

# An Observational Analysis of Genetic Operators

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## ABSTRACT

Genetic algorithm is a search heuristic that mimics the natural process of evolution and it generates solution to a very complex NP-Hard problems. Genetic algorithm belongs to the class of evolutionary algorithms (EA) and it generates solution by using nature inspired techniques like selection, crossover and mutation. The performance of the genetic algorithm is mainly depends on the genetic operators. Genetic operators have the capability to maintain the genetic diversity. This paper mainly describes the available selection mechanisms as well as the crossover and the mutation operators.

## Keywords

Genetic algorithm; Selection mechanism; Crossover; Mutation

## 1. INTRODUCTION

Genetic algorithm provides the solution to solve the complex real world optimization problems by mimicking the natural process such as genetic operators. Genetic operators have the capability to maintain the genetic diversity. Genetic diversity or variation is obligatory for the process of evolution. Genetic operator has the equivalent things which occur in the natural world. The main intention of the genetic operator is to create the new population. The main success of genetic algorithm depends on the unique cooperation between the genetic operators. The most commonly used genetic operators are selection or reproduction, crossover or recombination and finally the mutation. The genetic algorithm performance is mainly based on the crossover and mutation; these two are the most important parts of genetic algorithm [9]. In reproduction process, new individuals are created through crossover and mutation operators. Crossover operator blends the genetic information between the chromosomes in order to explore the search space while the mutation operator is used to maintain the genetic diversity in order to avoid the premature convergence problem [3]. Which is better Crossover or Mutation and which is needed? The selection of crossover or mutation is mainly depends on the problem. But in general, both the crossover and mutation is needed in order to achieve the good results. Both the crossover and mutation have different roles both are different. Before going into the discussion, we have to know the key terms exploration and exploitation. Exploration means discovering promising areas in the search space, i.e. gaining information on the problem. Exploitation means optimizing within a promising area, i.e. using the information. There is always cooperation and competition between both the exploration and exploitation. Crossover is explorative, i.e. it makes a big jump to an area somewhere in between two parents. Mutation is exploitative, i.e. it creates a random small diversion, and it stays near the parent. Only crossover can combine the information from two parents. Only mutation can introduce the new gene.

Crossover does not change the gene frequencies of the population. In order to hit the optimum solution, mutation is very important. Mutation and crossover is applicable only for bit string and integer representations [24].

## 2. SELECTION / REPRODUCTION

Selection follows the Darwinian evolution theory based on the principle of, "survival of the fittest", the best one should survive and it create offspring. Selection is the first operator applied on the population. From the population, chromosomes are selected to be as parents and it applies crossover and then it produces offspring [9]. The selection operator is proposed to improve the quality of the population by giving the high fit individuals to the next generation. The quality of an individual is determined by the fitness function. The balance between exploration and exploitation can be adjusted by the selection pressure of the selection operator or by the crossover operator [14]. The selection operator works at the level of chromosomes [10]. Before going into the selection methods, some important terms have to be discussed. *Loss of Diversity*: During each selection phase, low fit individuals are lost and it was replaced by the copies of better individuals; therefore some amount of genetic material was lost that was present in the bad individuals. The number of individuals that was replaced are corresponds to the strength of the loss of diversity [14]. *Selection Intensity or Selection Pressure*: The change of the average fitness of the population due to fitness is the most reasonable measure of selection intensity. The selection intensity was introduced in order to obtain a normalized and dimension-less measure [14]. The selection pressure determines the algorithm convergence. If the selection pressure is set as too low, then the rate of convergence towards the optimum solution is also too low. If the selection pressure is set as too high, then it easily stuck in the local optimum due to the loss of diversity in the population [10]. The selection intensity is mainly depends on the fitness distribution of the initial population [14]. *Selection Variance*: The selection variance is the normalized expected variance of the fitness distribution of the population after applying the selection method to the fitness distribution [14]. The selection methods are used to select the chromosomes for parents to apply crossover. The selection mechanism is classified into two categories [10]. Some of the existing selection methods are summarized as follows.

### Selection Mechanisms

#### a. Traditional Selection Mechanisms:

- Proportionate Selection Methods
- *Roulette Wheel (RW) selection / Fitness Proportionate Selection (FPS)*
- *Deterministic Sampling*
- *Stochastic Remainder Sampling*

- Stochastic Remainder selection with replacement
- Stochastic remainder selection without replacement
- Stochastic Universal Sampling (SUS) selection
- Ranking Selection Methods
  - Linear Ranking selection
  - Truncate selection
- Tournament Selection Methods
  - Binary Tournament Selection
  - Larger Tournament Selection
  - Boltzmann tournament selection
  - Correlative Tournament Selection
  - Restricted Tournament Selection

**b. Alternative Selection Mechanisms:**

- Range selection
- Gender-Specific Selection
- GR based selection
  - Fitness Uniform selection scheme (FUSS)
  - Reserve selection
- Boltzmann Selection
- CHC Selection
- Elitism Selection
- Sequential Selection
- Dominant Selection
- Kin Selection
- Random Selection
- Back Controlled Selection
- Diversity Oriented Selection
- Survivor / Replacement Selection
  - Age based replacement
  - Fitness based replacement
    - ✓ Elitism
    - ✓ Genitor

**Roulette Wheel selection or Fitness Proportionate Selection (FPS) Method**

Roulette wheel method is used to select the parents in a population for mating. In this method, the cumulative weight constructs the wheel. This method chooses the string based upon their relative cost or fitness values. This technique sorts the chromosomes in a population according to their fitness values. Then it assigns the area to every chromosome, where the chromosome with the highest fitness value has the largest area. Let  $g_i$  denote the fitness value of the  $i^{\text{th}}$  chromosome in a population and  $g_t$  denote the summation of the fitness value of all the chromosomes.

$$g_t = \sum_{i=1}^n g_i$$

The selected probability,  $P_{gi}$  of the  $i^{\text{th}}$  chromosome is denoted by

$$P_{gi} = \frac{g_i}{g_t}$$

When the selection operator is performed, then the system chooses a chromosome from a population according to its degree of probability. Therefore larger the selected probability of chromosome more is the opportunity of the chromosome to be chosen for the crossover operation [9].

