ÇUKUROVA UNIVERSITY
INSTITUTE OF NATURAL AND APPLIED SCIENCES

MSc THESIS

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ASSORTATIVE –DISASSORTATIVE SELECTION MECHANISMS FOR GENETIC ALGORITHMS

DEPARTMENT OF COMPUTER ENGINEERING

ADANA, 2013

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We certify that the thesis titled above was reviewed and approved for the award of degree of the Master of Science by the board of jury on / /2013

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ABSTRACT

MSc THESIS

ASSORTATIVE –DISASSORTATIVE SELECTION MECHANISMS FOR GENETIC ALGORITHMS

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Supervisor : Asst. Prof. Dr. Mustafa ORAL
Year: 2013, Page: 86
Jury : Asst. Prof. Dr. Mustafa ORAL
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The aim of this study is to improve the performance of Genetic Algorithm (GA) and extend the GA towards a more natural approach by incorporating "assortative & disassortative mating (ADM)" to the selection strategies.

In this study, a simple and efficient ADM based real-coded genetic algorithm (RCGA) is proposed and then employed to solve complex function optimization problems. The suggested DISASSORTATIVE mating approaches enhances the abilities of GAs in searching global optima as well as in speeding convergence by integrating the ASSORTATIVE mating search strategies. Eight different ADM strategies were proposed within this study. Using ten benchmark global optimization test functions, the performance of these strategies were evaluated. Results indicate that the disassortative based mating strategies are fast, accurate, and reliable, and outperform all the other GAs considered in the present study.

Key Words: Genetic algorithm, diversity, disassortative mating, assortative mating.

ÖZ

YÜKSEK LİSANS TEZİ

GENETİK ALGORİTMALAR İÇİN ASSORTATİF- DİSASSORTATİF SEÇİLİM MEKANİZMALARI

Serkan KARTAL

ÇUKUROVA ÜNİVERSİTESİ
FEN BİLİMLERİ ENSTİTÜSÜ
BİLGİSAYAR MÜHENDİSLİĞİ ANABİLİM DALI

Danışman :Yrd. Doç. Dr. Mustafa ORAL
Yıl: 2013, Sayfa: 86
Jüri : Yrd. Doç. Dr. Mustafa ORAL
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Bu çalışmanın amacı, Genetik Algoritma (GA)' nın performansını arttırmak ve seçim mekanizmasını "benzer birey - farklı birey eş seçimi (ADM)" ile birleştirerek daha doğal bir yaklaşım haline getirmektir.

Bu çalışmada, basit ve etkili bir ADM tabanlı, sürekli değerlerle kodlanmış genetik algoritma (RCGA) öne sürülmüş ve daha sonra karmaşık optimizasyon problemlerini çözmek için kullanılmıştır. Öne sürülen farklı birey eş seçim yaklaşımı GA'nın genel en iyiyi arama yeteneğini arttırdığı gibi benzer birey eş seçiminin eklenmesi de en iyiye yakınsama hızını arttırmaktadır. Çalışmada sekiz farklı ADM stratejisi önerilmiştir. Öne sürülen stratejilerin performansları, on farklı genel optimizasyon değerlendirme fonksiyonu kullanılarak değerlendirilmiştir. Sonuçlar farklılık tabanlı eş seçim stratejisinin daha hızlı, tutarlı, güvenilir olduğunu ve bu çalışmadaki diğer tüm GA'lardan daha iyi sonuç verdiğini göstermektedir.

Anahtar Kelimeler: Genetic algoritma, farklı birey eş seçimi, benzer birey eş seçimi.

ACKNOWLEDGEMENTS

I would like to express my sincere gratitude to my advisor Assist.Prof. Dr. Mustafa ORAL for his supervision guidance, encouragements, patience, motivation, useful suggestions and his valuable time for this work.

I would like to thank members of MSc thesis jury, Assoc. Prof. Dr. Zekeriya TÜFEKÇİ and Assoc. Prof. Dr.Hakan YAVUZ for their suggestions and corrections.

Special thanks to Buse Melis Özyıldırım for her endless support, patience and motivation.

Finally, I would like to thank my family, who have supported me throughout entire process, both by their love and encouragements.

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LIST OF SYMBOLS / ABBREVIATIONS

(RC)-SGA	: Real Coded Standard Genetic Algorithm
ADMS	: Assortative-Dissortative Mating Strategy
ADM	: Assortative-Dissortative Mating
BCGA	: Binary-Coded Genetic Algorithm
DCGA	: Diversity Control Oriented Genetic Algorithm
GA	: Genetic Algorithm
GID	: Genotypic Individual Dissimilarity
GIS	: Genotypic Individual Similarity
GPD	: Genotypic Population Diversity
GPS	: Genotypic Population Similarity
EA	: Evolutionary Algorithm
PID	: Phenotypic Individual Dissimilarity
PIS	: Phenotypic Individual Similarity
PPD	: Phenotypic Population Dissimilarity
PPS	: Phenotypic Population Similarity
RBSM	: Rank-Based Selection Mechanism
RCGA	: Real-Coded Genetic Algorithm
RW	: Roulette Wheel
RWSM	: Roulette-Wheel Selection Mechanism
SM	: Selection Mechanisms
SP	: Selective Pressure
SGA	: Standard Genetic Algorithm
SSM	: Standard Selection Mechanism
TSM	: Tournament Selection Mechanism

1. INTRODUCTION

Traditional GAs perform selection process independent from individual's genotypic or phenotypic similarities. In nature it is called as random mating (Russel, 1998; Smith, 1980). However selection of the individuals according to their kinship or likeness is more common in natural system (Fernandes et. al., 2009).

In random mating better individuals should be favoured more often than the weaker ones for recombination process. However there are better selection mechanisms for recombination, in nature. For instance, humans usually select their mate outside of their family tree (Fernandes and Rosa, 2008). This type of non-random mating is called as *outbreeding* mating and it is opposite of the *inbreeding* where individuals mate preferentially with their relatives. It is reported that *outbreeding* usually increase the diversity in the population while *inbreeding* decreases (Russel, 1998).

In non-random mating, parenthood or likeness based mating is performed (Fernandes and Rosa, 2008). For example, disassortative mating is a specific type of non-random mating that may improve EAs performance by maintaining the genetic diversity of the population at a higher level during the search process. Another non-random mating mechanism is the assortative mating (AM) where the individuals choose their mates according to similarities (Russel, 1998). For example the existence of correlations between same certain aspects of couples, such as: heights, intelligence, behaviour, etc., can be viewed as an instance of AM among humans.

Previous studies view that mating is very unlikely to be random in nature. Assortative and disassortative selection mechanisms (SMs) may produce higher survival rates among individuals evolving in static and dynamic environments, respectively. These mechanisms bring to mind two major topics: selective pressure and genetic diversity. Pressure and diversity are closely related with the terms of exploration and exploitation which are needed in order to have safe search and avoid from premature convergence in GAs.

Premature convergence to local optima is one of the most frequently encountered difficulties that arise when applying GAs to complex problems.

Premature convergence is directly related with loss of diversity. When the individuals are in the solution space is too alike, then genetic operators can not generate offspring that are better than their suboptimal parents. On the other hand, higher population diversity can cause to a dramatic deterioration of GA's productivity. Therefore, an important issue in the design and application of GAs is the trade-off between exploitation of the best individuals and exploration of alternative regions of the search space.

In this study, we investigated the inclusion of assortative-disassortative selection mechanism to achieve a proper balance between exploitation and exploration. In addition to this, assortative-disassortative selection may overcome the problem of the standard GAs that usually get stuck on the local optimum rather than the global optimum. With disassortative mate selection, individual selects the least similar co-candidate for itself. In this way, individuals with rare traits are in the advantage of individuals without the rare trait. In addition to this, assortative mate selection provides advantages to similar individuals. Promoting mating among the similar individuals provides narrowing down the spread of search space. That yields exploitation of a certain region.

