Survival of the Fittest Bits

In Darwinian terms, life is a struggle in which only the fittest survive to reproduce. What has proved successful to life is also useful to problem solving on a computer. In particular, programs using so-called genetic algorithms find solutions by applying the strategies of natural selection. The algorithm first advances possible answers. Then, like biological organisms, the solutions "cross over," or exchange "genes," with every generation. Sometimes there are mutations, or changes, in the genes. Only the "fittest" solutions survive so that they can reproduce to create even better answers [see "Genetic Algorithms," by John Holland; page 66].

One way to understand how genetic algorithms work is to implement a simple one and use it in some experiments. I chose the C language for my algorithm, but any other computer language would do as well. It took me two days to complete the version described here. I spent the most time by far writing the utilities to make the program easy to run, to change parameter settings and to display the population and statistics about its performance.

I recommend developing a genetic algorithm in two steps. First, write utilities (some are described below) to track the population's average fitness and the most fit members of each generation. Your version should generate random populations of individuals and have subroutines to assign fitness. The program should also display the individuals and their fitnesses, sort by fitness and calculate the average fitness of the population. Second, add subroutines to implement the genetic algorithm itself. That is, your program should select parents from the current population and modify the offspring of those parents through crossover and mutation.

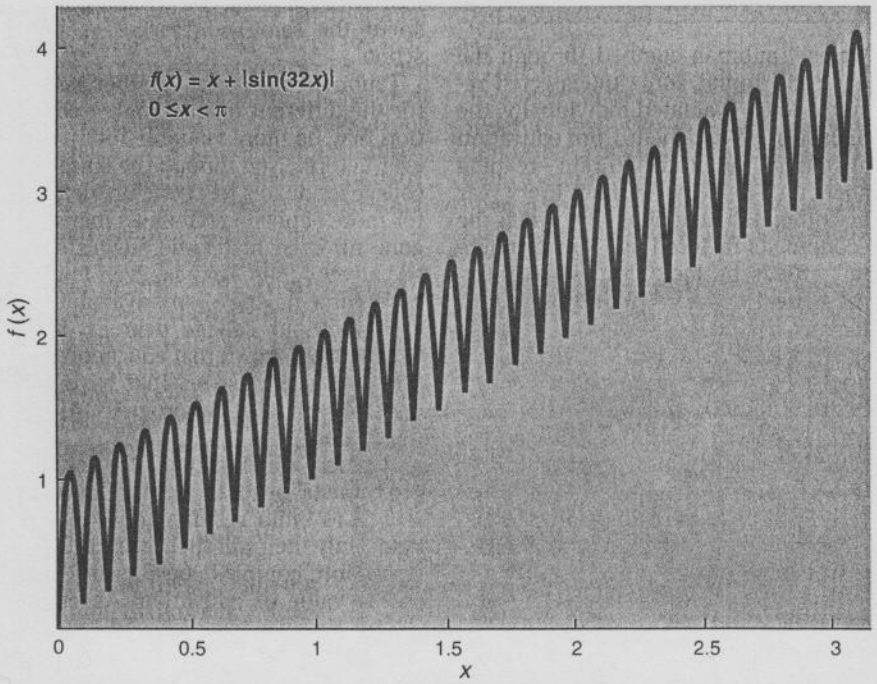
In writing a genetic algorithm for the first time, I found it best to use a simple problem for which I know the answer. This approach made it easier to debug and to understand the algorithm. Adjusting it for more complex problems is not too difficult.

I chose the problem of finding the optimum value of the function $f(x) = x + |\sin(32x)|$. I limited the values of x (the domain) to between 0 and π (I am working in radians, where $\pi = 180$ degrees.) Thus, this function has 32 regular oscillations added to the straight line $f(x) = x$ [*see illustration below*]. Because $f(x)$ is always positive, it can be used directly as a measure of fitness. The goal is to find an individual string (a value of x) that yields the largest $f(x)$.

