Module VI

Introduction to genetic algorithm, operators in genetic algorithm - coding - selection - cross over – mutation, Stopping condition for genetic algorithm flow,Genetic neuro hybrid systems, Genetic-Fuzzy rule based system.

Genetic Algorithmsare adaptive heuristic search algorithms based on the evolutionary ideas of natural selection and generics.
As such they represent an intelligent exploitation of a random search used to solve
Ahhough randomized, GAs are by no means random; instead iliey exploit historical information to direct
the search imo the region of better performance within the search space. The basic techniques of the GAs
are designed to simulate processes in natural systems necessary for evolution, especially those that follow the
principles first laid down by Charles Darwin, "survival of the fittest," because in narure, competition among
individuals for seamy resources results in the fittest individuals dominating over the weaker ones.

OPERATORS IN GENETIC ALGORITHM

1) Encoding

Encoding is a process of representing individual genes. The process can be performed using bits, numbers,trees, arrays, lists or any other objects. The encoding depends mainly on solving the problem. For example, one can encode directly real or integer numbers.

Binary Encoding

The most common way of encoding is a binary string, which would be represented *as* in Figure below.

Chromosome 1	1 1 0 1 0 0 0 1 1 0 1 0
Chromosome 2	0 1 1 1 1 1 1 1 1 1 0 0

Each chromosome encodes a binary (bit) string. Each bit in the string can represent some characteristics ofthe solution. Every bit string therefore is a solution but not necessarily the best solution.

Another possibility isthat the whole string can represent a number. The way bit strings can code differs from problem to problem.

Binary encoding gives many possible chromosomes with a smaller number of alleles. On the other hand, this encoding is not natural for many problems and sometimes corrections must be made after generic operationis completed. Binary coded strings with 1s and 0s are mostly used. The length of the string depends on theaccuracy. In such coding

1. Integers are represented exactly.
2. Finite number of real numbers can be represented.
3. Number of real numbers represented increases with string length.

Octal Encoding

This encoding uses string made up of octal numbers (0-7)

Chromosome 1	03467216
Chromosome 2	15723314

Hexadecimal Encoding

This encoding uses string made up of hexadecimal numbers (0-9, A-F).

Chromosome 1	9CE7
Chromosome 2	3DBA

Permutation Encoding (Real Number Coding)

Every chromosome is a string of numbers, represented in a sequence. Sometimes corrections have to be doneafter generic operation is complete. In permutation encoding, every chromosome is a suing of integer/realvalues, which represents number in a sequence.

Permutation encoding is only useful for ordering problems. Even for this problem,sometypes of crossover and mutation corrections must be made to leave the chromosome consistent (i.e., have realsequence in it).

Chromosome A	1 5 3 2 6 4 7 9 8
Chromosome B	8 5 6 7 2 3 1 4 9

Value Encoding

Every chromosome is a string of values and the values can be anything connected to the problem. This encoding produces best results for some special problems. On the other hand, it is often necessary to developnew genetic operator's

specific to the problem. Direct value encoding can be used in problems, where somecomplicated values, such as real numbers, are used. Use of binary encoding for this type of problems wouldbe very difficult.

In value encoding, every chromosome is a string of some values. Values can be anythingconnected to problem, form numbers, real numbers or characters to some complicated objects. Value encoding is very good for some special problems. On the other hand, for this encoding it is often necessary to developsome new crossover and mutation specific for the problem.

Chromosome A	1.2324 5.3243 0.4556 2.3293 2.4545
Chromosome B	ABDJEIFJDHDIERJFDLDFLFEGT
Chromosome C	(back), (back), (right), (forward), (left)

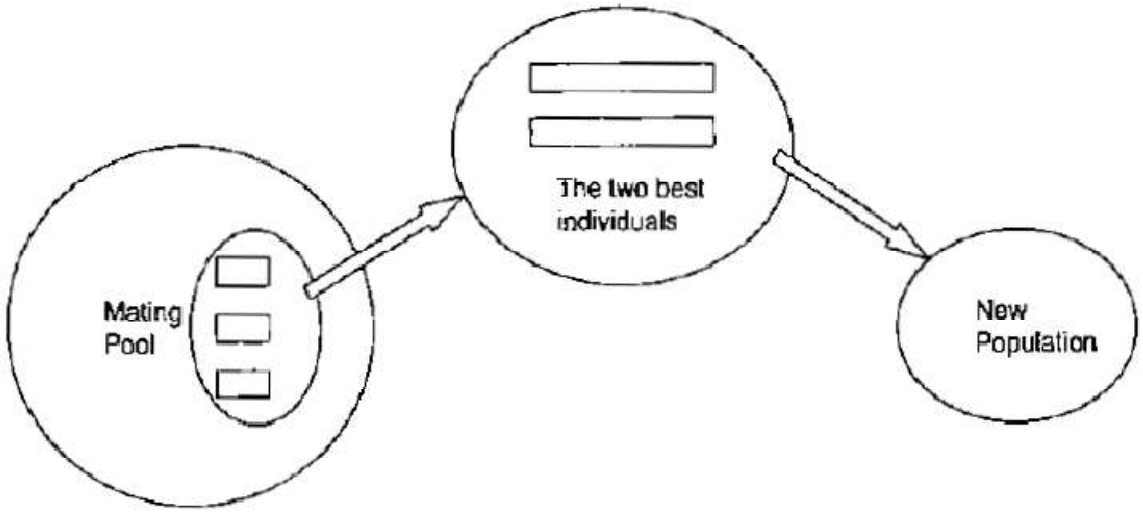
Tree Encoding

This encoding is mainly used for evolving program expressions for genetic programming. Every chromosomeis a tree of some objects such as functions and commands of a programming language.

Selection

Selection is the process of choosing two parents from the population for crossing. After deciding on anencoding, the next step is to decide how to perform selection, i.e., how *to* choose individuals in the populationthat will create offspring for the next generation_ and how many offspring each will create. The purpose of selection is to emphasize fitter individuals in the-population in hopes that their offspring have higher fitness.

Chromosomes are selected from the initial population to be parents for reproduction. The problem is how toselect these chromosomes. According to Darwin's theory of evolution the best ones survive to create newoffspring. Figure below shows the basic selection process.



