

25

Learning by Simulating Evolution

In this chapter, you learn how search can be done using procedures that are inspired by natural evolution. These procedures, commonly called *genetic algorithms*, rest on ideas that are analogous, in some ways, to *individuals*, *mating*, *chromosome crossover*, *gene mutation*, *fitness*, and *natural selection*.

You learn that natural selection often performs terribly when simple selection mechanisms are used. To do better, you need to devise a selection mechanism that takes note of *diversity among individuals*, as well as of individual performance. Such a diversity-noting selection measure can change the way that you think about local maxima. Instead of trying to escape from them, you populate them with sacrificial individuals who themselves get trapped, but who keep other evolving individuals at a distance.

By way of illustration, you see how to construct a genetic algorithm to optimize the quantities of flour and sugar used in the production of cookies. This optimization problem is like many others for which overall performance has a complicated dependence on various controllable factors that include temperatures, pressures, flow rates, and the like.

First, you review the most conspicuous mechanisms involved in evolution. Then, you see how simple procedures may exhibit similar properties.

Once you have finished this chapter, you will know how genetic learning procedures work, when they can be effective, and why they often break down.

SURVIVAL OF THE FITTEST

Every living thing consists of one or more cells, but beyond that, there are exceptions to just about every rule in biology. Nevertheless, certain characteristics of heredity and evolution seem to be universal or nearly so. In this section, you learn about those characteristics.

Chromosomes Determine Hereditary Traits

In higher plants and animals, each cell contains a single nucleus, which, in turn, contains **chromosomes**, often many of them. Late in the nineteenth century, chromosomes were identified as the custodians of the trait-determining factors, traditionally called **genes**, that are passed on when cells divide and when offspring are parented. Genes are strung along chromosomes like cars on a railroad train.

The chromosomes are usually paired, with each parent contributing one chromosome to each pair. The pairs are said to be **homologous**, meaning that, for each gene in one paired chromosome, there is a gene in the other corresponding chromosome that has the same purpose. Cells that contain paired, homologous chromosomes are said to be **diploid** cells.

In preparation for mating, homologous chromosomes are brought together, duplicated, and formed into bundles that look a bit like four ropes twisted together. Somehow, the twisting seems to produce stresses that lead to a great deal of cleavage and reconnection, thereby scrambling the genes on the chromosomes involved. This scrambling is called **crossover**.

Once duplication and crossover occur, there are two complete sets of scrambled chromosome pairs. The sets are herded to opposite ends of the nucleus, whereupon the nucleus divides, initiating the division of the entire cell. The two resulting cells then have the normal number of chromosomes, but they are not ordinary because the chromosomes have undergone crossover.

Next, the cells divide again; unlike in normal cell division, however, there is no chromosome duplication. Instead, one chromosome from each pair ends up in each of the two new cells. These new cells, either eggs or sperm, are said to be **haploid** cells because, in contrast to diploid cells, they exhibit no chromosome pairing.

Mating produces a fertilized, diploid egg, initiating the development of a new individual. Subsequent cell division in the course of development is much simpler. Chromosomes are copied, herded, and assigned to two distinct cells, but there is no crossover.

Occasionally, the chromosome-copying process goes astray, producing an altered gene that is slightly different from the corresponding gene in the contributing parent. This never-before-seen gene is called a **mutation**.

If the purpose of the unmutated gene is to dictate the shape of, say, a crucial enzyme, the mutated gene may dictate a better enzyme; more

often, the mutated gene produces either no enzyme or one with greatly diminished activity.

Fortunately, a bad mutation in one chromosome of a diploid pair need not be fatal, because the other, homologous chromosome is generally normal. Inbreeding can lead to tragedy, however, because the same, defective gene may end up on both of the two homologous chromosomes.

In lower plants and animals, chromosomes are paired only briefly, during reproduction. Most often, reproduction involves just one parent, whose chromosomes are copied in preparation for cell division, with the original set of chromosomes going into one of the two new cells, and the copied set going into the other. Occasionally, however, reproduction involves two parents, each of which contributes a set of chromosomes to the other, whereupon homologous chromosomes are paired, crossed, and separated in preparation for cell division.

The Fittest Survive

In his magnum opus, *The Origin of Species*, published in 1859, Charles Darwin championed the principle of **evolution through natural selection**, which subsequently, after much heated argument, became generally accepted among scientists:

- Each individual tends to pass on its traits to its offspring.
- Nevertheless, nature produces individuals with differing traits.
- The fittest individuals—those with the most favorable traits—tend to have more offspring than do those with unfavorable traits, thus driving the population as a whole toward favorable traits.
- Over long periods, variation can accumulate, producing entirely new species whose traits make them especially suited to particular ecological niches.

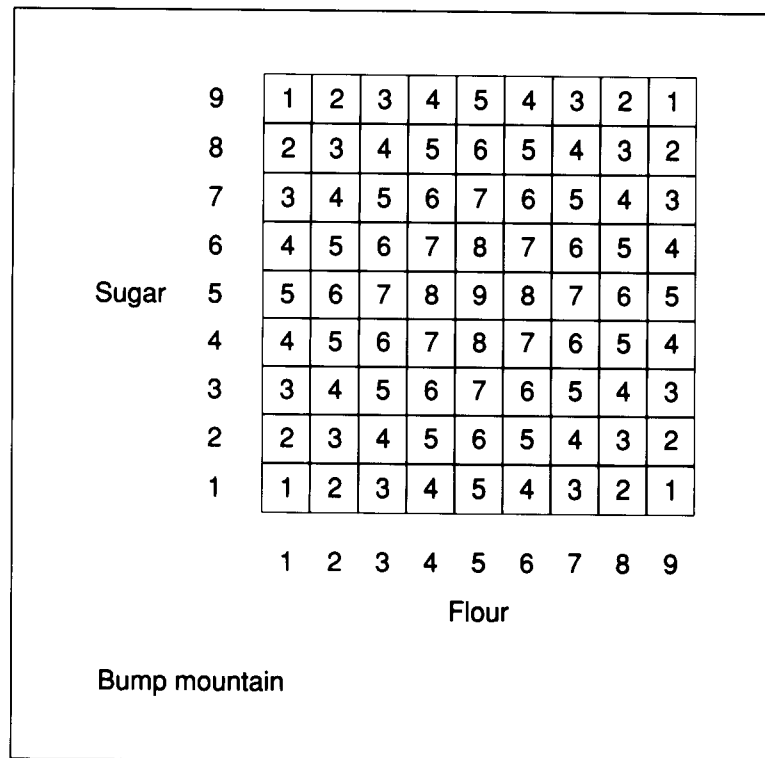
Of course, every horse breeder knows that traits are passed on and that traits vary; and every horse breeder arranges for faster horses to breed more. Darwin's contribution was to exhibit evidence that the same principles account for the great variation seen in living things.

