

1 Genetic Algorithms

The genetic algorithm (GA) was first introduced by John Henry Holland, even though he did not call it the genetic algorithm at the time. This section gives an overview of the workings and most important operations of the genetic algorithm. If not otherwise stated, everything in this section is based on Holland's book "Adaptation in natural and artificial systems" as well as Goldberg's book "Genetic algorithms in search, optimization and machine learning" [J. Holland, 1975] [D. Goldberg 1989].

1.1 Simple Genetic Algorithm

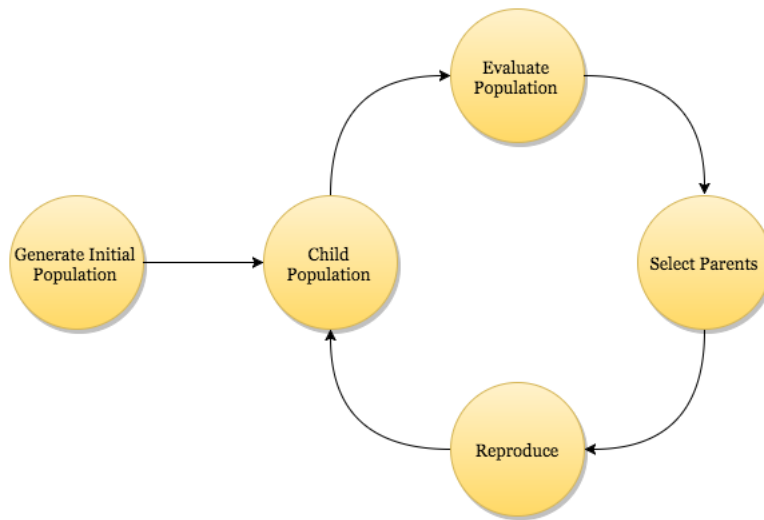


Figure 1: Overview of the phases of the genetic algorithm. First an initial population is generated and initialized as the first child population. Second, each individual in the child population is evaluated. Third, based on their evaluation, individuals are selected to become parents for the next generation. Forth, a new generation is generated by reproduction, and fifth, the newly generated population becomes the child population.

1.1.1 Representation

1.1.2 Operations

1.1.2.1 Selection

1.1.2.2 Mutation

In biology, mutation is defined as a permanent alteration in the DNA sequence that makes up a gene. Mutations vary in size, sometimes just a small base pair of the gene is altered, while other times the mutation can alter large parts of a chromosome. There are many different forms of

mutations. Sometimes it can simply mean changing the value of a nucleotide to its complement (nucleotides are the building blocks of DNA and consists of the values A, C, G and T), other times it can mean insertion of extra nucleotides into the DNA, deleting some of the nucleotides from the DNA, or inversion of nucleotides [P. Compeau, 2014].

In genetic computation the mutation process is simplified. Since the search space only consist of strings of bits with constant size, a mutation in genetic computing simply consists of flipping of bits, this is called single point mutation. In Figure 2 we have a bit string of size 8, where the 6th element is mutated from the value 1 to the value 0. Mutation is usually implemented by having a given probability of each value in the genotype being flipped.

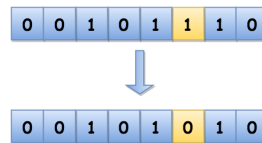


Figure 2: Mutation of a single bit. The bit in position 6 at the upper bit string has the value 1 before the mutation, while after mutation the value is flipped into 0.

Mutation is important because without mutation a population can converge to a population of individuals where each genotype has the same value at a given position. Since every individual has the same value in their genotype, reproduction will never be able to make a new individual that doesn't also have the same value at the same position. With mutation however, there is always a probability of the value being flipped, mutation is therefore crucial for maintaining diversity in the population.

Even though mutation is important, the probability of mutation needs to be kept low. If the mutation rate is very high, the genotype of a new individual will almost be a random bit string. Remember that a new individual is made by reproduction between two individuals with high fitness in the previous population, if mutation heavily changes the new individual, it will not inherit the good features of its parents and the whole point of evolutionary search will be gone.

1.1.2.3 Crossover

As in nature, we want individuals of the evolutionary search to inherit features from individuals in the previous population. In genetic algorithms this is performed by applying the crossover operation. Crossover is a simple method where a new individual gets some parts of its genotype from one parent, and the other parts from its other parent. Figure 3 illustrates the crossover operation. Before crossover is performed one needs to decide at which position it will be performed. If we are operating with genotypes of length 8 as in figure 3 there will be 7 possible crossover positions, one between each of the 8 values of the genotype. In figure 3 position 4 is picked as the crossover position, therefore the first of the newly produced individuals will have a genotype consisting of the first 4 values of the first individual of the old population and the 4 last values of the second individual of the old population, while the second newly generated individual will get the opposite genotype.

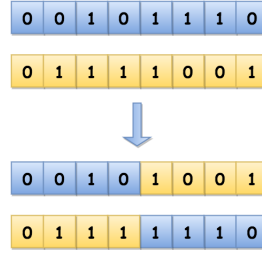


Figure 3: Single point crossover at position 4.

The crossover in figure 3 is called a single point crossover, because crossover is only performed at one position. It is also possible to have multiple crossover positions as shown in figure 4, where a double point crossover is performed with crossover positions 2 and 5.

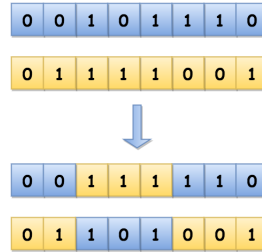


Figure 4: Double point crossover at position 2 and 5.

Crossover probability is usually kept high because one is hoping that combining to good solutions from the previous population will produce even better solutions for the next population. However, it is desirable to keep some solutions from the previous population as they are, because they might be better than combination of two of them.

Goldberg performs a very interesting analysis of the crossover operation by studying the probability of surviving a crossover operation for different schemata. A schema is a string taken from the library $\{0, 1, *\}$. A shema of size 8 could therefore for example look like this $0011****$, where 0 and 1 represents letters with values 0 and 1, while $*$ represents letters that we don't care about. This means that both strings 00110000 and 00111111 are covered by the given schema. If desirable features are represented by schemata it is easy to see that some features are much more likely to survive a single point crossover operation than others. Lets study the shemata $s_1 = 11*****$ and $s_2 = 1*****1$. Both has size 8, meaning that there are 7 possible crossover positions. However, only one of the crossover positions will destroy s_1 while all 7 positions will break up s_2 . This means that the genetic search would converge faster if s_1 was the desirable feature, then if s_2 was.