Selection is a method that randomly picks chromosomes out of the population according *to* their evaluationfunction. The higher the fitness function the better chance that an individual will be selected. The selectionpressure is defined as the degree to which the better individuals are favored. The higher theselection pressured,the more the better individuals are favored. This selection pressure drives the GA to improve the population
fitness over successive generations.

The convergence rate ofGA is largely determined by the magnitude of the selection pressure, with higherselection pressures resulting in higher convergence rates. *GAs* should be able to identify optimal or nearlyoptimal solutions under a wide range of selection scheme pressure. However, if the selection pressure is too low the convergence rate will be slow, and the GA will take unnecessarily longer to find the optimal solution.

If the selection pressure is too high, there is an increased change of the GA prematurely converging to anincorrect (sub-optimal) solution. In addition to providing selection pressure, selection schemes should alsopreserve population diversity, as this helps to avoid premature convergence.

Typically we can distinguish two types of selection scheme:

- proportionate-based selection and
- ordinalbasedselection.

Proportionate-based selection picks out individuals based upon their fitness values relative to the fitness of the other individuals in the population. Ordinal-based selection schemes select individuals norupon their raw fitness, bur upon their rank within the population. This requires that the selection pressureis independent

of the fitness distribution of the population, and is solely based upon the relative ordering(ranking) of the population.

Roulette Wheel Selection

Roulette selection is one of the traditional GAselection techniques. The commonly used reproduction operatoris the proportionate reproductive operator where a string is selected from the mating Pool with a probabilityproportional to the fitness. The principle of Roulette selection is a linear search through a Roulette wheel withthe slots in the wheel weighted in proportion to the individual's fitness values.

A target value is set, which isa random proportion of the sum of the fit nesses inthe population. The population is stepped through untilthe target value is reached. This is only a moderately strong selection technique, since for individuals are not guaranteed to be selected for, bur somewhat have a greater chance. A fit individual will contribute more to the target value, but if it does not exceed it, the next chromosome in line has a chance, and it may be weak.

It is essential that the population not be sorted by fitness, since this would dramatically bias the selection.The Roulette process can also be explained as follows: The expected value of an individual is individual'sfitness divided by the actual fitness of the population. Each individual is assigned a slice of the Roulette wheel,the size of the slice being proportional to the individual's fitness. The wheel is spun *N* times, where *N* is thenumber of individuals in the population. On each spin, the individual under the wheel's marker is selected to be in the pool of parents for the next generation. This method is implemented as follows:

1. Sum the total expected value of the individuals in the population. Let it beT.
2. Repeat *N* times:

i. Choose a random integer *"r"* between 0 and *T.*

ii. Loop through the individuals in the population, summing the expected values, until the sum is greater than or equal to *"r."* The individual whose expected value puts the sum over this limit is the oneselected.

Roulette wheel selection is easier to implement bur is noisy. The rate of evolution depends on the varianceof fitness's in the population.

Random Selection

This technique randomly selects a parent from the population. In terms of disruption of generic codes, random selection is a little more disruptive, on average, than Roulette wheel selection.

Rank Selection

The Roulette wheel will have a problem when the fitness values differ very much. If the best chromosomefitness is 90%, its circumference occupies 90% of Roulette wheel, and then other chromosomes have too fewchances to be selected. Rank Selection ranks the population and every chromosome receives fitness from theranking. The worst has fitness 1 and the best has fitness *N*. It results in slow convergence but prevents tooquick convergence. It also keeps up selection pressure when the fitness variance is low. It preserves diversityand hence leads to a successful search. In effect, potential parents are selected and a tournament is heldto decide which of the individuals will be the parent.

There are many ways this can be achieved and twosuggestions are:

1. Select a pair of individuals at random. Generate a random number *R* between 0 and 1. If *R* <ruse thefirst individual *as* a parent. If the *R* ≥ *r*then use the second individual as the parent. This is repeated toselect the second parent. The value of *r* is a parameter to this method.

2. Select two individuals at random. The individual with the highest evaluation becomes the parent. Repeatto find a second parent.

Tournament Selection

An ideal selection strategy should be such that it is able to adjust its selective pressure and population diversity so as to fine-tune GA search performance. Unlike, the Roulette wheel selection, the tournament selectionstrategy provides selective pressure by holding a tournament competition among **Nu**individuals.

The best individual from the tournament is the one with the highest fitness, who is the winner of *Nu.*Tournament competitions and the winner are then inserted into the mating pool. The tournament competitionis repeated until the mating pool for generating new offspring is filled. The mating pool comprising thetournament winner has higher average population fitness. The fitness difference provides the selection pressure,which drives GA to improve the fitness of the succeeding genes. This method is more efficient and leads toan optimal solution.

Boltzmann Selection

In Boltzmann selection, a continuously varying temperature controls the rate of selection according to a preset schedule. The temperature starts out high, which means that the selection pressure is low. Thetemperature is gradually lowered, which gradually increases the selection pressure, thereby allowing the GAto narrow in more closely to the best part of *the* search space while maintaining the appropriate degree ofdiversity.

A logarithmically decreasing temperature is found useful for convergence without getting stuck co a localminima state. However, it takes rime to cool down the system to the equilibrium state.

Let f_{max} be the fitness of the currently available best string. If the next string has fitness $f(X_i)$ such that $f(X_i) > f_{max}$ then the new string is selected. Otherwise it is selected with Boltzmann probability

$$P = \exp[-\{f_{max} - f(X_i)\}/T]$$

Where, $T = T_0(1-\alpha)^k$ and $k = (1 + 100 * g/G)$; g is the current generation number; G the maximum valueof g. The value of α can be chosen from the range [0, 1] and that of T_0 from the range [5, 100]. The final state is reached when computation approaches zero value *of* T_1, i.e., the global solution is achieved at this point.

