AN INTRODUCTION TO GENETIC ALGORITHMS

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An Introduction to Genetic Algorithms

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Chapter 1: Genetic Algorithms: An Overview

Overview

Science arises from the very human desire to understand and control the world. Over the course of history, we humans have gradually built up a grand edifice of knowledge that enables us to predict, to varying extents, the weather, the motions of the planets, solar and lunar eclipses, the courses of diseases, the rise and fall of economic growth, the stages of language development in children, and a vast panorama of other natural, social, and cultural phenomena. More recently we have even come to understand some fundamental limits to our abilities to predict. Over the eons we have developed increasingly complex means to control many aspects of our lives and our interactions with nature, and we have learned, often the hard way, the extent to which other aspects are uncontrollable.

The advent of electronic computers has arguably been the most revolutionary development in the history of science and technology. This ongoing revolution is profoundly increasing our ability to predict and control nature in ways that were barely conceived of even half a century ago. For many, the crowning achievements of this revolution will be the creation—in the form of computer programs—of new species of intelligent beings, and even of new forms of life.

The goals of creating artificial intelligence and artificial life can be traced back to the very beginnings of the computer age. The earliest computer scientists—Alan Turing, John von Neumann, Norbert Wiener, and others—were motivated in large part by visions of imbuing computer programs with intelligence, with the life−like ability to self−replicate, and with the adaptive capability to learn and to control their environments. These early pioneers of computer science were as much interested in biology and psychology as in electronics, and they looked to natural systems as guiding metaphors for how to achieve their visions. It should be no surprise, then, that from the earliest days computers were applied not only to calculating missile trajectories and deciphering military codes but also to modeling the brain, mimicking human learning, and simulating biological evolution. These biologically motivated computing activities have waxed and waned over the years, but since the early 1980s they have all undergone a resurgence in the computation research community. The first has grown into the field of neural networks, the second into machine learning, and the third into what is now called "evolutionary computation," of which genetic algorithms are the most prominent example.

1.1 A BRIEF HISTORY OF EVOLUTIONARY COMPUTATION

In the 1950s and the 1960s several computer scientists independently studied evolutionary systems with the idea that evolution could be used as an optimization tool for engineering problems. The idea in all these systems was to evolve a population of candidate solutions to a given problem, using operators inspired by natural genetic variation and natural selection.

In the 1960s, Rechenberg (1965, 1973) introduced "evolution strategies" (*Evolutionsstrategie* in the original German), a method he used to optimize real−valued parameters for devices such as airfoils. This idea was further developed by Schwefel (1975, 1977). The field of evolution strategies has remained an active area of research, mostly developing independently from the field of genetic algorithms (although recently the two communities have begun to interact). (For a short review of evolution strategies, see Back, Hoffmeister, and Schwefel 1991.) Fogel, Owens, and Walsh (1966) developed "evolutionary programming," a technique in which candidate solutions to given tasks were represented as finite−state machines, which were evolved by randomly mutating their state−transition diagrams and selecting the fittest. A somewhat broader formulation of evolutionary programming also remains an area of active research (see, for example, Fogel and Atmar 1993). Together, evolution strategies, evolutionary programming, and genetic algorithms form the backbone of the field of evolutionary computation.

Several other people working in the 1950s and the 1960s developed evolution−inspired algorithms for optimization and machine learning. Box (1957), Friedman (1959), Bledsoe (1961), Bremermann (1962), and Reed, Toombs, and Baricelli (1967) all worked in this area, though their work has been given little or none of the kind of attention or followup that evolution strategies, evolutionary programming, and genetic algorithms have seen. In addition, a number of evolutionary biologists used computers to simulate evolution for the purpose of controlled experiments (see, e.g., Baricelli 1957, 1962; Fraser 1957 a,b; Martin and Cockerham 1960). Evolutionary computation was definitely in the air in the formative days of the electronic computer.

Genetic algorithms (GAs) were invented by John Holland in the 1960s and were developed by Holland and his students and colleagues at the University of Michigan in the 1960s and the 1970s. In contrast with evolution strategies and evolutionary programming, Holland's original goal was not to design algorithms to solve specific problems, but rather to formally study the phenomenon of adaptation as it occurs in nature and to develop ways in which the mechanisms of natural adaptation might be imported into computer systems. Holland's 1975 book *Adaptation in Natural and Artificial Systems* presented the genetic algorithm as an abstraction of biological evolution and gave a theoretical framework for adaptation under the GA. Holland's GA is a method for moving from one population of "chromosomes" (e.g., strings of ones and zeros, or "bits") to a new population by using a kind of "natural selection" together with the genetics−inspired operators of crossover, mutation, and inversion. Each chromosome consists of "genes" (e.g., bits), each gene being an instance of a particular "allele" (e.g., 0 or 1). The selection operator chooses those chromosomes in the population that will be allowed to reproduce, and on average the fitter chromosomes produce more offspring than the less fit ones. Crossover exchanges subparts of two chromosomes, roughly mimicking biological recombination between two single−chromosome ("haploid") organisms; mutation randomly changes the allele values of some locations in the chromosome; and inversion reverses the order of a contiguous section of the chromosome, thus rearranging the order in which genes are arrayed. (Here, as in most of the GA literature, "crossover" and "recombination" will mean the same thing.)