From a molecular point of view, natural selection is enabled by the variation that follows from crossover and mutation. Crossover assembles existing genes into new combinations. Mutation produces new genes, hitherto unseen.

GENETIC ALGORITHMS

In this section, you learn how it is possible to simulate certain characteristics of heredity and evolution.

Figure 25.1 Cookie quality is dependent on the number of kilograms of flour and sugar per batch. Evidently, the best-quality cookies are produced when there are five kilograms of each, for then the judged quality of the cookies is maximized.



Genetic Algorithms Involve Myriad Analogs

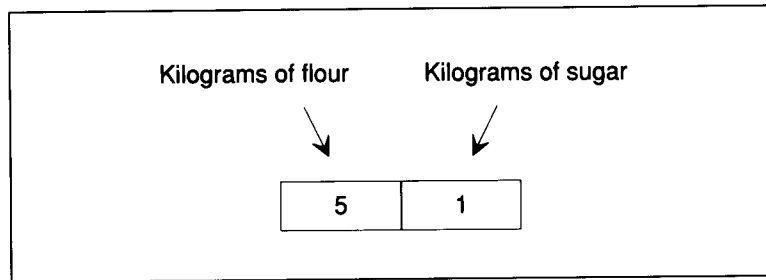
To understand natural selection from a computational point of view, consider the problem faced by Kookie, a cookie maker, who is trying to optimize the amount of sugar and flour in his cookies.

Essentially, Kookie is trying to find the optimal combination in the two-dimensional space illustrated in figure 25.1. One axis is the number of kilograms of flour per batch, and the other is the number of kilograms of sugar; the quality of the resulting cookies, somehow determined, is given as a function of the other two. In this example, the quality function resembles a smooth bump.

In this illustration, Kookie could, of course, just try every combination, noting that there are only 81, but as the number of options is increased, or as the number of dimensions is increased, brute-force testing eventually becomes impracticable.

Accordingly, assume Kookie wants to find a good combination without trying every combination. Kookie could try one of the search procedures described in Chapter 4. Assume, however, that Kookie is studying artificial intelligence, and he has just learned that search can be performed using **genetic algorithms**. Inspired by the miracle of evolution, Kookie decides to try a genetic algorithm on his cookie problem.

Figure 25.2 A chromosome in the cookie world consists of two numbers, which act as gene analogs. The first determines how much flour to use; the second determines how much sugar to use.



To begin, Kookie has to develop analogs to individuals, chromosomes, mutation, crossover, fitness, and natural selection. Analogs for individuals, chromosomes, mutation, and crossover are straightforward, and are easy for Kookie to establish. Kookie first decides that each batch of cookies is an “individual.” Then he decides, as illustrated in figure 25.2, that a “chromosome” consists of two “genes,” each of which is a number from 1 to 9. The first of these genes prescribes the amount of flour to use, and the second prescribes the amount of sugar. Kookie appears, therefore, to be adhering to the following specification:

A **chromosome** is a representation

In which

- ▷ There is a list of elements called genes.
- ▷ The chromosome determines the overall fitness manifested by some mechanism that uses the chromosome’s genes as a sort of blueprint.

With constructors that

- ▷ Create a chromosome, given a list of elements—this constructor might be called the genesis constructor
- ▷ Create a chromosome by crossing a pair of existing chromosomes

With writers that

- ▷ Mutate an existing chromosome by changing one of the genes

With readers that

- ▷ Produce a specified gene, given a chromosome
-

Next, Kookie decides that each individual will have only one copy of one chromosome, thus following the pattern of lower plants and animals whose chromosomes have no homologous partners except during mating.

To mimic chromosome mutation, Kookie selects one of the chromosome’s two genes randomly, and alters it randomly by adding or subtracting

1, taking care to stay within the 1-to-9 range. Figure 25.3 illustrates how two chromosomes might evolve through a series of four extremely lucky mutations, producing increasingly high-quality individuals.

Strictly speaking, individuals, which correspond to cookie batches, are the entities that are associated with quality. Chromosomes, which correspond to recipes for the flour and sugar contents of cookies, determine quality indirectly by specifying the characteristics of the individuals. Nevertheless, it is not necessary to be obsessive about the distinction, because the characteristics of individuals are so tightly determined by the nature of the chromosomes. Accordingly, in the rest of this chapter, chromosomes are said to have certain **quality scores**, rather than to produce individuals that have those quality scores. Similarly, chromosomes are said to constitute **populations**, even though it is really the chromosome-determined individuals that constitute populations.

To mimic the crossover involved in mating, Kookie cuts two chromosomes in the middle and rejoins them as illustrated in figure 25.4. Then, Kookie retains both in the hope that at least one will be a fortunate combination. For cookies, the 5-4 chromosome is the fortunate combination, for a 5-4 chromosome is just one mutation step away from the 5-5 combination which yields optimum, quality 9 cookies. On the other hand, the 2-1 chromosome is the unfortunate combination, for a 2-1 chromosome yields horrible, quality 2 cookies.

Of course, with just two genes, there is just one place to cut and rejoin; in general, however, there are many places, and many possible procedures for determining how many places to crossover and where exactly to crossover.

The Standard Method Equates Fitness with Relative Quality

Once Kookie has decided how to mimic mutation and crossover, he must decide on analogs to “fitness” and “natural selection.” These choices are far less straightforward, however, for there are many alternative approaches.

In general, the fitness of a chromosome is the probability that the chromosome survives to the next generation. Accordingly, you need a formula that relates the fitness of the i th chromosome, f_i , a probability ranging from 0 to 1, to the quality of the corresponding cookies, q_i , a number ranging from 1 to 9. The following formula, in which the sum is over all candidates, is one possibility:

$$f_i = \frac{q_i}{\sum_j q_j}.$$

Henceforth, the use of this formula is referred to as the **standard method** for fitness computation.

Suppose, for example, that a population consists of four chromosomes, collectively exhibiting 1-4, 3-1, 1-2, and 1-1 chromosomes. By inspecting

Figure 25.3 Two chromosomes undergoing a series of mutations, each of which changes one gene by adding or subtracting 1. Both original chromosomes are 1-1 chromosomes, which produce quality 1 cookies. One final chromosome is a 5-1 chromosome and the other is a 2-4 chromosome, both of which yield quality 5 cookies.