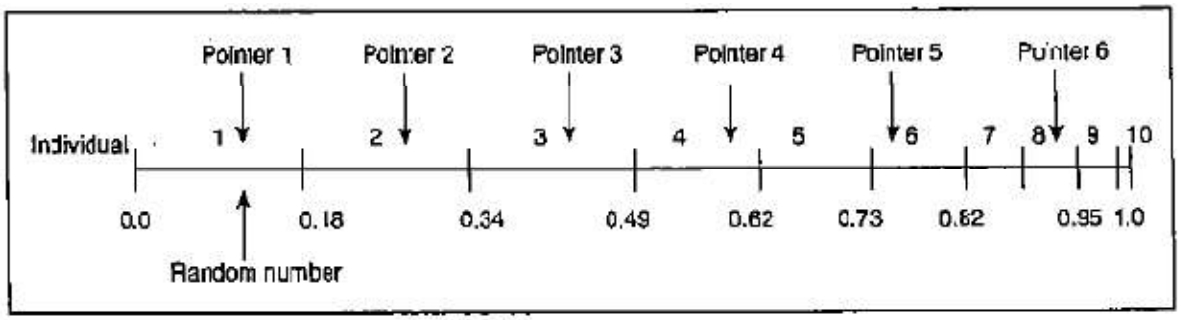
Elitism

The first best chromosome or the few best chromosomes are copied to the new population. The rest is donein a classical way. Such individuals can be lost if they are not selected to reproduce or if crossover or mutationdestroys them. This significantly improves-the GA's performance.

Stochastic Universal Sampling

Stochastic universal sampling provides zero bias and minimum spread. The individuals are mapped to contiguous segments of a line, such that each individual's segment is equal in size to its fitness exactly as in Roulette wheel selection. Here equally spaced pointers are placed over the line, as many as there are individuals to be selected. Consider NPointerthe number of individuals to be selected, then the distance betweenthe pointers are *1/NPointer*and the position of the first pointer is given by a randomly generated number inthe range

[0,1/*NPointer]*. For 6 individuals to be selected, the distance between the pointers is 1/6 = 0.167.Figure below shows the selection for the above example.



Sample of 1 random number in the range [0, 0.167]: 0.1.
After selection the mating population consists of the individuals,

1,2,3,4,6,8

Crossover (Recombination)

Crossover is the process of taking two parent solutions and producing from them a child. After the selection(reproduction) process, the population is enriched with better individuals. Reproduction makes clones ofgood strings but does not create new ones.

Crossover operator is applied to the mating pool with the hopethat it creates a better offspring.

Crossover is a recombination operator that proceeds in three steps:

1. The reproduction operator selects at random a pair of two individual strings for the mating.
2. A cross site is selected at random along the string length.
3. Finally, the position values are swapped between the two strings following the cross site.

That is the simplest way how to do that is to choose randomly some crossover point and copy everything before this point from the first parent and then copy everything after the crossover point from the otherparent.

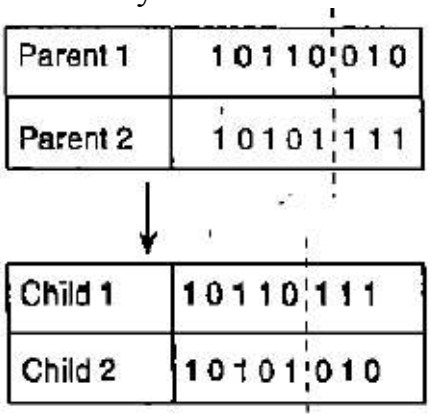
The various crossover techniques are in the following:

Single-Point Crossover

The traditional genetic algorithm uses single-point crossover, where the two mating chromosomes are occuronce at corresponding points and the sections after the cuts exchanged. Here, a cross site or crossover pointis selected randomly along the length of the mated strings and bits next to the cross sites are exchanged.

If appropriate site is chosen, better children can be obtained by combining good parents, else it severelyhampers string quality.

The Figure belowillustrates single point crossover and it can be observed that the bits next to the crossoverpoint are exchanged to produce children. The crossover point can be chosen randomly.

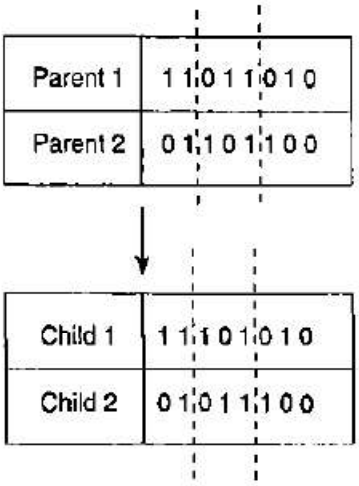


Two Point Crossover

Apart from single point crossover, many different crossover algorithms have been devised, often involvingmore than one cut point. It should be noted that adding further crossover points reduces the performance ofthe GA. The problem with adding additional crossover points is that building blocks are more likely to be disrupted. However, an advantage of having more crossover points is that the problem space may be searchedmore thoroughly.

In two-point crossover, two crossover points are chosen and the contents between these points are exchangedbetween two mated parents.

In Figure below the dotted lines indicate the crossover points. Thus the contents between these points areexchanged between the parents to produce new children for mating in the next generation.



Multipoint Crossover (N-Point Crossover)

There are two ways in this crossover. One is even number of cross sites and the other odd number of cross sites.

In the case of even number of cross sires, the cross sites are selected randomly around a circle and informationis exchanged.

In the case of odd number of cross sites, a different cross point is always assumed at the stringbeginning.

Uniform Crossover

Uniform crossover is quite different from the N-point crossover. Each gene in the offspring is created bycopying the corresponding gene from one or the other parent chosen according to a random generated binarycrossover mask of the same length as the chromosomes. Where there is a 1 in the crossover mask, the gene is copied from the first parent, and where there is a 0 in the mask the gene is copied from the second parent.

Anew crossover mask is randomly generated for each pair of parents. Offspring, therefore, contain a mixtureof genes from each parent. The number of effective crossing point is not fixed, but will average L/2 (where Lis the chromosome length).

In Figure below, new children are produced using uniform crossover approach. It can be noticed thatwhile producing child 1, when there is a I in the mask, the gene is copied from parent 1 else it is copied fromparent 2. On producing child 2, when there is a 1 in the mask, the gene is copied from parent 2, and when there is a 0 in the mask, the gene is copied from the parent 1.