We tested GA for different selection mechanisms; standard selection mechanism(SM) and proposed selection mechanisms. These mechanisms were tested on standard GA test functions (for two dimensions).

Clear winner is the disassortative based SMs to attain global optimum by promoting genetic diversity. Using some combinations of assortative and disassortative approaches are also give better results than standard SM for GA.

2. PRELIMINARY WORKS

In general, a typical RCGA involves three main operators: selection, crossover, and mutation to evolve the population towards global optimum. This method can be viewed as an evolutionary process. The crossover operation is used to create new offspring (solutions). Crossover is one of the key operators to increase the diversity of the population, hence enabling GAs to explore promising areas of the search space. For common diversity based crossover operations, sharing, diversity control oriented GA, restricted mating and assortative - disassortative mating can be found.

Goldberg and Deb (1991) described the sharing method as; each individual is forced to share its fitness value with its neighbours. So, the rare or deviant solutions will have selective advantages with respect to the common solutions. The neighbourhoods of the solutions are evaluated with Euclidian distance between their locations in phenotype (fitness) space.

Fitness sharing and niching methods are also used by Sareni and Krahenbuhl (1998). Niching method maintains population diversity and permits the GA to investigate many peaks in parallel. It can be viewed as a subspace in the environment that can support different types of life. In this way it also prevents the GA from being trapped in local optima.

Shimodaira proposed Diversity Control Oriented Genetic Algorithm (DCGA) to maintain population diversity (Shimodaira, 1997). In the DCGA the population that needed for the next generation is created by merging the population of parents and their offspring by eliminating duplicate solutions based on the selection probability, which is calculated using the Hamming distance between the candidate individual and the best. In another study Mauldin used the Hamming distance restriction to avoid the coexistence of similar individuals (Mauldin, 1984).

Following the concept of Assortative-Dissortative Mating in biological systems, Fernandes first used directed Assortative-Dissortative (positive and negative assortative) Mating technique to improve standard genetic algorithms (SGAs) (Fernandes et. al., 2001). First, for each recombination event an individual is selected

as first parent by using Roulette Wheel (RW) method. Then N genomes are selected by the same method. Additionally, the similarity between each of N genomes and the first parent is computed. Statistical measure of similarity of two codebooks based on the magnitude of the signal and the mean, variance and correlation of the code words' coordinates is used. Then individuals are selected depending on selected method (positive- negative assortative) and their similarity.

De et al. introduced genotypic and phenotypic assortative mating where the partners are chosen based on either their genotypic similarity or their phenotypic similarity (De et. al., 1998). The first parent is selected according to the fitness value. Then candidate partner is determined by considering the Hamming distance (genotypic) or the fitness distance (Phenotypic) to the first one. This approach provides exploitation of current search space. The aim of this selection is, exchange information with two genomes without losing any information. In nature, it is noticed that individuals select their partners with similar characteristic.

Matsui defined dissortative (disassortative) mating within the tournament selection strategy (Matsui, 1999). At first, one individual is selected as the first parent with standard tournament selection. Then N candidate individuals are selected for selection pool. After that correlation is measured between first parent and N candidate individuals. Later, the total of the fitness value and the Hamming Distance is used to determine second parent.

Fernandes introduced a different version of the dissortative (disassortative) selection to prevent the genetic diversity (Fernandes et. al., 2009). Firstly two parents are selected but crossover is performed if the Hamming distance between them is found to be above a threshold value. Otherwise, the recombination event is considered as "failed" and new pair is selected until N/2 pairs have tried to recombine (N is the population size). After the reproduction cycle, a new population is created by selecting the best N members amongst the parents and newly generated offspring. Then, the threshold is incremented or decremented, according to the number of successful and failed events. Thus, the population diversity can be controlled depending on the threshold value.

Another interesting approach is the multi-parental crossover with distance dependence alternation model that utilizes distance information among individuals (Takahashi et. al., 1999). First m+2 parents are randomly selected from population and selected parents generate several children. Then algorithm selects the elite solution from the children and finds the parent nearest to elite one. If the elite child is better than the parent then parent is replaced with the child. Else, the algorithm selects another parent randomly and processes the same procedure. The results showed it that the algorithm outperformed traditional GAs.

Jassadapakorn and Chongstitvatana introduced diversity adaptation in genetic algorithms with preference mating (Jassadapakorn and Chongstitvatana, 2011). The study is based on modified restricted mating which is called as “preference mating”. First individual is selected by the traditional SM. The selection chance of the second individual, depends on the difference function and the fitness value.

Another approach is introduced by Garcia-Martinez et al, for RCGA (2008). The authors indicate that the inclusion of that mating strategy increases the performance of the GA on a set of proposed problems. It uses the parent-centric real parameter crossover operators that create the offspring in the neighbourhood of the female parent. The other parent, the male one, defines the range of the neighbourhood. Before this process, a female and male differentiation determines the individuals in the population that may become female or/and male parents.

Unlike most of the previous methods, the algorithm ADM proposed in this thesis for RCGAs, which has the general distance functions is based on normal distribution and independent from the problem space. As shown above, disassortative mating maintains genetic diversity at a higher level. In addition, assortative mating is used to make more sensitive search which is based on the same distance measurements.

3. MATERIALS AND METHOD

3.1. Materials

3.1.1. Genetic Algorithm

Genetic Algorithms (GAs) are well known heuristic search and optimization algorithm for solving both constrained and unconstrained function optimization problems. GAs are inspired from Darwin's Theory of Evolution and aimed to find optimum solution by searching problem space randomly (Beasley at. al., 1993; Jaffe, 2002).

SGA starts with randomly creating a set of candidate solutions that is called initial population. Algorithm operates on the population applying the principle of survival of the fittest to produce better approximations for the solution. At each generation, a new set of chromosomes are produced by the process of selecting individuals depending on their fitness score in the problem domain and breeding them among themselves. This process leads the population evolve towards the better individuals by modelling natural processes, such as selection, recombination and mutation (Beasley at. al., 1993).

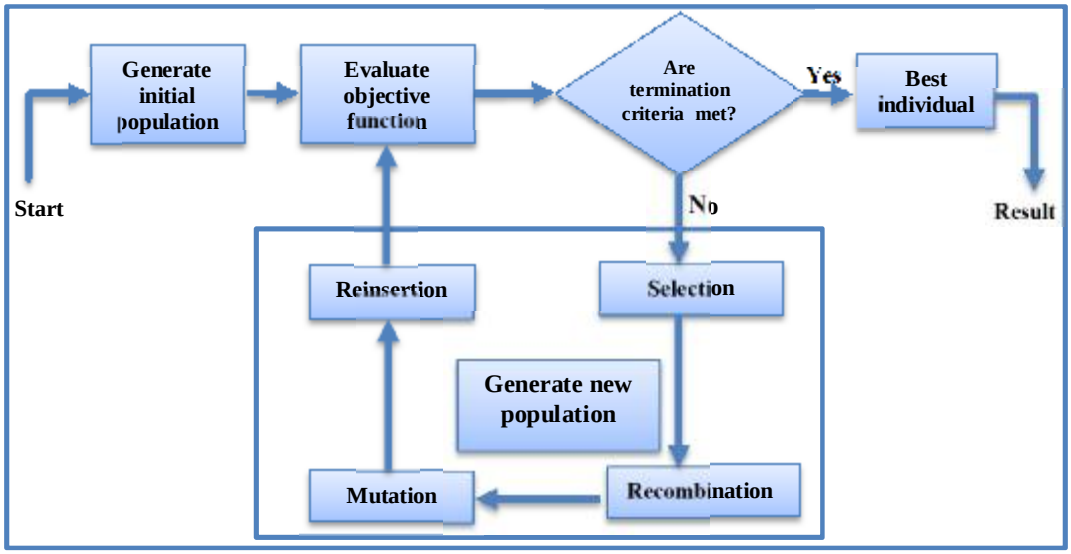


Figure 3.1. Structure of Genetic Algorithm

3.1.2. Basic GA

Basic GA follows common steps illustrated in Figure 3.1. At the first step, many chromosomes which represent the solutions are randomly generated to form an initial population. Discrete or continuous search spaces can be used for gene representation. The population size depends on the nature of the problem and generally a predefined constant population size is used. Then the objective function is used to evaluate the fitness of individuals. If the desired solution is, by chance, in the initial population, there is no need to proceed further. The algorithm should terminate straight away.