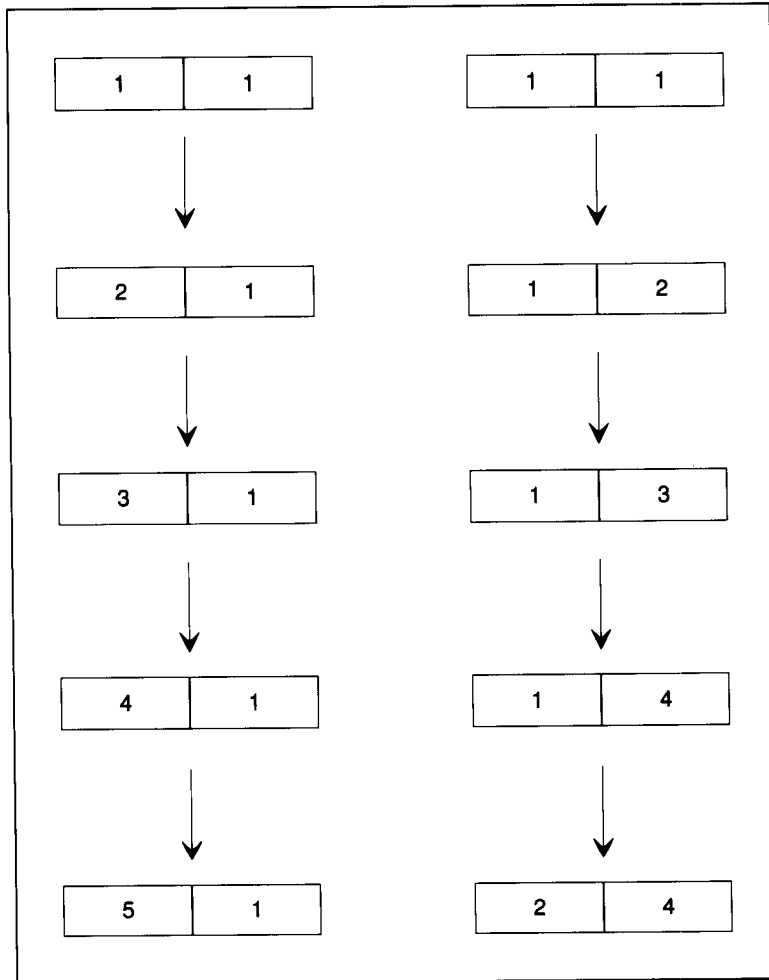
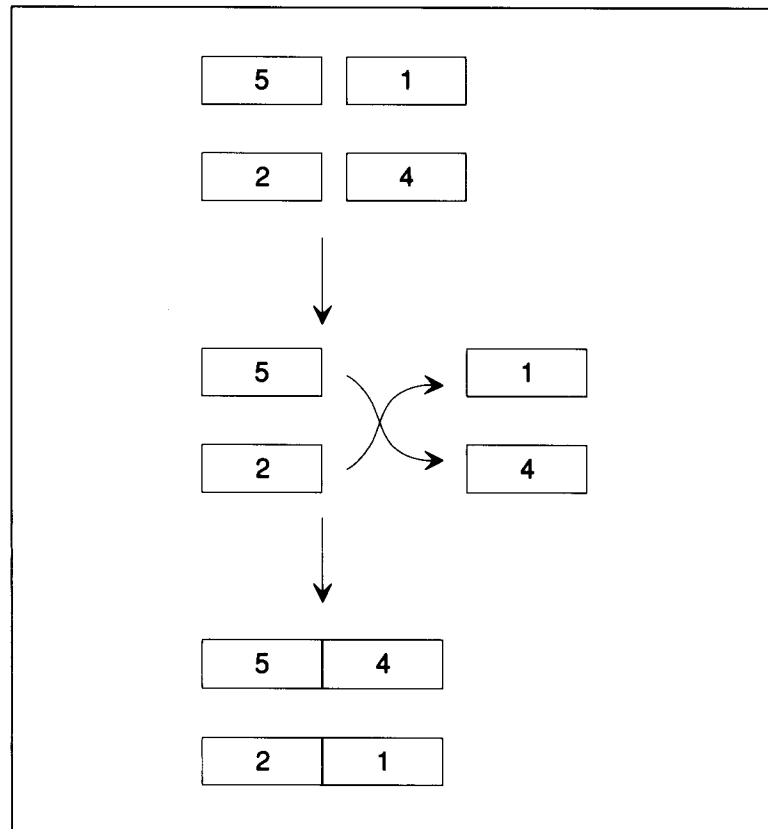


figure 25.1, you can see that their qualities and corresponding fitnesses are as shown in the following table:

Chromosomes	Quality	Standard fitness
1 4	4	0.40
3 1	3	0.30
1 2	2	0.20
1 1	1	0.10

With a fitness analog established, one way that Kookie can mimic natural selection is as follows:

Figure 25.4 Two chromosomes undergoing crossover, each of which is cut in the middle and reattached to the other chromosome. One of the two original chromosomes is a 5-1 chromosome, and the other is a 2-4 chromosome. One of the two new chromosomes is a 5-4 chromosome, which yields quality 8 cookies.



To mimic natural selection in general,

- ▷ Create an initial “population” of one chromosome.
- ▷ Mutate one or more genes in one or more of the current chromosomes, producing one new offspring for each chromosome mutated.
- ▷ Mate one or more pairs of chromosomes.
- ▷ Add the mutated and offspring chromosomes to the current population.
- ▷ Create a new generation by keeping the best of the current population’s chromosomes, along with other chromosomes selected randomly from the current population. Bias the random selection according to assessed fitness.

Genetic Algorithms Generally Involve Many Choices

Even after Kookie decides to deploy a genetic algorithm using the standard method for computing fitness, many decisions remain.

- How many chromosomes are to be in the population? If the number is too low, all chromosomes will soon have identical traits and crossover will do nothing; if the number is too high, computation time will be unnecessarily excessive.
- What is the mutation rate? If the rate is too low, new traits will appear too slowly in the population; if the rate is too high, each generation will be unrelated to the previous generation.
- Is mating allowed? If so, how are mating pairs selected, and how are crossover points determined?
- Can any chromosome appear more than once in a population?

Generally speaking, it is helpful to know the shape of the space to be searched, which is a variant of the principle that it is always nice to know the answer before you work the problem.