Parent 1	1 0 1 1 0 0 1 1
Parent 2	0 0 0 1 1 0 1 0
Mask	1 1 0 1 0 1 1 0
Child 1	1 0 0 1 1 0 1 0
Child 2	0 0 1 1 0 0 1 1

Three-Parent Crossover

In this crossover technique, three parents are randomly chosen. Each bit of the first parent is compared withthe bit of the second parent. If both are the same,

the bit is taken for the offspring, otherwise the bit from thethird parent is taken for the offspring. This concept is illustrated in Figure below.

Parent 1	1 1 0 1 0 0 0 1
Parent 2	.0 1 1 0 1 0 0 1
Parent 3	0 1 1 0 1 1 0 0
Child	0 1 1 0 1 0 0 1

Crossover with Reduced Surrogate

The reduced surrogate operator constraints crossover to always produce new individuals wherever possible.This is implemented by restricting the location of crossover points such that crossover points only occur wheregene values differ.

Shuffle Crossover

Shuffle crossover is related to uniform crossover. A single crossover position (as in single-point crossover) is selected. But before the variables are exchanged, they are randomly shuffled in both parents. After recombination, the variables in the offspring are unshuffled. This removes positional bias as the variables are randomly reassigned each time crossover is performed.

Precedence Preservative Crossover

Precedence preservative crossover (PPX) was independently developed for vehicle routing problems. The operator passes onprecedence relations of operations given in two parental permutations to one offspring at the same race, whileno new precedence relations are introduced.

PPX is illustrated below for a problem consisting of six operationsA-F. The operator works as follows:

l. A vector oflength Sigma, sub i = 1 to mi, representing the number of operations involved in the problem,is randomly filled with elements of the set {1, 2).

2. This vector defines the order in which the operations are successively drawn from parent 1 and parent 2.

3. We can also consider the parent and offspring permutations as lists, for which the operations "append"and "delete" are defined.

4. First we start by initializing an empty offspring.

5. The leftmost operation in one of the two parents is selected in accordance with the order of parents givenin the vector.

6. After an operation is selected, it is deleted in both parents.

7 · Finally the selected operation is appended to the offspring.

8. Step 7 is repeated until both parents are empty and the offspring contains all operations involved.

PPX does not work in a uniform-crossover manner due to the "deletion-append" scheme used.Example is shown in Figure below.

Parent permutation 1	A	B	C	D	E	F
Parent permutation 2	C	A	B	F	D	E
Select parent no. (1/2)	1	2	1	1	2	2
Offspring permutation	A	C	B	D	F	E

Ordered Crossover

Ordered two-point crossover is used when the problem is order based, for example in U-shaped assemblyline balancing, etc.Given two parent chromosomes, two random crossover points are selected partitioning them into a left, middle and right portions. The ordered two-point crossover behaves in the following way:

child 1 inherits its left and right section from· parent l, and its middle section is determined by the genes inthe middle section of parent 1 in the order in which the values appear in parent 2. A similar process is appliedto determine child 2. This is shown in Figure below.

Parent 1: 4 2 | 1 3 | 6 5 Child 1: 4 2 | 3 1 | 6 5

Parent 2: 2 3 | 1 4 | 5 6 Child 2: 2 3 | 4 1 | 5 6

Partially Matched Crossover

Partially matched crossover (PMX) can be applied usefully in the TSP. Indeed, TSP chromosomes are simplysequences of integers, where each integer represents a different city and the order represents the time at which acity is visited. Under this representation, known as permutation encoding, we are only interested in labels andnot alleles.

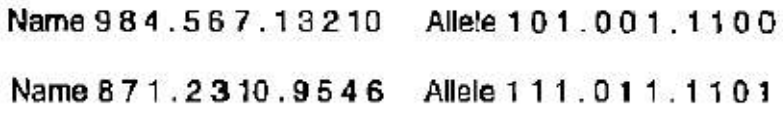
It may be viewed as a crossover of permutations that guarantees that all positions arc found exactlyonce in each offspring, i.e., both offspring receive a full complement of genes, followed by the correspondingfilling in of alleles from their parents.

PMX proceeds as follows:

I. The two chromosomes are aligned.

2. Two crossing sires are selected uniformly at random along the strings, defining a marching section.

3. The matching section is used to effect a cross through position-by-position exchange operation.
4. Alleles are moved to their new positions in the offspring.
The following illustrates how PMX works.



Consider the two strings shown in Figure above, where the dots mark the selected cross points. The marchingsection defines the position-wise exchanges that must take place in both parents to produce the offspring.

The exchanges are read from the marching section of one chromosome to that of the other. In the exampleillustrate in Figure above, the numbers that exchange places are 5 and 2, 6 and 3, and 7 and 10. The resultingoffspring are as shown in Figure below.

Crossover Probability

The basic parameter in crossover technique is the crossover probability (Pt). Crossover probability is a parameterto describe how often crossover will be performed. If there is no crossover, offspring are exact copiesof parents. If there is crossover, offspring are made from parts of both parents' chromosome. If crossover probability is 100%, then all offspring are made by crossover. If it is 0%, whole new- generation is made fromexact copies of chromosomes from old population. Crossover is made in hope that new chromosomes will contain good pam of old chromosomes andtherefore the new chromosomes will be better. However, it is good to leave some part of old population surviveto next generation.

Mutation

After crossover, the strings are subjected to mutation. Mutation prevents the algorithm to be trapped in a localminimum. Mutation plays the role of recovering the lost genetic materials as well as for randomly distributinggeneric information. It is an insurance policy against the irreversible loss of genetic material. Mutation has beentraditionally considered as a simple search operator. If crossover is

supposed to exploit the current solutionto find better ones, mutation is supposed to help for the exploration of the whole search space.

Mutation isviewed as a background operator to maintain genetic diversity in the population. It introduces new genericstructures in the population by randomly modifying some of its building blocks. Mutation helps escape fromlocal minima's trap and maintains diversity in the population.

There are many different forms of mutation for the different kinds of representation. For binary representation,a simple mutation can consist in inverting the value of each gene with a small probability.

