

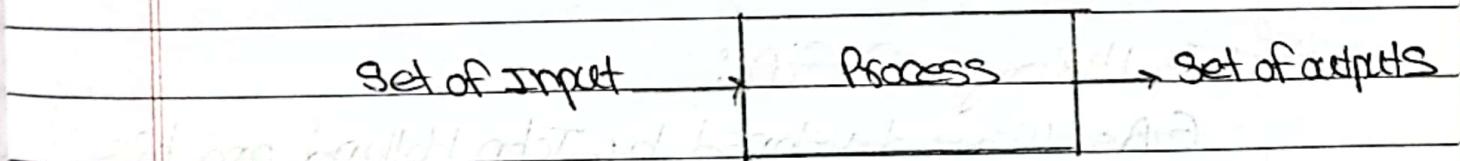
## GA - Introduction

### \* Definition:

- Genetic Algorithm (GA) is a Search-based optimization technique based on the principles of Genetics & Natural selection.
- Genetic Algorithm is not Gene Coding rather they are Computer algorithm that resides or based on principles of genetics & Evolution.
- It is frequently used to find optimal or near-optimal solutions to difficult problems which otherwise would take a lifetime to solve.
- It is frequently used to solve optimization problems, in machine learning.
- GAs are a subset of a much larger branch of computation known as Evolutionary Computation.
- Focus on: Optimization & Searching.

### \* Optimization:

- Optimization is the process of making something better.  
e.g.: In any process, we have a set of inputs & a set of outputs as shown in the figure.



optimization refers to finding the values of inputs in such a way that we get the "best" output values.

- The definition of "best" varies from problem to problem, but in mathematical terms, it refers to maximizing or minimizing one or more objective functions, by varying the input parameters.
- The set of all possible solutions or values which the inputs can take make up the search space. In this search space, lies a point or a set of points which gives the optimal solution. The aim of optimization is to find that point or set of points in the search space.

### \* Searching:

- The process of finding a solution of the given problem can be defined as searching.

for e.g:- Starting point is given we need to find the target point.

### \* Concept of Survival of the fittest:

- The main principle of evolution used in GA is "Survival of the fittest"
- The good solution survive, while bad one die.

### \* The History of GA:

GANs were developed by John Holland and his students & colleagues at the University of Michigan, in 1975.

- Until ~~80's~~ early 80's, the concept was studied theoretically,
- In 80's, the first "real world" GAs were designed. Since then GAs are tried on various optimization problems with a high degree of success.

### \* How GAs Works?

In GAs, we have a pool or a population of possible solutions to the given problem. These solutions then undergo crossover & mutation (like in natural genetics) producing new children, the process is repeated over various generations. Each individual (or candidate solution) is assigned a fitness value (based on its objective function value) and the fitter individuals are given a higher chance to mate and yield more "fitter" individuals. This is in line with the Darwinian Theory of "Survival of the fittest".

In this way we keep "evolving" better individuals or solutions over generations, till we reach a stopping criteria.

Genetic Algorithms are sufficiently randomized in nature, but they perform much better than random local search (in which we just try various random solutions, keeping track of the best so far).

Initialize the population.

→ select individuals for the mating pool

Perform Crossover

perform mutation

In Set offsping into the population

No

Stop

? Yes

The End

Flow:- Algorithmic phases of GIA.

### \* Advantages of GIA:

GIA's have various advantages which have made them immensely popular. These includes:

- i) Does not require any prior or derivative information (which may not be available for many real-world problems).
- ii) It is faster & more efficient as compared to the traditional methods.
- iii) It has very good parallel capabilities,
- iv) It can optimize both continuous & discrete functions

and also multi-objective problems.

- v) It provides a list of "good solutions", not just a single solution.
- vi) It always gets an answer to the problem, which gets better over the time.
- vii) Mostly useful when the search space is very large & there are a large number of parameters involved.

### \* Limitations of GAs:

- i) GAs are not suited for all problems, especially problems which are simple & for which derivative information is available.
- ii) Fitness value is calculated repeatedly which might be computationally expensive for some problems.
- iii) Being stochastic, there are no guarantees on the optimality or the quality of the solution.
- iv) If not implemented properly, the GA may not converge to the optimal solution.

### \* GA-Motivation:

→ Genetic Algorithms have the ability to deliver a "good-enough" solution "fast-enough". Which makes genetic algorithms attractive for use in solving optimization problems.

Some of the reasons why GAs are needed are as follow:

## i) Solving difficult Problems:

In Computer Science, there is a large set of problems, which are NP-Hard, which means, even with the most powerful computing systems it take a very long time (even years) to solve that problem.

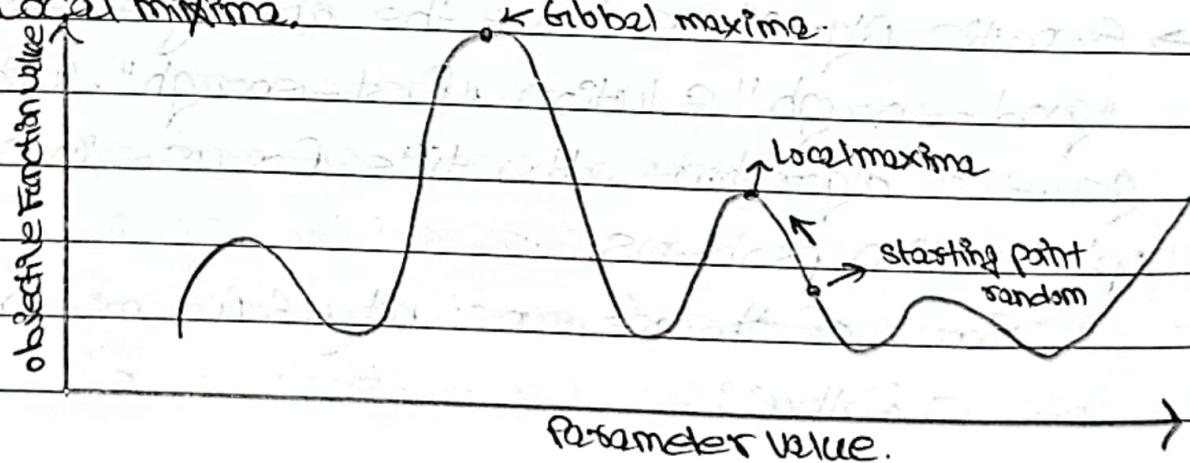
In such scenario, GAs prove to be an efficient tool to provide usable near-optimal solutions in a short amount of time.

## ii) Failure of Gradient Based Methods: (Hill climbing problem)

Traditional calculus based methods work by starting at a random point and by moving in the direction of the gradient, till we reach the top of the hill.

This technique is efficient & works very well for single-peaked objective functions like the Cost function in Linear regression.

But in most real-world situations, we have a very complex problem called as landscapes, which are made of many peaks & many valleys, which causes such methods to fail as they get stuck at the local minima.



### iii) Getting a Good Solution Fast :

Some difficult problems like the Travelling Salesperson problem (TSP), have real-world applications like path finding & VLSI (Very Large Scale Integration) Design.

Mostly used in GPS system for finding the quickest & shortest path from source to destination.

## \* Basic Terminology:

Before beginning a discussion on Genetic Algorithm it is essential to be familiar with some basic terminology which will be used throughout this tutorial.

### i) Population :

It is a subset of all the possible (encoded) solutions to the given problem. The population for a GA is similar to the population for human beings except that instead of human beings, we have candidate solutions representing human beings.