Holland's introduction of a population−based algorithm with crossover, inversion, and mutation was a major innovation. (Rechenberg's evolution strategies started with a "population" of two individuals, one parent and one offspring, the offspring being a mutated version of the parent; many−individual populations and crossover were not incorporated until later. Fogel, Owens, and Walsh's evolutionary programming likewise used only mutation to provide variation.) Moreover, Holland was the first to attempt to put computational evolution on a firm theoretical footing (see Holland 1975). Until recently this theoretical foundation, based on the notion of "schemas," was the basis of almost all subsequent theoretical work on genetic algorithms

In the last several years there has been widespread interaction among researchers studying various evolutionary computation methods, and the boundaries between GAs, evolution strategies, evolutionary programming, and other evolutionary approaches have broken down to some extent. Today, researchers often use the term "genetic algorithm" to describe something very far from Holland's original conception. In this book I adopt this flexibility. Most of the projects I will describe here were referred to by their originators as GAs; some were not, but they all have enough of a "family resemblance" that I include them under the rubric of genetic algorithms.

1.2 THE APPEAL OF EVOLUTION

Why use evolution as an inspiration for solving computational problems? To evolutionary−computation researchers, the mechanisms of evolution seem well suited for some of the most pressing computational problems in many fields. Many computational problems require searching through a huge number of possibilities for solutions. One example is the problem of computational protein engineering, in which an algorithm is sought that will search among the vast number of possible amino acid sequences for a protein with specified properties. Another example is searching for a set of rules or equations that will predict the ups and downs of a financial market, such as that for foreign currency. Such search problems can often benefit from an effective use of parallelism, in which many different possibilities are explored simultaneously in an efficient way. For example, in searching for proteins with specified properties, rather than evaluate one amino acid sequence at a time it would be much faster to evaluate many simultaneously. What is needed is both computational parallelism (i.e., many processors evaluating sequences at the same time) and an intelligent strategy for choosing the next set of sequences to evaluate.

Many computational problems require a computer program to be *adaptive*—to continue to perform well in a changing environment. This is typified by problems in robot control in which a robot has to perform a task in a variable environment, and by computer interfaces that must adapt to the idiosyncrasies of different users. Other problems require computer programs to be innovative—to construct something truly new and original, such as a new algorithm for accomplishing a computational task or even a new scientific discovery. Finally, many computational problems require complex solutions that are difficult to program by hand. A striking example is the problem of creating artificial intelligence. Early on, AI practitioners believed that it would be straightforward to encode the rules that would confer intelligence on a program; expert systems were one result of this early optimism. Nowadays, many AI researchers believe that the "rules" underlying intelligence are too complex for scientists to encode by hand in a "top−down" fashion. Instead they believe that the best route to artificial intelligence is through a "bottom−up" paradigm in which humans write only very simple rules, and complex behaviors such as intelligence emerge from the massively parallel application and interaction of these simple rules. Connectionism (i.e., the study of computer programs inspired by neural systems) is one example of this philosophy (see Smolensky 1988); evolutionary computation is another. In connectionism the rules are typically simple "neural" thresholding, activation spreading, and strengthening or weakening of connections; the hoped−for emergent behavior is sophisticated pattern recognition and learning. In evolutionary computation the rules are typically "natural selection" with variation due to crossover and/or mutation; the hoped−for emergent behavior is the design of high−quality solutions to difficult problems and the ability to adapt these solutions in the face of a changing environment.

Biological evolution is an appealing source of inspiration for addressing these problems. Evolution is, in effect, a method of searching among an enormous number of possibilities for "solutions." In biology the enormous set of possibilities is the set of possible genetic sequences, and the desired "solutions" are highly fit organisms—organisms well able to survive and reproduce in their environments. Evolution can also be seen as a method for *designing* innovative solutions to complex problems. For example, the mammalian immune system is a marvelous evolved solution to the problem of germs invading the body. Seen in this light, the mechanisms of evolution can inspire computational search methods. Of course the fitness of a biological organism depends on many factors—for example, how well it can weather the physical characteristics of its environment and how well it can compete with or cooperate with the other organisms around it. The fitness criteria continually change as creatures evolve, so evolution is searching a constantly changing set of possibilities. Searching for solutions in the face of changing conditions is precisely what is required for adaptive computer programs. Furthermore, evolution is a massively parallel search method: rather than work on one species at a time, evolution tests and changes millions of species in parallel. Finally, viewed from a high level the "rules" of evolution are remarkably simple: species evolve by means of random variation (via mutation, recombination, and other operators), followed by natural selection in which the fittest tend to survive and reproduce, thus propagating their genetic material to future generations. Yet these simple rules are thought to be responsible, in large part, for the extraordinary variety and complexity we see in the biosphere.

1.3 BIOLOGICAL TERMINOLOGY

At this point it is useful to formally introduce some of the biological terminology that will be used throughout the book. In the context of genetic algorithms, these biological terms are used in the spirit of analogy with real biology, though the entities they refer to are much simpler than the real biological ones.

All living organisms consist of cells, and each cell contains the same set of one or more *chromosomes*—strings of DNA—that serve as a "blueprint" for the organism. A chromosome can be conceptually divided into *genes*— each of which encodes a particular protein. Very roughly, one can think of a gene as encoding a *trait*, such as eye color. The different possible "settings" for a trait (e.g., blue, brown, hazel) are called *alleles*. Each gene is located at a particular *locus* (position) on the chromosome.