The probability is usually taken about $1/L$, where L is the length of the chromosome. It is also possible to implement kindof hill climbing mutation operators that do mutation only if it improves the quality of the solution. Such an operator can accelerate the search; however, care should be taken, because it might also reduce the diversityin the population and make the algorithm converge toward some local optima. Mutation of a bit involves flipping a bit, changing 0 to 1 and vice-versa.

Flipping

Flipping of a bit involves changing 0 to 1 and 1 to 0 based on a mutation chromosome generated. Figure below explains mutation-flipping concept.

Parent	1 0 1 1 0 1 0 1
Mutation chromosome	1 0 0 0 1 0 0 1
Child	0 0 1 1 1 1 0 0

A parent is considered and a mutation chromosome is randomly generated.For a 1 in mutation chromosome, the corresponding bit in parent chromosome is flipped (0 to 1 and1 to 0) and child chromosome is produced. In the case illustrated in Figure 15-30, 1 occurs at 3 places ofmutation chromosome, the corresponding bits in parent chromosome are flipped and the child is generated.

Interchanging

Two random positions of the string are chosen and the bits corresponding to those positions are interchanged shown in Figure below.

Parent	1 0 1 1 0 1 0 1
Child	1 1 1 1 0 0 0 1

Reversing

A random position is chosen and the bits next tothat position are reversed and child chromosome is produced as shown Figure below.

Parent	1 0 1 1 0 1 0 1
Child	1 0 1 1 0 1 1 0

Mutation Probability

An important parameter in the mutation technique is the mutation probability(P_m). It decides how often partsof chromosome will be mutated. If there is no mutation, offspring are generated immediately after crossover(or directly copied) without any change. If mutation is performed, one or more parts of a chromosome arechanged.

If mutation probability is 100%, whole chromosome is changed; if it is 0%, nothing is changed. Mutation generally prevents the GA from falling into local extremes. Mutation should not occur very often,because then GA will in fact change to random search.

STOPPING CONDITION FOR GENETIC ALGORITHM FLOW

The various stopping condition are listed as follows:

1. Maximum generations:. The GA stops when the specified number of generations has evolved.

2. Elapsed time: The generic process will end when a specified rime has elapsed.

3. No change in fitness: The genetic process will end if there is no change to the population's best fitness fora specified number of generations.

4. **Stall generations:**The algorithm stops if there is no improvement in the objective function for a sequenceof consecutive generations of length "Stall generations."

5. Stall time limit: The algorithm stops if there is no improvement in the objective function during an interval oftime in seconds equal to "Stall time limit."·

The termination or convergence criterion finally brings the search to a halt. The following are the fewmethods of termination techniques.

Best Individual

A best individual convergence criterion stops the search once the minimum fitness in the population dropsbelow the convergence value. This brings the search toa faster conclusion, guaranteeing at least one good solution.

Worst Individual

Worst individual terminates the search when the least fir individuals in the population have fitness less thanme convergence criteria.

This guarantees the entire population tobe of minimum standard, although thebest individual may not be significantly better than the worst. In this case, a stringent convergence value maynever be met, in which case the search will terminate after the maximum has been exceeded.

Sum of Fitness

In this termination scheme, the search is considered to have satisfaction converged when the sum of thefitness in the entire population is less than or equal to the convergence value in the population record.

This guarantees that virtually all individuals in the population will be within a particular fitness range, althoughit is better to pair this convergence criteria with weakest gene replacement, otherwise a few unfit individuals in the population will blow out the fitness sum. The population size has to be considered while setting theconvergence value.

Median Fitness

Here at least half of the individuals will be better than or equal to the convergence value, which should givea good range of solutions to choose from.

GENETIC NEURO HYBRID SYSTEMS

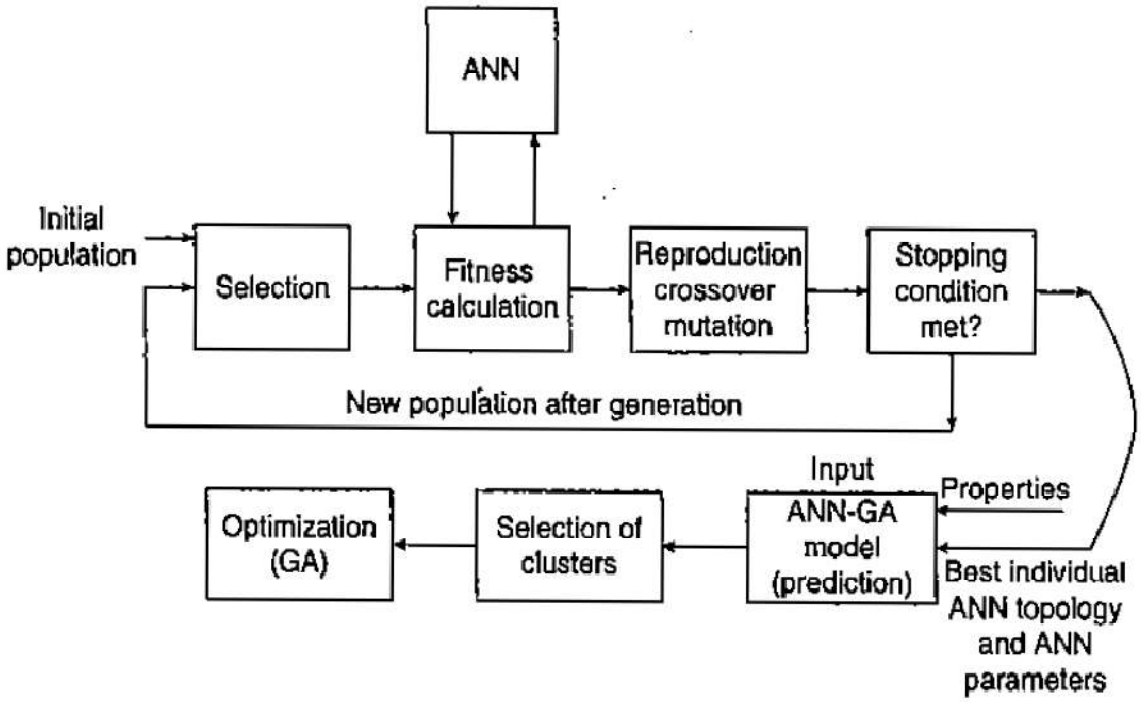
A neuro-genetic hybrid or a genetic-neurohybrid system is one in which a neural network employs a geneticalgorithm to optimize its structural parameters that define its architecture.