### ii) Chromosome:

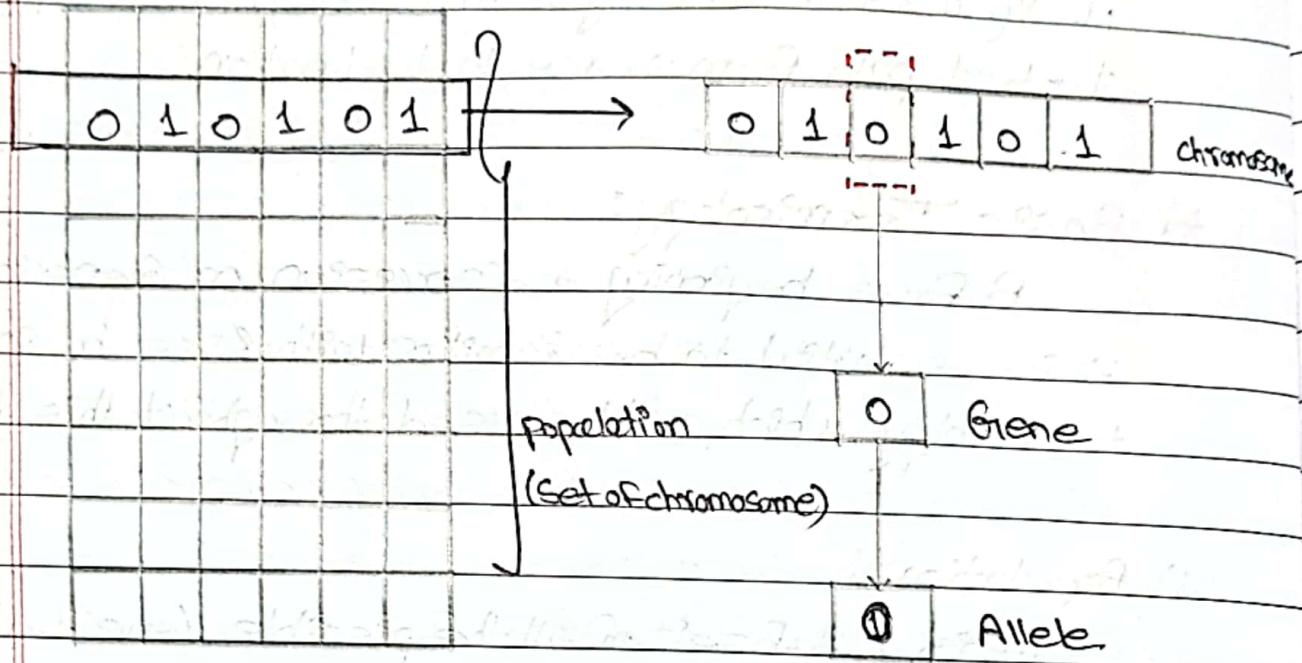
A chromosome is one such solution to the given problem.

### iii) Gene:

A gene is one element position of a chromosome.

#### iv) Allele:

It is the value a gene takes for a particular chromosome.



#### v) Genotype:

Genotype is the population in the Computational space. In the Computational space, the solutions are represented in a way which can be easily understood & manipulated using a computing system.

#### vi) Phenotype:

Phenotype is the population in the actual real world Solution / Solution space in which solutions are represented in a way that are represented in real world situations.

e.g:-  
(dominant)  $T$

$t$  (dwarf)

$Tt$  (hybrid tall)

$Tt$

$TT$

$Tt$

$tT$

$tt$

(hybrid tall dwarf)

Genotype: 1 2 1 0 0 0

phenotype: 3:1

### \* Encoding & Decoding:

For simple problems, the phenotype & genotype spaces are the same. However, in most of the cases, the phenotype & genotype spaces are different.

#### i) Decoding:

- Decoding is a process of transforming a solution from the genotype to the phenotype space.
- Decoding should be fast as it is carried out repeatedly in a GA during the fitness value calculation

Genotype → Phenotype

## ii) Encoding:

→ Encoding is a process of transforming the solution from the phenotype to genotype space.

Phenotype  $\rightarrow$  Genotype

\* For example:-

Consider the 0/1 Knapsack problem. The phenotype space consists of solutions which just contain the item numbers of items to be picked.

i.e.  $\{1, 2, 3, 4, 5\}$

Sack = 10 kg

(Capacity)

Kg	5	3	6	4	2	{ phenotype space solution }
Values	6	7	12	7	5	

However, the genotype space it can be represented as a binary string of length  $n$  (where  $n$  is the number of items).

A 1 at position  $x$  represents that  $x^{\text{th}}$  item is picked while a 0 represents the reverse.

This is a case where genotype & phenotype spaces are different.

Solution 1: 1 1 1 0 0 1

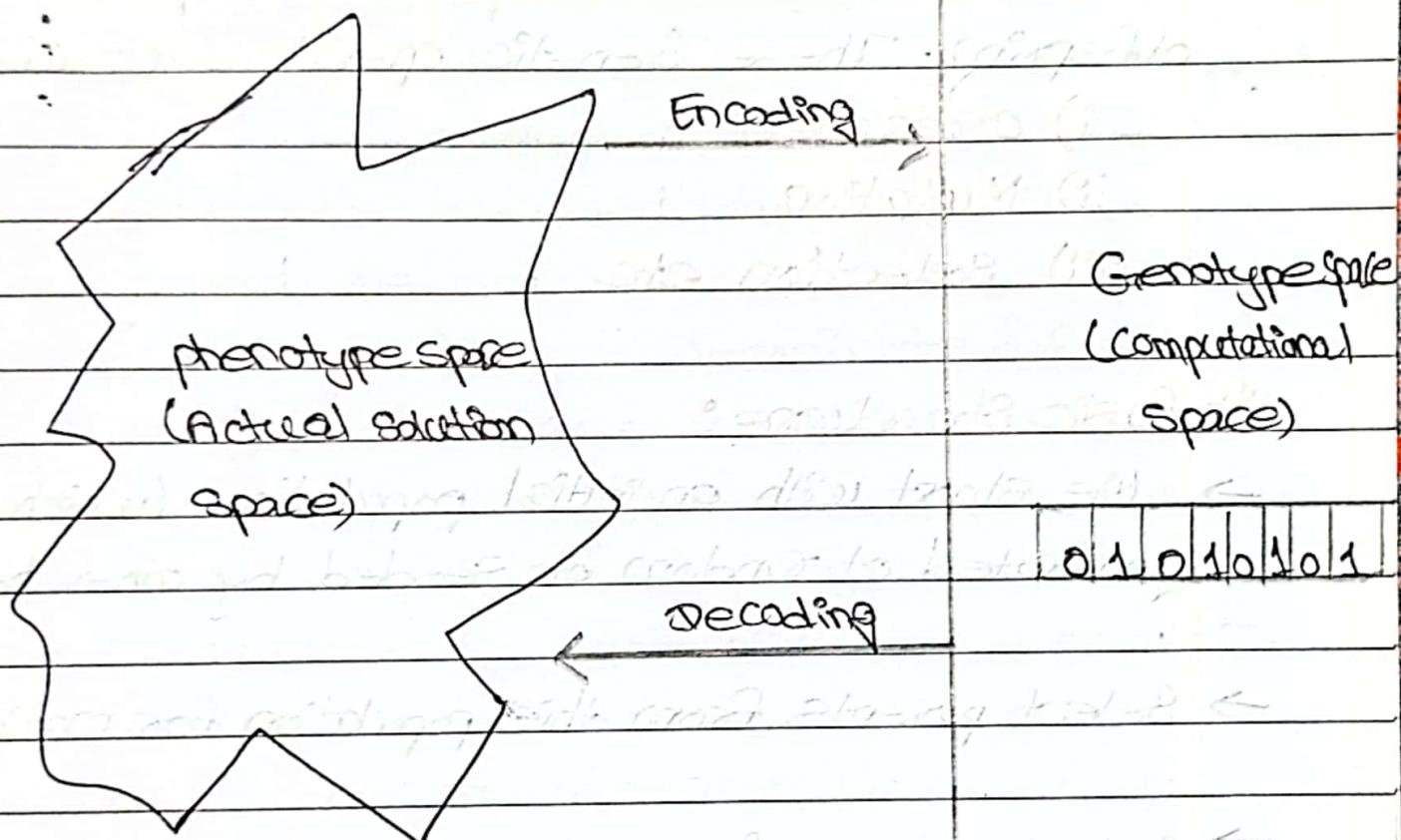
Solution 2: 1 0 0 1 0

Genotype space  
selection.