**Deterministic Sampling Method**

In this method, the average fitness of the population  $P_{select_i}$  is calculated as the ratio between the fitness associated with each individual to the average fitness.

$$P_{select_i} = \frac{\text{fitness associated with each individual}}{\text{average fitness}}$$

Here only the integer part of this result is taken to select the individuals for the next generation population. The whole fraction is used to sort the individuals. From the sorted list the greatest fraction value individuals is taken to fill the remaining places in the new population [10].

**Stochastic Remainder Sampling**

Stochastic Remainder Sampling has similar concepts which are used in the deterministic sampling method, and the population is formed with the integer part of the expression

$$\frac{a_{pi}}{a_{pavg}}$$

Here the remaining free places are filled based on the roulette wheel selection method. In remainder selection mechanism, the expected number of copies of a string is

calculated by  $m_i = \frac{f_i}{f}$ . It assigns parents deterministically from the integer part of each individual scaled value  $m_i$  and then it uses roulette wheel selection on the remaining fractional part. After the parents have been assigned according to the integer parts of the scaled value, then the rest of the parents are chosen stochastically. Stochastic means it generates and uses random values. The probability of a selected parent is proportional to the fractional part of its scaled value [10].

**Stochastic Remainder Sampling with replacement**

If the stochastic remainder sampling is done with replacement means then the remainder is used to size the slots of a roulette wheel selection process [10].

**Stochastic Remainder Sampling without replacement**

If the stochastic remainder sampling is done without replacement means then each remainder is used to bias the flip of a coin that determines whether the part receives another copy or not [10].

**Stochastic Universal Sampling (SUS) selection**

SUS uses N equally spaced pointers where N is the number of required selections. In roulette wheel selection method single selection pointer is used. In SUS the population is shuffled randomly and a single random number pointer1 (0,

1/N) is generated. Then N individuals are chosen by generating N pointers, starting with pointer1 and spaced by 1/N and selecting the individuals whose fitness spans the positions of the pointers [10][15].

#### Ranking Selection

In this selection method, it first ranks the population and then every chromosome receives fitness from this ranking. The worst individual will have fitness 1 and then the second worst will have fitness 2 and then the best individual will have the fitness N, where N is the number of chromosomes in the population.

#### Linear Ranking Selection

In this method, the individuals are ranked according to their fitness value. The high fit individuals will have high rank and then the low fit individual will have low rank. Then the individuals are selected with a probability that is linearly proportional to the rank of the individuals in the population [10].

#### Truncate Selection

In Truncate Selection, the candidate solutions are ordered by fitness and some proportion p (where  $p=1/2$ ,  $p=1/3$ ), then the fittest individuals are selected and it reproduced  $1/p$  times. This method is less complicated than many other selection methods and it is not used in practice [10].

#### Tournament Selection

In this method, the size of the tournament is a very important factor to select the individuals for reproduction to next generation. Initially the tournament size is selected with lower value of two individuals, which will carry out a tournament between two individuals and it will select one individual who has higher fitness than the other one. The same principle is applied to various sizes of tournament selection method; the only thing is the size is going to be varied. The larger size increases the diversity in the population.

#### Binary Tournament Selection

In this method, two individuals are randomly selected and the better of the two individuals is selected with a fixed probability p,  $0.5 < p < 1$  [10].

#### Larger Tournament Selection

In order to analyze the performance of the tournament selection with any size of tournament, it is easier to conduct the doughnut hole rather than the doughnut itself [10].

#### Boltzmann Selection

Boltzmann Selection method is motivated by simulated annealing (SA) algorithm. This SA method simulates the process of slow cooling of molten metal to achieve the minimum value in the minimization problem. The cooling phenomenon is simulated by controlling the temperature. The temperature is controlled by the Boltzmann probability distribution. The system in thermal equilibrium at a temperature T has its energy distribution based on the probability and it was defined by the expression

$$p(E) = \exp\left(\frac{-E}{kT}\right)$$

where k is the Boltzmann constant. The above expression implies that a system at a higher temperature has almost uniform probability at any stage, but at a lower temperature it has a small probability of being at a higher energy state. Thus by controlling the temperature T and assuming that the search process follows Boltzmann probability distribution, and then the convergence of the algorithm is controlled [9].

#### Boltzmann Tournament Selection

Boltzmann Tournament Selection (BTS) method is motivated by simulated annealing (SA) algorithm. In BTS, in each generation, a three way competition or tournament is held for each generation slot. The first individual is chosen uniformly at random, second individual with an objective function value which is different from the first by a threshold amount x. Half of the time, choose the third individual with an objective function value which is totally different from the first and the second individuals by the threshold amount; this is called strict choice and the other half of the time, choose the third individual with an objective function value which is different by the threshold amount from the first individual alone; this is called as relaxed choice. If the algorithm is successful, it will create a steady proportion of individuals according to the Boltzmann distribution [10].

#### Correlative Tournament Selection

It is an extension of the ordinary tournament selection method. This Correlative Tournament selection method selects a pair of parents instead of selecting two parents for crossover. By selecting a pair of parents which are highly correlative in nature and it will exhibit an effective crossover. This method is similar to seduction. The selection of the second parent is closely dependent on the first parent distinct the former where the seduce function is independent of the first parent. Hamming distance is used as a correlation function (similar function has a correlation value to each other) [10].

#### Restricted Tournament Selection

Restricted Tournament Selection (RTS) adapt standard tournament selection for multimodal optimization. Crowding methods uses RTS technique to find the uniqueness of each individual. RTS initially selects two elements from the population to undergo crossover and mutation. After crossover, a random sample of CF individuals is taken from the population as in standard crowding. Each offspring competes with the closest sample element. The winners are inserted in the population. This procedure is repeated  $N/2$  times. The order of complexity of RTS is  $O(CF \cdot N)$ . It can vary from  $O(N)$  to  $O(N^2)$  according to the crowding factor value CF.

#### CHC Selection

CHC stands for Cross generational elitist selection, Heterogeneous recombination and Cataclysmic mutation, which is used to restart the search when the population starts to converge. When the population converges to the point that it begins to more or less reproduce many of the same things. At this point CHC uses cataclysmic mutation. All strings undergo heavy mutation, except that the best string is preserved intact. Eshelman's CHC algorithm uses nontraditional form of selection whereby crossover is performed among the initial population and then the selection is performed without replacement from the combined population of parents and offspring. Whatever the crossover

operator is used, the CHC selection strategy should increase the performance.

#### Range Selection

Each individual in the population is assigned a numerical rank based on their fitness and the selection is based on the ranking [10].