In general, neural networks andgenetic algorithm refers to two distinct methodologies. Neural networks learn and execute different tasksusing several examples, classify phenomena, and model nonlinear relationships; that is neural networks solveproblems by self-learning and self-organizing.

Properties of Genetic Neuro-Hybrid Systems

1. The parameters of neural networks are encoded by generic algorithms as a string of properties of thenetwork, that is, chromosomes. A large population of chromosomes is generated, which represent themany possible parameter sets for the given neural network.
2. Genetic Algorithm- Neural Network, or GANN, has the ability to locate the neighborhood of the optimalsolution quickly, compared to other conventional search strategies.

The Figure below shows the block diagram for the genetic-neuro-hybrid systems.



Drawbacks:

- the largeamount of memory required for handling and manipulation of chromosomes for a given network;
- the question of scalability of this problem as the size of the networks become large.

Genetic Algorithm Based Back-Propagation Network (BPN)

BPN is a method of reaching multi-layer neural networks how to perform a given task. Here learning occursduring this training phase.

The limitations ofBPN are as follows:

1. BPN do not have the ability to recognize new patterns; they can recognize patterns similar to those theyhave learnt.

2. They must be sufficiently trained so that enough general features applicable to both seen and unseeninstances can be extracted; there may be undesirable effects due to over training the network.

Before a genetic algorithm is executed,

l. A suitable coding for the problem has to be devised.
2. A fitness function has to be formulated.
3. Parents have to be selected for reproduction and then crossed over to generate offspring.

Coding

Assume a BPN configuration n-l-m where n is the number of neurons in the input layer, lis the numberof neurons in the hidden layer and m is the number of output layer neurons. The number of weights to bedetermined is given by

$$(n + m)!$$

Weight Extraction

In order to determine the fitness values, weightsare extracted from each chromosome. Let $a_1, a_2, \ldots, a_d, \ldots, a_L$ represent a chromosome and let $a_{pd+1}, a_{pd+2}, \ldots, a_{(p+1)d}$ represent pth gene $(p \geq 0)$ in the chromosomes.

The actual weight *Wp*is given by

$$w_p = \begin{cases} -\dfrac{a_{pd+2}10^{d-2} + a_{pd+3}10^{d-3} + \cdots + a_{(p+1)d}}{10^{d-2}} & \text{if } 0 \le a_{pd+1} < 5 \\ +\dfrac{a_{pd+2}10^{d-2} + a_{pd+3}10^{d-3} + \cdots + a_{(p+1)d}}{10^{d-2}} & \text{if } 5 \le a_{pd+1} \le 9 \end{cases}$$

Fitness Function

A fitness has to be formulated for each and every problem to be solved. Consider the matrix given by

$$\begin{Bmatrix} (x_{11}, x_{21}, x_{31}, \ldots, x_{n1}) & (y_{11}, y_{21}, y_{31}, \ldots, y_{n1}) \\ (x_{12}, x_{22}, x_{32}, \ldots, x_{n2}) & (y_{12}, y_{22}, y_{32}, \ldots, y_{n2}) \\ (x_{13}, x_{23}, x_{33}, \ldots, x_{n3}) & (y_{13}, y_{23}, y_{33}, \ldots, y_{n3}) \\ \vdots & \vdots \\ (x_{1m}, x_{2m}, x_{3m}, \ldots, x_{nm}) & (y_{1m}, y_{2m}, y_{3m}, \ldots, y_{nm}) \end{Bmatrix}$$

where*X* and Yare the inputs and targets, respectively. Compute initial population Io of size *'j'*. Let $O_{10}, O_{20}, \ldots, O_{j0}$ represent*'j'* chromosomes of the initial population Io. Let the weights extracted for eachof the chromosomes uptojth chromosome be $w_{10}, w_{20}, w_{30}, \ldots, w_{j0}$.For *n* number of inputs and *m* numberof outputs, let the calculated output of the considered BPN be

$$\begin{Bmatrix} (c_{11}, c_{21}, c_{31}, \ldots, c_{n1}) \\ (c_{12}, c_{22}, c_{32}, \ldots, c_{n2}) \\ (c_{13}, c_{23}, c_{33}, \ldots, c_{n3}) \\ \vdots \\ (c_{1m}, c_{2m}, c_{3m}, \ldots, c_{nm}) \end{Bmatrix}$$

*As*a result, the error here is calculated by

$$ER_1 = (y_{11} - c_{11})^2 + (y_{21} - c_{21})^2 + (y_{31} - c_{31})^2 + \cdots + (y_{n1} - c_{n1})^2$$
$$ER_2 = (y_{12} - c_{12})^2 + (y_{22} - c_{22})^2 + (y_{32} - c_{32})^2 + \cdots + (y_{n2} - c_{n2})^2$$
$$\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots$$
$$\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots$$
$$ER_m = (y_{1m} - c_{1m})^2 + (y_{2m} - c_{2m})^2 + (y_{3m} - c_{3m})^2 + \cdots + (y_{nm} - c_{nm})^2$$

The fitness function is further derived from this root mean square error given by

$$FF_n = \frac{1}{E_{rmse}}$$

The process has to be carried out for all the total number of chromosomes.

Reproduction of Offspring

In this process, before the parents produce the offspring with better fitness, the mating pool has to beformulated. This is accomplished by neglecting the chromosome with minimum fitness and replacing it with a chromosome having maximum fitness, In other words, the fittest individuals among the chromosomes willbe given more chances to participate in the generations and the worst individuals will be eliminated. Oncethe mating pool is formulated, parent pairs are selected' randomly and the chromosomes of respective pairs arecombined using crossover technique to reproduce offspring. The selection operator is suitably used to selectthe best parent to participate in the reproduction process.

Convergence

The convergence for generic algorithm is the number of generations with which the fitness value increases towards the global optimum. Convergence is the progression towards increasing uniformity. When about 95%of the individuals in the population share the same fitness value then we say that a population has converged.