Solution 3: 0 1 1 0 0

Solution 4: 1 0 1 1 1 0

Solution 5: 1 1 1 0 0 X exceeds the 10 kg



### vii) Fitness Function:

A fitness function is a function which takes the solution as input and produces the suitability of the solution as the output.

In some cases, the fitness function and the objective function may be the same, while in others it might be different based on the problems.

### viii) Genetic operators:

These alter the genetic composition of the offspring. These Genetic operators include:

- i) crossover,
- ii) Mutation,
- iii) Selection etc.

### \* Basic Structure:

- We start with an initial population (which may be generated at random or seeded by other heuristics).
- Select parents from this population for mating.
- Apply crossover & mutation operators on the parents to generate new off-springs.
- Finally, these off-springs replace the existing.

individuals in the population and the process repeats.

In this way genetic algorithms actually try to mimic the human evolution to some extent.

Population Initialization

Fitness Function

calculation

Loop until

crossover and mutation

termination

criteria reached

Mutation

Survivors Selection

Terminate & Return

Fig of Basic Structure of GA.



## Genotype Representation:

One of the most important decisions to make while implementing a genetic algorithm is deciding the representation that we will use to represent our solutions. It has been observed that improper representation can lead to poor performance of the GAs.

Therefore, choosing a proper representation, having a proper definition of the mappings between the phenotype & genotype spaces is essential for the success of GAs.

In this, we present some of the most commonly used representations for genetic algorithms.

However, representation is highly problem specific and the reader might find that another representation or a mix of the representations mentioned here might suit their problem better.

### i) Binary Representation:

This is one of the simplest & most widely used representation in GAs. In this type of representation the genotype consists of bit strings.

For some problems when the solutions space consists of Boolean decision variables - Yes or no, the binary representation is best suited.

Take for example the 0/1 Knapsack problem, If there are  $n$  items, we can represent a solution by a binary string of  $n$  elements, where the  $x^{\text{th}}$  element tells whether the item  $x$  is picked (1) or not(0).

0	0	1	0	1	1	1	0	0	1
---	---	---	---	---	---	---	---	---	---

For other problems, specifically those dealing with numbers, we can represent the numbers with their binary representation. The problem with this kind of encoding is that different bits have different significance and therefore mutation & crossover operators can have undesired consequences. This can be resolved to some extent by using Gray Coding, as a change in one bit does not have a massive effect on the solution.

### i) Real valued Representation:

For problems where we want to define the genes using continuous rather than discrete variables, the real valued representation is the best suited. The precision of these real valued or floating point numbers is however limited to the computer.

0.5	0.2	0.6	0.8	0.7	0.4	0.3	0.2	0.1	0.9
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

iii)

### Integer Representation:

For discrete valued genes, we cannot always limit the solution space to binary 'Yes' or 'No'.

For example, if we want to encode the four directions - East, West, North, South?, we can encode them as  $0, 1, 2, 3$ . In such cases, integer representation is ~~desirable~~, best suited.

1	2	3	4	3	2	4	1	2	1
---	---	---	---	---	---	---	---	---	---

### iv) Permutation Representation:

In many problems, the solution is represented by an order of elements. In such cases permutation representation is the most suited.

A classical example of this representation is the travelling salesman problem (TSP). In this the salesman has to take a tour of all the cities visiting each city exactly once and come back to the starting city. The main aim of this problem is the total distance of the tour has to be minimized.

The solution to this TSP is naturally an ordering or permutation of all the cities and therefore using a permutation representation makes sense for this problem.

1	5	9	8	7	4	2	3	6	0
---	---	---	---	---	---	---	---	---	---

### \* Population :

Population is a subset of solutions in the current generation. It can also be defined as a set of chromosomes. There are several things to be kept in mind when dealing with GA population, i.e.:

- i) The diversity of the population should be maintained otherwise it might lead to premature convergence.
- ii) The population size should not be kept very large as it can cause a GA to slow down, while a smaller population might not be enough for a good mating pool.

Therefore, an optimal population size needs to be decided by trial and error.

The population is usually defined as a two-dimensional array of :- i) Size population,



## \* Population Initialization:

These are two primary methods to initialize a population in a GA. They are:

### i) Random Initialization:

Populate the initial population with completely random Solutions.

### ii) Heuristic Initialization:

Populate the initial population using a known heuristic for the problem.

→ It has been observed that the entire population should not be initialized using a heuristic, as it can result in the population having similar solutions and very little diversity.

→ It has been experimentally observed that the random Solutions are the ones to drive the population to optimality.

→ Therefore, with heuristic initialization, we just seed the population with a couple of good Solutions, filling up the rest with random Solutions rather than filling the entire population with heuristic based Solutions.

It has also been observed that heuristic initialization in some cases, only affects the initial fitness of the population, but in the end, it is the diversity of the solutions which lead to optimality.

## \* Population Models:

There are two population models widely in use:

### i) Steady State:

In Steady state GA, we generate one or two off-springs in each iteration & they replace one or two individuals from the population.

A steady state GA is also known as **Incremental GA**.

### ii) Generational :

In a generational model, we generate ' $n$ ' off-springs, where  $n$  is the population size, and the entire population is replaced by the new one at the end of the iteration.

## \* Fitness Function:

A fitness function simply defined is a function which takes a candidate solution to the problem as input & produces an output and also determines how "fit" or how "good" the solution is with respect to the problem in consideration.

The calculation of fitness value is done repeatedly in a GA and therefore it should be sufficiently fast. A slow computation of the fitness value can adversely affect a GA and make it exceptionally slow.

In most cases the fitness function and the objective function are the same as the objective is to either maximize or minimize the given objective function. However, for more complex problems with multiple objectives & constraints, an algorithm designer might choose to have a different fitness function.

### ~~V. 3) When the objective Function map to Fitness Function~~

When the objective of the problem is to find optimal or maximize value both objective function & fitness function can be same.

for e.g:- 0/1 knapsack problems.

Both objective & Fitness Function: Maximum or optimal value.

but when the objective is to find the minimize value objective function & fitness function are different as fitness function always find the optimal solution. So in this case, the objective Function can't be map with Fitness Function.

Ex:- Travelling Salesman problem

Objective Function : Minimise value

Fitness Function : Maximise value

### \* Characteristics:

A fitness Function should possess the following characteristics:

- i) The fitness function should be sufficiently fast to compute
- ii) It should quantitatively measure how fit a given solution is or how fit individuals can be produced from the given Solution.

In some cases, calculating the fitness function directly might not be possible due to the inherent complexities of the problem at hand. In such cases, we do fitness approximation to suit our needs.

\* Example:

The following image shows the fitness calculation for a solution of the 0/1 Knapsack. It is a simple fitness function which just sums the profit values of the items being picked (which have a 1), Scanning the elements from left to right till the Knapsack is full.

Item Number.: 

0	1	2	3	4	5	6
---	---	---	---	---	---	---

chromosome: 

0	1	1	1	1	0	0
---	---	---	---	---	---	---

Profit values: 

2	9	8	5	4	0	2
---	---	---	---	---	---	---

Weight values: 

7	5	3	1	5	9	8
---	---	---	---	---	---	---

Knapsack capacity: 15 (14 taken with max profit)

Total resultant profit: 26

## \* Parent Selection:

Parent selection is the process of selecting parents which mate together to create off-spring for the next generation. Parent selection is very crucial to the convergence rate of the GA as good parents ~~divide~~ drive individuals to a better & fitter solutions.

However, care should be taken to prevent one extremely fit solution from taking over the entire population in a few generations, as this leads to the solutions being close to one another in the solution space thereby leading to a loss of diversity. This taking up of the entire population by one extremely fit solution is known as **Premature Convergence** and is an undesirable condition in a GA. Maintaining good diversity in the population is extremely crucial for the success of a GA.

### 1) \* Fitness Proportionate Selection:

Fitness Proportionate Selection is one of the most popular ways of parent selection. In this every individual can become a parent with a probability which is proportional to its fitness.

Therefore, fitter individuals have a higher chance of mating & propagating their features to the next generation. This kind of selection strategy

applies the selection of the more fit individuals from the population, evolving better individuals over time.