The first step is deciding how to represent structures from the domain in a form your genetic algorithm can process. I represented the values of x as binary strings, as described in Holland's article. For my initial experiments, I chose the length, L, of my strings to be 16 bits ($L = 16$). I thus have $2^L = 2^{16} = 65{,}536$ possible values of x. (Increasing the length of the string improves the precision of the solution.) I assigned these 2^L string values to values of x: I let the string 0000000000000000 represent $x = 0$, 0000000000000001 to be $x = 1(\pi/2^L)$, 0000000000000010 to be $x = 2(\pi/2^L)$, and so on, all the way to 1111111111111111, which represents the maximum value of the domain, $x = (2^L - 1)(\pi/2^L) = \pi - \pi/2^L$. (The value of π itself is excluded because there is no string left to represent it.) To test your intuition, what value of x does the string 1000000000000000 represent?

In short, the binary strings represent 2^L values of x that are equally spaced between 0 and π. Hence, as the algorithm searches the space of binary strings, it is in effect searching through the possible values of x. The C fragment on page 116 (the mapping algorithm) shows one way to implement this mapping from a binary string, which is stored as a char array in C. For example, it will map 1000000000000000 onto (approximately) $\pi/2$. The fitness of an individual binary string S is just $f(x)$, where $x = \text{MapStringToX}(S)$.

Given this mapping from binary strings to the domain of $f(x)$, it is instructive to map schemata, or target regions, as specified by Holland. For



FITTEST SOLUTION of f(x) = x + |sin (32x)| *is the value of* x *that yields the highest* f(x). *The answer is* x = 3.09346401 *(in radians), represented by* 1111110000010100.

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example, the schema 0********** consists of all the strings that start with 0. The * is the "don't care" placeholder: it does not matter whether it is 0 or 1. The schema 0********** maps into the first half of the domain—that is, between 0 and $\pi/2$. The schema 1********** corresponds to the other half, between $\pi/2$ and π. For the function $f(x)$, the average value of $f(x)$ over 1********** is greater than that over 0**********. Thus, in a random population of strings, you should find that the average fitness of individuals in the former region is greater than that of members in the latter.

My implementation includes some subroutines that track individuals in any schemata specified by the user (for example, all strings that start with 1 or all that end in 001 and so forth). At each generation, the program will count the number of individuals in the population that are members of each region. It will also calculate the average fitness of those individuals, thus explicitly estimating the fitness of the regions.

To further hone your intuition, try mapping some other schemata into the domain x and examine the random individuals that fall into those regions. Can you specify schemata that partition each oscillation in $f(x)$ into eight contiguous regions? What is the average fitness of individuals in each region?

Once you are confident the first version of your program is working, you should add the subroutines that implement the heart of the genetic algorithm. The algorithm I used appears on the next page.

The EvaluatePopulation subroutine simply loops over all the individuals in the population, assigning each an $f(x)$ value as a measure of fitness. The DoTournamentSelection subroutine conducts a series of tournaments between randomly selected individuals and usually, but not always, copies the fittest individual of the pair (i,j) to NewPop. A sample tournament selection algorithm appears on the next page. In the algorithm, URand01 returns a (uniformly distributed) random value between 0 and 1. The net effect is that more fit individuals tend to have more offspring in the new population than do less fit ones. You may find it useful, nonetheless, to copy the fittest individual into the new populations every generation.

Note that if URand01 is greater than 0.75, the selective pressure will be greater (it will be harder for less fit strings to be copied into NewPop), whereas a smaller value will yield less selective pressure. If 0.5 is used, there will be no selective pressure at all.

The ModifyPopulation subroutine should randomly perform the crossover operation on some of the pairs in NewPop; a typical crossover rate is 0.75 (that is, cross 75 percent of the pairs). I used the "single point" crossover operation described in Holland's article. My version also mutates a small, randomly selected number of bits in the individual strings, changing the value from 1 to 0, or vice versa. A typical mutation rate is 0.005 per bit—in other words, each bit has a 0.005 chance of being mutated.