If the termination condition is not reached, the next generation should be generated. The reproducing of the new generation starts with selecting parents from the current population through a fitness-based process. Various selection methods can be used for this operation. Such as, rank-based selection, roulette wheel selection, tournament selection, etc.

The selected individuals (parents) undergo recombination process. Recombination aims to produce offspring by combining two or more individuals. The parents are not necessarily combined to produce offspring. The crossover probability p_c determines whether recombination will be performed or not. If the process should not be performed, the two offspring would be exact copy of their parents. The most common real valued recombination methods are, intermediate recombination and line recombination.

All offspring are taken into mutation process with certain probability. The aim of the mutation is to alter individuals randomly. It is applied to the individuals with very low probability. This value may vary in the interval of [0, 1] (Shopova and Vaklieva-Bancheva, 2006). However it is recommended to use low values, such as 0.01, 0.1, etc. The significance of mutation is to provide exploration of the search space.

After the offspring have been produced, they are used to form the next generation. In the case of producing less offspring than the size of the original population, in order to preserve the size of the original population, combination of

the offspring and the old population is used. This process is called reinsertion. Global reinsertion and local reinsertion are the well-known reinsertion methods in the literature.

This cycle is performed until termination criteria are met. Generally genetic algorithms are run over a predefined number of generations or until problem specific termination criteria are reached. Typical termination criteria are: stop after a fixed number of generations, stop when a chromosome reaches a specified fitness level, stop when a chromosome succeeds in solving the problem within a specified tolerance or stop if there is no improvement on the solution in a certain amount of generation.

Previous works show that the behaviour and performance of GAs are strongly influenced by the representation scheme used for the problem (Goldberg, 1989; Liepins and Vose, 1990). So, to make the application successful, often considerable effort is needed to customize the GA to suit the problem. For example representation of the problem can be achieved by coding the chromosomes as binary, integer, real-valued, messy or tree structure. Among of them, the binary coded and real-valued representations are the most important and widely used coding schemes.

3.1.2.1. Binary Coded GA

Binary encodings are the most commonly used and nature-inspired representations for EAs, especially for GAs (Goldberg, 1989). It was proposed based on some theoretical guidance and existing recommendations for designing efficient genetic representations. In BCGA each chromosome has one binary string. Each bit in this string represents the characteristic of the related solution. Two chromosomes with binary coding are given below as an example:

Chromosome A	10110010110010101110010 1
Chromosome B	11111110000011000001111 1

When encoding real-valued problems with binary representations, different types of binary representations can be used. The most common binary representations are binary, gray and unary encodings (Liang et. al., 2007).

3.1.2.2. Real Coded GA

In real-coded genetic algorithm (RCGA), a solution is directly represented with the real number variables. So, the use of real-parameter makes it possible to use large domains for variables (Herrera et. al., 1998).

The main purpose of the RCGA implementation is to move the genetic algorithm closer to the problem space. The real coding is used to represent a solution for a given problem to decrease computing burden in most of the GA applications.

3.1.2.3. Binary versus Real Coding

Perhaps, the most basic decision for the GA designer is whether to use, binary or real coding. The traditional GA uses binary coding (Holland, 1975). On the other hand, in many applications real coding is used (Michalewicz, 1996). Various arguments are given as to whether binary or real coding should be used, but it is not exactly clear which coding method should be adopted.

Binary coded representation has been demonstrated as the most appropriate one and is easy to implement (Goldberg, 1991). However, the GA's good properties do not stem from the use of bit strings (Antonisse, 1989; Radcliffe, 1992). The binary representation encounters with certain difficulties when dealing with continuous search space and numerical precision is required.

On the other hand, real coding would seem more natural to represent the genes directly as real numbers for optimization problems in continuous search space. Each gene represents a variable of the problem. The use of real parameters makes it possible to use large domains for the variables, which is difficult to achieve in binary representation. One of the other advantages of the real coding is a slight change in variable corresponds to a slight changes in the function. In this way, it is possible to

make local tuning on the solutions. There is no difference between the genotype (coding) and the phenotype (search space). Therefore, the coding and decoding processes that are needed in the BCGAs are avoided, and that enhances the GA's speed. For these reasons, in this study the use of real coded representations is preferred for optimization problems.

3.1.3. Factors Influencing GA

Traditional genetic algorithms use random solutions to create initial population. If the population is not spread to search space, it can be difficult to find the desired solution for the problem. Therefore, some factors should be considered while generating the new population. These factors are: size of the search space, and the population size, the selection pressure, the diversity, etc. (Diaz-Gomez and Hougen, 2007). However, in this thesis just the diversity factor will be taken into account.

3.1.3.1. Search Space

The size of the search space is an important aspect to reach optimum solution. If the space is too large, EA may not be able to come close to optimum point. It is likely that it will get stuck on a local minimum. Therefore, if it is possible, one should try to decrease the number of parameters affecting the problem. If this is not possible it may be a good idea to narrow down the range of each dimension. This would result in a smaller search space.

Furthermore the landscape of the search space plays an effective role in the success of EA. If the space contains numerous local minimums a good EA should be able to avoid such traps.

In most of the cases, one cannot choose the landscape of the search space. Therefore while developing an EA, one should select challenging search spaces in order to show the algorithm's superiority.

3.1.3.2. Population Size

Population size is another aspect that affects the performance of an EA. In order to explore search space a large amount of candidate solutions should be generated. However this comes with the price of decreased speed of convergence.

Inevitably, the amount of time to evaluate large number of solutions (population) will slow down the algorithm. On the other hand having a small sized population most probably would result with early convergence on a local minimum. Since the search space may not be well explored with such number of solutions.

Therefore the population size should be selected carefully while optimizing the speed and the exploration power.

3.1.3.3. Selective Pressure

Selective Pressure (SP) is the tendency to select the best individuals of the population for the recombination to direct the GA better solutions. Too much selective pressure cause to premature convergence. However, low selective pressure inhibits GA to converge optimum solution in a reasonable time.

3.1.3.4. Diversity

Diversity is the major topic that affects the GA's performance (Guptai and Ghafir, 2012). The maintenance of diversity of the population is essential to ensure that all solution space is efficiently searched. Loosing population diversity may be a major reason for the premature convergence. Not being capable of producing distinct individuals will result in almost identical chromosomes that exploit only a limited portion of the search space. So the genetic operators can no longer produce offspring that outperform their parents. Generally, this situation cause to stuck on a local optimum and to scarify exploration that a good search algorithm should never give up (DeJong, 1975; Guptai and Ghafir, 2012).

3.1.3.4.(1). Diversity Measurement Methods

Measures to evaluate the diversity of a set of solutions in search space play an important role in EAs. Measurement methods can be classified according to representation scheme of the solution. Hamming distance and Euclidean distance are the most common techniques for the binary and real coded GAs.

3.1.3.4.(1).a. Hamming Distance

Hamming distance is the most widely used technique for measuring the similarity of two binary strings (Hamming, 1980). It is used to measure distance between two genotypes by counting the number of different bits (Banzhaf et. al., 1998). In other words, Hamming distance describes how many bits are different in two binary strings. The below illustration shows how to calculate Hamming distance as an example.

A	1	1	1	1	0	0	1	0	0	1
B	1	0	1	1	0	0	0	0	1	1

Hamming distance is equal to 3.Total Hamming distance can be computed by the following formula:

$$D_v(P) = \sum_{i=1}^{N-1} \sum_{j=i+1}^{N} \mathrm{hd}(C_i, C_j)$$

$$\mathrm{hd}(C_i, C_j) = \sum_{a=0}^{tgens} \left| C_{i,a} - C_{j,a} \right|$$

where tgens is total gene count in a chromosome C_i,and $C_{i,a}$, $C_{i,j}$ correspond to a^{th} genes in i^{th} and j^{th} chromosomes respectively, and $\mathrm{hd}(C_i, C_j)$ is the Hamming distance between two chromosomes c_i and c_j of a population P= $\{C_1, C_2, \ldots, C_N\}$, $D_v(P)$ is the total hamming distance between all chromosomes.