It Is Easy to Climb Bump Mountain Without Crossover

Recall that the problem is to find an optimum mix of ingredients given the relation between cookie quality and ingredients shown in figure 25.1.

To keep method comparison simple, suppose that Kookie decides to specialize the general method for mimicking natural selection as follows:

- Kookie starts with a single chromosome located at 1-1.
- No chromosome is permitted to appear more than once in each generation.
- A maximum of four chromosomes survive from one generation to the next.
- Each survivor is a candidate for survival to the next generation, along with any new chromosomes produced.
- One gene is selected at random in each of the survivors, and is mutated at random. If the mutant is different from any candidate accumulated so far, that mutant is added to the candidates.
- There is no crossover.
- The chromosome with the highest score survives to the next generation.
- The remaining survivors from one generation to the next are selected at random from the remaining candidates, according to the standard method for fitness computation.

Now recall that Kookie not only wants good cookies, but also wants to learn more about how genetic algorithms work. Accordingly, he might propose to improve his cookies 1000 times, starting from a single 1-1 chromosome each time.

If Kookie were to go to all that trouble, he would find the best combination of ingredients, on average, at generation 16. Among 1000 simulation experiments performed by Kookie, the luckiest produced the best

combination eight generations after starting at generation 0 with a one 1-1 chromosome, which produces quality 1 cookies:

Generation 0:

Chromosome	Quality
1 1	1

A favorable mutation produced a 1-2 chromosome, which was added to the population, producing two members:

Generation 1:

Chromosome	Quality
1 2	2
1 1	1

The 1-2 chromosome mutated to 1-3, which was added to the population. The 1-1 chromosome mutated to 1-2, which was already in the population. Accordingly, the next generation had just one new member:

Generation 2:

Chromosome	Quality
1 3	3
1 2	2
1 1	1

Now 1-3 mutated to 1-4; 1-2 mutated to 2-2; and 1-1 mutated to 2-1. For the first time, the population exceeded the four-chromosome population limit. Hence, the best plus three more chromosomes had to be selected from the following six:

Chromosome	Quality
1 4	4
2 2	3
1 3	3
2 1	2
1 2	2
1 1	1

The four that happened to be selected, using the standard fitness method, were as follows:

Generation 3:

Chromosome	Quality
1 4	4
1 3	3
1 2	2
2 1	2

Now mutation produced three new chromosomes:

Chromosome	Quality
2 4	5
2 3	4
3 1	3

From the total of seven, four were selected for the next generation:

Generation 4:

Chromosome	Quality
2 4	5
1 4	4
1 3	3
2 1	2

Next, all chromosomes mutated, and the new chromosomes happened to be selected for the next generation:

Generation 5:

Chromosome	Quality
2 5	6
1 5	5
2 3	4
2 2	3

Once again, all chromosomes mutated, but this time one of the existing chromosomes—the 1-5 chromosome—survived to the next generation:

Generation 6:

Chromosome	Quality
3 5	7
1 5	5
3 2	4
1 4	4

This time, 3-5 mutates to 4-5, and 3-2 mutated to 3-1. The other two—1-5 and 1-4—happened to mutate into each other. Accordingly, four chromosomes had to be selected from the following six:

Chromosome	Quality
4 5	8
3 5	7
1 5	5
3 2	4
1 4	4
3 1	3

These were selected:

Generation 7:

Chromosome	Quality
4 5	8
1 5	5
1 4	4
3 1	3

Now 4-5 mutated into 5-5, the optimum, terminating the experiment with the optimum chromosome included in the population:

Generation 8:

Chromosome	Quality
5 5	9
4 5	8
2 5	6
2 1	2

Evidently, for straightforward bumplike terrain, crossover is not at all necessary.

Crossover Enables Genetic Algorithms to Search High-Dimensional Spaces Efficiently

Now suppose Kookie wants to see whether crossover does any good. To decide which chromosomes to cross, Kookie proceeds as follows:

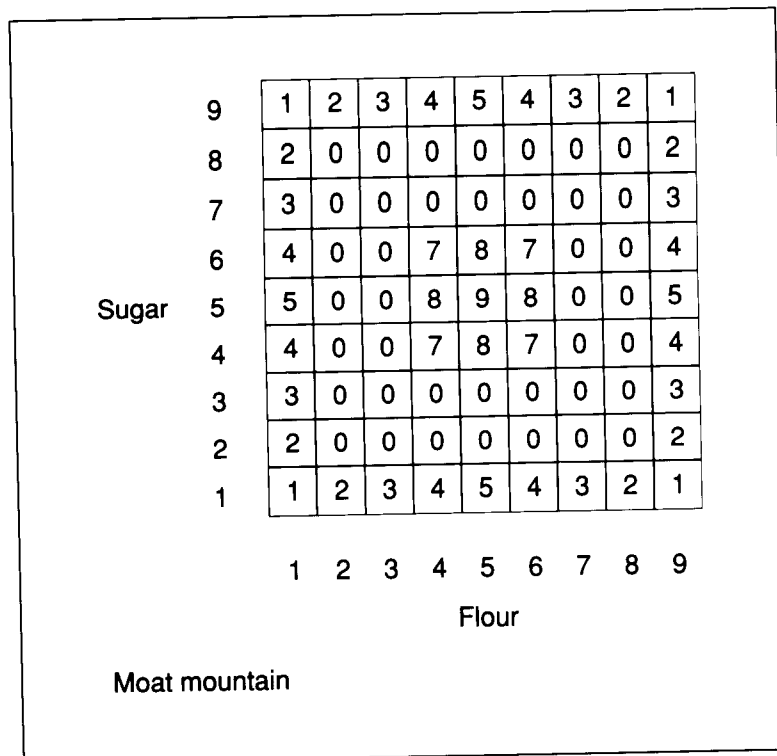
- Kookie considers only the chromosomes that survived from the previous generation.
- For each such chromosome, Kookie selects a mate from among the other survivors. Mate selection is done at random, in keeping with the standard method for computing fitness.
- Each mating pair is crossed in the middle, producing two crossed, offspring chromosomes. If an offspring chromosome is different from any candidate accumulated so far, that offspring chromosome is added to the candidates.

Using this crossover method, Kookie finds the best combination of ingredients on bump mountain, on average, at generation 14, two generations sooner than without crossover.

The reason for this speedup is that crossover can unite an individual that is doing well in the flour dimension with another individual that is doing well in the sugar dimension. If crossover carries a good flour gene and a good sugar gene into a new individual, the new individual has two good genes.