#### Gender Specific Selection

The brainwave of this selection method comes from the concept of sexual selection in the population genetics where the process of choosing the mating partner is modulated differently for male and female individuals. Sexual selection uses two different selection methods to select the parents for crossover. So it is possible to simulate the concept of male vigor and female choice by random selection as the first selection schemes and the selection pressure is the second one. The second selection can be roulette wheel selection or linear rank selection. By using the above two different selection concepts simultaneously a GA user can simultaneously influence the selection pressure level of a GA so that GA runs more accurately [10].

#### GR based selection

The Generic Relatedness (GR) is introduced to define the relationship existing between the individuals that have the common ancestor [10].

#### Fitness Uniform Selection Scheme (FUSS)

FUSS was proposed by Hutter in the year 2002. FUSS method is based on the concept of preserving the genetic diversity by using the individuals' fitness in order to estimate their similarity. The similarity is found by calculating the distance between two individuals  $i$  and  $j$  with the fitness  $f(i)$  and  $f(j)$ . A uniform random number is chosen in the interval  $(f_{min}, f_{max})$  where  $f_{min}$  and  $f_{max}$  are the minimum and maximum fitness values in the current population. Then the fitness nearest to this number is chosen to be the fitness level for this generation. The individuals for the next generations are selected randomly from each of the fitness level [6] [10].

#### Reserve Selection

This method is based on the technique called 'Process Segmentation'. Process segmentation means the process of splitting into reserved and non-reserved area. The Non-reserved area consists of high fit individuals and the reserved area consists of low fit individuals [10]. This selection prevents the premature convergence problem in the global optimization [16]. Non-Reserved Area (NRA) worked as an intensified searcher. Here the offsprings are produced by the high fit individuals and then NRA applies elite and tournament selection techniques [16]. Reserved area is mainly designed to set up in order to reserve the building blocks buried in poor individuals and thus it maintain a diversified search so as to *explore* the global optimum. The reserved area size is generally known as *reserve size*. The offspring in the reserved area normally derive exclusively from those not having been selected yet in producing non-reserved area, which are of low fitness values. While doing this, a record called *selected table* is used to label the individuals selected in producing non-reserved area, with  $O(N)$  space complexity where  $N$  is the population size. Restricted area helps to restrict the loss of genetic information. The way of segmentation, or the choice of reserve size, and it totally depends on the various demands

and therefore a balance between exploitation and exploration is obtained. In general, when reserve size becomes zero, the implementation completely reduces to a conventional GA [16].

#### Steady state selection

The key idea of this selection is that, the big part of chromosomes should survive to the next generation. In the steady state genetic algorithm we select one member at random, replicate it and replace another random member with the copy in each time.

#### Sequential Selection

In this method the individuals in the population are arranged in the form of order from the best to the worst according to the fitness values. A copying number is assigned to the individuals with a decreasing function. The most common linear assignment function is used here. The copying numbers assigned by this function is used to form a new population [4].

#### Dominant Selection Operator (DSO)

This selection method includes roulette wheel, tournament, top percent and best selection. This method cannot produce a new schema but it eliminates some less useful ones. This is the main reason that premature convergence occurs. Low fit individuals are tend to die before they sufficiently mature to pass on their genes. This DSO method strengthens the action of dominant individuals and weakens the effect of the inferior individuals in the process of evolution [4].

#### Hybrid Selection

This method uses the combination of both roulette wheel and the tournament selection methods. There are two types of hybrid selection operator's namely single level and two level hybrid selection operators. In the single level hybrid selection operator, first 50% of the population size tournament selection method is used and the remaining 50% roulette wheel selection method is used. The two level hybrid selection operator, uses tournament selection for 25% of the population size followed by the use of roulette wheel selection for a further 25% and then repeats the process by using tournament selection which is followed by the roulette wheel selection for the remaining 25% of the population size [4].

#### Kin Selection

This selection method is controlled by a kin probability variable, which serves the same purpose as the crossover probability or mutation probability variables in the PGA. The chromosome to be sacrificed is selected randomly from the solutions pool. It is replaced by a copy of another chromosome having the least non-zero Hamiltonian distance from the original chromosome. If more than one chromosome is present means, the lower fitness value is selected. If more than one chromosome is having same lowest fitness value, then any one of them is randomly selected [4].

#### Back Controlled Selection Operator (BCSO)

This selection method is different from the previous selection methods. In BCSO the fitness value of the individual is compared from the previous generation. If the fitness value of the individual is more than one in the preceding generation means the individual would keep the own position. Otherwise if the fitness value of the same individual is less than or equal to the preceding generation,

this individual would be discarded from the population. Then individual would be copied to the population in the preceding generation to replace this individual [4].

#### Random Selection

The selection method works by generating two random integer numbers. Here each number represents a chromosome. Find the fitness for each chromosome. Then the fitness values of both the chromosomes are compared with each other, the one with the best fitness will go into the mating pool. This randomly selected chromosomes mechanism will be repeated until the population in the mating pool equals to the initial chromosomes population [26].

#### Diversity-oriented selection (DOS)

DOS was proposed by Shimodaira in the year 1999. The parent selection mechanisms are defined by using both the fitness function and a measure that evaluates the diversity; which was introduced by the competing chromosomes in the population (Bonham and Parmee, 1999; De Jong et al., 2001; Ichikawa and Ishiiolland, 1993; Lee, 2003; Mori et al., 1995; Shimodaira, 1999; Toffolo and Benini, 2003). Their main purpose is to support the individuals with both high fitness function values and high diversity contributions [6].

#### Survivor Selection

Survivor selection is also known as Replacement selection. It determines who survives into next generation and it reduces  $(m+1)$  to  $m$ ; where  $m$  is the population size and  $l$  is the number of offspring at end of generation. It has several replacement strategies. Survivor selection can be divided into two approaches: Age-Based Selection (FIFO and Replace random) and the other one is Fitness-Based Selection (Elitism and the other one is GENITOR) [23].

- Age-Based Replacement

Here the fitness not taken into account. Each individual exists for same number of generations while in SGA each individual exists only for one generation [23].

- Fitness-Based Replacement

- Elitism Method

It always keeps the best or the best few of the fittest solution so far and it ensures that the best found solutions are never lost [23]. Genetic algorithm saves the best solution from one generation to the next generation by elitism. Elitism should be there in order to achieve better solutions. Elitist selection is suitable for locating the optimum of unimodal benchmark functions.