3.1.3.4.(1).b. Euclidean Distance

One of the most frequently used technique for measuring the similarity for the RCGA individuals is based on summing (averaging) the Euclidean distances from every point (gen) to the center-point (average gen value) (Ursem, 2002; Wineberg and Oppacher, 2003a; Barker and Martin, 1999; Barker and Martin, 2000; Wineberg and Oppacher, 2003b,).

$$D_v\big(P(X,N)\big) = \sum_{i=1}^{N} \|C_i - \overline{C_\iota}\|$$

where $\overline{C_\iota}$ is the centroid of the population in each dimension. Another popular measure is based on summing (averaging) the Euclidean distances between all pairs of points:

$$D_v\big(P(X,N)\big) = \sum_{i=1}^{N-1} \sum_{j=i+1}^{N} \big\|C_i - C_j\big\|$$

For example, C_i and C_j are arbitrary individuals and $\big\|C_i - C_j\big\|$ is the Euclidean distance between C_i and C_j.

3.1.3.4.2. Methods for Maintaining Diversity

Maintaining population diversity is important factor in enhancing the performance of the Genetic Algorithms. Diversity-preserving mechanisms can enhance global exploration of the problem domain and favour dissimilar individuals for recombination. These methods can help to the performance of the algorithm by supporting global exploration and escaping from local extreme (Friedrich et. al., 2009). Methods for preserving diversity are mentioned below.

3.1.3.4.(2).a. Niching

"Niching" method was described by DeJong (DeJong, 1975). A niche can be considered as a subspace in the search space that can support different types of life.

Each species is formed by a group of individuals with similar biological features which are capable of interbreeding among them but that are unable to breed with individuals outside their group. For each group the physical resources are finite and must be shared among the individuals of that niche. Niching methods have been developed to permit the GA to investigate many peaks parallel and prevent GAs to stuck on local optima (Sareni and Krahenbuhl, 1998).

3.1.3.4.(2).b. Crowding

Later, DeJong presented another approach called “crowding”. This mechanism eliminates the most similar individuals when a new one enters to the subpopulation. Crowding has some restrictions on the selection methods. There are various types of crowding:

In standard crowding, in each generation only a specified percentage of the population is used for replacement. In order to insert an offspring into the population, first, randomly select a group of individuals and then calculate the similarities. Then identify the most similar individuals and replace the offspring with one of these. The size of this subpopulation is called crowding factor.

Another type of crowding approach assumes that offspring compete directly with their parents. In each generation population is divided into pairs for recombination. After recombination, each offspring compares with its parent and if the offspring is better it replaces with one of its parent.

3.1.3.4.(2).c. Restricted Mating

Another approach is proposed to maintain the genetic diversity is called “restricted mating”. While selecting an individual as a mate for another one, some restrictions, such as hamming distance are used. If the candidate mate satisfies the conditions it will be granted for the mating (Guptai and Ghafir, 2012).

3.1.3.4.(2).d. Sharing

In **"**sharing method", each individual receives a fitness value by dividing its fitness by the number of similar individuals. Thus the rare individuals get more change to reproduce and it tends to encourage search in unexplored area of the search space. However, high computational cost of sharing is considered as its most important drawback (Snijders, 2005).

3.1.3.4.(2).e. By Multiploidy

Traditional GAs are based on haploid genotypes. However in nature many organism uses "multiploid" genotypes (poly-poid) which is formed from a set of chromosomes. This mechanism provides a number of advantages on the nature, mainly by enhancing population diversity. So the multiploidy method can be used in GAs for maintaining diversity and avoid premature convergence. The results from the set of experiments demonstrated that multiploid GAs more capable of finding the optimum than a haploid GA (Collingwood and Ross, 1996).

3.1.3.4.(2).f. Ranked space

"Ranked space" uses the two ranks in selection phase, first one is the quality and the second one is the diversity rank. The combination of these two ranks is used to change selection probability of the individuals in the population. In this mechanism, the fitter individual is selected by the first rank and population diversity is preserved and getting rid of the identical chromosomes (Jassadapakorn and Chongstitvatana, 2011).

3.1.3.4.(2).g. DCGA

"DCGA" (Diversity control oriented GA) is based on elimination of the duplicated individuals from merged population of the parents and their offspring.

The elimination operation is performed according the Hamming distance between the candidate individual and the best individual. The idea is to use even the worse solutions instead of discarding them (Shimodaira, 1997).

3.1.3.4.(2).h. Elitist

In the “Elitist” method the best two individuals, from the group of parent and their offspring, are selected for the next generation. No additional selection or recombination phase is performed. So the diversity is maintained and the best solution is never lost unless even better solutions are created. However, each family competes within themselves.

3.1.3.4.(2).i. Injection

“Injection” strategy is based on injection of the randomly created individuals to the population for maintaining the population diversity. The injection is used for certain number of generations. But the new individual can overlap the current one so an appropriate sorting strategy should be used together (Sultan et. al., 2006).

3.1.3.4.(2).j. Removal of Genotype or Fitness Duplicate

Another way to prevent population diversity is using a “restrictive method” which does not allow to genotype duplicates within the population. The population diversity is maintained by preventing identical copies from entering within the population. In addition, another restriction mechanism called fitness duplicate can be used as genotype duplicate to avoid from multiple individuals with the same fitness (Friedrich et. al., 2009).

3.1.4. GA Standard Test Functions

To investigate the performance of the ADM, ten real valued, well known benchmark test functions were employed (Tang et. al., 2009). These global optimization test problems consist of different levels of complexity and multimodality including unimodal and multimodal functions. The corresponding test function and its features are listed in Table 3.1.

Table 3.1. Test functions with their features

Function	Definition	Multimodal	Separable
f_1	Rosenbrock	no	no
f_2	Rastrigin	yes	yes
f_3	Schwefel	yes	yes
f_4	Ackley	yes	no
f_5	Langerman	yes	no
f_6	Fifth function of De Jong	yes	no
f_7	Drop wave	yes	no
f_8	Shekel	yes	no
f_9	Griewangk	yes	no
f_{10}	Deceptive	yes	no

The separability is closely related to the concept of interrelation among the variables of the function. In the GA, the interrelation measures how much the contribution of a gene to the fitness of the individual depends on the values of other genes. The non-separable functions are more difficult to optimize as the accurate search direction. On the other hand, separable functions can be optimized for each variable one by one.

A function is called multimodal if it has two or more local optima. The problem is even more difficult if the function is also multimodal. In order to come close to the global optimum, the search process must be able to avoid the regions around local minima. The most complex situation appears when the local optima are

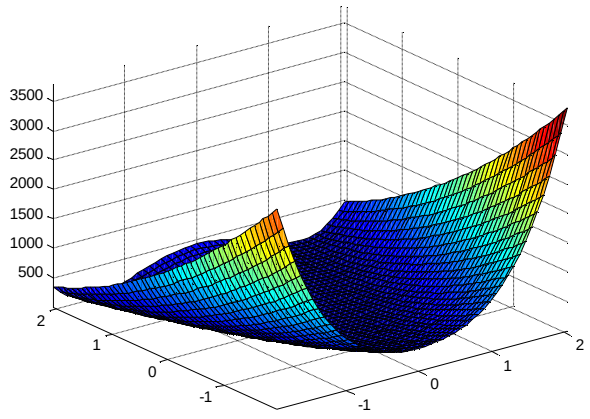
randomly distributed in the search space. All the test functions except Rosenbrock's function are multimodal.

In the following section, the detailed view of each test function is given. The section is divided into sub sections that include a plot of each function in the range of the problem space.