For this crossover improvement to work, of course, the search space must be such that you can search the global maximum by searching for the maximum in each dimension independently. Essentially, crossover reduces the dimensionality of the search space.

Figure 25.5 In this example, the function relating cookie quality to cookie ingredients exhibits a moat. Crossover helps you to jump over.



Crossover Enables Genetic Algorithms to Traverse Obstructing Moats

Suspending disbelief, suppose the relation between cookie quality and ingredients is given by the moatlike function in figure 25.5. Under these circumstances, it is not possible for a series of random mutations to lead a population from outside the moat to inside given just one mutation per generation. The reason is that the necessary intermediate chromosomes—the ones producing cookies in the moat—have 0 quality, and hence 0 fitness, and hence 0 chance of surviving to the next generation.

On the other hand, given two well-situated parents, with 1-5 and 5-1 chromosomes, a single mating can create a trans-moat offspring. No zero-fitness intermediates ever need to survive. Evidently, for terrain with moats, crossover can be more than just helpful.

Unfortunately, Kookie still does extremely poorly on moat mountain, even after adding a crossover to each generation, because the population as a whole tends to crawl along the flour axis or up the sugar axis, with all four chromosomes bunching up with 5-1 chromosomes or 1-5 chromosomes. Mutations into the moat die immediately. Mutations that take a chromosome toward 1-1 and beyond tend to die before they get to a favorable position for crossover.

When Kookie tried 1000 times to find the optimum starting with a 1-1 chromosome, he found the best combination, on average, only after 155 generations.

The Rank Method Links Fitness to Quality Rank

The standard method for determining fitness provides you with no way to influence selection. One alternative is to use the **rank method**, which not only offers a way of controlling the bias toward the best chromosome, but also eliminates implicit biases, introduced by unfortunate choices of the measurement scale, that might otherwise do harm.

Basically, the rank method ignores quality measurements except insofar as those measurements serve to rank the candidates from the highest quality to the lowest quality. Then, the fitness of the highest-quality candidate among the ranked candidates is some fixed constant, p . If the best candidate, the one ranked number 1, is not selected, then the next best candidate, the one ranked number 2, is selected with fitness p . This selection process continues until a candidate is selected or there is only one left, in which case that last-ranked candidate is selected, as indicated in the following procedure:

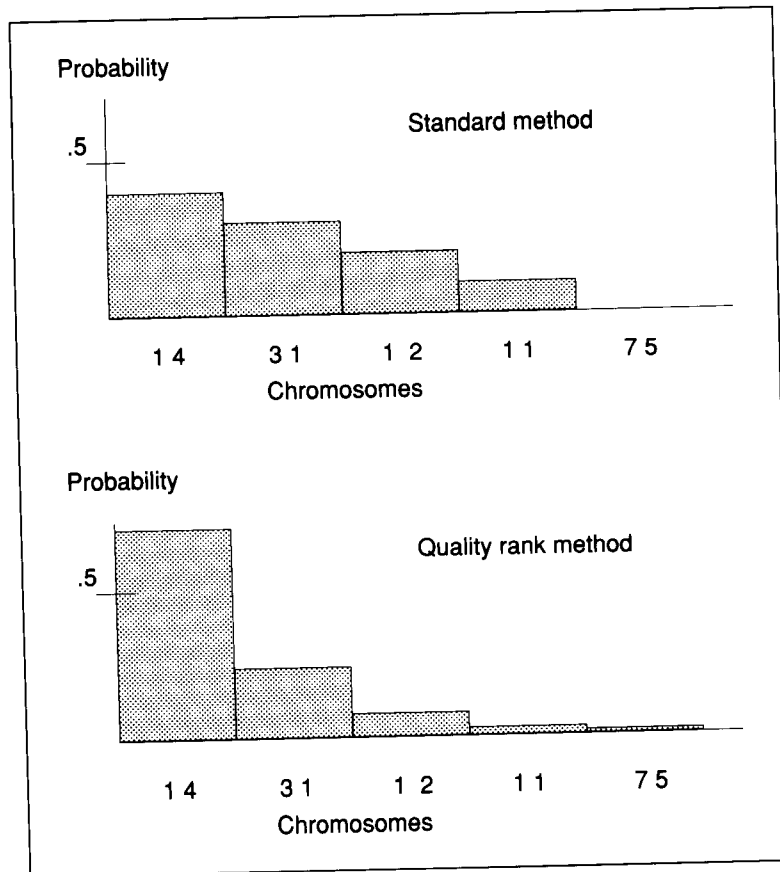
To select a candidate by the rank method,

- ▷ Sort the n individuals by quality.
 - ▷ Let the probability of selecting the i th candidate, given that the first $i - 1$ candidates have not been selected, be p , except for the final candidate, which is selected if no previous candidate has been selected.
 - ▷ Select a candidate using the computed probabilities.
-

Suppose, for example, that $p = 0.667$. Next, assume you are interested in the same chromosomes—1-4, 3-1, 1-2, and 1-1—used before to illustrate the standard method, but this time in the context of moat mountain. Further assume that those four chromosomes are augmented by 7-5, which produces quality 0 cookies on moat mountain. The following table and figure 25.6 show the chromosomes' rank fitnesses, along with their standard fitnesses for comparison.

Chromosome	Quality	Rank	Standard fitness	Rank fitness
1 4	4	1	0.40	0.667
3 1	3	2	0.30	0.222
1 2	2	3	0.20	0.074
1 1	1	4	0.10	0.025
7 5	0	5	0.0	0.012

Figure 25.6 Fitnesses for five chromosomes, as measured by both the standard method and the rank method, using quality scores as determined by moat mountain. In contrast to the standard method, the rank method shows nonzero fitness for all chromosomes, even for the one that produces quality 0 cookies.



When Kookie tried 1000 times to find the optimum, using the rank method, starting with a 1-1 chromosome, he found the best combination, on average, after 75 generations. Thus, the rank method provides a considerable improvement, on the moat-mountain problem, over the standard method, which takes, on average, 155 generations.

Unfortunately, 75 generations is still a lot through which to work. All four chromosomes still tend to bunch up around either the 5-1 chromosome or the 1-5 chromosomes. Now, however, it is possible to tunnel through the 0-quality moat, because the lowest fitness of any chromosome is determined indirectly, by quality rank, rather than directly, by quality score. Accordingly, no chromosome can have a fitness of 0, whereas with the standard method, chromosomes in the moat have a fitness of exactly 0.

