evolution of these functions could probably be made in a manner similar to those made on the linkage, and the homogeneity effect could be more closely modeled armed with such a theory. We do not proceed further along that line of inquiry as we have established what we had set out to do— to show that the mechanics of the first mechanism change under the homogeneity effect.

7.2 Linkage Shift

In the second mechanism we showed a tendency for crosses from the deceptive building block over onto the optimal building block to lead to a higher linkage in the building blocks that survive. We can come up with an approximation to the effect that a violation in our assumption has on our calculations. Recall that the probability of survival in this case was unrelated to the building block's level of linkage and equaled $1/(k + 1)$ where k was the building block's order. Now, assuming that the donating building block has a proportion p of its genes in agreement with the optimal building block, then only the remaining $(1 - p)k$ of the bits have to be excluded in the exchange for survival of the optimal building block. We calculate the proportion of non-destructive crossovers occurring under the original conditions to the total number of successful crossovers. We do this by comparing the original survival rate to the new survival rate:

The original survival rate was $1/(k + 1)$

The new survival rate is $1/((1 - p)k + 1)$

The ratio of the two rates is then $((1 - p)k + 1)/(k + 1)$

As k becomes large, we conservatively approximate this proportion by $1 - p$. Therefore a proportion equal to $1 - p$ of the population is doing what we had expected it to do under the original calculations. On the other hand, the other p of the crossovers are injecting genetic material into the optimal building blocks at random positions throughout the coding string. We conservatively assume that this injection of random material causes the optimal building block to revert back to its random linkage value of $2/(k + 1)$. Under these conditions, the new conservative difference equation for the average linkage value under the second mechanism becomes:

$$L(t + 1) = p(2/(k + 1)) + (1 - p)(L(t) + (1 - L(t)) * 2/(k + 2)(k + 3))$$

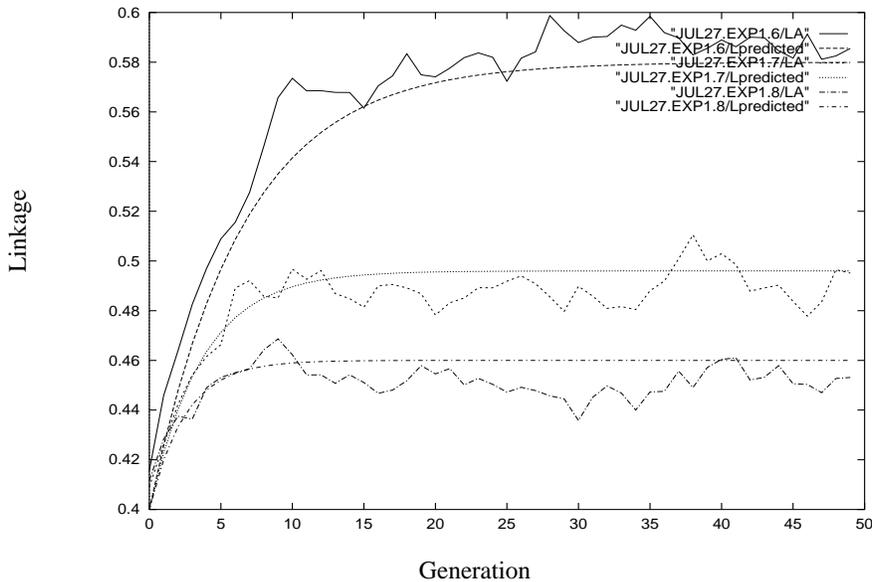


Figure 8: Linkage shift under various levels of the homogeneity effect.

Even with a small p this difference equation is significantly slower than the one where $p = 0$. Furthermore, L is bounded under this equation at a value less than 1. To see this we set $L(t+1) = L(t)$ and solve for $L(t)$.

$$\begin{aligned}
 L &= 2p/(k+1) + (1-p)(L + (1-L)2/((k+2)(k+3))) \Rightarrow \\
 L - (1-p)L + L(1-p)(2/((k+2)(k+3))) &= 2p/(k+1) + (1-p)(2/((k+2)(k+3))) \Rightarrow \\
 L &= (2p/(k+1) + (1-p)(2/((k+2)(k+3))))/(p + 2(1-p)/((k+2)(k+3)))
 \end{aligned}$$

For example, the maximum values attained for $p = 0, 0.1, 0.2$ and 0.3 and $k = 4$ are $0.58, 0.496$ and 0.46 respectively.

To confirm this analysis, we repeat the same kind of experiment we did when confirming our initial difference equation. Instead of using deceptive attractors as the originator of genetic material, this time we use building blocks containing a proportion p of their genes coinciding with the optimal building block. We look at a 4 bit trap function again with a deceptive to optimal fitness ratio of 0.6 . We use a chromosome length of 150 and a population size of 200 optimal building blocks. Each generation, perform exchange on these building blocks with our constructed building block being the originator of the genetic material. We repeat this experiment 30 times to gather averages of the linkage levels for each of 50 generations and 3 different levels for p of $.1, .2$ and $.3$. Figure 8 shows the results of this experiment. As we see, our intuition is validated in that our model is reasonably accurate over the range of violations of our assumptions.

8 Summary and Conclusion

In this paper, we have defined a new crossover operator capable of operating on structurally heterogeneous chromosomes, and analyzed a new measure of linkage appropriate for our defined operator. We have seen that under certain conditions the use of this operator demonstrates an advantage for and a tendency to drift towards tight linkage. We have also quantified and empirically verified the above advantage and drift.

The race between selection and linkage-learning still prevents this advantage from manifesting itself in an uncontrolled setting. What advantage, we can ask, does this hold over inversion which is also plagued by the same problem? First, the use of a crossover operator means that linkage can be learned concurrently over multiple building blocks. All the inversion-based schemes convert one parent to the form of the other before crossover — destroying any information contained in the second parent. Second, the time to solve the linkage problem using the exchange operator is around k^2 generations, with k being the order of the building block attempted. Since only the first mechanism identified in this paper comes into play using inversion, this time is likely faster than that of inversion alone; though these calculations have yet to be made.

Both of these reasons imply that the linkage-learning induced by this crossover operator is faster than that induced by inversion. Thus, we have less work to do in matching its time scale with that of selection. Indeed, the practical implementation of a working version of the exchange operator has recently become possible. Work in this area will be presented in a later paper.

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