- GENITOR Method

It follows the “delete-worst” strategy. Rapid takeover takes place and it is used with large populations or it follows “no duplicates” policy. There is a fast increase in the population mean and the premature convergence is possible [23].

### 3. CROSSOVER/ RECOMBINATION

Crossover is a genetic operator that combines (mates) two chromosomes from the parents and it produce a new chromosome called offspring. The crossover will produce best offspring if both the taken parents have best characteristics. It

takes place during evolution according to a user definable crossover probability [9].

#### Crossover Mechanism

The exchange of structured data performed by the crossover operator is based on three different selection mechanisms [18] and they are MSM, OGM and OSM.

##### *Mating selection mechanism (MSM)*

MSM is the process in which the chromosomes are mated before applying crossover operator on them. Here also the common random procedure is applied to select the parents. Examples for MSM are: Elitist selection and age based selection [18].

##### *Offspring generation mechanism (OGM)*

This mechanism enables the genetic material to be transferred from parents to offspring. In this later case, the value of the gene analogous to a position in the offspring is obtained by combining the values of the genes of the parents in that same position (Herrera et al. 1998) [18].

##### *Offspring selection mechanism (OSM)*

Departing from the offspring generated for each set of parents this mechanism chooses the individuals that will become population members. One of the most widely used OSMs chooses a core of best offspring to form the next population (Wright 1991; Conceição António and Lhate 2003) [18].

From the taxonomy analysis presented by Herrera et al. (2003) the crossover operators based on application to two parents are grouped as DCO, ABCO and NBCO [18]:

##### *a)Discrete crossover operators (DCOs)*

A general property of the DCO is that the value of each gene in the offspring chromosome coincides with the value of the same gene in one of the parents. There is no numerical transformation is needed in order to obtain the offspring gene values from the parents’ genes. It considers the two-point and uniform crossover operators [18].

##### *b)Aggregation based crossover operators (ABCOs)*

ABCO uses an aggregation function to combine numerically the values of the genes of the parents in order to produce the value of the offspring genes (Michallewicz et al. 1996) [18].

##### *c)Neighbourhood-based crossover operators (NBCOs)*

In NBCO, the offspring genes are obtained from intervals defined in neighbourhoods associated with the genes of the parents throughout probability distribution functions. Examples of NBCOs are BLX- $\alpha$ , simulated binary crossover and fuzzy recombination (Voigt et al. 1995), which is based on uniform, polynomial and triangular probability distributions [18].Some of the available crossover operators are summarized below:

#### Crossover Operators

- Discrete crossover operators
- Aggregation based crossover operators
- Neighbourhood-based crossover operators
- One Point Crossover
- Two Point Crossover
  - Two Point Crossover operator (Version 1)

- Two Point Crossover operator (Version 2)
- Two Point Crossover operator (Version 3)
- Three parent crossover operator
- N-point Crossover Operator / Multi Parent Crossover
- Cut and Splice Crossover Operator
- Uniform Crossover Operator (UX)
- Half Uniform Crossover Operator (HUX)
- Cycle Crossover Operator
- Arithmetic Crossover Operator
- Heuristic Crossover Operator
- Order Crossover Operator
  - Position Based Crossover Operator
  - One point order crossover operator
  - Two point order crossover operator
  - Edge Recombination Crossover Operator
  - Order based crossover operator (OBX)
  - Linear order crossover operator (LOX)
- Partially Mapped Crossover Operator (PMX)
- Self adaptive crossover operator
- Knowledge based crossover operator
- Sense Crossover Operator
- Middle point crossover
- Guided Crossover (GC)
- Simplex crossover (SPX)
- Scanning Crossover
  - Uniform Scanning Crossover (U-Scan)
  - Occurrence- Based Scanning Crossover (OB-Scan)
- Diagonal Crossover (Diagonal)
- Unimodal Normally Distributed Crossover operator (UNDX)
- Simulated Binary Crossover
- Laplace Crossover
- Parent-centric crossover operator
- Intermediate Crossover
- Ring Crossover

The detailed description of the crossover operators are given as follows:

#### One Point Crossover

In One point crossover operator, a single crossover point on both the parents is selected. All the data beyond that point in the string is swapped between the two parents [1] [2] [9].

#### Two Point Crossover

Two point crossover operator randomly selects two crossover points within a chromosome then interchanges the two parent chromosomes between these points to produce two new offspring [2] [9].

#### Two Point Crossover operator (Version 1)

It was proposed by Murata and Ishibuchi. First two crossover points have to be randomly selected. The symbols outside the selected two points are inherited from one parent to the offspring. The remaining symbols are placed in the order which was appeared in the other parent. After changing the roles of both the parents, the same procedure is applied to produce the second offspring [1].

#### Two Point Crossover operator (Version 2)

It was proposed by Murata and Ishibuchi. Version 2 is same as the version 1 except the inherited symbols of the first parent. In this two point version 2 crossover operator, the symbols between the randomly selected points are inherited from one parent to the offspring [1].

#### Two Point Crossover operator (Version 3)

It was proposed by Murata and Ishibuchi. Version 3 is the mixture of both version 1 and version 2 of the two point crossover operators. These two crossovers are applied to each pair of selected parents with the same probability. Take 0.5 crossover probability for each parent [1].

#### Three parent crossover operator

In this operator, the child is derived from three parents; they are randomly selected. Each bit of the first parent is checked with the second parent whether they are same or not. If it is same that bit is taken for the offspring else the bit from the third parent is taken for the offspring.

#### N-point Crossover Operator

N point crossover operator was applied to more than one point on each parent individuals. The segment after the cut points are swapped and produce offspring.

#### Cut and Splice Crossover Operator

This operator results in a change in length of the children strings. The main cause of this difference is that each parent string has a separate choice of crossover point.

#### Uniform Crossover Operator (UX)

Uniform crossover operator is drastically different to one point crossover. Each gene in the offspring is created by copying the equivalent gene from the parents, and they select according to a randomly generated crossover. Uniform crossover operator does not select a set of crossover points. Uniform crossover outperforms both one point and two point crossover operators. In this uniform crossover operator, individual bit strings are compared between the two parents and then the bits are swapped with a fixed probability, usually 0.5 is taken as crossover probability. This uniform crossover is a dynamic and less deterministic method, since the algorithm does not decide how many positions to replace or what to replace [2].