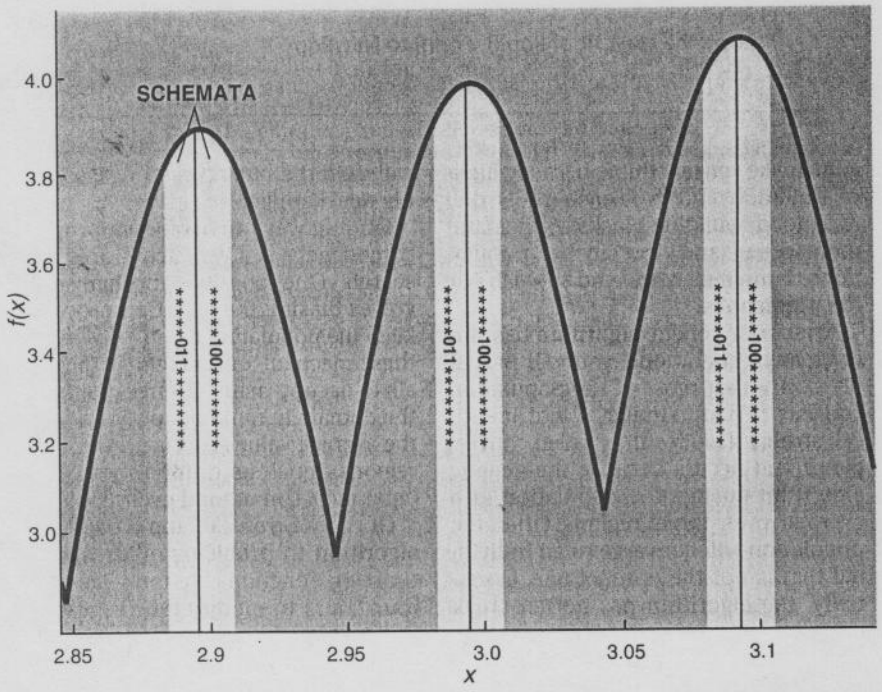
Once the implementation is complete, you can begin to run experiments. Try starting the system with a random population of 200 individuals and run it for 50 generations, collecting statistics on how the average fitness changes and noting the highest individual fitness found at each generation. You might compare the results you get with different population sizes and with crossover and mutation rates. I found it best to compare average results from several runs started with different seeds of the random number generator.

One especially useful experiment for understanding the dynamics of how populations evolve is to track the individuals in the eight regions that partition the 32 oscillations of $f(x)$, to which I referred earlier. The regions are defined by the schemata *****000********, *****001******** and so on, to *****111********. Notice that *****011******** and *****100******** occupy the center part of each peak, which includes the points of highest fitness.

In an initially random population, there should be approximately equal numbers of individuals in each of the eight schemata. As the genetic algorithm runs, you should see, on average, more individuals in the two center schemata than in the other six. This result happens even though many members of the center schemata map into low values of x and so have low fitnesses. The reason is that the average fitness in the center schemata is higher than that in the others.

Using these eight schemata, I tried to track how well the algorithm can bias its search for individuals of higher fitness. I set up my program to record at each generation the number of individuals in each schema, the average fitness of the individuals in those regions and the average fitness for the population as a whole. The theorems mentioned in Holland's article predict that the number of individuals in regions with an estimated average fitness above the population average should increase and the number of those in regions having below-average fitness should decrease.

For a population of 400, a crossover rate of 0.75 and a mutation rate of 0.001, the program confirmed the predictions about 67 percent of the time. I found that the greater the mutation and crossover rates and the smaller the population size, the less frequently the predictions were confirmed. These re-



TWO SCHEMATA occupy the central regions of each peak in f(x). *They include the points of highest fitness. Only the last three peaks are illustrated.*

Programming Fragments

MAPPING ALGORITHM—allows binary strings to represent values of x (Note: the compiler defines M_PI as π)

```
double scalefactor = (double) M_PI / pow ((double) 2.0,(double) L);
double MapStringToX ( char *S )
{ /* put bits from S in rightmost end of r and move them left */
  int i, r;
  for ( i = r = 0; i < L; ++i, ++S ) {
    r << = 1;    /* shift bits left, place 0 in right bit */
    if ( *S == '1' ) /* if S has a 1, then... */
      ++r;       /* change rightmost bit to 1 */
  }
  return ( (double) r * scalefactor );
}
```