SURVIVAL OF THE MOST DIVERSE

Fitness, as measured so far, ignores **diversity**, which you can think of as the degree to which chromosomes exhibit different genes. Accordingly,

chromosomes tend to get wiped out if they score just a bit lower than does a chromosome that is close to the best current chromosome. Even in large populations, the result is uniformity.

On a larger scale, however, unfit-looking individuals and species in nature survive quite well in ecological niches that lie outside the view of other, relatively fit-looking individuals and species:

The diversity principle:

▷ It can be as good to be different as it is to be fit.

In this section, you learn that being different can be incorporated into an overall measurement of fitness, and you learn that this observation creates a different perspective on what to do with local maxima.

The Rank-Space Method Links Fitness to Both Quality Rank and Diversity Rank

When you are selecting chromosomes for a new generation, one way to measure the diversity that would be contributed by a candidate chromosome is to calculate the sum of the inverse squared distances between that chromosome and the other, already selected chromosomes. Then, the **diversity rank** of a chromosome is determined by that inverse squared distance sum:

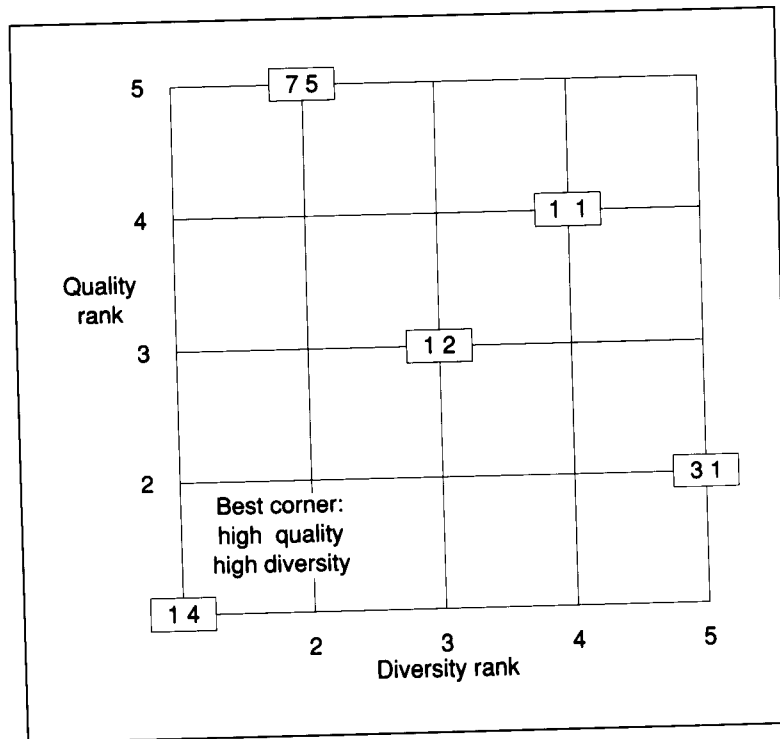
$$\sum_i \frac{1}{d_i^2}.$$

Consider again the set of six candidates that include 5-1, 1-4, 3-1, 1-2, 1-1, and 7-5. The highest-scoring candidate is 5-1. Ranking the other five by quality and inverse squared distances to 5-1 yields the following table:

Chromosome	Score	$\frac{1}{d^2}$	Diversity rank	Quality rank
1 4	4	0.040	1	1
3 1	3	0.250	5	2
1 2	2	0.059	3	3
1 1	1	0.062	4	4
7 5	0	0.050	2	5

One simple way to combine rank by quality and rank by diversity into a combined rank is to rank each chromosome according to the sum of its quality rank and its diversity rank using one or the other of the two rankings to break ties, as indicated in the following procedure:

Figure 25.7 Rank space enables two chromosomes to be compared in both quality and diversity.

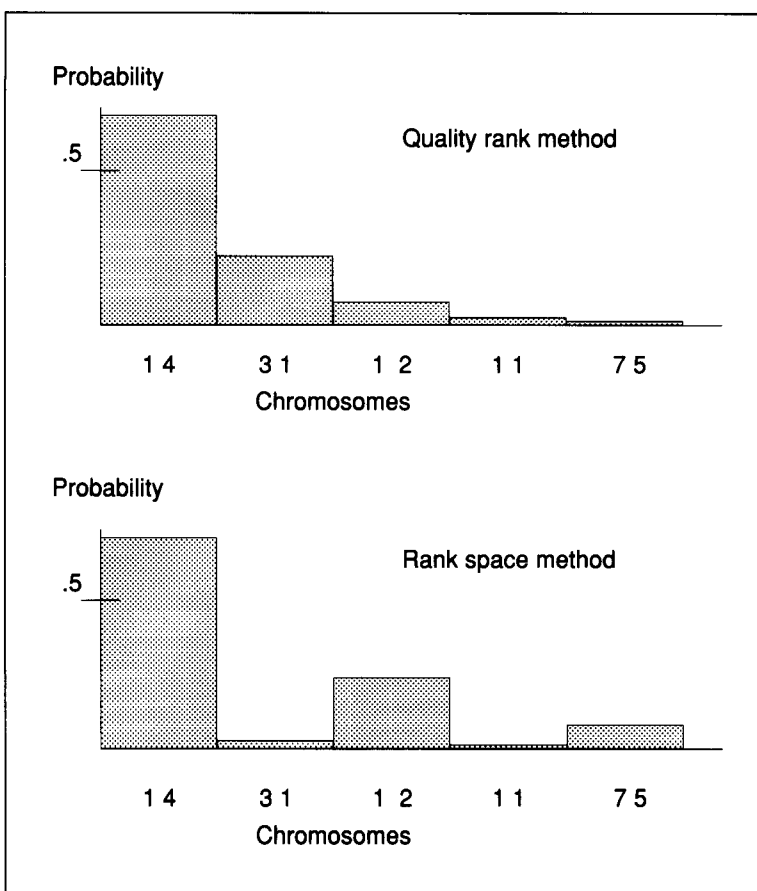


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- To select a candidate by the rank-space method,
- ▷ Sort the n individuals by quality.
 - ▷ Sort the n individuals by the sum of their inverse squared distances to already selected candidates.
 - ▷ Use the rank method, but sort on the sum of the quality rank and the diversity rank, rather than on quality rank.
-

Figure 25.7 illustrates this procedure. With diversity rank given by one axis and quality rank by another, it is natural to call the diagram a **rank space**, and to refer to the method as the **rank-space method**. Clearly, it is best to be in the lower-left corner of rank space, where a chromosome will be if it ranks well in terms of both quality and diversity.