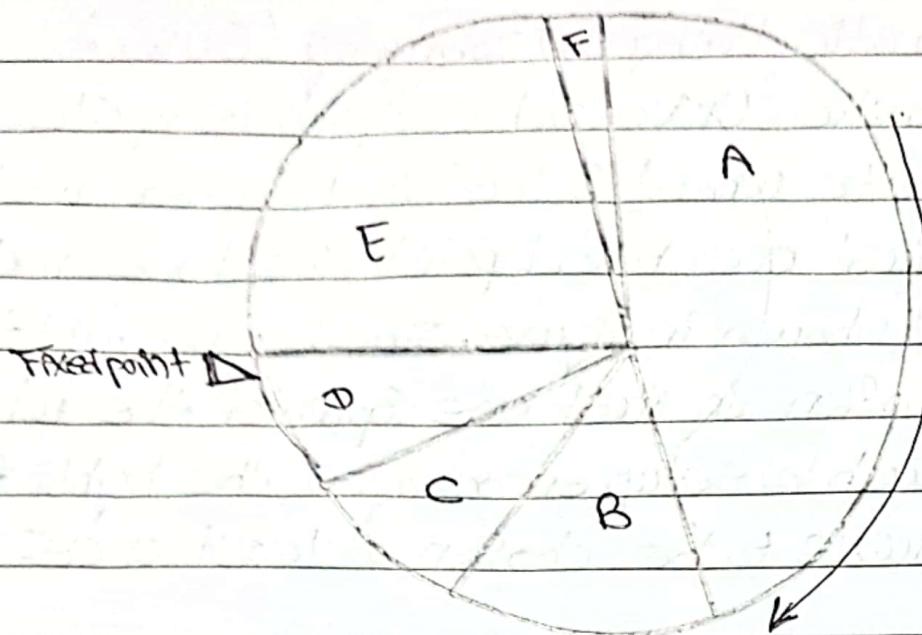
Consider a circular wheel. The wheel is divided into  $n$  pieces, where  $n$  is the number of individuals in the population. Each individual gets a portion of the circle which is proportional to their fitness values.

Two implementations of fitness proportionate Selection are:

- i) Roulette Wheel Selection,
- ii) Stochastic Universal Sampling (SUS),

### i) Roulette Wheel Selection:

In Roulette Wheel Selection, the circular wheel is divided into slots of region as described earlier. A fixed point is chosen on the wheel circumference as shown and wheel is rotated. The region of the wheel which comes in front of the fixed point is chosen as the parent. For the second part, the same process is repeated.



choose D as the parent.

It is clear that a fitter individual has a greater position on the wheel and therefore a greater chance of landing in front of the fixed point when the wheel is rotated.

Therefore, the probability of choosing an individual depends directly on its fitness.

#### \*Implementation:

We use the following steps:

Calculate  $S = \text{the sum of all fitnesses}$ .

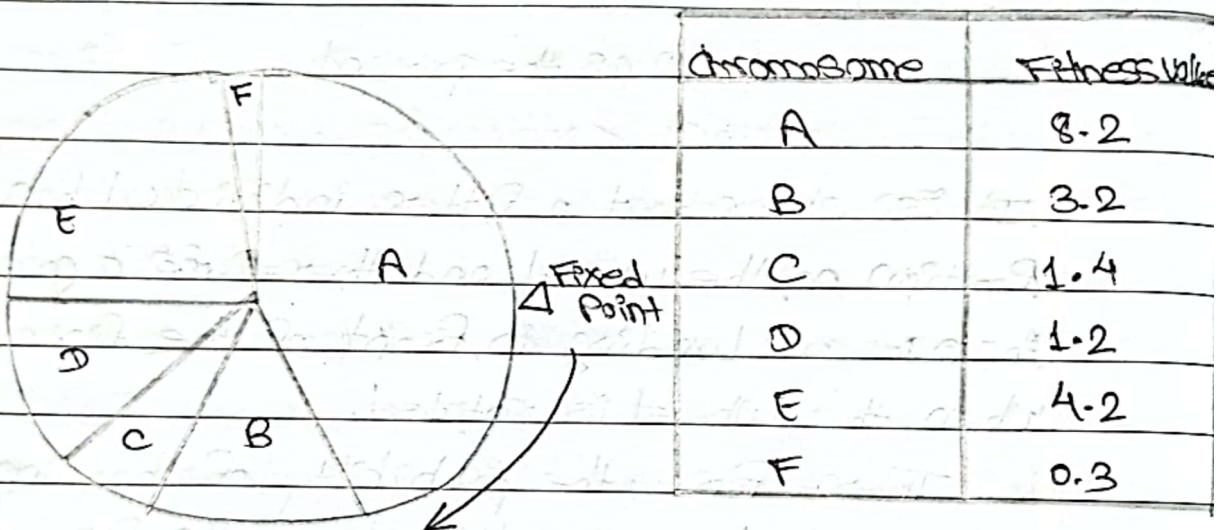
Generate a random number between 0 & S.

Starting from the top of the population, keep adding the fitnesses to the partial sum P, till  $P \leq S$ .

The individual for which P exceeds S is the chosen individual.

## ii) Stochastic Universal Sampling (SUS):

Stochastic Universal Sampling is quite similar to Roulette Wheel Selection, however instead of having just one fixed point, we have multiple fixed point as shown in figure. Therefore, all the parents are chosen in just one spin of the wheel. Also, such a setup encourages the highly fit individuals to be chosen at least once.



**Note:** It is to be noted that fitness proportionate Selection methods don't work for cases where the fitness can take a negative value.

## 2) Tournament Selection:

In K-way tournament Selection, we select K individuals from the population at random & select the best out of these to become a parent. The same process is repeated for selecting the next parent.

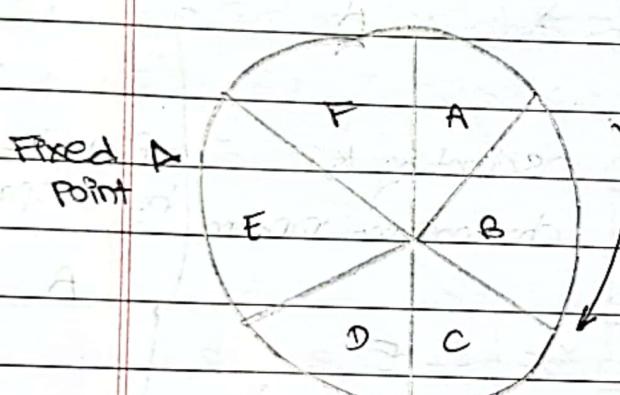
Tournament Selection is also extremely popular in literature as it can even work with negative fitness values.

Fitness      chromosome

1	Q			Fitness value = 5
5	A	→	A	
9	Z			
8	W			Selecting K
7	S			chromosome random
4	X			Pick the best as parent
2	E	→	E	
3	F			
6	R			
2	T	→	T	
2	Y			
1	V			
0	I			

### 3) Rank Selection:

Rank Selection also works with negative fitness values & is mostly used when the individuals in the population have very close fitness values. This leads to each individuals having an almost equal share of the pie (like in case of fitness proportionate selection) as shown in the following figure & hence each individual in the population has same probability of getting selected as a parent. This in turn leads to a loss in the selection pressure towards fitter individuals, making the GA to make poor parent selections in such situations.



No selection pressure.

	chromosome	Fitness value
A	A	8.1
B	B	8.0
C	C	8.05
D	D	7.95
E	E	8.02
F	F	7.99

In this, we remove the concept of a fitness value while selecting a parent. However, every individual in the population is ranked according to their fitness.

The selection of the parents depends on the rank of each individual & not the fitness. The higher ranked

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individuals are preferred more than the lower ranked ones.

chromosome	Fitness value	Rank
A	8.1	1
B	8.0	4
C	8.05	2
D	7.95	6
E	8.02	3
F	7.99	5

#### 4) Random Selection:

In this strategy we randomly select parents from the existing population. There is no selection pressure towards fitter individuals and therefore this strategy is usually avoided.