Furthermore optimum point(s) is/are also pointed out. It should be mentioned here that the range of functions are not always the ones defined in the literature. They have been changed to make the functions more challenging.

3.1.4.1. Detailed View to the Test Functions

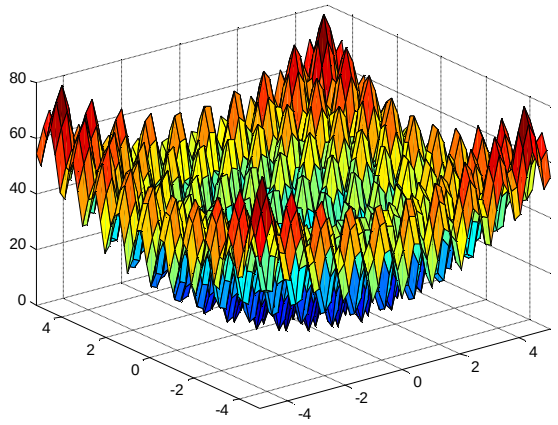
3.1.4.1.(1). F_1: Rosenbrock's valley



$$f_1 = \sum_{i=1}^{n-1}[100(x_{i+1} - x_i^2)^2 + (1 - x_i)^2]$$

Test area is usually restricted to -2.048≤ x_i≤2.048, i = 1...., n. Its global minimum equal f(x) = 0 is obtainable at (x^*) = (1, 1).

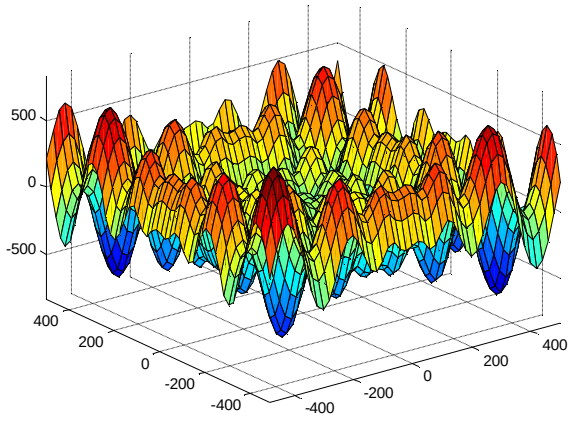
3.1.4.1.(2). F_2: Rastrigin



$$f_2 = 10n + \sum_{i=1}^{n}[x_i^2 - 10\cos(2\pi x_i)]$$

Test area is usually restricted to -5.12≤ x_i≤ 5.12, i = 1...., n. Its global minimum equal f(x) = 0 is obtainable for (x^*) = (0, 0).

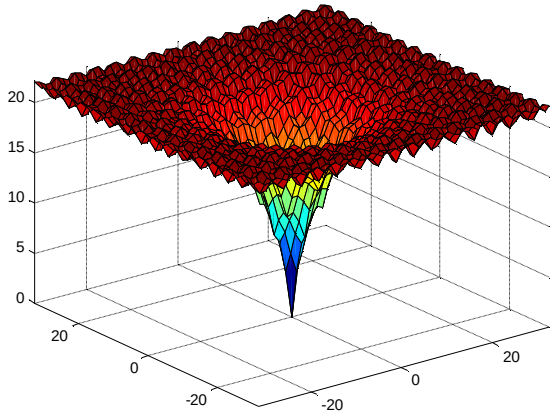
3.1.4.1.(3). F_3: Schwefel



$$f_3 = \sum_{i=1}^{n}[-x_i sin(\sqrt{|x_i|})]$$

Test area is usually restricted to -500≤ x_i≤ 500, i = 1,..., n. Its global minimum equal f(x) = -418.9829n is obtainable for (x^*) = (420.9687, 420.9687).

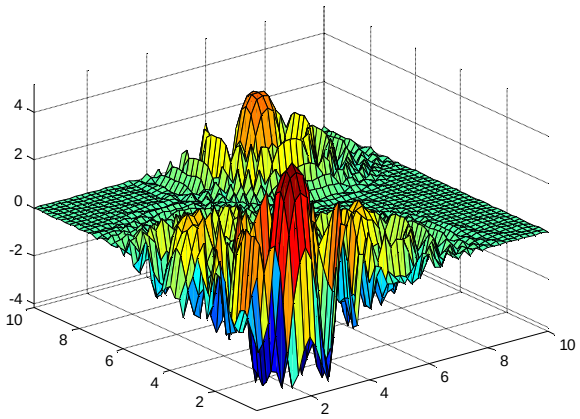
3.1.4.1.(4). F_4: Ackley



$$f_4 = -a * \exp\left(-b * \sqrt{\frac{1}{n}\sum_1^n x_i^2}\right) - \exp\left(\frac{1}{n}\sum_{i=1}^n \cos(cx_i)\right) + a + \exp(1)$$

Test area is usually restricted to -32.768≤ x_i≤ *32.768*, i = 1,..., *n*. Its global minimum equal *f*(*x*) = 0 is obtainable for (x^*) = (0, 0).

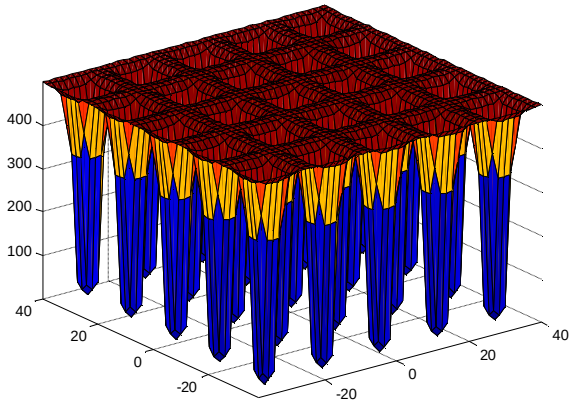
3.1.4.1.(5). F_5: Langerman



$$f_5 = \sum_{i=1}^m c_i \exp[-\frac{1}{\pi}\sum_{j=1}^n (x_i - a_{ij})^2] \cos[\pi \sum_{j=1}^n (x_i - a_{ij})^2]$$

Where m=5, a=[3,5,2,1,7], b=[5,2,1,4,9], c=[1,2,5,2,3]. Test area is usually restricted to 0≤ x_i≤ 10, i = 1,..., n. Its global minimum equal f(x) = -4.15 is obtainable for (x^*) = (2.8, 1.6).

3.1.4.1.(6). F_6: Fifth Function of De Jong

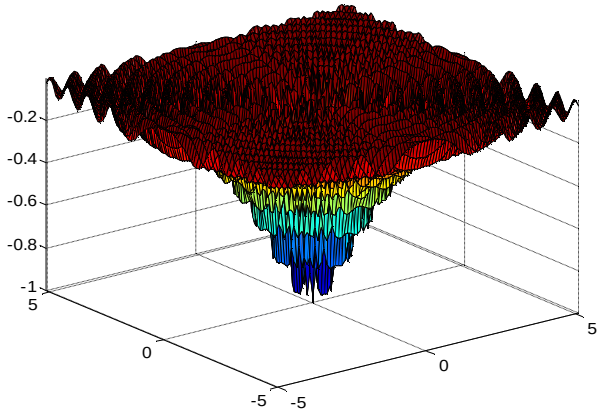


$$f_6 = \{0.002 + \sum_{j=1}^{25}[j + (x_1 - a_{1j})^6 + (x_2 - a_{2j})^6]^{-1}\}^{-1}$$

Where $(a_{ij}) = \begin{pmatrix} -32 & -16 & 0 & 16 & 32 & -32 & \dots & 0 & 16 & 32 \\ -32 & -32 & -32 & -32 & -32 & -16 & \dots & 32 & 32 & 32 \end{pmatrix}$

Test area is restricted to $-40 \leq x_i \leq 40$, i = 1....n. Its global minimum equal f(x) = 0.998 is obtainable for (x^*) = (-32, 32).