Advantages of Neuro-Genetic Hybrids

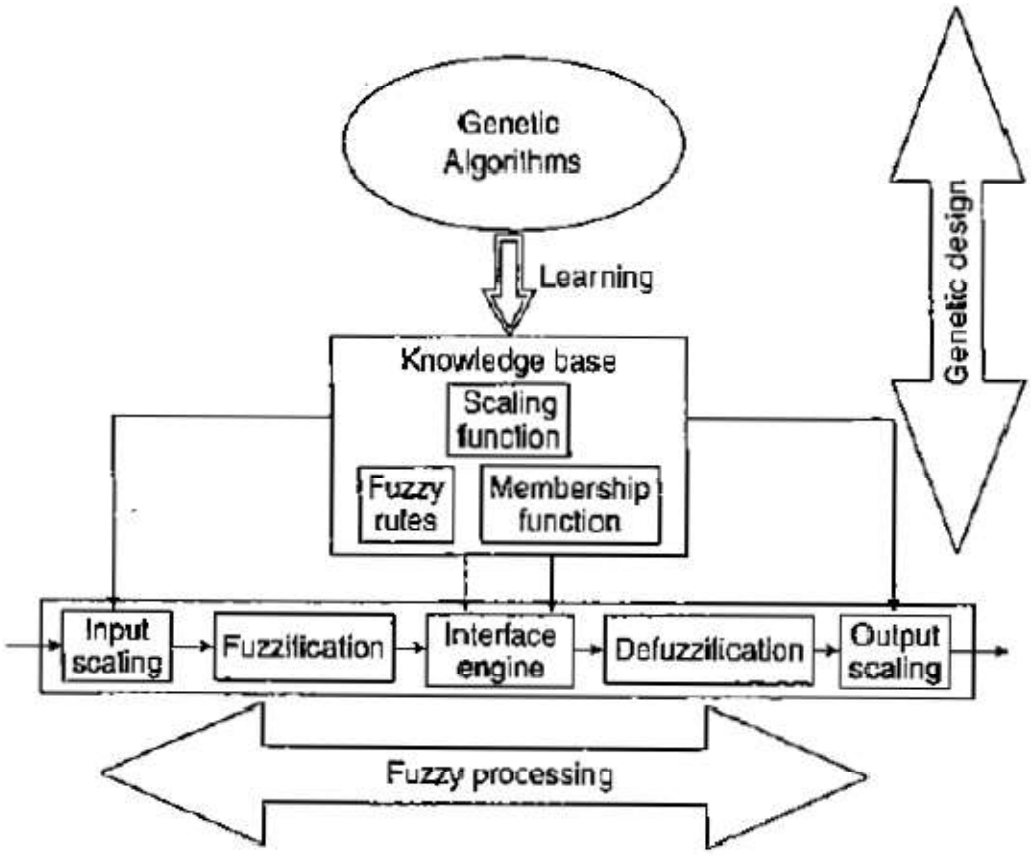
1) GA performs optimization of neural network parameters with simplicity, ease of operation, minimal requirements and global perspective.

2) GA helps to find om complex structure of ANN for given input and the output data set by using its learning rule as a fitness function.
3) Hybrid approach ensembles a powerful model that could signif1camly improve the predictability of the system under construction.

The hybrid approach can be applied to several applications, which include: load forecasting, stock forecasting,cost optimization in textile industries, medical diagnosis, face recognition, multi-processor scheduling, jobshop scheduling, and so on.

GENETIC FUZZY RULE BASED SYSTEMS (GFRBSS)

For modeling complex systems in which classical tools are unsuccessful, due to them being complex orimprecise, an important tool in the form of fuzzy rule based systems has been identified. Figure below shows a system where genetic design and fuzzy processingare the two fundamental constituents. Inside GFRBSs, it is possible to distinguish between either parameteroptimization or rule generation processes, that is, adaptation and learning.



The main objectives of optimization in fuzzy rule based system are as follows:
l. The task of finding an appropriate knowledge base (KB) for a particular problem. This is equivalent toparameterizing the fuzzy KB (rules and membership functions).
2. To find those parameter values that are optimal with respect to the design criteria.

In this phase.it is important to distinguish between tuning {alternatively. adaptation) and learningproblems.

Tuning

- It is concerned with optimization of an existing FRRS.
- Tuning processes assume <1 predefined RB and have theobjective to find a set of optimal parameters for the membershipand/or the scaling functions, DB parameters.

Learning Problems

It constitutean automated design method for fuzzy rule sets that start from scratch.

Learning processes perform a more elaborated search in the space of possible RRs or whole KB and do notdepend on a predefined set of rules.

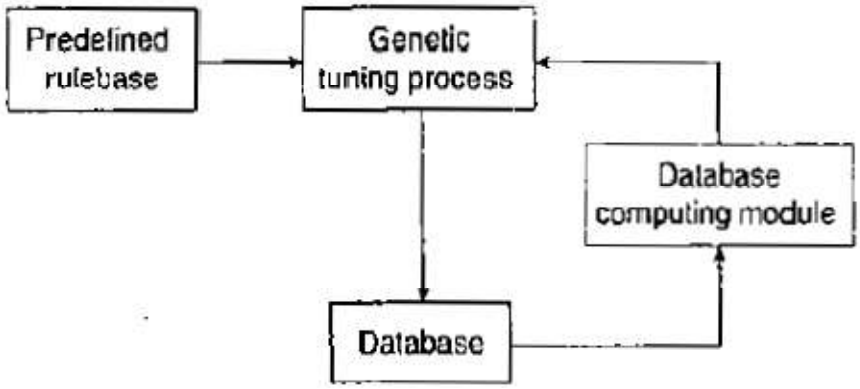
Genetic Tuning Process

The task of tuning the scaling functions and fuzzy membership function is important in FRBS design.

The adoption of parameterized scaling functions and membership functions by the GA is based on thefitness function that specifies the design criteria quantitatively.

The responsibility of finding a set of optimalparameters for the membership andfor the scaling functions rests with the tuning processes which assume apredefined rule base.