#### Half Uniform Crossover Operator (HUX)

In HUX operator, half of the non matching bits are swapped. The number of differing bits is calculated by using hamming distance; that number has to divide by two. The resulting number is how many of the bits that do not match between the two parents will be swapped.

### Cycle Crossover Operator

Cycle Crossover Operator was originally developed by Oliver et al. This operator starts the procedure by finding the cycle; which was defined by the equivalent positions of symbols between the parents. This cycle operator always starts from the first position. The symbols in the cycle of one parent are copied to the same position of the offspring; and the symbols are deleted from the other parent; and then the remaining symbols of the other parents are copied to the offspring. After changing the roles of the parents, the same procedure is applied to produce the second offspring [1].

### Order Crossover Operator

Order crossover was developed by Davis. In this operator, first two crossover points have to be randomly selected and then the symbols between these positions are copied to the same positions of the offspring. The copied symbols are deleted from the other parent, and then the remaining symbols are inherited, starting with the first position followed by the second crossover point. After changing the roles of the parents, the same procedure is applied to produce the second offspring [1].

### Arithmetic Crossover Operator

This operator linearly combines two parent chromosome vectors to produce two new offspring according to the following equations

$$\text{Offspring 1} = a \times \text{parent 1} + (1 - a) \times \text{parent 2}$$

$$\text{Offspring 2} = (1 - a) \times \text{parent 1} + a \times \text{parent 2}$$

Where  $a$  is the random weighting factor chosen before each crossover operator [9].

### Heuristic Crossover Operator

Heuristic crossover was first introduced by Wright and later by Michealwicz et al. This operator uses the fitness values of the two parent chromosomes in order to find the direction of the search space. Michealwicz applied heuristic crossover operator to solve non linear constrained optimization problems. The offspring is created according to the following equations

$$\text{Offspring 1} = \text{Best parent} + r \times (\text{Best parent} - \text{Worst parent})$$

$$\text{Offspring 2} = \text{Best parent}$$

where  $r$  is the random number between 0 and 1 [3] [9].

### Position Based Crossover Operator

instead of circular. First the two crossover points have to be selected randomly. The symbols of the second parent In this operator, the parent's individuals are arranged and kept in the form of order. Here the crossover is based on the position which was already defined by the parent 1 and it is not based on the crossover points. The genes from the respective positions of the parent 1 are transferred to the child and the remaining portions of the child are filled from the parent 2 [1].

### One point order crossover operator

In this operator, both the parents' individuals are arranged and kept in the form of order. The crossover point is fixed on parent 1 but not on parent 2. The segment before the cut point is transferred to its child and the remaining portion of the

child is filled from the parent 2. The segment after the cut point in the parent 1 is not moved to the child.

### Two point order crossover operator

In this operator, both the parents' individuals are arranged and kept in the form of order. The two crossover points are fixed on parent 1 but not on parent 2. The segment between the boundaries is cut and it is transferred to its child and the remaining portion of the child is filled from the parent 2 orderly.

### Edge Recombination Crossover Operator

Edge Recombination Crossover Operator was developed by Whitley et al. This operator emphasizes adjacency information. Very first the edge table is built by determining symbols adjacent to each symbol in both the parents. The starting symbol has to produce randomly. Until the completion of the offspring, the symbols that have link to the previous symbol, the element is selected randomly. If the symbol has no link to the previous one, any symbol from the remaining symbol is selected randomly. By using this method, any number of offspring can be produced [1].

### Order based crossover operator (OBX)

This crossover operator was proposed by Syswerda and it is a small variation of the position based crossover operator. In this operator, the order of the symbols in the position selected in one parent is imposed on the equivalent position in the other parent. First, each position is selected in turn and independently marked in the first parent with the crossover probability of 0.5 and the symbols in the unmarked positions are placed in the position which they appeared in the second parent. Finally, marked symbols of the first parent are copied into the vacant positions of the offspring by preserving their absolute order in the first parent [1].

### Linear order crossover operator (LOX)

Linear order crossover is a tailored version of the order crossover operator, and the chromosome is arranged in the linear fashion between the two crossover points are deleted from the first parent, and the holes created are slid from the extremities toward the centre until they reach the cross section. By copying the symbols of the second parent between the two crossover points to the same positions of the first parent, the first offspring is produced. After changing the roles of parents, the same procedure is applied to produce the second offspring [1].

### Partially Mapped Crossover Operator (PMX)

This PMX operator was proposed by Goldberg and Lingle. Two crossover points have to be randomly selected. The substrings which was defined by the two crossover points are called mapping sections. The two substrings are exchanged to produce the protochildren. The mapping relationship between the two mapping sections is determined, and by using this relationship, offspring's are officially recognized [1].

### Self adaptive crossover operator

This operator is mainly restricted due to the control of the crossover probability  $P_c$ . The first attempt to integrate self adaptation into crossover was punctuated crossover and it was proposed by Schaffer and Morishima.

### Knowledge based crossover operator

This operator is mainly used to solve the constraint specification problem. The constraint specification problem is

very difficult to solve by the standard genetic crossover operation. This knowledge based crossover operator is best suitable with respect to preference settings problem on individuals.

#### Sense Crossover Operator

It is a new crossover operator for the genetic algorithm process. This operator improves the performance of the genetic algorithm process both in terms of the quality as well as the speed. This operator has a different mechanism of combining solutions. Here the crossover takes place in the problem space rather than the chromosome space. This sense operator can be used as the complete replacement for the traditional crossover operator or it can be combined with it.

#### Middle point crossover

Middle point crossover operator randomly selects two parent chromosomes from the previous generations. The daughter chromosome inherits the first half section directly from the father. As the labels in the sequence cannot be duplicated, the daughter will inherit the labels which have not appeared in its first half section from the mother chromosome in the same order they appeared in the mother chromosome. Similarly, the son chromosome inherits its first-half section completely from the mother and the second-half section from the father [19].

#### Guided Crossover (GC)

Guided crossover is having the capable of improving the steady state error of a genetic algorithm optimizer i.e. the distance between the best point found and the global optimum of the search space, in a continuous space, without having to use gradient information or gradient based methods.