## \* Crossover:

### # Introduction:

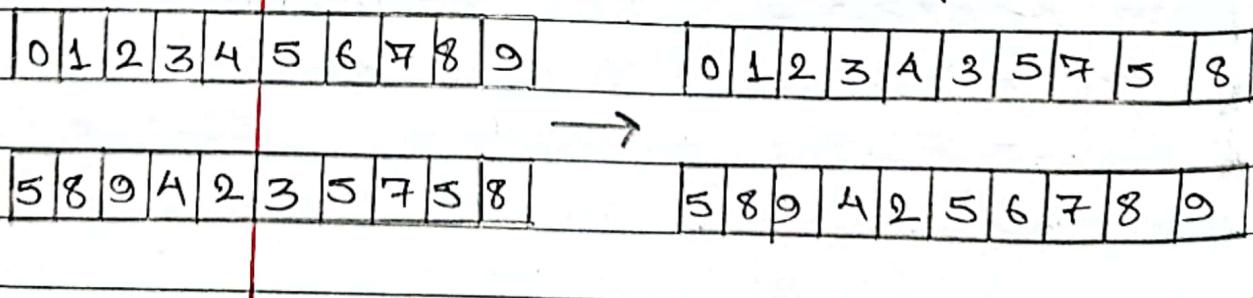
The Crossover operator is similar to reproduction & biological crossover. In this more than one parent is selected and ~~most~~ one or more off-springs are produced using the genetic material of the parents. Crossover is usually applied in a GA with a high probability.

### \* Crossover Operators:

In this we will discuss some of the most popularly used crossover operators. It is to be noted that these crossover operators are very generic & the GA designer might choose to implement a problem-specific crossover operator as well.

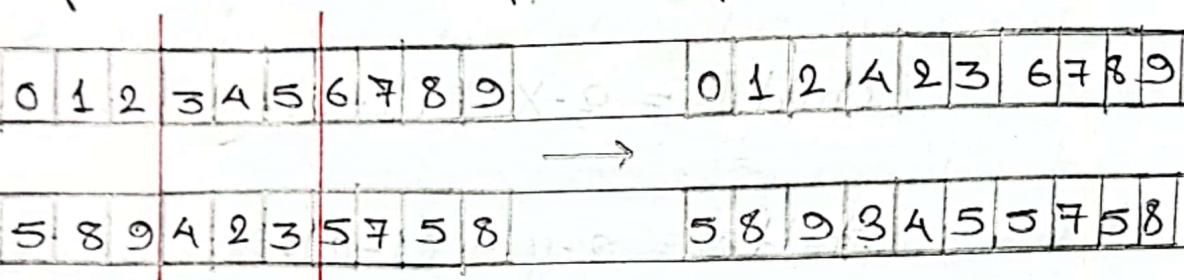
#### i) One-point crossover:

In this one-point crossover, a random crossover point is selected and the tails of its two parents are swapped to get new off-springs.



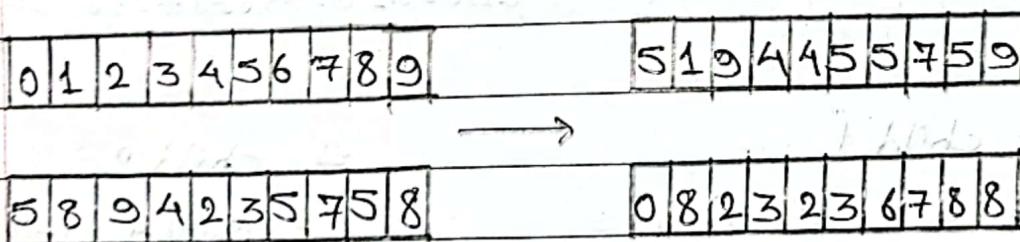
### ii) Multi-Point Crossover:

Multi-point crossover is a generalization of the one-point crossover where the alternating segments are swapped to get new off-springs.



### iii) Uniform Crossover: (3-point)

In a uniform crossover, we don't divide the chromosome into segments, rather we treat each gene separately. In this, we essentially flip a coin for each gene to decide whether or not it'll be included in the off-spring. We can also bias the coin to one parent, to have more genetic material in the child from that parent.



### v) Whole Arithmetic Recombination:

This is commonly used for integer representations & works by taking the weighted average of the two parents by using the following formula:

$$\text{child 1} = \alpha \cdot x + (1-\alpha) \cdot y$$

$$\text{child 2} = \alpha \cdot y + (1-\alpha) \cdot x$$

where,  $\alpha \in [0, 1]$

Also, when  $\alpha = 0.5$

Then, both the children will be identical as shown in the following,

0.1 0.1 0.2 0.2 0.3 0.3 0.4 0.4 0.5 0.5	0.15 0.2 0.2 0.2 0.3 0.25 0.3 0.2 0.35
---	--

0.2 0.3 0.2 0.2 0.3 0.2 0.3 0.2 0.2 0.2	0.15 0.2 0.2 0.2 0.3 0.25 0.35 0.3 0.2 0.35
---	---

\* = child 1

# = child 2

$$= \alpha \cdot X + (1-\alpha) \cdot Y$$

$$= \alpha \cdot Y + (1-\alpha) \cdot X$$

$$= 0.5 \times 0.1 + (1-0.5) \times 0.2$$

$$= 0.5 \times 0.2 + (1-0.5) \times 0.1$$

$$= 0.05 + 0.1$$

$$= 0.1 + 0.05$$

$$= 0.15$$

$$= 0.15$$

\* similarly for all genes

## v) Davis' Order Crossover (OX1):

### i) OX1 (Order crossover):

OX1 is used for permutation based crossovers with the intention of transmitting information about relative ordering to the off-springs.

#### \* How it works :

- Create two random crossover points in the parent & copy the segment between these crossover points from first parent to the first child.
- Now, starting from the second crossover point in the second parent , copy the remaining unused gene numbers from the second parent to the first child, wrapping around the list.
- Repeat for the second child with the parent's role reversed.

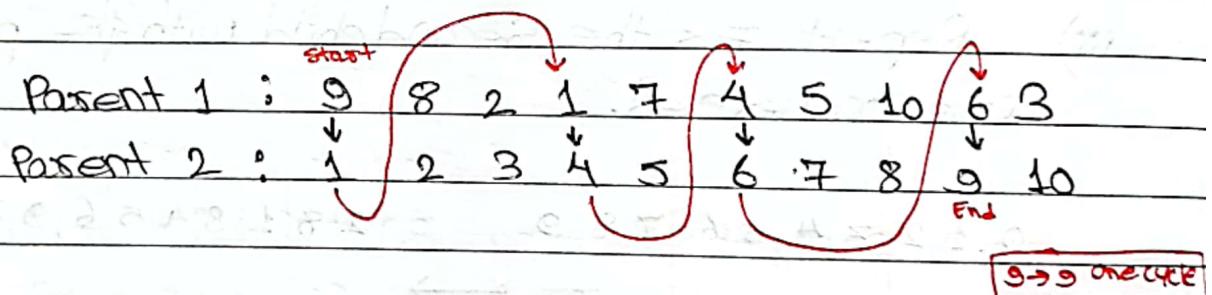
0   1   2   3   4   5   6   7   8   9	2   8   1   3   4   5   6   9   7   0
0   7   0   2   8   1   4   3   5   6	3   5   6   2   8   1   4   7   9   0

## ii) CX (cyclic crossovers):

Cyclic crossover is also a type of Permutation based crossovers. It is specifically applied to problems that involve permutations, such as Travelling Salesman problem (TSP) or job scheduling.

### \* How it works:

- i) The cyclic crossover starts by identifying cycles within the parent solutions. A cycle is a sequence of elements that cycle through the permutations of the two parents.
- ii) The child or offspring are created by swapping the elements between the two parents within the identified cycles.



Child 1 : 9 2 3 1 5 4 7 8 6 10

Child 2 : 1 8 2 4 7 6 5 10 9 3

### iii) PMX (Partially Matched Crossover):

Partially matched crossover is also one of the type of permutation based crossovers.