Many organisms have multiple chromosomes in each cell. The complete collection of genetic material (all chromosomes taken together) is called the organism's *genome*. The term *genotype* refers to the particular set of genes contained in a genome. Two individuals that have identical genomes are said to have the same genotype. The genotype gives rise, under fetal and later development, to the organism's *phenotype*—its physical and mental characteristics, such as eye color, height, brain size, and intelligence.

Organisms whose chromosomes are arrayed in pairs are called *diploid*; organisms whose chromosomes are unpaired are called *haploid*. In nature, most sexually reproducing species are diploid, including human beings, who each have 23 pairs of chromosomes in each somatic (non−germ) cell in the body. During sexual reproduction, *recombination* (or *crossover*) occurs: in each parent, genes are exchanged between each pair of chromosomes to form a *gamete* (a single chromosome), and then gametes from the two parents pair up to create a full set of diploid chromosomes. In haploid sexual reproduction, genes are exchanged between the two parents' single−strand chromosomes. Offspring are subject to *mutation*, in which single nucleotides (elementary bits of DNA) are changed from parent to offspring, the changes often resulting from copying errors. The *fitness* of an organism is typically defined as the probability that the organism will live to reproduce (*viability*) or as a function of the number of offspring the organism has (*fertility*).

In genetic algorithms, the term *chromosome* typically refers to a candidate solution to a problem, often encoded as a bit string. The "genes" are either single bits or short blocks of adjacent bits that encode a particular element of the candidate solution (e.g., in the context of multiparameter function optimization the bits encoding a particular parameter might be considered to be a gene). An allele in a bit string is either 0 or 1; for larger alphabets more alleles are possible at each locus. Crossover typically consists of exchanging genetic material between two singlechromosome haploid parents. Mutation consists of flipping the bit at a randomly chosen locus (or, for larger alphabets, replacing a the symbol at a randomly chosen locus with a randomly chosen new symbol).

Most applications of genetic algorithms employ haploid individuals, particularly, single−chromosome individuals. The genotype of an individual in a GA using bit strings is simply the configuration of bits in that individual's chromosome. Often there is no notion of "phenotype" in the context of GAs, although more recently many workers have experimented with GAs in which there is both a genotypic level and a phenotypic level (e.g., the bit−string encoding of a neural network and the neural network itself).

1.4 SEARCH SPACES AND FITNESS LANDSCAPES

The idea of searching among a collection of candidate solutions for a desired solution is so common in computer science that it has been given its own name: searching in a "search space." Here the term "search space" refers to some collection of candidate solutions to a problem and some notion of "distance" between candidate solutions. For an example, let us take one of the most important problems in computational bioengineering: the aforementioned problem of computational protein design. Suppose you want use a computer to search for a protein—a sequence of amino acids—that folds up to a particular three−dimensional shape so it can be used, say, to fight a specific virus. The search space is the collection of all possible protein sequences—an infinite set of possibilities. To constrain it, let us restrict the search to all possible sequences of length 100 or less—still a huge search space, since there are 20 possible amino acids at each position in the sequence. (How many possible sequences are there?) If we represent the 20 amino acids by letters of the alphabet, candidate solutions will look like this:

A G G M C G B L….

We will define the distance between two sequences as the number of positions in which the letters at corresponding positions differ. For example, the distance between A G G M C G B L and MG G M C G B L is 1, and the distance between A G G M C G B L and L B M P A F G A is 8. An algorithm for searching this space is a method for choosing which candidate solutions to test at each stage of the search. In most cases the next candidate solution(s) to be tested will depend on the results of testing previous sequences; most useful algorithms assume that there will be some correlation between the quality of "neighboring" candidate solutions—those close in the space. Genetic algorithms assume that high−quality "parent" candidate solutions from different regions in the space can be combined via crossover to, on occasion, produce high−quality "offspring" candidate solutions.

Another important concept is that of "fitness landscape." Originally defined by the biologist Sewell Wright (1931) in the context of population genetics, a fitness landscape is a representation of the space of all possible genotypes along with their fitnesses.

Suppose, for the sake of simplicity, that each genotype is a bit string of length *l*, and that the distance between two genotypes is their "Hamming distance"—the number of locations at which corresponding bits differ. Also suppose that each genotype can be assigned a real−valued fitness. A fitness landscape can be pictured as an (*l* + 1)−dimensional plot in which each genotype is a point in *l* dimensions and its fitness is plotted along the (*l* + 1)st axis. A simple landscape for *l* = 2 is shown in figure 1.1. Such plots are called landscapes because the plot of fitness values can form "hills," "peaks," "valleys," and other features analogous to those of physical landscapes. Under Wright's formulation, evolution causes populations to move along landscapes in particular ways, and "adaptation" can be seen as the movement toward local peaks. (A "local peak," or "local optimum," is not necessarily the highest point in the landscape, but any small

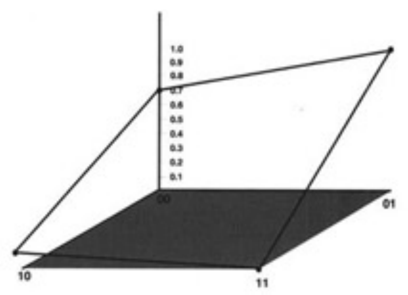


Figure 1.1: A simple fitness landscape for l = 2. Here f(00) = 0.7, f(01) = 1.0, f(10) = 0.1, and f(11) = 0.0.

movement away from it goes downward in fitness.) Likewise, in GAs the operators of crossover and mutation can be seen as ways of moving a population around on the landscape defined by the fitness function.

