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APPRAISAL OF GENETIC ALGORITHM: AN OPTIMIZATION AND EVOLUTIONARY TECHNIQUE

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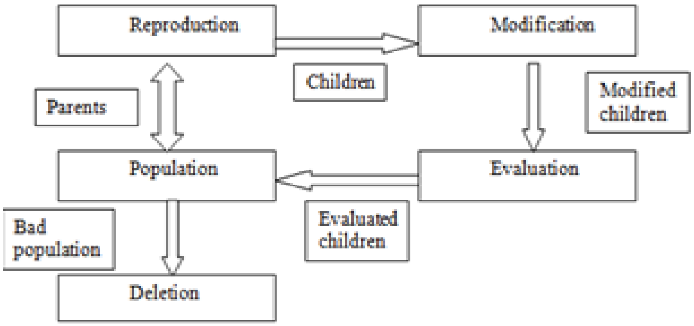
Abstract:

In this paper we discussed about optimization techniques and its methods. There are different types of optimization techniques are available like ant colony, simulated annealing, greedy approach and genetic algorithm. Among this genetic algorithm is meta heuristics search for different types of optimization. It is one of the most persistent techniques in Artificial Intelligence. It is mainly used in Biology, Biotechnology, computer engineering, economics, chemistry, manufacturing, Mathematics, medicine and pharmacology [11]. In my proposed system i prepared modified Quick reduct algorithm for optimization of risk factor analysis in Diabetics. And the genetic algorithm is used for evolutionary function to identify the best factors.

Key Words: Optimization, Genetic Algorithm & Operators

1. Introduction:

Genetic algorithm is a part of soft computing that deals with exploring the search space and select the best solution. It was designed by John Holland at 1970's. Genetic algorithm is a subset of the evolutionary algorithm set. It is based on processes which occur in living organisms in nature, for example Genes, selection, reproduction, cross over, mutation, and fitness calculation [3]. It explores search space for finding global optimization solution by iterative evolution. This paper presents appraisal of genetic algorithm for optimization.



Process of genetic algorithm

2. Literature Survey:

Gopesh Joshi presented a brief explanation about "Review of Genetic Algorithm: An Optimization Technique" [1]. He discuss about pseudo code for genetic algorithm and explained about operators. M. Melanie, "An Introduction to Genetic Algorithms" gives functions of Genetic algorithm [2]. E. Sreedeve "A Threshold Genetic Algorithm for Diagnosis of Diabetes using Minkowshi Distance Method" used modified algorithm with Minkowshi Distance method to find the distance between two objects. It gives high accuracy and low error rate in prediction of diabetics [3]. T. Keerthika, Dr. K. Premalatha (2015) discussed about evolutionary Techniques for medical Domain using Feature Selection and find the best Feature selection method [12]. This approach approved with PIMA data set.

3. Basic concept of Genetic Algorithm:

The main terms in genetic algorithm are gene, chromosome, individual, population. Gene is small unit of information. Individual is a set of genes. Combinations of individual are called population[1][2]. Here optimization is a process of modifying the inputs of a device, mathematical process to obtain minimum or maximum of the output. It is important to solve the unsolvable or hard problems. Types of optimization are one dimension, dynamic, discrete variable, constrained and global optimization [8].

4. Genetic Algorithm Applications:

Evolvable Hardware Applications [5]: Automatically develop new configurations based on the old configurations. **Example**: Robot, such a robot will be able to alter its configuration to a newer version if it meets a situation where it is requires more functionality to perform its tasks. It can also find optimal path to the target without disturb the objects.

Engineering Design: It uses the minimum resources to deliver the maximum output is even much complex. Fields like telecommunication routing, trip and shipment routing, gaming, encryption and code breaking, chemical analysis, finance strategies, marketing strategies, which also uses the GA.

Data Encryption [6]: In the field of cryptology, Genetic Algorithm is being used to produce a new advance encryption by using the operations of Crossover and Mutation.

Computer Gaming [7]: The learning technique allows the AI to avoid repeating past mistakes, which therefore increase the playability of the game.