The tuning process can he performed a priori also. This can be done if asubsequent process derives the RB once the DB has been obtained, thatisa priori generic DB learning. Figure below illustrates the process of genetic tuning.



Tuning Scaling Functions

In case of linear scalingthe scaling functions are parameterized by a single scaling factor or either by specifying a lower and upper bound. On the other hand, in case of non-linear scaling, the scaling functions are parameterized by one or several contraction/dilationparameters.

These parameters are adapted such thatthe scaled universe of discourse marches the underlyingvariable range.

Ideally, in these kinds of processes the approach is to adapt one to four parameters per variable:

one when using a scaling factor,

two for linear scaling,

and three or four :Or non-linear scaling.

This approach leads toa fixed length code as the number of variables is predefined as is the number of parameters required to codeeach scaling function.

Tuning Membership Functions

It can be noted that during the tuning of membership functions, an individual represents the entire DB. This is because its chromosome encodes the parameterized membership functions associated to the linguistic termsin every fuzzy partition considered by the fuzzy rule based system. Triangular (either isosceles or asymmetric),Trapezoidal, or Gaussian functions are the most common shapes for the membership functions (in GFRBSs).

The number of parameters per membership function can vary from one to four and each parameter can beeither binary or real coded.

For FRBSs of the descriptive (using linguistic variables) or the approximate (using fuzzy variables) type, thestructure of the chromosome is different. In the process of tuning the membership functions in a linguisticmodel, the entire fuzzy

partitions are encoded into the chromosome and in order to maintain the globalsemantic in the RB, it is globally adapted. These approaches usually consider a predefined number of linguisticterms for each variable- with no requirement to be the same for each of them -which leads to a code of fixedlength in what concerns membership functions. Despite this, it is possible to evolve the number of linguisticterms associated to a variable; simply define a maximum number (for the length of the code) and let someof the membership functions be located out of the range of the linguistic variable (which reduces the actualnumber oflinguistic terms).

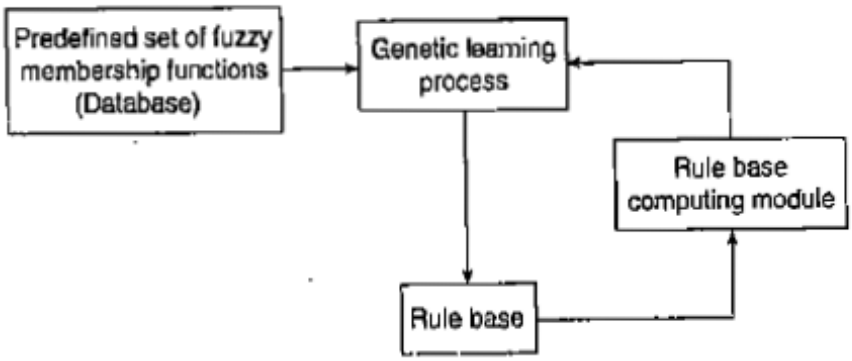
Descriptive fuzzy systems working with strong fuzzy partitions, is a particular case where the number ofparameters to be coded is reduced. Here, the number of parameters to code is reduced to the ones defining thecore regions of the fuzzy set: the modal point for triangles and the extreme points of the core for trapezoidalshapes .

Tuning the membership functions of a model working with fuzzy variables (scatter partitions), on the otherhand, is a particular instance of knowledge base learning. This is because, instead of referring to linguisticterms in the DB, the rules are defined completely by their own membership functions.

Genetic Learning of Rule Bases

As shown in Figure below, genetic learning of rule bases assumes a predefined set of fuzzy membership functionsin the DB to which the rules refer, by means of linguistic labels. As in the approximate approach adaptingrules, it only applies to descriptive FRBSs, which is equivalent to modifying the membership functions. Whenconsidering a rule based system and focusing on learning rules, there are three main approaches that have been applied in the literature:

1. Pittsburgh approach.
2. Michigan approach.
3. Iterative rule learning approach.

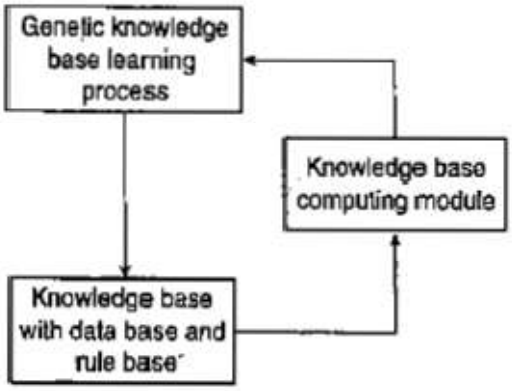


- The Pittsburgh approach is characterized by representing an entire rule set as a generic code {chromosome),maintaining a population of candidate rule sets and using selection and generic operators to produce newgenerations of rule sets.
- The Michigan approach considers a different model where the members of thepopulation are individual rules and a rule set is represented *by* the entire population.
- In the third approach, the iterative one, chromosomes code individual rules, and a new rule is adapted and added to the rule set, inan iterative fashion, in every run of the genetic algorithm.

Genetic Learning of Knowledge Base

Genetic learning of a KB includes different generic representations such as variable length chromosomes,multi-chromosome genomes and chromosomes encoding single rules instead of a whole KB as it deals withheterogeneous search spaces. As the complexity of the search space increases, the computational cost of thegeneric search also grows. To combat this issue an option is to maintain a GFRBS that encodes individualrules rather than entire KB. In this manner one can maintain a flexible, complex rule space in which the searchfor a solution remains feasible and efficient.

The three learning approaches as used in case of rule base canalso be considered here: Michigan, Pittsburgh, and iterative rule learning approach. Figure below illustrates thegeneric learning ofKB.



Advantages of Genetic Fuzzy Hybrids

GAs allow us to represent different kinds of structures, such as weights, features together withrule parameters, etc., allowing us m code multiple models of knowledge representation. This provides awide variety of approaches where it is necessary in design specific generic components for evolving a specificrepresentation.

Generic algorithm efficiently optimizes the rules, membership functions, DB and KB of fuzzy systems. Themethodology adopted is simple and the fittest individual is identified during the process.