The idea of evolution moving populations around in unchanging landscapes is biologically unrealistic for several reasons. For example, an organism cannot be assigned a fitness value independent of the other organisms in its environment; thus, as the population changes, the fitnesses of particular genotypes will change as well. In other words, in the real world the "landscape" cannot be separated from the organisms that inhabit it. In spite of such caveats, the notion of fitness landscape has become central to the study of genetic algorithms, and it will come up in various guises throughout this book.

1.5 ELEMENTS OF GENETIC ALGORITHMS

It turns out that there is no rigorous definition of "genetic algorithm" accepted by all in the evolutionary−computation community that differentiates GAs from other evolutionary computation methods. However, it can be said that most methods called "GAs" have at least the following elements in common: populations of chromosomes, selection according to fitness, crossover to produce new offspring, and random mutation of new offspring.Inversion—Holland's fourth element of GAs—is rarely used in today's implementations, and its advantages, if any, are not well established. (Inversion will be discussed at length in chapter 5.)

The chromosomes in a GA population typically take the form of bit strings. Each locus in the chromosome has two possible alleles: 0 and 1. Each chromosome can be thought of as a point in the search space of candidate solutions. The GA processes populations of chromosomes, successively replacing one such population with another. The GA most often requires a fitness function that assigns a score (fitness) to each chromosome in the current population. The fitness of a chromosome depends on how well that chromosome solves the problem at hand.

Examples of Fitness Functions

One common application of GAs is function optimization, where the goal is to find a set of parameter values that maximize, say, a complex multiparameter function. As a simple example, one might want to maximize the real−valued one−dimensional function

$$f(y) = y + |\sin(32y)|, \quad 0 \leq y < \pi$$

(Riolo 1992). Here the candidate solutions are values of *y*, which can be encoded as bit strings representing real numbers. The fitness calculation translates a given bit string *x* into a real number *y* and then evaluates the function at that value. The fitness of a string is the function value at that point.

As a non−numerical example, consider the problem of finding a sequence of 50 amino acids that will fold to a desired three−dimensional protein structure. A GA could be applied to this problem by searching a population of candidate solutions, each encoded as a 50−letter string such as

IHCCVASASDMIKPVFTVASYLKNWTKAKGPNFEICISGRTPYWDNFPGI,

where each letter represents one of 20 possible amino acids. One way to define the fitness of a candidate sequence is as the negative of the potential energy of the sequence with respect to the desired structure. The potential energy is a measure of how much physical resistance the sequence would put up if forced to be folded into the desired structure—the lower the potential energy, the higher the fitness. Of course one would not want to physically force every sequence in the population into the desired structure and measure its resistance—this would be very difficult, if not impossible. Instead, given a sequence and a desired structure (and knowing some of the relevant biophysics), one can estimate the potential energy by calculating some of the forces acting on each amino acid, so the whole fitness calculation can be done computationally.

These examples show two different contexts in which candidate solutions to a problem are encoded as abstract chromosomes encoded as strings of symbols, with fitness functions defined on the resulting space of strings. A genetic algorithm is a method for searching such fitness landscapes for highly fit strings.

GA Operators

The simplest form of genetic algorithm involves three types of operators: selection, crossover (single point), and mutation.

Selection This operator selects chromosomes in the population for reproduction. The fitter the chromosome, the more times it is likely to be selected to reproduce.

Crossover This operator randomly chooses a locus and exchanges the subsequences before and after that locus between two chromosomes to create two offspring. For example, the strings 10000100 and 11111111 could be crossed over after the third locus in each to produce the two offspring 10011111 and 11100100. The crossover operator roughly mimics biological recombination between two single−chromosome (haploid) organisms.

Mutation This operator randomly flips some of the bits in a chromosome. For example, the string 00000100 might be mutated in its second position to yield 01000100. Mutation can occur at each bit position in a string with some probability, usually very small (e.g., 0.001).

1.6 A SIMPLE GENETIC ALGORITHM

Given a clearly defined problem to be solved and a bit string representation for candidate solutions, a simple GA works as follows:

1. Start with a randomly generated population of *n* *l*−bit chromosomes (candidate solutions to a problem).

2. Calculate the fitness $f(x)$ of each chromosome x in the population.

3. Repeat the following steps until *n* offspring have been created:

    a. Select a pair of parent chromosomes from the current population, the probability of selection being an increasing function of fitness. Selection is done "with replacement," meaning that the same chromosome can be selected more than once to become a parent.

    b.

With probability p_c (the "crossover probability" or "crossover rate"), cross over the pair at a randomly chosen point (chosen with uniform probability) to form two offspring. If no crossover takes place, form two offspring that are exact copies of their respective parents. (Note that here the crossover rate is defined to be the probability that two parents will cross over in a single point. There are also "multi−point crossover" versions of the GA in which the crossover rate for a pair of parents is the number of points at which a crossover takes place.)

c.
Mutate the two offspring at each locus with probability p_m (the mutation probability or mutation rate), and place the resulting chromosomes in the new population.