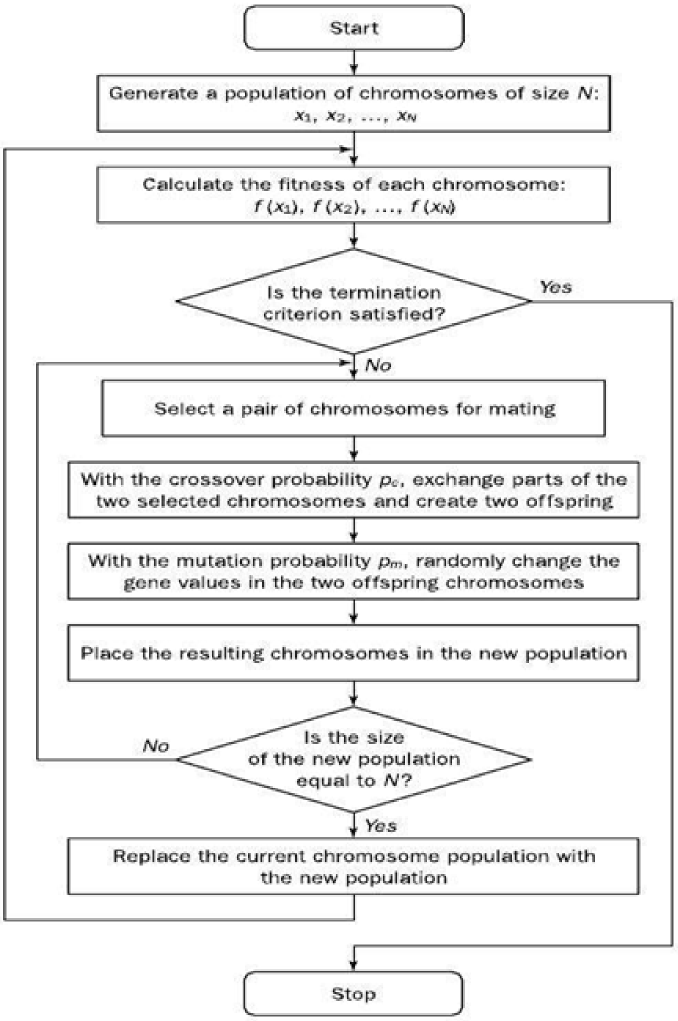
5. Selection Techniques:

Roulette Wheel Selection: Parents selected depends fitness.

- ✓ Find the sum of all chromosomes fitness in the population
- ✓ Generate random number within population interval
- ✓ Go through the entire population and sum the fitness. When the sum is greater than fitness criteria value, stop and return

Rank Selection Method: The individuals in a population are ranked according to the fitness and the expected value of each individual depends on its rank rather than its absolute fitness.

Steady State Selection: It replaces few individuals in each generation. Larger part of chromosome should retain to successive population.



6. Genetic Algorithm [1]:

Encoding: Phenotype is mapped to genotype (ie) Data is represented in genes

Initialization: Input parameters

- ✓ Population size
- ✓ Crossover probability
- ✓ Mutation probability
- ✓ Number of generation

Evaluation: Find the fitness values for each individual set of Genes

Selection: Retain best fitness individuals. Eliminate bas population.

Crossover: Recombination (Crossover two selected parents)

Mutation: Mutation is adding new features from outside.

Iterate: Step 3 to 6 until terminate the loop

Decoding: Back to phenotype.

7. Methods Used to Find Fitness:

Euclidean Distance [10]:

- ✓ Euclidean distance or the L_2 norm of the difference vector is most commonly used to compute distances and has an intuitive appeal but the largest valued attribute may dominate the distance[4].

$$D(x, y) = (\Sigma (x_i – y_i)^2)^{½}$$

- ✓ This method is more appropriate when the data is not standardized.

Manhattan Distance:

- ✓ Manhattan distance also called the L_1 norm of the difference vector. Mostly, the results obtained by this measure are similar to those obtained by using the Euclidean distance [4].
- ✓ The largest-valued attribute can dominate the distance, although not as much as in the Euclidean distance.

$$D(x, y) = \sum_{i} | x_i – y_i |$$

Chebychev Distance:

- ✓ This distance metric is based on the maximum attribute difference. Also called the L_∞ norm of the difference vector.

$$D(x, y) = \text{Max} | x_i – y_i |$$

Categorical Data Distance:

- ✓ This distance measure may be used if many attributes have categorical values with only a small number of values (e.g. binary values).
- ✓ Let N be the total number of categorical attributes.

$$D(x, y) = (\text{number of } x_i – y_i) / N$$

Minkowski Distance:

The Minkowski distance is a generalized metric that includes others as special cases of the generalized form.

$$Dist_{XY} = \left(\sum_{K=1}^{d} |X_{ik} - X_{jk}|^{\frac{1}{P}} \right)^{P}$$

8. Review of Genetic Operation:

Evaluation: In population of size n there are n individuals. Each will have their own fitness value.