Eg:-

Parent 1 : 9 8 4 5 6 7 1 3 2 10

Parent 2 : 8 7 1 2 3 10 9 5 4 6

child 1 : 9 8 4 2 3 10 1 6 5 7

child 2 : 8 10 1 5 6 7 9 2 4 3

② Another eg - when the segment is large:

Parent 1 : 9 8 4 5 6 7 1 3 2 10

Parent 2 : 8 7 1 2 3 10 9 5 4 6

child 1 : 1 8 6 2 3 10 9 5 4 7

child 2 : 8 10 9 5 6 7 1 3 2 4

③ Parent 1 : A B | C D E F G

Parent 2 : F D | F G B A C

child 1 : C F E G B A D

child 2 : B G C D E F A

other crossover also exists like shuffle crossover, ring crossovers etc.

### \* Mutation:

In simple terms, mutations may be defined as a small random twist in the chromosome, to get a new solution. It is used to maintain and introduce diversity in the genetic population & is usually applied with a low probability. If the mutation probability is very high, the GA gets reduced to a random search.

Mutation is also the part of the GA which is related to the "exploration" of the search space. It has been observed that mutation is essential to the convergence of the GA while crossover is not.

### \* Mutation Operators:

We will discuss some of the most commonly used mutation operators. Like the crossover operators, this is not an exhaustive list & the GA designer might find a combination of these approaches or a problem-specific mutation operator more useful.

### i) Bit-Flip Mutation:

In this bit flip mutation, we select one or more random bits & flip them. This is used for binary encoded GAs.

$\begin{array}{ccccccccc} 0 & 0 & 1 & \textcolor{red}{1} & 0 & 1 & 0 & 0 & 1 & 0 \end{array} \rightarrow \begin{array}{ccccccccc} 0 & 0 & 1 & \textcolor{red}{0} & 0 & 1 & 0 & 0 & 1 & 0 \end{array}$

### ii) Random Resetting:

Random Resetting is an extension of the bit flip for the integer representation. In this, a random value from the set of allowed values is assigned to a randomly chosen gene.

i.e.  $1 \rightarrow 0$       { Reset to 0 where  
 $0 \rightarrow 0$       }  $0 \in$  allowed values set  
 $8 \rightarrow 0$

### iii) Swap Mutation:

In Swap mutation, we select two position on the chromosome at random, and interchange their values. This is commonly used in Permutation based encodings.

$\begin{array}{ccccccccc} 1 & 2 & 3 & 4 & 5 & \textcolor{red}{6} & 7 & 8 & 9 & 0 \end{array} \rightarrow \begin{array}{ccccccccc} 1 & 6 & 3 & 4 & 5 & \textcolor{red}{2} & 7 & 8 & 9 & 0 \end{array}$

#### iv) Scramble Mutation:

Scramble mutation is popular with Permutation representations. In this, a subset of gene is chosen from the entire chromosome and their value are Scrambled or shuffled randomly.

0	1	2	3	4	5	6	7	8	9
0	1	3	6	4	2	5	7	8	9

#### v) Inversion Mutation:

In inversion mutation, we select a subset of genes like in Scramble mutation, but instead of shuffling the subset, we merely invert the entire string in the subset.

0	1	2	3	4	5	6	7	8	9
0	1	6	5	4	3	2	7	8	9

#### \* Wild Mutation:

- Introduces Diversity in Selection Set,
- Helps to Stop Premature Convergence.
- Helps to move the Solution from the domain of Local maxima to Global maxima.

## \* Survivor Selection:

The Survivor selection Policy determines which individuals are to be kicked out and which are to be kept in the next generation. It is crucial in GFA as it should ensure that the fitter individuals are not kicked out of the population, while at the same time diversity should be maintained in the population.

Some GFAs employs **Elitism**. In simple terms, it means that the current fittest member of the population is always propagated to the next generation i.e., under any circumstances the fittest member of the current population can't be replaced.

The easiest approach for Survivor selection is to kick out random members out of the population, but such an approach frequently has convergence issues.

Some of the widely used strategies of Survivor selection are as follow:

### i) Age-Based Selection:

In Age-Based Selection, we don't have any idea of a fitness. It is based on the premise that each individual is allowed in the population for a finite generation where it is allowed to reproduce, after that, it is kicked out of the population no matter how good its fitness is.

Example:

For instance, in the following example, the age is the number of generations for which the individual has been in the population. The oldest members of the population i.e.  $P_4$  &  $P_7$  are kicked out of the population and the ages of the rest of the individuals are incremented by +1.

Age      Fitness value      chromosome

6      1       $P_1$

8      5       $P_2$

5      9       $P_3$

10      8       $P_4$

2      7       $P_5$

3      4       $P_6$

9      2       $P_7$

2      2       $P_8$

5      1       $P_9$

4      0       $P_{10}$

Fitness value      chromosome

8       $C_1$

+       $P_5$

9       $C_2$

OFFSPRINGS

Existing Population

Date: .....

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Age	Fitness value	chromosome	
7	1	P <sub>1</sub>	
9	5	P <sub>2</sub>	
6	9	P <sub>3</sub>	
* 0	8	C <sub>1</sub>	
3	7	P <sub>5</sub>	
4	4	P <sub>6</sub>	
* 0	9	C <sub>2</sub>	
3	2	P <sub>8</sub>	
6	1	P <sub>9</sub>	
5	0	P <sub>10</sub>	

New population.

## ii) Fitness Based Selection:

In this fitness based selection, the children or the offsprings tend to replace the least fit individuals in the population. The selection of the least fit individuals may be done using a variation of any of the selection policies described before - Tournament Selection, fitness proportionate selection, etc.

\* For example :

In the following figure, the children replaces the least fit individuals P<sub>1</sub> & P<sub>10</sub> of the population. It is also to be noted that since

$P_1$  &  $P_9$  have same fitness value, the decision to remove which individuals from the population is arbitrary.

Fitness chromosome  
value

1	$P_1$
---	-------

5	$P_2$
---	-------

0	$P_3$
---	-------

8	$P_4$
---	-------

7	$P_5$
---	-------

4	$P_6$
---	-------

2	$P_7$
---	-------

2	$P_8$
---	-------

1	$P_9$
---	-------

0	$P_{10}$
---	----------

Fitness  
value.

8	$C_1$
---	-------

9	$C_2$
---	-------

OFFSPRINGS

Fitness chromosome  
value

8	$C_1$
---	-------

5	$P_2$
---	-------

9	$P_3$
---	-------

8	$P_4$
---	-------

7	$P_5$
---	-------

4	$P_6$
---	-------

2	$P_7$
---	-------

2	$P_8$
---	-------

1	$P_9$
---	-------

9	$C_2$
---	-------

Existing population      New population

From above 25% mating will start with  $P_1$

25% each will mate with  $P_2$  to get offsprings

25% each will mate with  $P_3$  to get offsprings

25% each will mate with  $P_4$  to get offsprings

25% each will mate with  $P_5$  to get offsprings

25% each will mate with  $P_6$  to get offsprings

25% each will mate with  $P_7$  to get offsprings

25% each will mate with  $P_8$  to get offsprings

25% each will mate with  $P_9$  to get offsprings

## \* Termination Condition:

The termination condition of a Genetic Algorithm is important in determining when a GA run will end. It has been observed that initially, the GA progresses very fast with better solutions coming in every few iterations, but this tends to slowdown in the later stages where the improvements are very small.

We usually want a termination condition such that our solution is close to the optimal at the end of the run.

Usually, we keep one of the following termination conditions:

- i) When there has been no improvement in the population for  $X^{\text{th}}$  iterations.
- ii) When we reach an absolute number of generations.
- iii) When the objective function value has reached a certain pre-defined value.

For example, in a genetic algorithm we keep a counter which keeps track of the generation for which there has been no improvement in the population. Initially, we set this counter to zero. Each time when we don't generate offsprings which are better than the individuals in the populations, we increment the counter.

However, if the fitness of any of the off-springs is better, then we reset the counter to zero, and the algorithm terminates when the counter reaches a predetermined value.

Like other parameters of a GA, the termination condition is also highly problem specific and the GA designer should try out various options to see what suits his particular problem the best.