Next, with a combined rank that combines the influence of quality and diversity, selection can be done as before, setting the fitness of the first candidate to p . Thus, the rank sum, combined rank, and fitnesses for the five chromosomes is given by the following table. Note that there is a rank-sum tie between 3-1 and 7-5. To break the tie, you judge the chromosome with the better diversity rank to have a better combined rank.

Figure 25.8 Fitnesses for five chromosomes, as measured by the quality-rank method and the rank-space method, using the qualities provided by moat mountain. In contrast to both the standard method and the rank method, the rank-space method takes diversity into account.



Chromosome	Rank sum	Combined rank	Fitness
1 4	2	1	0.667
3 1	7	4	0.025
1 2	6	2	0.222
1 1	8	5	0.012
7 5	7	3	0.074

Figure 25.8 compares fitness measured by combined rank with fitness measured by quality rank.

Suppose that the most probable chromosome—the 1-4 chromosome—is selected to accompany the 5-1 chromosome into the next generation. Two more remain to be selected. Now, however, the next one selected should be far from both 5-1 and 1-4. Accordingly, instead of measuring the inverse squared distance to just one reference chromosome, you sum the inverse squared distances from both reference chromosomes, 5-1 and 1-4. At this

point, the rank sums are all the same, but using diversity rank as the tie breaker yields the following table:

Chromosome	$\sum_i \frac{1}{d_i^2}$	Diversity rank	Quality rank	Combined rank	Fitness
3 1	0.327	4	1	4	0.037
1 2	0.309	3	2	3	0.074
1 1	0.173	2	3	2	0.222
7 5	0.077	1	4	1	0.667

Again suppose that the most probable chromosome—this time the 7-5 chromosome—is selected to accompany the 5-1 and 1-4 chromosomes into the next generation. Then, the ranks relevant to the final choice are determined by the following table; again, you break the rank-sum ties by appealing to diversity rank as the tie breaker. This time, 1-1 is the most probable chromosome:

Chromosome	$\sum_i \frac{1}{d_i^2}$	Diversity rank	Quality rank	Combined rank	Fitness
3 1	0.358	3	1	3	0.111
1 2	0.331	2	2	2	0.222
1 1	0.190	1	3	1	0.667

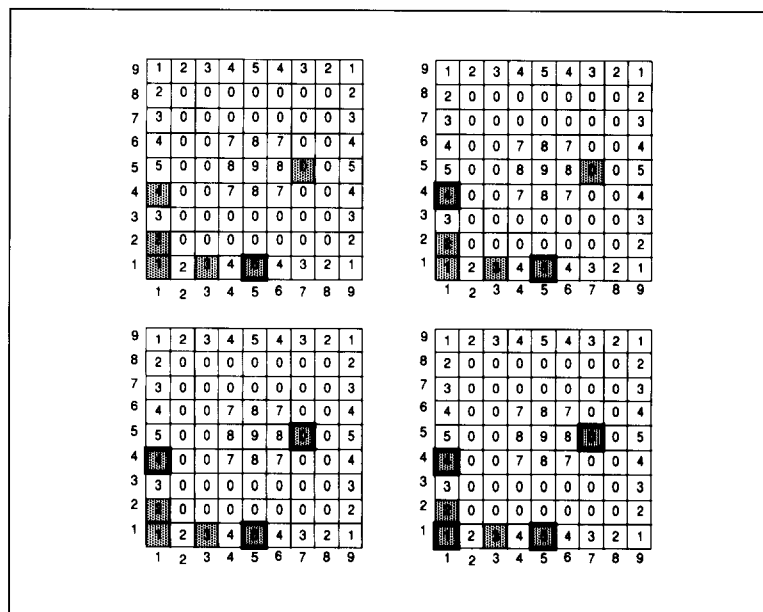
Figure 25.9 illustrates how all this computation is progressing. Note that the rank-space method tends to maintain diversity relative to the standard method, which would never select 7-5, and to the plain rank method, which would select 7-5 last, rather than third.

In summary, if you assume that the most probable chromosome is selected at each point following the automatic selection of the highest scoring chromosome, 5-1, then 1-4, 7-5, and 1-1 are selected for the next generation, in that order. Had you just examined quality alone, then the order would have been 5-1, 1-4, 3-1, and 1-2.

The Rank-Space Method Does Well on Moat Mountain

If Kookie were to try 1000 times to find the optimum, using the rank-space method, starting with a 1-1 chromosome and $p = 0.66$, he would find the best combination, on average, after about 15 generations. Thus, the rank-space method provides a considerable improvement, on the moat problem, over both the standard method and the rank method. The following table summarizes the improvement:

Figure 25.9 The sequence of three most probable choices drawn from a set of five candidates. Using the rank-space method, selections are made so as to retain diversity.



Mountain	Standard method	Quality rank	Rank space
Bump	14	12	12
Moat	155	75	15

Among 1000 simulation experiments performed by Kookie using the rank-space method, the luckiest produced the best combination after just seven generations, after starting at generation 0 with one 1-1 chromosome, which produces quality 1 cookies:

Generation 0:
 Chromosome Quality
 1 1 1

At this point, a favorable mutation produced a 2-1 chromosome, which was added to the population, producing two members. Crossover did not add anything during this generation, because there was just one chromosome:

Generation 1:
 Chromosome Quality
 2 1 2
 1 1 1

Next, mutation added a 3-1 chromosome. Crossover did not add anything during this generation, because both chromosomes in the current population had the same second gene, a 1.