Selection: Retain the best fit individual and eliminate rest.

Crossover: Reproduction

One-Point Crossover: A random position is selected for crossover.

PARENT 1 111 |1111
PARENT 2 000 |0000
CHILD 1 111 |0000
CHILD2 000 |1111

Single point crossover

Two-Point Crossover: Select two random points for crossover such that child 1 adopt middle portion of parent 2 and rest from parent 1, similar for child 2.

PARENT 1 11 | 111 | 11
PARENT 2 00 | 000 | 00
CHILD 1 11 | 000 | 11
CHILD2 00 | 111 | 00

Two point crossover

Uniform Crossover: Uniformly spread across the chromosome that is either even or odd ordering.

PARENT 1 1 | 1 | 1 | 1 | 1 | 1 | 1
PARENT 2 0 | 0 | 0 | 0 | 0 | 0 | 0
CHILD 1 1 | 0 | 1 | 0 | 1 | 0 | 1
CHILD 2 0 | 1 | 0 | 1 | 0 | 1 | 0

Mutation: Modifies the solution

Insert Mutation: Random changes occur at gene.

BEFORE MUTATION A B C D E F
AFTER MUTATION A B **P D** E **Q**

Swap Mutation: Gene at random locations is replaced with each other.

BEFORE MUTATION A B C D E F
AFTER MUTATION P Q **E** S **C** U

Jumble Mutation: Rearrangement are done so new outcome will result.

BEFORE MUTATION A B C D E F
AFTER MUTATION **C A F C D E**

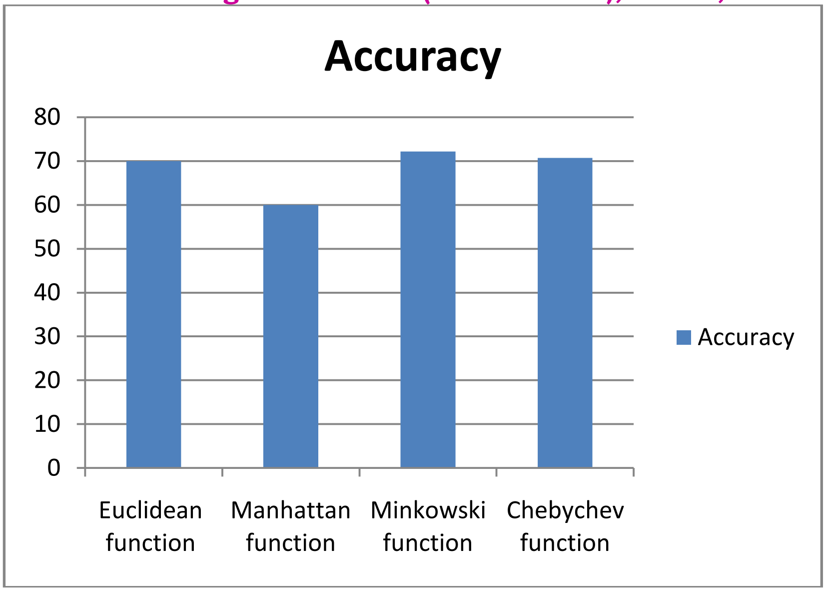
Inverse Mutation: It is a new approach where all values from left are moved to right.

BEFORE MUTATION A B C D E F
AFTER MUTATION F E D C B A

9. Sample Results and Analysis:

The PIMA diabetes dataset is used. The training and testing datasets are arranged by normalizing the instances of the data (ie) each field values are converted into 0 to 1. The analysis has been made by different distance methods. The accuracy of each distance is given in tabular and chart. Here Minkowski function is best.

Distance Methods	Accuracy
Euclidean function	70
Manhattan function	60
Minkowski function	72.2
Chebychev function	70.7



10. Conclusion:

Here we evaluate the genetic algorithm for the optimization problem. It described how genetic algorithms are originated, the basic concepts, genetic algorithm applications and the working of genetic algorithm. The basic distance methods and its accuracy are discussed. Genetic algorithm is best optimization technique. Sample for each operator is explained. In my research I implement modified quick reduct to optimization of risk factor analysis in diabetics and use Genetic algorithm for evolutionary task.

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