The working procedure of guided crossover is summarized as follows:

- One candidate point is selected from the GA population by using Rank selection technique and it is called as candidate<sub>1</sub>.
- The second candidate point is selected from the GA population but in a different fashion: for each point X in the GA population other than candidate<sub>1</sub>, a quantity Mutual\_fitness(X, candidate<sub>1</sub>) is computed where

$$\text{Mutual}_{\text{fitness}(A,B)} = \frac{(\text{fitness}(A) - \text{fitness}(B))^2}{\text{Euclidean}_{\text{distance}(A,B)}^2}$$

- Candidate<sub>1</sub> and candidate<sub>2</sub> are swapped if necessary; to make the candidate<sub>1</sub> point that has the highest fitness among the two.
- The result of the crossover is a point along the line joining candidate<sub>1</sub> to candidate<sub>2</sub> which is selected randomly from the small region around candidate<sub>1</sub> ( it has the better point ) is given as follows:

$$\text{Result} = L \times \text{candidate}_1 + (1 - L) \times \text{candidate}_2$$

where L is a uniformly distributed random number in the interval  $[1 - 0.2 \times x, 1 + x]$  and x is a function of the number of elapsed iterations  $I_e$  and the total allowed number of iterations

$$I_t \text{ such that: } x = 0.75 \times \frac{(I_t - I_e)}{I_t} + 0.25$$

This is the working procedure of guided crossover [17].

#### Scanning Crossover

The scanning crossover operator was proposed by Eiben et al; first it takes n parents and it create a child by scanning the parents genes deciding at each gene which parent can deliver its allele to its child. In general, the choice mechanism is not defined. The choice can be uniform random choice or a random fitness proportional choice [27] [29].

#### Uniform Scanning Crossover (U-Scan)

U-Scan is the generalization of the two parent uniform crossover. U-Scan uses a method that one of the selected parents randomly determines the value of the offspring. Therefore each parent has the same probability to be the dominator of the value inherited by the offspring. This U-Scan breaks the traditional two parents approach and can extend the number of parents to an arbitrary number [29].

#### Occurrence- Based Scanning Crossover (OB-Scan)

OB-Scan relies on parental occurrence in order to find the offspring values. In general, each parent votes and the values inherited will be the one privileged by the majority of the parents [29].

#### Diagonal Crossover (Diagonal)

Diagonal Crossover is the generalization of the one point crossover. For s parent solutions, the diagonal crossover divides each parents into s sections through s - 1 crossover points. Then each section has the same length except the last section containing the surplus variables when divided unevenly. The offspring is constructed through extracting in a diagonal fashion correspondingly one section from each parent [29].

#### Laplace Crossover

Laplace crossover was proposed by K.Deep and M.Thakur which uses laplace distribution. It is a parent centric operator. This operator shows self adaptive behavior [3].

#### Intermediate Crossover

Intermediate crossover operator produces offsprings by a weighted average of the parents. Intermediate crossover (IC) is controlled by a single parameter *Ratio*.

$$\text{Offspring} = \text{parent1} + \text{rand}(\epsilon) \cdot \text{Ratio} \cdot (\text{parent2} - \text{parent1})$$

If the *Ratio* is in the range of [0, 1] then the produced offsprings are within the hypercube defined by the parents locations at opposite vertices. *Ratio* can be a scalar or a vector of length

number of variables. If the obtained *Ratio* is a scalar, then all of the offsprings will lie on the line between the parents. If the obtained *Ratio* is a vector then the resultant children can be any point within the hypercube [11].

#### Ring Crossover

Ring Crossover consists of four steps. They are

*Step-1:* Two parents such as parent1 and parent2 have to be considered for the crossover process.

*Step-2:* The two parent's chromosomes are firstly combined with a form of ring. Later, a random cutting point is decided in any point of ring.

*Step-3:* The children are created with a random number generated in any point of ring according to the length of the combined two parental chromosomes. With reference to the cutting point in step 2, one of the children is created in the

clockwise direction, and the other one is created in the anti-clockwise direction.

*Step-4:* Swapping and reversing process takes place in this step. In the swapping process, a number of genes are swapped in the crossed parents. In the reversing process, the remaining genes are reversed in crossed parents. As the length of ring is equal to the total length of both of parents and the children are created according to a random point of ring, so that more variety can be provided in possible number of children by the ring crossover operator according to single point and two point crossover operators [11].

Recombination operators such as unimodal normal distribution crossover (UNDX), simplex crossover (SPX), and blend crossover (BLX) are mean-centric approaches, whereas the simulated binary crossover (SBX), fuzzy recombination and parent centric crossover (PCX) are parent-centric approaches.

Unimodal Normally Distributed Crossover operator (UNDX)

UNDX was proposed by Ono and Kobayashi. The UNDX operator generates offspring by using normal distribution and it was defined by three parents. Offspring are generated around the line segment connecting the two parents, namely Parent 1 and Parent 2. The third parent, Parent 3, is used to decide the standard deviation of the distance to the axis connecting Parent 1 and Parent 2. This operator has a feature of independence from coordinate systems and is excellent in characteristics preservation for function optimization. UNDX was implemented in the steady state genetic algorithm and it is used to solve three difficult large optimization problems [3][29].

Simplex crossover (SPX)

Simplex crossover was proposed by Tsutsui et al, which is a multi-parent crossover operator; and it uses the property of a simplex in the search space. In general, SPX has the capability to provide the balance between exploration and exploitation, and it is independent from coordinating systems in generating offspring. The experimental results clearly explaining that it has high performance on test functions with multimodality or epistasis with a medium number of parents. i.e three parents on a low 10 dimensional functions and four parents on a high 20 dimensional functions [3][27].

Simulated Binary Crossover

Simulated binary crossover was developed by Deb and Agarwal. This operator follows the working principle of the single point crossover operator on the binary strings in continuous domain. It takes a pair of parents and it produces two offspring's [3].

Parent-centric crossover operator

This PCCO assign more probability to generate the offspring near the female parent than anywhere in the search space. The ranges of these probability distributions depend on the distance among the genes of the female parent and the genes of the male parent. The common example is SBX (Deb and Agrawal, 1995) [6].

Advantages of the parent-centric crossover operators

Deb et al. (2002) carried out the experiments and showed that PCCO has the capability to

solve the real-parameter optimization problems. Most of us think that these results are due to those PCCOs combine two advantageous features:

- PCCOs behave like a mutation operator.
- PCCOs are self-adaptive crossover operators [6].