If n is odd, one new population member can be discarded at random.

4.
Replace the current population with the new population.

5.
Go to step 2.

Each iteration of this process is called a *generation*. A GA is typically iterated for anywhere from 50 to 500 or more generations. The entire set of generations is called a *run*. At the end of a run there are often one or more highly fit chromosomes in the population. Since randomness plays a large role in each run, two runs with different random−number seeds will generally produce different detailed behaviors. GA researchers often report statistics (such as the best fitness found in a run and the generation at which the individual with that best fitness was discovered) averaged over many different runs of the GA on the same problem.

The simple procedure just described is the basis for most applications of GAs. There are a number of details to fill in, such as the size of the population and the probabilities of crossover and mutation, and the success of the algorithm often depends greatly on these details. There are also more complicated versions of GAs (e.g., GAs that work on representations other than strings or GAs that have different types of crossover and mutation operators). Many examples will be given in later chapters.

As a more detailed example of a simple GA, suppose that l (string length) is 8, that $f(x)$ is equal to the number of ones in bit string x (an extremely simple fitness function, used here only for illustrative purposes), that n(the population size)is 4, that $p_c = 0.7$, and that $p_m = 0.001$. (Like the fitness function, these values of l and n were chosen for simplicity. More typical values of l and n are in the range 50–1000. The values given for p_c and p_m are fairly typical.)

The initial (randomly generated) population might look like this:

Chromosome label	Chromosome string	Fitness
A	00000110	2
B	11101110	6
C	00100000	1
D	00110100	3

A common selection method in GAs is *fitness−proportionate selection*, in which the number of times an individual is expected to reproduce is equal to its fitness divided by the average of fitnesses in the population. (This is equivalent to what biologists call "viability selection.")

A simple method of implementing fitness−proportionate selection is "roulette−wheel sampling" (Goldberg 1989a), which is conceptually equivalent to giving each individual a slice of a circular roulette wheel equal in area to the individual's fitness. The roulette wheel is spun, the ball comes to rest on one wedge−shaped slice, and the corresponding individual is selected. In the $n = 4$ example above, the roulette wheel would be spun four times; the first two spins might choose chromosomes B and D to be parents, and the second two spins might choose chromosomes B and C to be parents. (The fact that A might not be selected is just the luck of the draw. If the roulette wheel were spun many times, the average results would be closer to the expected values.)

Once a pair of parents is selected, with probability p_c they cross over to form two offspring. If they do not cross over, then the offspring are exact copies of each parent. Suppose, in the example above, that parents B and D cross over after the first bit position to form offspring E = 10110100 and F = 01101110, and parents B and C do not cross over, instead forming offspring that are exact copies of B and C. Next, each offspring is subject to mutation at each locus with probability p_m. For example, suppose offspring E is mutated at the sixth locus to form E' = 10110000, offspring F and C are not mutated at all, and offspring B is mutated at the first locus to form B' = 01101110. The new population will be the following:

Chromosome label	Chromosome string	Fitness
E'	10110000	3
F	01101110	5
C	00100000	1
B'	01101110	5

Note that, in the new population, although the best string (the one with fitness 6) was lost, the average fitness rose from 12/4 to 14/4. Iterating this procedure will eventually result in a string with all ones.

1.7 GENETIC ALGORITHMS AND TRADITIONAL SEARCH METHODS

In the preceding sections I used the word "search" to describe what GAs do. It is important at this point to contrast this meaning of "search" with its other meanings in computer science.

There are at least three (overlapping) meanings of "search":

Search for stored data Here the problem is to efficiently retrieve information stored in computer memory. Suppose you have a large database of names and addresses stored in some ordered way. What is the best way to search for the record corresponding to a given last name? "Binary search" is one method for efficiently finding the desired record. Knuth (1973) describes and analyzes many such search methods.

Search for paths to goals Here the problem is to efficiently find a set of actions that will move from a given initial state to a given goal. This form of search is central to many approaches in artificial intelligence. A simple example—all too familiar to anyone who has taken a course in AI—is the "8−puzzle," illustrated in figure 1.2. A set of tiles numbered 1–8 are placed in a square, leaving one space empty. Sliding one of the adjacent tiles into the blank space is termed a "move." Figure 1.2a illustrates the problem of finding a set of moves from the initial state to the state in which all the tiles are in order. A partial search tree corresponding to this problem is illustrated in figure 1.2b The "root" node represents the initial state, the nodes branching out from it represent all possible results of one move from that state, and so on down the tree. The search algorithms discussed in most AI contexts are methods for efficiently finding the best (here, the shortest) path in the tree from the initial state to the goal state. Typical algorithms are "depth−first search," "branch and bound," and "A*."