Generation 2:

Chromosome	Quality
3 1	3
2 1	2
1 1	1

Next, mutation added a 2-2 chromosome and a 4-1 chromosome. Again, crossover added nothing. Of the existing and mutated chromosomes, the 2-1 chromosome was lost in forming the third generation:

Generation 3:

Chromosome	Quality
4 1	4
3 1	3
1 1	1
2 2	0

At this point, mutation produces three new chromosomes: 5-1, 1-2, and 2-3. Crossover of the 2-2 and 4-1 chromosomes produced a 2-1 chromosome and a 4-2 chromosome. All the rest of the mutation and crossover results were already in the current population. Accordingly, the next generation was selected from nine chromosomes:

Chromosome	Quality
4 1	4
3 1	3
1 1	1
2 2	0
5 1	5
1 2	2
2 3	0
2 1	2
4 2	0

Of these, the following were retained:

Generation 4:

Chromosome	Quality
5 1	5
3 1	3
1 2	2
2 3	0

Now 5-1 mutated to 6-1, 1-2 mutated to 2-2, 3-1 mutated to 3-2, and 2-3 mutated to 2-4. Also, various crossovers yielded five new chromosomes, 2-1, 1-1, 5-2, 3-2, and 5-3. Accordingly, the next generation was selected from 13 possibilities:

Chromosome	Quality
5 1	5
3 1	3
1 2	2
2 3	0
6 1	4
2 2	0
3 2	0
2 4	0
2 1	2
1 1	1
5 2	0
3 2	0
5 3	0

Of these, four were selected for the next generation, as usual:

Generation 5:

Chromosome	Quality
5 1	5
3 1	3
1 2	2
2 4	0

For the next generation, there was a considerable improvement as a consequence of mating 5-1 with 2-4, which led to a 5-4 chromosome in the next generation:

Generation 6:

Chromosome	Quality
5 4	8
1 4	4
3 1	3
1 2	2

Finally, 5-4 mutated to 5-5 in the final generation:

Generation 7:

Chromosome	Quality
5 5	9
1 4	4
1 2	2
5 2	0

Figure 25.10 shows graphically how this evolution occurred. Note that the rank-space method tends to keep the chromosomes apart. Because there is some randomness in the selection of candidates, however, some bunching still occurred.

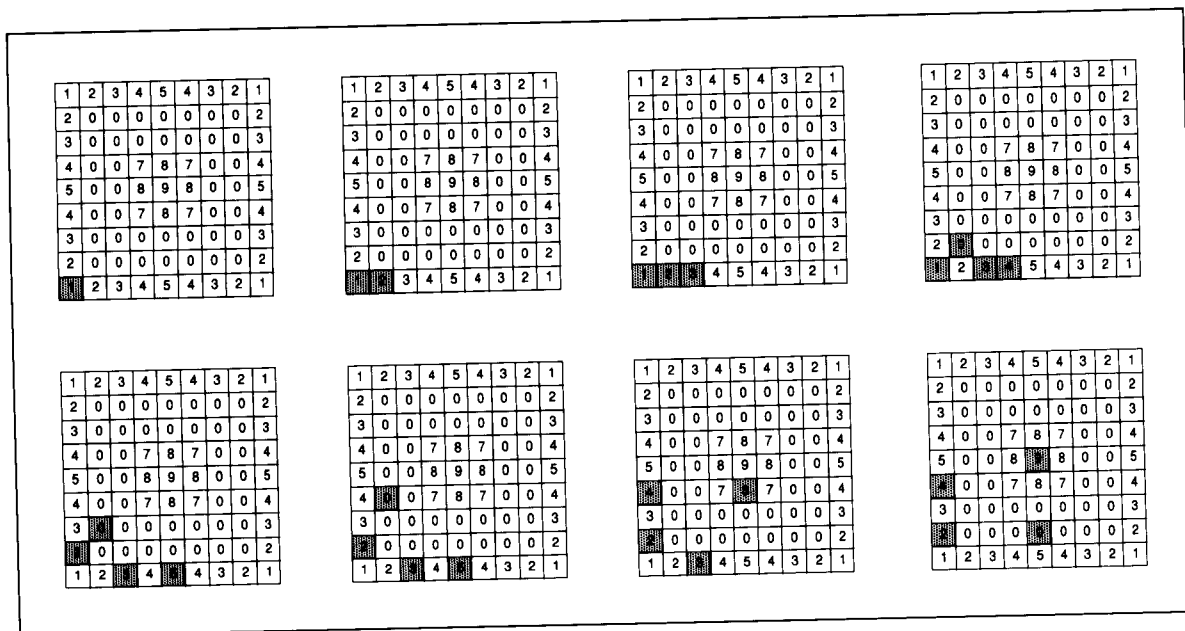


Figure 25.10 The results of a lucky experiment using the rank-space method. The optimum point was found in the seventh generation.

Local Maxima Are Easier to Handle when Diversity Is Maintained

Most approaches to search take the position that local maxima are traps. Accordingly, some approaches involve trap-escaping mechanisms such as backtracking and initially large, ever-shrinking step size. Other approaches involve parallel search with a large number of random starting positions in the hope that one of the parallel searches will get trapped on the local maximum that happens to be the global maximum as well.

In contrast, if a genetic algorithm treats diversity as a component of fitness, then some of the individuals in a population tend to hover around already-discovered local maxima in quality or diversity, driving off other, still peripatetic, individuals. As long as there are enough individuals to populate all the local maxima sufficiently, there is a reasonable chance that one individual will find its way to the global maximum.

The populate-and-conquer principle:

- ▷ Local maxima should be populated, not avoided, when you are seeking a global maximum.

SUMMARY

- One way to learn may be to imitate natural evolution, using the notion that survival is biased toward the fittest to guide a massive search.

- Chromosomes determine hereditary traits. Genetic learning algorithms modify analogs to chromosomes through analogs to mutation and mating, thus creating new individuals that may be fitter than their parents.
- The standard method for determining fitness equates fitness to a measure of quality. The rank method links fitness to quality rank, thus preventing the particular scale used to measure quality from having deleterious effects.
- The rank-space method links fitness to both quality rank and diversity rank, thus promoting not only the survival of individuals that are extremely fit from the perspective of quality, but also the survival of individuals that are both quite fit and different from other, even more fit individuals.
- It can be as good to be different as it is to be fit. When diversity is maintained, local maxima can be populated, rather than avoided altogether. By embodying this idea, the rank-space method solves problems that are beyond both the standard method and the rank method.

BACKGROUND

The Origin of Species is considered to be among the most influential scientific works of all time [Charles Darwin 1859].

Recently, new light has been shed on evolution by scientists equipped with ideas that have emerged with the dawn of the computer age. In particular, the idea of the importance of neutral mutations is becoming more appreciated. See, for example, the work of Motoo Kimura [1983].

John Holland is one of the pioneers of modern work on natural adaptation algorithms, and is a frequent contributor to the literature [1975, 1986].

An important paper by Jim Antonisse [1989] corrects a long-standing supposition that binary representations are best for genetic algorithms.

Michael de la Maza and Bruce Tidor show how time-varying selective pressure provides a way to maintain diversity on a variety of sample optimization problems, including problems of protein recognition [1991].

A fascinating account of how the speed of evolution can be increased using coevolving parasites appears in a paper by W. Daniel Hillis [1990].

To learn about molecular biology in detail, you should read the comprehensive textbook volumes by James D. Watson et al. [1987].