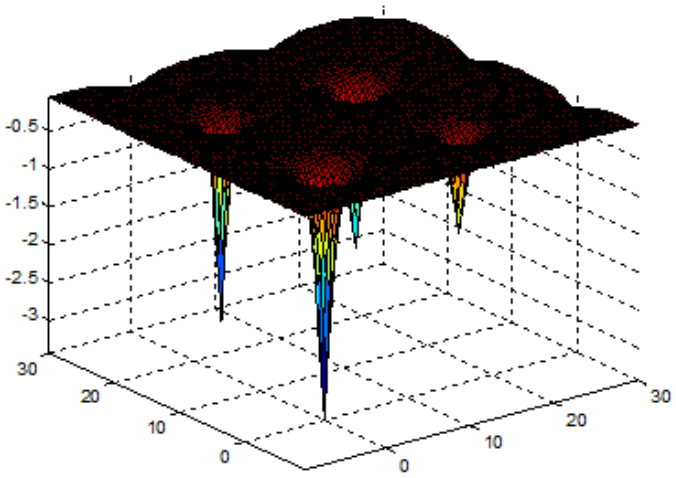
3.1.4.1.(7). F_7: Drop Wave



$$f_7 = -\frac{1+\cos\left(12\sqrt{x_1^2+x_2^2}\right)}{\frac{1}{2}(x_1^2+x_2^2)+2}$$

Test area is restricted to $-5.12 \leq x_i \leq 5.12$, i = 1,..., n. Its global minimum equal f(x) = -1 is obtainable for $(x^*) = (0, 0)$.

3.1.4.1.(8). F_8: Shekel

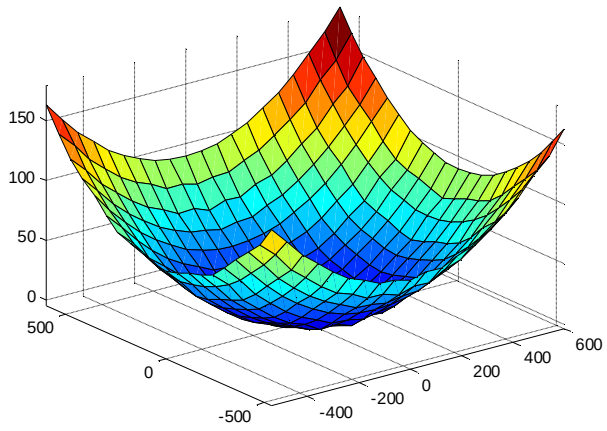


$$f_8 = -\sum_{i=1}^{m}(\sum_{j=1}^{n}[(x_i - a_{ij})^2 + c_{ij}])^{-1}$$

Where $(a_{ij}) = \begin{pmatrix} -32 & -16 & 0 & 16 & 32 & -32 & \dots & 0 & 16 & 32 \\ -32 & -32 & -32 & -32 & -32 & -16 & \dots & 32 & 32 & 32 \end{pmatrix}$

Test area is usually restricted to -10≤ x_i≤ 30, i = 1,..., n. Its global minimum equal f(x) = -3.43 is obtainable for (x^*) = (0, 0).

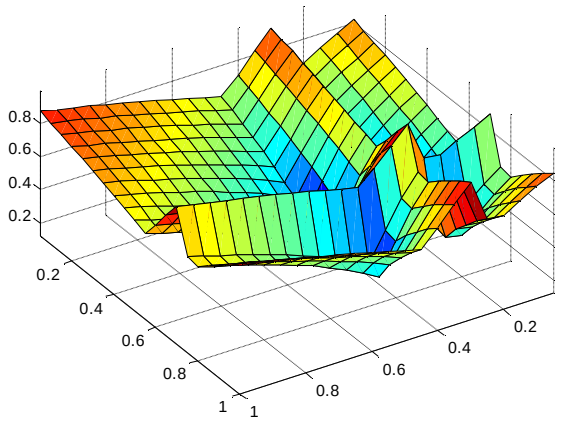
3.1.4.1.(9). F_9: Griewangk



$$f_9 = \frac{1}{4000}\sum_{i=1}^{n} x_i^2 - \prod_{i=1}^{n}\cos\left(\frac{x_i}{\sqrt{i}}\right) + 1$$

Test area is usually restricted to -600≤ x_i≤ 600, i = 1,..., n. Its global minimum equal f(x) = 0 is obtainable for $(x^*) = (0, 0)$.

3.1.4.1.(10). F_{10}: Deceptive



$$f_{10} = -\left[\frac{1}{n}\sum_{i=1}^{n} g_i(x_i)\right]^{\beta}$$

$$g_i(x_i) = \begin{cases} -\dfrac{x}{\alpha_i} + \dfrac{4}{5} & if\ -0 \le x_i \le \dfrac{4}{5}\alpha_i \\ \dfrac{5x}{\alpha_i} - 4 & if\ \dfrac{4}{5}\alpha_i \le x_i \le \alpha_i \\ \dfrac{5(x-\alpha_i)}{\alpha_i - 1} + 1 & if\ \alpha_i \le x_i \le \dfrac{1+4\alpha_i}{5} \\ \dfrac{x-1}{1-\alpha_i} + \dfrac{4}{5} & if\ \dfrac{1+4\alpha_i}{5} \le x_i \le 1 \end{cases}$$

Test area is usually restricted to $0 \le x_i \le 1$, i = 1,..., n *where* $\alpha_1 = 0.3$, $\alpha_2 = 0.7$ and $\beta = 2.5$. Its global minimum equal f(x) = 0 is obtainable for $(x^*) = (0.44, 0.76)$.

3.2. Method

3.2.1. Fitness Based Selection Mechanism

Fitness Based Selection aims to identify better individuals of the population that might be suitable for recombination. In SGA, selection is carried out in compliance with a fitness value. Fitness function is used to assign a selection probability to each individual. Tournament, Ranking and Roulette Wheel are the most common selection methods employed in many GA applications.

3.2.1.1. Roulette Wheel Selection Mechanism

The simplest selection scheme is Roulette-Wheel Selection Mechanism (RWSM). Each individual gets a selection probability proportional to its fitness value. RWSM emphasizes the better individuals in the population. This mechanism speeds up convergence to better solutions. On the other hand, this could cause loss of genetic diversity and may lead getting stuck on local optima.

3.2.1.2. Rank Based Selection Mechanism

In Rank-Based Selection Mechanism (RBSM), an individual's rank score (instead of the fitness value) is used to calculate selection probability. Firstly, individuals are arranged according to their fitness values. Then, a selection probability is assigned to each individual proportional to its rank in the population. This mechanism relatively protects the population diversity when compared to RWSM.

3.2.1.3. Tournament Selection Mechanism

In Tournament Selection Mechanism (TSM), a number of individuals, that is called tournament size, are chosen randomly from the population and the one which

has the highest fitness value is selected as one of the parents. The tournament size can vary from two to up any reasonable number.

3.2.1.4. Which Selection Mechanism?

Based on the selection schemes mentioned above, several researchers have attempted to derive good techniques to build better selection schemes for solving constrained problems. Jadaan et al. compared the results of GA between RWSM and RBSM using several optimization functions and reported that rank-based selection outperformed roulette based in number of generations to find the optimum solution (Jadaan et. al., 2005). The study demonstrated that RBSM is faster and more robust in the direction of the optimum solutions than fitness proportional RWSM.

Furthermore, Zhong et al. compared TSM with RWSM at seven general test functions and concluded tournament selection strategy is more efficient in converging to optimum solution than that of RWSM (Zhong et. al., 2005).

However, Julstrom analyzed the computing time efficiency of two types of rank-based selection probabilities; linear ranking and exponential ranking probabilities and compared them with TSM (Julstrom, 1999). The study revealed that TSM should be preferred to RBSM, because repeated tournament selection is a lot faster than sorting the whole population to assign rank-based probabilities.