## 4. MUTATION

The term mutation represents *innovation*. Mutation is a very important operator and hence it is used to enhance the search. Some of the evolutionary algorithms are there they used mutation operator only for searching purpose [12]. Mutation alters one or more gene values in a chromosome from its initial state so it will produce a new gene values which is being added to the gene pool; based on the new gene values, genetic algorithm may have the capability to obtain a optimal better solution than previous one [9]. Generally crossover is called as recombination but in paper [12] the author said that mutation is another recombination technique and it is used to ensure that all the elements in the population are not homogeneous and finally the mutation is used to maintain the genetic diversity [9] [12] [13]. Mutation helps to prevent the genetic algorithm to fall from local optima while searching for global optima [9] [12] [13]. The mutation rate is usually less than 30%. The MultiNonUniform is used at the rate of 5% in some experiments [12]. Mutation randomly adds the new information to the genetic search process [13]. Mutation may produce different individuals of chromosomes from their parent individuals [13]. Mutation is a process and it is used to randomly distribute the genetic information [13]. The very important term mutation probability is going to be discussed here. Mutation operates at the bit level; when the bit in the chromosome is being copied from current to the next string there is a probability that the bit become mutated. That probability value is usually small and it is called as mutation probability  $p_m$  [13]. Some of the mutation operators are summarized as follows;

### Mutation Operators

- Flip Bit Mutation or Bit-Flip Mutation
- Random Mutation
- Boundary Mutation
- Uniform Mutation
- Non- Uniform Mutation
- Gaussian Mutation
- Novel Mutation
- Bit String Mutation
- Single Point Mutation
- Double Point Mutation
- Adjacent Mutation
- Arbitrary Mutation
- Shift Mutation
- Exchange Mutation
- Scramble sublist mutation
- Makinen, Periaux and Toivanen Mutation (MPTM)
- Insert mutation

- Swap mutation
- Inversion mutation
- Scramble mutation

#### Flip Bit Mutation or Bit-Flip Mutation

Bit flip is the classical mutation operator. Flip bit mutation operator basically inverts the value of the selected gene. i.e it changes the value from 0 to 1 otherwise from 1 to 0. This operator can be used only for binary genes [9] [21].

#### Random Mutation

It is the simplest form of mutation, which flips one of the bits in a random fashion with a certain probability [2].

#### Boundary Mutation

Boundary mutation operator replaces the value of the selected gene with either the upper bound or the lower bound of that gene. It can be done randomly. It can be used only for integer and float genes [9].

#### Uniform Mutation

Uniform mutation operator replaces the value of the selected gene with a uniform random value selected between user specified upper and lower bounds of that gene. It can be used only for integer and float genes [9].

#### Non- Uniform Mutation

Non-uniform mutation operator increases the probability such that the amount of the mutation will be close to 0 as the generation number increases. It can be used only for integer and float genes [9].

#### Gaussian Mutation

Gaussian mutation operator adds a unit Gaussian distributed random value to that selected gene. The new gene value is clipped if it falls outside of the user specified lower or upper bound of that gene. It can be used only for integer and float genes [9].

#### Inversion Mutation

Inversion mutation operator is easy to operate. This operator selects two points in a parent and it inverts the genes between the two points to produce an offspring [5].

#### Novel Mutation

Novel mutation operator is based on the immunity operation. The traditional mutation operators are inefficient to solve complex global optimization problem. In order to overcome all those problem novel mutation operator was proposed. This novel mutation operator utilizes the available knowledge to intervene the global parallel process, in order to overcome the blindness in the mutation actions. This operator involves five steps. They are [7]

- Preparation
- Knowledge Discovering
- Mutation
- Selection
- and
- Repetition.

#### Bit String Mutation

The mutation of the bit strings ensue through bit flips at random positions. The probability of a mutation of a bit is  $1/l$ , where  $l$  is the length of the binary vector. Thus a mutation rate of 1 per mutation and individual selected for mutation is reached.

#### Single Point Mutation

In single point mutation, the selected gene from the chromosome is being mutated from 1 to 0 and the resultant offspring 0 is produced.

#### Double Point Mutation

In Double point mutation, the two selected genes from the chromosome is being mutated from 1 to 0 or from 0 to 1 and the resultant offspring 0 or 1 is produced.

#### Adjacent Mutation

Adjacent mutation operator exchanges the adjacent genes in the parent individual.

#### Arbitrary Mutation

Arbitrary mutation operator randomly chooses two positions of the genes in the parent individual and exchanges those genes to produce offspring.

#### Shift Mutation

Shift mutation operator acts like a single point mutation operator. In shift mutation operator, it randomly chooses a value in the parent individual and inserts this value to the randomly selected point and the rest of the genes next to insertion are shifted to the right.

#### Exchange Mutation

Exchange mutation is the process of interchanging two randomly selected genes of the permutation [2] [25]. The remaining genes in the chromosome are kept intact. From the experimental results, we can analyze that exchange mutation has the capacity to provide better performance [2].

#### Scramble sublist mutation

This operator randomly selects two points in the string or chromosome and then it randomly permuting the elements or genes between these two positions [25].

#### Makinen, Periaux and Toivanen Mutation (MPTM)

This mutation operator was proposed by Makinen et al.; they applied in a genetic algorithm to solve multidisciplinary shape optimization problems in aerodynamics and electromagnetic as well as large set of constrained optimization problem. The specific name was not given by the authors so (Makinen, Periaux and Toivanen) became the authors of this MPT mutation. The strength of MPT does not decrease as the generation number increases [3].

#### Mutation operators for Permutations

Normal mutation operators lead to inadmissible solutions. Example: Bit wise mutation. Mutation parameter reflects the probability that some operator is applied only once to the whole string rather than individually in each position [24].

#### Insert mutation for permutations

Select two gene values randomly. Move the second gene to follow the first gene and then shift the remaining genes. This process conserves most of the order and the adjacency information [2] [24].

#### Swap mutation for permutations

Select two gene values randomly and swap their positions. This process conserves most of the adjacency information (it will break 4 links) and it interrupts the order [20] [24].

#### Inversion mutation for permutations

Select two gene values randomly and then invert the substring between them. This process conserves most of the adjacency information (it will break 2 links) and it interrupts the order [24].

#### Scramble mutation for permutations

Select the subset of genes randomly and then rearrange the genes in those positions [24].