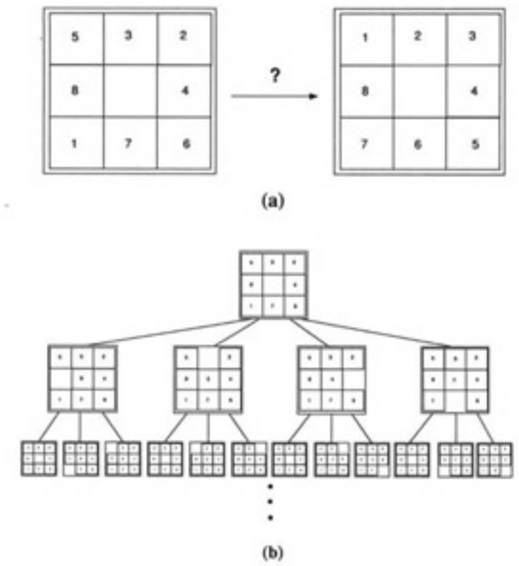


Figure 1.2: The 8−puzzle. (a) The problem is to find a sequence of moves that will go from the initial state to the state with the tiles in the correct order (the goal state). (b) A partial search tree for the 8−puzzle.

Search for solutions This is a more general class of search than "search for paths to goals." The idea is to efficiently find a solution to a problem in a large space of candidate solutions. These are the kinds of search problems for which genetic algorithms are used.

There is clearly a big difference between the first kind of search and the second two. The first concerns problems in which one needs to find a piece of information (e.g., a telephone number) in a collection of explicitly stored information. In the second two, the information to be searched is not explicitly stored; rather, candidate solutions are created as the search process proceeds. For example, the AI search methods for solving the 8−puzzle do not begin with a complete search tree in which all the nodes are already stored in memory; for most problems of interest there are too many possible nodes in the tree to store them all. Rather, the search tree is elaborated step by step in a way that depends on the particular algorithm, and the goal is to find an optimal or high−quality solution by examining only a small portion of the tree. Likewise, when searching a space of candidate solutions with a GA, not all possible candidate solutions are created first and then evaluated; rather, the GA is a method for finding optimal or good solutions by examining only a small fraction of the possible candidates.

"Search for solutions" subsumes "search for paths to goals," since a path through a search tree can be encoded as a candidate solution. For the 8−puzzle, the candidate solutions could be lists of moves from the initial state to some other state (correct only if the final state is the goal state). However, many "search for paths to goals" problems are better solved by the AI tree−search techniques (in which partial solutions can be evaluated) than by GA or GA−like techniques (in which full candidate solutions must typically be generated before they can be evaluated).

However, the standard AI tree−search (or, more generally, graph−search) methods do not always apply. Not all problems require finding a path from an initial state to a goal. For example, predicting the threedimensional structure of a protein from its amino acid sequence does not necessarily require knowing the sequence of physical moves by which a protein folds up into a 3D structure; it requires only that the final 3D configuration be predicted. Also, for many problems, including the protein−prediction problem, the configuration of the goal state is not known ahead of time.

The GA is a general method for solving "search for solutions" problems (as are the other evolution−inspired techniques, such as evolution strategies and evolutionary programming). Hill climbing, simulated annealing, and tabu search are examples of other general methods. Some of these are similar to "search for paths to goals" methods such as branch−and−bound and A*. For descriptions of these and other search methods see Winston 1992, Glover 1989 and 1990, and Kirkpatrick, Gelatt, and Vecchi 1983. "Steepest−ascent" hill climbing, for example, works as follows:

1. Choose a candidate solution (e.g., encoded as a bit string) at random. Call this string *current−string*.
2. Systematically mutate each bit in the string from left to right, one at a time, recording the fitnesses of the resulting one−bit mutants.
3. If any of the resulting one−bit mutants give a fitness increase, then set *current−string* to the one−bit mutant giving the highest fitness increase (the "steepest ascent").
4. If there is no fitness increase, then save *current−string* (a "hilltop") and go to step 1. Otherwise, go to step 2 with the new *current−string*.
5. When a set number of fitness−function evaluations has been performed, return the highest hilltop that was found.

In AI such general methods (methods that can work on a large variety of problems) are called "weak methods," to differentiate them from "strong methods" specially designed to work on particular problems. All the "search for solutions" methods (1) initially generate a set of candidate solutions (in the GA this is the initial population; in steepest−ascent hill climbing this is the initial string and all the one−bit mutants of it), (2) evaluate the candidate solutions according to some fitness criteria, (3) decide on the basis of this evaluation which candidates will be kept and which will be discarded, and (4) produce further variants by using some kind of operators on the surviving candidates.

The particular combination of elements in genetic algorithms—parallel population−based search with stochastic selection of many individuals, stochastic crossover and mutation—distinguishes them from other search methods. Many other search methods have some of these elements, but not this particular combination.

1.9 TWO BRIEF EXAMPLES

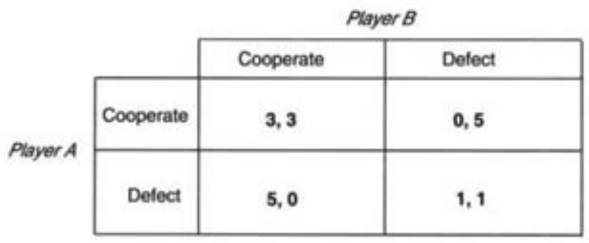
As warmups to more extensive discussions of GA applications, here are brief examples of GAs in action on two particularly interesting projects.