BASIC GENETIC ALGORITHM—performs crossover, mutation and selection operations repeatedly

```
/* create structure to store the populations */
struct PopStr {
  char  Genome[L + 1]; double  Fitness;
} Pop[PopSize], NewPop[PopSize];
/* implement algorithm */
GenerateRandomPopulation ( Pop );
EvaluatePopulation ( Pop );
while ( Not_Done ) {
  DoTournamentSelection ( Pop, NewPop );
  ModifyPopulation ( NewPop );
  Switch ( Pop, NewPop );
  EvaluatePopulation ( Pop );
}
```

TOURNAMENT SELECTION ALGORITHM—selects for and copies the more fit individuals into the next generation

```
while ( NewPopNotFull ) {
  /* pick two individuals from Pop at random */
  i = random() % PopSize; j = random() % PopSize;
  /* return a random value between 0 and 1 */
  if ( URand01() < 0.75 )
    copy the most fit of Pop[i], Pop[j] to NewPop
  else
    copy the least fit of Pop[i], Pop[j] to NewPop
}
```

sults make sense, I think, because higher mutation and crossover rates disrupt good "building blocks" (schemata) more often, and, for smaller populations, sampling errors tend to wash out the predictions.

After your genetic algorithm has run for many generations, you will probably notice that most of the population consists of very similar, if not identical, strings. This result is called convergence and occurs because the genetic algorithm pushes the population into ever narrower target regions. Often the population will converge to an individual that is not the optimal one. Essentially, the algorithm has gotten stuck on a local optimum. Convergence can be particularly debilitating, because it means that crossover will not contribute much to the search for better individuals. Crossing two identical strings will yield the same two strings, so nothing new happens.

Finding ways to avoid inappropriate convergence is a very active area of research. One possible mechanism involves biasing the selection process to keep the population diverse. In essence, these mechanisms encourage individuals to occupy many different regions in the domain in numbers proportional to the average value associated with those regions, much as different species inhabit niches in natural evolution.

Of course, you can apply the genetic algorithm to problems other than optimizing functions. It took me about four hours to modify the program described here to create a version in which the individuals represent strategies for playing a form of the Prisoner's Dilemma. In this game, two prisoners face a choice: cooperate with the other (by remaining silent about the crime) and receive a three-year sentence, or try to get off free by "defecting," or squealing. Unfortunately, you do not know what the other player is going to do: if you cooperate and he defects, then you get a 10-year sentence and he goes free. If you both defect, then you both get seven years.

My modified genetic algorithm explored the strategies involved in playing the game many times with the same opponent. Each individual's binary string represents two numbers (p, q), where p is the probability the individual will cooperate if the opponent cooperated on the previous play and q is the probability of cooperation if the opponent had defected. For instance, the strategy (1,0) is tit for tat, and (0.1,0.1) is approximately the "always defect" approach.

The genetic algorithm generates some very interesting dynamics in the evolution of populations of such strategies, especially if each individual's binary string also contains some bits that specify an arbitrary "tag." Another set of bits could then indicate the propensity of the individual to play only with those that have a similarly tagged string. In effect, the population can evolve individuals that recognize external "markings" (the tags) associated with tit-for-tat players. Thus, they can prosper by looking for cooperative individuals and by avoiding defectors.

From relatively simple gene structures, complicated evolutionary dynamics may emerge. For instance, mimicry and other forms of deception may evolve: a defector could have a tag associated with cooperators. With some imagination, you can construct other simple gene structures and use the genetic algorithm to coax complex evolution out of your computer.

For a copy of the optimization program (written in C language), please write to: The Amateur Scientist, Scientific American, 415 Madison Avenue, New York, NY 10017-1111.

FURTHER READING

A COMPARATIVE ANALYSIS OF SELECTION SCHEMES USED IN GENETIC ALGORITHMS. David E. Goldberg and Kalyanmoy Deb in *Foundations of Genetic Algorithms.* Edited by Gregory J. E. Rawlins. Morgan Kaufmann, 1991.

HANDBOOK OF GENETIC ALGORITHMS. Edited by Lawrence Davis. Van Nostrand Reinhold, 1991.

TIT FOR TAT IN HETEROGENEOUS POPULATIONS. Martin A. Nowak and Karl Sigmund in *Nature,* Vol. 355, No. 6357, pages 250–253; January 16, 1992.