## 5. CONCLUSION

In this paper, an observational analysis of genetic operators (Selection, Crossover and Mutation) was briefly discussed and the maximum number of available genetic operators was briefly presented. The selection of appropriate genetic operators has to be chosen carefully for the specific problem in order to achieve the optimal solution.

## 6. REFERENCES

- [1] Talip Kellego'z<sup>a,\*</sup>, Bilal Toklu<sup>b</sup>, John Wilson<sup>c</sup>, "Comparing efficiencies of genetic crossover operators for one machine total weighted tardiness problem", Applied Mathematics and Computation 199 (2008) 590–598.
- [2] Chao-Hsien Chu<sup>1</sup>, G. Premkumar<sup>\*</sup>, Hsinghua Chou<sup>2</sup>, "Digital data networks design using genetic algorithms", European Journal of Operational Research 127 (2000) 140±158.
- [3] Kusum Deep, Manoj Thakur<sup>\*</sup>, "A new crossover operator for real coded genetic algorithms", Applied Mathematics and Computation 188 (2007) 895–911.
- [4] Mustafa Kaya, "The effects of a new selection operator on the performance of a genetic algorithm", Applied Mathematics and Computation 217 (2011) 7669–7678.
- [5] Yong Xu<sup>a,b,\*</sup>, Shen-Chu Xu<sup>a</sup>, Bo-Xi Wu<sup>a</sup>, "Traffic grooming in unidirectional WDM ring networks using genetic algorithms", Computer communications 25 (2002) 1185-1194.
- [6] C.Garci'a-Martí'nez<sup>a,\*</sup>, M. Lozano<sup>b</sup>, F. Herrera<sup>b</sup>, D. Molina<sup>c</sup>, A.M. Sánchez<sup>d</sup>, "Global and local real-coded genetic algorithms based on parent-centric crossover operators", European Journal of Operational Research 185 (2008) 1088–1113.
- [7] Li-Ning Xing<sup>a,b,\*</sup>, Ying-Wu Chen<sup>a</sup>, Ke-Wei Yang<sup>a</sup>, "A novel mutation operator based on the immunity operation", European Journal of Operational Research 197 (2009) 830–833.
- [8] A.W.M. Ng<sup>a,\*</sup>, B.J.C. Perera<sup>b</sup>, "Selection of genetic algorithm operators for river water quality model calibration", Engineering Applications of Artificial Intelligence 16 (2003) 529–541.
- [9] RC Chakraborty, "Fundamentals of Genetic Algorithms".
- [10] R.SIVARAJ, Dr.T.RAVICHANDRAN, "A REVIEW OF SELECTION METHODS IN GENETIC ALGORITHM", R.Sivaraj et al. / International Journal of Engineering Science and Technology (IJEST).
- [11] Yılmaz KAYA<sup>1</sup>, Murat UYAR<sup>2</sup>, Ramazan TEKĐN<sup>3</sup>, "A Novel Crossover Operator for Genetic Algorithms: Ring Crossover".
- [12] Dr. Elgasim Elamin Elnima Ali, "A Proposed Genetic Algorithm Selection Method".
- [13] Tom V. Mathew, "Genetic Algorithm".
- [14] Tobias Blickle, Lothar Thiele, "A Comparison of Selection Schemes used in Genetic Algorithms".
- [15] <sup>1</sup>Omar Al Jadaan, <sup>2</sup>Lakshmi Rajamani, <sup>3</sup>C. R. Rao, "IMPROVED SELECTION OPERATOR FOR GA", Journal of Theoretical and Applied Information Technology © 2005 – 2008, JATIT.
- [16] Yang Chen<sup>\*</sup>, Jinglu Hu<sup>†</sup>, Kotaro irasawa<sup>‡</sup>, "GARS: An Improved Genetic Algorithm with Reserve Selection for Global Optimization".
- [17] Khaled Rasheed, "Guided Crossover: A New Operator for Genetic Algorithm Based optimization".
- [18] Carlos Conceição António, "A study on synergy of multiple crossover operators in a hierarchical genetic algorithm applied to structural optimization", Struct Multidisc Optim (2009) 38:117–135, DOI 10.1007/s00158-008-0268-x.
- [19] Andrew Lim<sup>a</sup>, Brian Rodrigues<sup>b</sup>, Fei Xiao<sup>c</sup>, "A Genetic Algorithm with Hill Climbing for the Bandwidth Minimization Problem".
- [20] Sandeep Rajoria<sup>1</sup>, Carlos Soares<sup>2</sup>, Jorge Pinho de Sousa<sup>3</sup>, and Joydip Dhar<sup>4</sup>, "Predicting the Outcome of Mutation in Genetic Algorithms".
- [21] Wilhelm Erben, HTWG Konstanz, "Genetic Algorithms", wilhelm.erben@htwg-konstanz.de.
- [22] Kamaljit Kaur, Amit Chhabra & Gurvinder Singh, "Heuristics Based Genetic Algorithm for Scheduling Static Tasks in Homogeneous Parallel System", International Journal of Computer Science and Security (IJCSS), Volume (4): Issue (2) 183.
- [23] Dr. Masoud Yaghini, "Genetic Algorithms Part 3: The Component of Genetic Algorithms", Spring 2009.
- [24] Dr. Masoud Yaghini, "Chapter 3: Genetic Algorithms", Spring 2009.
- [25] "Tutorial: Genetic Algorithm"
- [26] Muhammad Tami Al-Hajri, M. A. Abido, "Assessment of Genetic Algorithm Selection, Crossover and Mutation Techniques in Reactive Power Optimization", 978-1-4244-2959-2/09/\$25.00\_c 2009 IEEE.
- [27] Shigeyoshi Tsutsui, Masayuki Yamamura, Takahide Higuchi, "Multi-parent Recombination with Simplex Crossover in Real Coded Genetic Algorithms", Ministry of Education, Science, Sports and Culture of Japan under Grant-in-Aid for Scientific Research number 10680396.
- [28] A.E.Eiben, C.H.M.van Kemenade, "Performance on Multi-Parent Crossover Operators on Numerical Function Optimization Problems".
- [29] Yang Wang, Zhipeng L'u, and Jin-Kao Hao, "A Study of Multi-parent Crossover Operators in a Memetic Algorithm" R. Schaefer et al. (Eds.): PPSN XI, Part I, LNCS 6238, pp. 556–565, 2010. @Springer-Verlag Berlin Heidelberg 2010.