To have a better understanding of the working of a GA, let us consider the following steps:

- Initial population: The first step in any optimization problem is to generate an initial population of chromosomes. This population consists of several individuals, each represented by a string of binary digits. The length of this string depends on the number of variables in the problem. For example, if there are two variables, then each individual will consist of two binary digits.
- Selection: In this step, the fittest individuals from the population are selected based on their fitness values. The fitness value of an individual is determined by its performance in the optimization process. It is usually calculated by summing up the squared differences between the actual output and the desired output.
- Crossover: In this step, two individuals are selected from the population and their genetic material is exchanged to produce new individuals. This process is called crossover. Crossover can be done in various ways, such as single-point crossover, multi-point crossover, etc.
- Mutation: In this step, some individuals in the population undergo random changes in their genetic material. These changes are usually small and random, but they help in exploring the search space and avoiding local optima.
- Replacement: The new individuals produced in the previous step are added to the population, and the least fit individuals are removed. This process is called replacement or elitism. The population size remains constant throughout the process.

## \* Mathematical Foundation of Genetic algorithm & building block hypothesis:

We will discuss about Schema, NFL theorem with building block hypothesis.

### \* Schema Theorem:

- The Schema is a "similarity template".
- Formally, it is a string over the alphabet = {0, 1, \*} where, \* is don't care & can take any values.

For ex:-

\* 10 \* 1 could mean i.e. possible  $2^2 = 4$  chromosomes

① 01001

② 01011

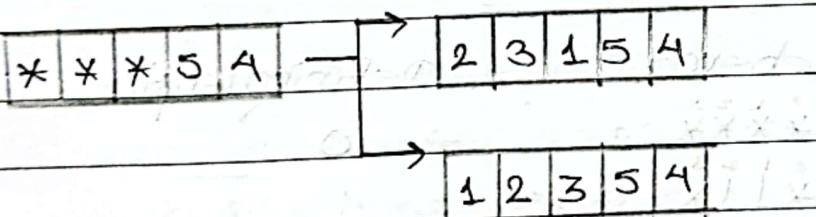
③ 11001

(A) 11011

→ The schema is represented by H

$$H = * 11 * 0 *$$

→ In case of Permutation i.e.,



i.e.,  $3 \times 2 \times 1 = 6$  possibilities of chromosome

→ It should represent the solution which belongs to the solution set.

### \* Order of Schema:

- Order of Schema is the number of specified fixed position in a gene; Schema.
- It is denoted by  $o(H)$ .

i.e.

Schema	order
***	0
101	3
*11	2
1**	1

### \* Defining length:

- Defining length is the distance between the first and last specific string position.
- It can also defined as the distance between the two furthest fixed symbols in the genes or Schema.

Schema	Defining length
• 1 2 3 *** 0	0
• 1 2 3 *11*	(2-1)=1
• 1 2 3 1 * 0 *	(2-0)=2
• 1 2 3 1 1 1	(3-0)=3

- It is denoted by  $\delta(H)$ .

\* How many schemes are possible:

$$\text{no. of schemes} = (n(A) + 1)^L - 1$$

where,

$L$  = length

$A = \{0, 1\}$ , set of values of gene

$$\text{for, binary encoding } = 3^L - 1$$

\* Building Block Hypothesis:

→ Building Block are short defining length & low order schemata with the fitness value above the average fitness has high chances of surviving in the offspring.

→ The building block hypothesis say that such schemes serves as foundation for i) G/A Succession & ii) Adaptation in G/A.

\* Let see an example:

$$\text{Schema 1} = 1 * * * 0 * 1 = H_1 \quad O(H_1) = 3, S(H_1) = 6$$

$$\text{Schema 2} = * * 1 0 * * * = H_2 \quad O(H_2) = 2, S(H_2) = 1$$

① From  $H_1 (1 * * * 0 * 1)$

$$P_1 = 1 0 0 1 0 1 1 \quad C_1 = \begin{matrix} * \\ 1 0 0 1 0 0 1 \end{matrix} \quad ? H_1 \text{ survive}$$

$$P_2 = 1 1 0 1 0 0 1 \quad C_2 = \begin{matrix} * \\ 1 1 0 1 0 1 1 \end{matrix} \quad *$$

② From  $H_1 (1***0*1)$  generate  $P_1$

From  $H_2 (* * 10 * **)$  generate  $P_2$

i.e.,

$$P_1 = 1001011 \quad C_1 = 1001100 \quad \text{only } H_2 \text{ survives}$$

$$P_2 = 0110100 \quad C_2 = 0110011 \quad \text{**}$$

J.U.I

\* Mathematical building block of Schema & mathematical Process of Probability of Survival of Schema.

= Effect of reproduction on Schema:

$m(H, t) \rightarrow$  no. of schema  $H$  in population  $A(t)$ ,  
are  $m$  in generation  $t$ .

Also,  $m(H, t+1) \rightarrow$  what would be the no. of schema  
 $H$  in next generation in population  
 $A(t)$

$$\text{i.e., } m(H, t+1) = m(H, t) \times \frac{f(H)}{\bar{f}}$$

where,

$f(H) =$  Fitness of Particular Schema

$$\bar{f} = \frac{\sum f}{n} \text{ (average fitness.)}$$

$$m(H, t+1) = m(H, t) \times \frac{f(H)}{\sum f}$$

$$= m(H, t) \times n \times \frac{f(H)}{\sum f}$$

now, probability of destroying of that schema in crossover is

$$P_c = \frac{s(H)}{L-1} \quad \text{i.e., long defining length has high probability of being destroyed.}$$

so, Probability of survival of that schema is.

$$1 - P_c \cdot \frac{s(H)}{L-1}$$

next, Probability of destroying of that schema in mutation is.

$$p = p_m \cdot o(H) \quad p_m \rightarrow \text{Probability of mutation.}$$

so,

Probability of surviving schema on mutation.

$$= 1 - p_m \cdot o(H)$$

now,

overall survival of schemata over crossover & mutation is

$$m(H, t+1) \geq m(H, t) * n * \frac{f(H)}{\sum f_i} \left[ 1 - P_c \frac{s(H)}{L-1} - p_m s(H) \right]$$

### \* Schema Processing at work : An Example by Hand Revisited.

\* problem : Find the optimal (best) value of  $x$  where,  $f(x) = x^2$  &  $x \in [0, 31]$

① Population size = 4

② Encoding = Binary encoding (use 5 bits since highest number is 31 in population to represent chromosomes)

③ Fitness ( $x$ ) =  $f(x) = x^2$

= Initially, we take: 13  $\rightarrow$  01101

24  $\rightarrow$  11000

8  $\rightarrow$  01000

19  $\rightarrow$  10011

String Processing

String No.	$x$ -value	Initial population (encoding)	Fitness	Probability	Expected Count
1	13	01101	163	14.1%	0.58
2	24	11.000	576	49.1%	1.96
3	8	01000	64	6.1%	0.22
4	19	10.011	361	31.1%	1.23
Sum			1170	100.1%	4
Average			293	25.1%	1
Max			576	49.1%	1.97

(based on experiment)

Actual Count

Crossover

New population value  $f(x) = ?$ 

1 2	4	01100	12	144
2 1,3	4	11001	25	625
0	2,4	11011	27	729
1	4	10600	16	256
Score	4			1754
Average	1			439
Max	2			729

Schema Processing

# Before Reproduction:

(From initial population)

Schema

String representation

Schema Average Fitness ( $f(x)$ ) $H_1: 1 * * * *$ 

2,4

 $(576 + 361)/2 = 469$  $H_2: * 10 **$ 

2,3

 $(576 + 64)/2 = 320$  $H_3: 1 * * * 0$ 

2

576

 $\rightarrow (1,11) \text{ or}$

### X After Reproduction:

Expected Count	Actual Count	String representation (New Population)
$(1.96 + 1.23) = 3.20$	3	2, 3, 4
$(1.96 + 0.22) = 2.18$	2	2, 3
1.96	2	4

### \* Actual Count:

- i) can be done by Round-off operation of Expected count
- ii) or using Formula:

i.e.