The fitness value of an individual does not entirely depend on the basic fitness value that is how good a solution is, in the proposed selection mechanisms. This might sound a little bit confusing. When one talks about the fitness value of an individual in SGA, it means how good the solution for the problem is. The individuals that have better basic fitness values have more probability for reproducing. However, if we are talking about Assortitative-Dissortitative Mating, one has to have some other qualities besides having better basic fitness value in order to be advantageous for reproducing. This can be easily observed in human population. If the basic goal is to survive and pass one's own DNAs to next generations, one should select a mate that is strong and healthy. However, human society demands more than that. The qualities like beauty, wealth, reputation,

religion, race, etc., have importance while selecting a mate. When we talk about basic fitness value, we talk about satisfying the basic goal, health and survival, respectively. However, if we talk about a proper mate for an individual, the fitness value of a candidate partner should be weighted sum of his/her health, wealth, beauty, reputation, religion, etc.

Evaluation of the qualities mentioned above is critical. They can be evaluated either locally or globally. If we are talking about SGA, then we should satisfy the whole population's needs, global needs, in this case. However calculation of such extra information, similarity/dissimilarity for example, requires extra work and computational time. Identification process of each individual's similarity and dissimilarity to every other individual in a population has $O(N^2)$ complexity. However, if we use TSM, as Julstrom suggested (Julstrom, 1999), for selecting a partner for an individual, computation time will be substantially reduced. All those measurements have to be carried out with O(N) complexity.

As a conclusion, to show the advantages and disadvantages of ADM against pure fitness based selection mechanisms, TSM will be preferred as default selection mechanism. While time complexity of RWSM and RBSM is $O(N^2)$, TSM outstands with O(N) complexity.

3.2.2. The Proposed ADM

3.2.2.1. Background

The objective of the present study is to introduce a new selection methodology for (RC)-SGA, namely ADM and to evaluate its performance. Despite of the discussions in the preceding section, ADM is also applicable to RWSM and RBSM as well as TSM.

The fundamental motivation that led us to investigate ADM is that do the common phrase "opposites attract each other" and the adage "Birds of a feather flock together" really hold in the sense of genetic algorithms? There are numerous reported studies in relationship research area that supports the principle "similar attract" since

1961 (Newcomb 1961; Byrne 1971). Byrne, for example, reported strong linear relationship between degree of similarity and liking. Tests of the idea that “opposites attract” have been reported unsuccessful in general, despite similarity-attraction effect is now well established (Berscheid and Reis, 1998; Byrne, 1997) and widely accepted. It has to be reminded that all these efforts are made in relationship research field. Are there such relationships in genotypic characteristics?

Hardy and Weinberg Principle states that the gene pool of a population, that is mating randomly and is not subject to any other evolutionary process, will remain in equilibrium. However, in evolutionary algorithms, it is strongly desired to evolve from a randomly generated gene pool to the best possible gene that is optimum solution for the problem at hand. SGA does not contradict with Hardy and Weinberg Principle, because it incorporates other evolutionary processes such as, mutation, selection (favouring one to another through phenotypic traits).

On the other hand, in all human populations, people usually select mates non-randomly. Assortative Mating is a non-random mating pattern in which individuals with similar genotypic and/or phenotypic traits mate with each other more frequently than in random mating pattern. The term "assortative" designates classifying and selecting characteristics. For example, it is common for individuals of similar body size to mate with one another. Less commonly, in disassortative mating, also referred as negative assortative mating, individuals with dissimilar qualities mate more frequently than what would be expected in random mating. Both mating strategies cause the frequency of certain genotypes to differ from the frequencies anticipated by the Hardy-Weinberg Principle. Plant and animal breeders usually employ controlled positive assortative mating to increase the frequency of certain characteristics of the species and to reduce genetic variation in a population. By contrast, disassortative mating results in a greater number of heterozygote that is an organism possessing two dissimilar forms of a gene for a heritable characteristic, which may therefore produce offspring differing from the parents and each other in that characteristic.

Assortative and Dissortative mating strategies may enhance the exploitation and exploration abilities of SGA, respectively. Assortative mating promotes

reproduction among similar alleles resulting with increased numbers of offspring that strongly resembles to their parents. This process is analogous to exploitation characteristic of a good search algorithm. Plant and animal breeders usually employ controlled assortative mating to increase the prevalence of certain traits and to reduce genetic variation in a population. This, however, suggest that if assortative mating is not supervised carefully, it may result with loss of genetic diversity that is the main reason for premature convergence. Dennis O'Neil (http://anthro.palomar.edu/synthetic/Default.htm, 2013) states that "If brothers and sisters are mated together every generation, it will only take 20 generations for all individuals in a family line to share 98+% of the same alleles—they essentially will be clones, and breeding results will be close to those resulting from self-fertilization." This exemplifies how catastrophic the results of assortative mating can be.

Dissortative mating, on the other hand, is analogous to exploration characteristic of a search algorithm. The offspring will be diverging from their parents and allowing exploration for SGA. If carefully devised Assortative and Dissortative Mating Strategy (ADMS) may enhance the search capabilities of Evolutionary Algorithms.

ADMS is devised to be based on similarity/dissimilarity of Phenotypic/Genotypic traits between individual-individual/individual-population. An individual that is selected somehow for reproduction seeks a mating partner through TSM. A number of candidates that is equal to tournament size are evaluated according to their Attraction Scores. Attraction Score of a candidate is calculated from mixture of the following:

- Similarity and/or Dissimilarity
- Based on Phenotypic and/or Genotypic traits.
- Targeted to Population and/or Individual

Genotypic similarity/dissimilarity is a measure derived from structure of genes. In section 3.1.3.4.1, it has been indicated that the measure of similarity and

dissimilarity for binary chromosomes are calculated from Hamming Distance (Banzhaf et. al., 1998; Hamming, 1980). However, quantifying similarity/dissimilarity measure of real coded genes is harder than binary counterparts. Details of calculations can be found in section 3.1.3.4.1.2. While selecting a suitable mate, two different strategies can be chosen; similar/dissimilar individuals to self or similar/dissimilar individuals to the population. Both strategies promise to reproduce offspring that differ from their parents and the normal of the population.

The above discussion is valid for phenotypic characteristics as well. Therefore eight different ADM strategy can be constructed from three main features; similarity/dissimilarity, phenotype/genotype and population/individual. Figure 3.2 displays tree structure of these characteristics. Eight ADM strategies for selection can be listed as;

- Genotypic, Population based Similarity (GPS)
- Genotypic, Population based Dissimilarity (GPD)
- Genotypic, Individual based Similarity (GIS)
- Genotypic, Individual based Dissimilarity (GID)
- Phenotypic, Population based Similarity (PPS)
- Phenotypic, Population based Dissimilarity (PPD)
- Phenotypic, Individual based Similarity (PIS)
- Phenotypic, Individual based Dissimilarity (PID)

While genotypic measurement can be done in one method, phenotypic measurements can be varied by future researchers. For example; sexuality, kinship, neighbourhood, lifetime etc., can be considered as phenotypic traits of an individual. In this thesis, the strategies are limited only to eight. However, by combining one or more of these strategies, we can expand the possibilities to 256 different ADM strategies. By switching on and off each strategy, 2^8=256 different strategies can be obtained. It may be a good idea to consider an individual's, similarity to one's self and dissimilarity to the population, while selecting a mate. On the other hand, it may

be just waste of time to employ all of them together for mate selection. For the sake of completeness, all the combinations will be experimented and discussed in this study.