Using GAs to Evolve Strategies for the Prisoner's Dilemma

The Prisoner's Dilemma, a simple two−person game invented by Merrill Flood and Melvin Dresher in the 1950s, has been studied extensively in game theory, economics, and political science because it can be seen as an idealized model for real−world phenomena such as arms races (Axelrod 1984; Axelrod and Dion 1988). It can be formulated as follows: Two individuals (call them Alice and Bob) are arrested for committing a crime together and are held in separate cells, with no communication possible between them. Alice is offered the following deal: If she confesses and agrees to testify against Bob, she will receive a suspended sentence with probation, and Bob will be put away for 5 years. However, if at the same time Bob confesses and agrees to testify against Alice, her testimony will be discredited, and each will receive 4 years for pleading guilty. Alice is told that Bob is being offered precisely the same deal. Both Alice and Bob know that if neither testify against the other they can be convicted only on a lesser charge for which they will each get 2 years in jail.

Should Alice "defect" against Bob and hope for the suspended sentence, risking a 4−year sentence if Bob defects? Or should she "cooperate" with Bob (even though they cannot communicate), in the hope that he will also cooperate so each will get only 2 years, thereby risking a defection by Bob that will send her away for 5 years?

The game can be described more abstractly. Each player independently decides which move to make—i.e., whether to cooperate or defect. A "game" consists of each player's making a decision (a "move"). The possible results of a single game are summarized in a payoff matrix like the one shown in figure 1.3. Here the goal is to get as many points (as opposed to as few years in prison) as possible. (In figure 1.3, the payoff in each case can be interpreted as 5 minus the number of years in prison.) If both players cooperate, each gets 3 points. If player A defects and player B cooperates, then player A gets 5 points and player B gets 0 points, and vice versa if the situation is reversed. If both players defect, each gets 1 point. What is the best strategy to use in order to maximize one's own payoff? If you suspect that your opponent is going to cooperate, then you should surely defect. If you suspect that your opponent is going to defect, then you should defect too. No matter what the other player does, it is always better to defect. The dilemma is that if both players defect each gets a worse score than if they cooperate. If the game is *iterated* (that is, if the two players play several games in a row), both players' always defecting will lead to a much lower total payoff than the players would get if they



		Player B	
		Cooperate	Defect
Player A	Cooperate	3, 3	0, 5
	Defect	5, 0	1, 1

Figure 1.3: The payoff matrix for the Prisoner's Dilemma (adapted from Axelrod 1987). The two numbers given in each box are the payoffs for players A and B in the given situation, with player A's payoff listed first in each pair.

cooperated. How can reciprocal cooperation be induced? This question takes on special significance when the notions of cooperating and defecting correspond to actions in, say, a real−world arms race (e.g., reducing or increasing one's arsenal).

Robert Axelrod of the University of Michigan has studied the Prisoner's Dilemma and related games extensively. His interest in determining what makes for a good strategy led him to organize two Prisoner's Dilemma tournaments (described in Axelrod 1984). He solicited strategies from researchers in a number of disciplines. Each participant submitted a computer program that implemented a particular strategy, and the various programs played iterated games with each other. During each game, each program remembered what move (i.e., cooperate or defect) both it and its opponent had made in each of the three previous games that they had played with each other, and its strategy was based on this memory. The programs were paired in a round−robin tournament in which each played with all the other programs over a number of games. The first tournament consisted of 14 different programs; the second consisted of 63 programs (including one that made random moves). Some of the strategies submitted were rather complicated, using techniques such as Markov processes and Bayesian inference to model the other players in order to determine the best move. However, in both tournaments the winner (the strategy with the highest average score) was the simplest of the submitted strategies: TIT FOR TAT. This strategy, submitted by Anatol Rapoport, cooperates in the first game and then, in subsequent games, does whatever the other player did in its move in the previous game with TIT FOR TAT. That is, it offers cooperation and reciprocates it. But if the other player defects, TIT FOR TAT punishes that defection with a defection of its own, and continues the punishment until the other player begins cooperating again.

After the two tournaments, Axelrod (1987) decided to see if a GA could evolve strategies to play this game successfully. The first issue was figuring out how to encode a strategy as a string. Here is how Axelrod's encoding worked. Suppose the memory of each player is one previous game. There are four possibilities for the previous game:

- *CC* (case 1),
- *CD* (case 2),
- *DC* (case 3),
- *DD* (case 4),

where *C* denotes "cooperate" and *D* denotes "defect." Case 1 is when both players cooperated in the previous game, case 2 is when player A cooperated and player B defected, and so on. A strategy is simply a rule that specifies an action in each of these cases. For example, TIT FOR TAT as played by player A is as follows:

- If *CC* (case 1), then *C*.
- If *CD* (case 2), then *D*.
- If *DC* (case 3), then *C*.
- If *DD* (case 4), then *D*.

If the cases are ordered in this canonical way, this strategy can be expressed compactly as the string *CDCD*. To use the string as a strategy, the player records the moves made in the previous game (e.g., *CD*), finds the case number *i* by looking up that case in a table of ordered cases like that given above (for *CD*, *i* = 2), and selects the letter in the *i*th position of the string as its move in the next game (for *i* = 2, the move is *D*).

Axelrod's tournaments involved strategies that remembered three previous games. There are 64 possibilities for the previous three games:

- *CC CC CC* (case 1),
- *CC CC CD* (case 2),
- *CC CC DC* (case 3),
    - î
- *DD DD DC* (case 63),
- *DD DD DD* (case 64).