$$m(H, t+1) = m(H, t) \cdot \frac{f(H)}{F}$$

So,  $m(H, t+1) = m(H, t) \cdot \frac{f(H)}{F}$

- ① For, Schema 1 ( $H_1$ ) =  $1 * * * *$ :

$$O(H_1) = 1 \quad F(H_1) = 0, \text{ String representation: } m(H_1, t) = 2$$

So,

$$\begin{aligned} m(H, t+1) &= \left[ m(H, t) \cdot \frac{f(H)}{F} \right] \cdot \frac{m(H, t) \cdot f(H)}{F} \\ &= m(H, t) \times n \times \frac{f(H)}{F} \end{aligned}$$

$$= \frac{2 \times 469}{293}$$

$$= 3.20$$

- ②  $H_2 = *10**$

$$O(H_2) = 2, F(H_2) = 1, \text{ String representation } = 2, 3$$

$$m(H, t) = 2$$

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So,

$$m(H, t+1) = m(H, t) \cdot \frac{F(H)}{F}$$

$$= 2 \times \frac{320}{293}$$

$$= 2.18$$

$$\Leftrightarrow H_3 = 1 * 2 * 0$$

$$O(H_3) = 2, S(H_3) = 4 \text{ & string representation} = 2 \\ \text{obviously } m(H, t) = 1$$

So,

$$m(H, t+1) = m(H, t) \cdot \frac{F(H)}{F}$$

$$= 1 \times \frac{576}{293}$$

$$= 1.96$$

\* Imp Questions?

i) How many Schemata exists in a binary string of length 10:

$$= \underline{\text{Sol}}$$

$$\text{length} = 10$$

we have two ways to find the no. of Schemata:

i) For binary String:

$$3^L - 1$$

$$= 3^{10} - 1$$

$$= 59048 \text{ schemata}$$

ii) For any string:

$$= (n(A)+1)^L - 1$$

$$= (2+1)^{10} - 1 \quad (\because n(A) = \{0, 1\}, \text{ for binary})$$

$$= 3^{10} - 1$$

$$= 59048 \text{ schemata.}$$

iii) How many Schemata exists in a binary string of order (i.e. 3 positions in chromosome are fixed) & length 10?

$$= \underline{\text{Sol.}}$$

$$\text{length} = 10$$

$$\text{order} = 3$$

We use combination which is:

$${}^n C_r = {}^{10} C_3$$

$$= \frac{10!}{(10-3)! 3!}$$

$$= .8 \times 5 \times 10 \\ 8 \times 2$$

= 120 Schemata.

ii) How many Schemata exists with population size of 50 & length of schema is 10? (MIN & MAX)

= Sol

length = 10

Population size = 50

So,

The MINIMUM number of schema is 5

= 10 (as there are 10 possible ways where any one position among 10<sup>th</sup> possible places can be fixed).

chromosome 1	1	*	*	*	*	*	*	*	*	*
chromosome 2	*	1	*	*	*	*	*	*	*	*
chromosome 3	*	*	1	*	*	*	*	*	*	*
chromosome 4	*	*	*	1	*	*	*	*	*	*
chromosome 5	*	*	*	*	1	*	*	*	*	*
chromosome 6	*	*	*	*	*	1	*	*	*	*
chromosome 7	*	*	*	*	*	*	1	*	*	*
chromosome 8	*	*	*	*	*	*	*	1	*	*
chromosome 9	*	*	*	*	*	*	*	*	1	*
chromosome 10	*	*	*	*	*	*	*	*	*	1

The Maximum possibilities is :

$$= 2^{10} \text{ (In case of binary Encoding)}$$

So, number of possibilities =  $n^{10}$  (In case of n-values)

Ans

Ques 2. State the 2x2x2x2x2x2x2x2x2x2 possibilities.

Ans 2. The above 2x2x2x2x2x2x2x2x2x2 possibilities are

1. 0000000000

2. 0000000001

3. 0000000010

4. 0000000011

5. 0000000100

6. 0000000101

7. 0000000110

8. 0000000111

9. 0000001000

10. 0000001001

11. 0000001010

12. 0000001011

13. 0000001100

14. 0000001101

15. 0000001110

16. 0000001111

17. 0000010000

18. 0000010001

19. 0000010010

20. 0000010011

21. 0000010100

22. 0000010101

23. 0000010110

24. 0000010111

25. 0000011000

26. 0000011001

27. 0000011010

28. 0000011011

29. 0000011100

30. 0000011101

31. 0000011110

32. 0000011111

33. 0000100000

34. 0000100001

35. 0000100010

36. 0000100011

37. 0000100100

38. 0000100101

39. 0000100110

40. 0000100111

41. 0000101000

42. 0000101001

43. 0000101010

44. 0000101011

45. 0000101100

46. 0000101101

47. 0000101110

48. 0000101111

49. 0000110000

50. 0000110001

51. 0000110010

52. 0000110011

53. 0000110100

54. 0000110101

55. 0000110110

56. 0000110111

57. 0000111000

58. 0000111001

59. 0000111010

60. 0000111011

61. 0000111100

62. 0000111101

63. 0000111110

64. 0000111111

65. 0001000000

66. 0001000001

67. 0001000010

68. 0001000011

69. 0001000100

70. 0001000101

71. 0001000110

72. 0001000111

73. 0001001000

74. 0001001001

75. 0001001010

76. 0001001011

77. 0001001100

78. 0001001101

79. 0001001110

80. 0001001111

81. 0001010000

82. 0001010001

83. 0001010010

84. 0001010011

85. 0001010100

86. 0001010101

87. 0001010110

88. 0001010111

89. 0001011000

90. 0001011001

91. 0001011010

92. 0001011011

93. 0001011100

94. 0001011101

95. 0001011110

96. 0001011111

97. 0001100000

98. 0001100001

99. 0001100010

100. 0001100011

101. 0001100100

102. 0001100101

103. 0001100110

104. 0001100111

105. 0001101000

106. 0001101001

107. 0001101010

108. 0001101011

109. 0001101100

110. 0001101101

111. 0001101110

112. 0001101111

113. 0001110000

114. 0001110001

115. 0001110010

116. 0001110011

117. 0001110100

118. 0001110101

119. 0001110110

120. 0001110111

121. 0001111000

122. 0001111001

123. 0001111010

124. 0001111011

125. 0001111100

126. 0001111101

127. 0001111110

128. 0001111111

129. 0010000000

130. 0010000001

131. 0010000010

132. 0010000011

133. 0010000100

134. 0010000101

135. 0010000110

136. 0010000111

137. 0010001000

138. 0010001001

139. 0010001010

140. 0010001011

141. 0010001100

142. 0010001101

143. 0010001110

144. 0010001111

145. 0010010000

146. 0010010001

147. 0010010010

148. 0010010011

149. 0010010100

150. 0010010101

151. 0010010110

152. 0010010111

153. 0010011000

154. 0010011001

155. 0010011010

156. 0010011011

157. 0010011100

158. 0010011101

159. 0010011110

160. 0010011111

161. 0010100000

162. 0010100001

163. 0010100010

164. 0010100011

165. 0010100100

166. 0010100101

167. 0010100110

168. 0010100111

169. 0010101000

170. 0010101001

171. 0010101010

172. 0010101011

173. 0010101100

174. 0010101101

175. 0010101110

176. 0010101111

177. 0010110000

178. 0010110001

179. 0010110010

180. 0010110011

181. 0010110100

182. 0010110101

183. 0010110110

184. 0010110111

185. 0010111000

186. 0010111001

187. 0010111010

188. 0010111011

189. 0010111100

190. 0010111101

191. 0010111110

192. 0010111111

193. 0011000000

194. 0011000001

195. 0011000010

196. 0011000011

197. 0011000100

198. 0011000101

199. 0011000110

200. 0011000111

201. 0011001000

202. 0011001001

203. 0011001010

204. 0011001011

205. 0011001100

206. 0011001101

207. 0011001110

208. 0011001111

209. 0011010000

210. 0011010001

211. 0011010010

212. 0011010011

213. 0011010100

214. 0011010101

215. 0011010110

216. 0011010111

217. 0011011000

218. 0011011001

219. 0011011010

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