Thus, a strategy can be encoded by a 64−letter string, e.g., *CDCCCDDCC CDD…*. Since using the strategy requires the results of the three previous games, Axelrod actually used a 70−letter string, where the six extra letters encoded three hypothetical previous games used by the strategy to decide how to move in the first actual game. Since each locus in the string has two possible alleles (*C* and *D*), the number of possible strategies is 2^{70}. The search space is thus far too big to be searched exhaustively.

In Axelrod's first experiment, the GA had a population of 20 such strategies. The fitness of a strategy in the population was determined as follows: Axelrod had found that eight of the human−generated strategies from the second tournament were representative of the entire set of strategies, in the sense that a given strategy's score playing with these eight was a good predictor of the strategy's score playing with all 63 entries. This set of eight strategies (which did *not* include TIT FOR TAT) served as the "environment" for the evolving strategies in the population. Each individual in the population played iterated games with each of the eight fixed strategies, and the individual's fitness was taken to be its average score over all the games it played.

Axelrod performed 40 different runs of 50 generations each, using different random−number seeds for each run. Most of the strategies that evolved were similar to TIT FOR TAT in that they reciprocated cooperation and punished defection (although not necessarily only on the basis of the immediately preceding move). However, the GA often found strategies that scored substantially higher than TIT FOR TAT. This is a striking result, especially in view of the fact that in a given run the GA is testing only $20 \times 50 = 1000$ individuals out of a huge search space of 2^{70} possible individuals.

It would be wrong to conclude that the GA discovered strategies that are "better" than any human−designed strategy. The performance of a strategy depends very much on its environment—that is, on the strategies with which it is playing. Here the environment was fixed—it consisted of eight human−designed strategies that did not change over the course of a run. The resulting fitness function is an example of a static (unchanging) fitness landscape. The highest−scoring strategies produced by the GA were designed to exploit specific weaknesses of several of the eight fixed strategies. It is not necessarily true that these high−scoring strategies would also score well in a different environment. TIT FOR TAT is a generalist, whereas the highest−scoring evolved strategies were more specialized to the given environment. Axelrod concluded that the GA is good at doing what evolution often does: developing highly specialized adaptations to specific characteristics of the environment.

To see the effects of a changing (as opposed to fixed) environment, Axelrod carried out another experiment in which the fitness of an individual was determined by allowing the individuals in the population to play with one another rather than with the fixed set of eight strategies. Now the environment changed from generation to generation because the opponents themselves were evolving. At every generation, each individual played iterated games with each of the 19 other members of the population and with itself, and its fitness was again taken to be its average score over all games. Here the fitness landscape was not static—it was a function of the particular individuals present in the population, and it changed as the population changed.

In this second set of experiments, Axelrod observed that the GA initially evolved uncooperative strategies. In the first few generations strategies that tended to cooperate did not find reciprocation among their fellow population members and thus tended to die out, but after about 10–20 generations the trend started to reverse: the GA discovered strategies that reciprocated cooperation and that punished defection (i.e., variants of TIT FOR TAT). These strategies did well with one another and were not completely defeated by less cooperative strategies, as were the initial cooperative strategies. Because the reciprocators scored above average, they spread in the population; this resulted in increasing cooperation and thus increasing fitness.

Axelrod's experiments illustrate how one might use a GA both to evolve solutions to an interesting problem and to model evolution and coevolution in an idealized way. One can think of many additional possible experiments, such as running the GA with the probability of crossover set to 0—that is, using only the selection and mutation operators (Axelrod 1987) or allowing a more open−ended kind of evolution in which the amount of memory available to a given strategy is allowed to increase or decrease (Lindgren 1992).

Hosts and Parasites: Using GAs to Evolve Sorting Networks

Designing algorithms for efficiently sorting collections of ordered elements is fundamental to computer science. Donald Knuth (1973) devoted more than half of a 700−page volume to this topic in his classic series *The Art of Computer Programming*. The goal of sorting is to place the elements in a data structure (e.g., a list or a tree) in some specified order (e.g., numerical or alphabetic) in minimal time. One particular approach to sorting described in Knuth's book is the *sorting network*, a parallelizable device for sorting lists with a fixed number n of elements. Figure 1.4 displays one such network (a "Batcher sort"—see Knuth 1973) that will sort lists of $n = 16$ elements (e_0–e_{15}). Each horizontal line represents one of the elements in the list, and each vertical arrow represents a comparison to be made between two elements. For example, the leftmost column of vertical arrows indicates that comparisons are to be made between e_0 and e_1, between e_2 and e_3, and so on. If the elements being compared are out of the desired order, they are swapped.

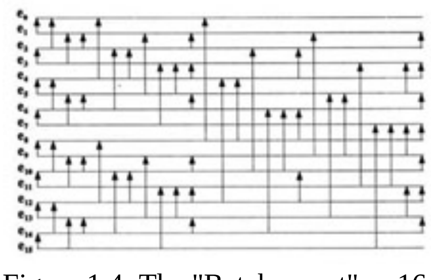


Figure 1.4: The "Batcher sort" n=16 sorting network (adapted from Knuth 1973). Each horizontal line