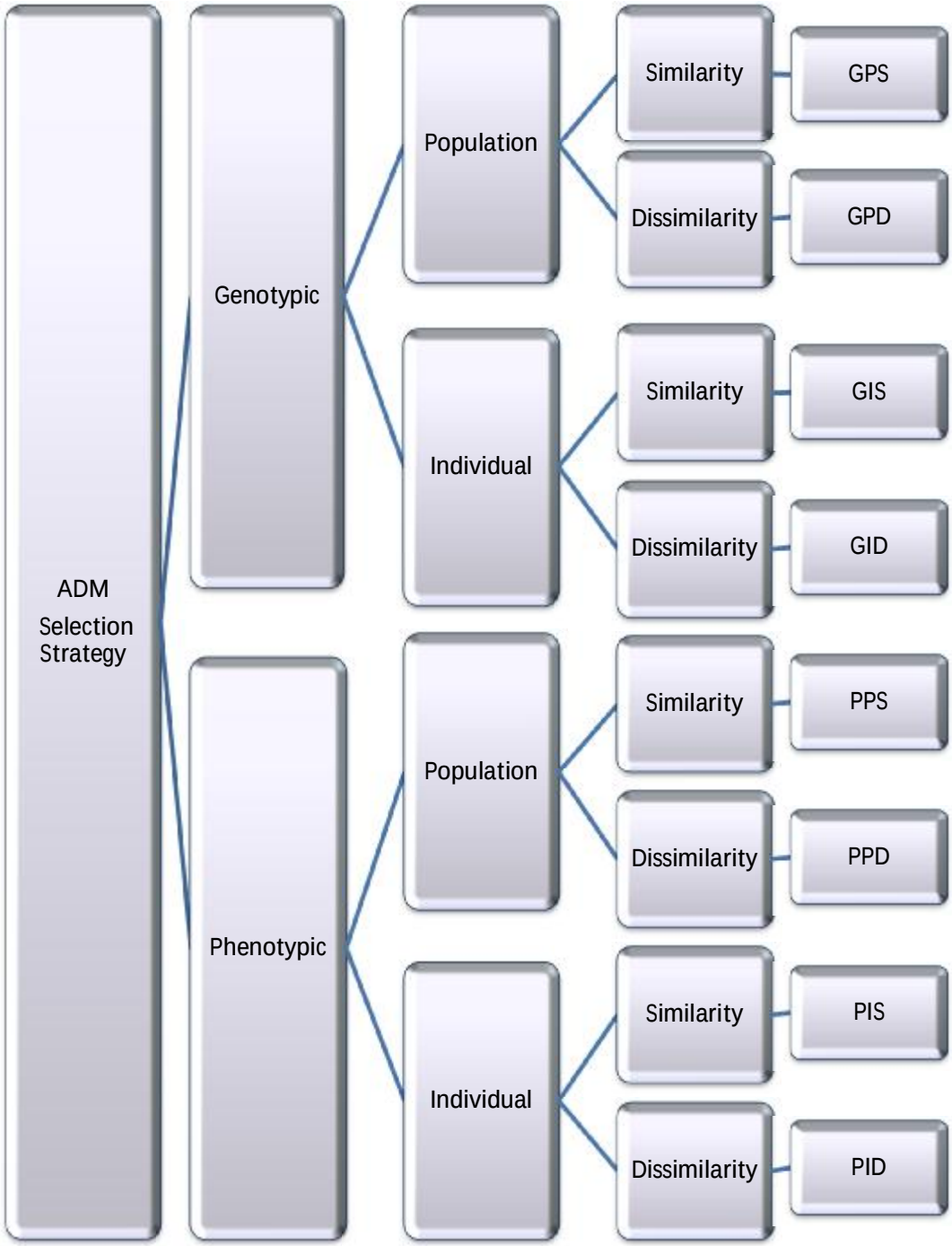


Figure 3.2 ADM selection strategy tree

3.2.2.2. Diversity Calculation

Diversity of two binary chromosomes can be calculated as the average dispersion of genes. It can be easily calculated from Hamming distance that is the sum of absolute difference of corresponding binary genes. However, for real coded genes, Hamming Distance is not applicable. In such cases Euclidian Distance, the most commonly used distance metric in the literature, can be used to measure the distance between two solutions points (chromosomes) in the search space. However, real coded genes may vary in extremely different ranges. While some of the genes may have values spanning in a narrow range with extremely small magnitudes, some others may have extremely large values with large dispersion. In such cases, the sum/average of Euclidian distances between corresponding genes may not reflect true diversity of chromosomes. Solution to this problem is the normalization of data prior to its usage.

In order to adjust values measured on different scales to a notionally common scale, often prior to averaging, is called normalization. Min-Max normalization, for example, is the process of taking data measured in its units and transforming it to a new value between 0.0 and 1.0. The lowest value in the data set is set to 0.0 and the highest value is set to 1.0. By this way, the values that are measured using different scales (for example degrees Celsius and degrees Fahrenheit) or different units of measure (speed and distance) can be comparable.

However, if there is a small number of data that substantially differ from the rest, normalization range [0-1] would not be used efficiently. For example, if the data set A={1,1000,1001,1002,1000,2000,90000} is Min-Max normalized, apart from minimum and maximum values, the remaining data will have new values in the range of (0.01-0.02). This displays that the full range would not be used. Considering GA problem, there is a strong possibility that some of the offspring or mutated individuals will be extremely differing from the population, especially after few generations. Existence of such extreme values in a data set makes the Min-Max minimization unsuitable for the purpose.

Standard score that measures the sigma distance of actual data from the average can be used instead of Min-Max normalization. It is, as desired, a dimensionless quantity derived by subtracting the population mean from an individual data and then dividing the difference by the population standard deviation. It is given as

$$z = \frac{d - \mu}{\sigma}$$

where; d is a data, μ is the mean of the population, σ is the standard deviation of the population and z is the standard score that can have negative and positive value. Figure 3.3 illustrates the normal distribution of the population around the mean value and z scores.

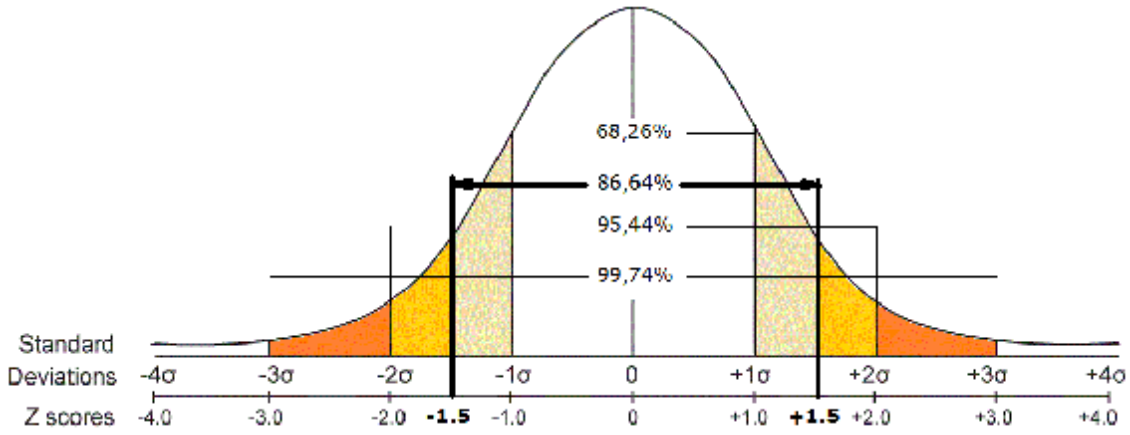


Figure 3.3. Plot of normal distribution

As it can be seen from the Fig. 3.3, one standard deviation around the mean covers 68.26% of whole population. Two and three standard deviations around the mean include 95.44% and 99.74% of the population, respectively.

Representing real valued genes with z scores allow us to use dimensionless values proportional to dispersion of population. Furthermore, regardless of how diverse are the range of the genes, we can confidently use arithmetical operations on the z scores. In the meantime, we desire to calculate a diversity score that is limited in the range of [0-1]. Depending on the value of a gene it may have such z scores that as big as tens, hundreds, thousands, even in extreme cases billions. This may sound

preposterous but that is possible if do not prevent such cases. Clipping-off the genes after a certain z score can guarantee not to face such cases. Then, a threshold z value (z_{th}) should be determined.

Since 99.74% of the population lay within z=±3, it may be plausible to set maximum and minimum values of a gene to +3 and -3 respectively. On the other hand, selecting z_{th}=±2 will still cover most of the population (as much as 95.44%). In case of z_{th}=±3 one third of whole ***z*** score range will be reserved for only 4.3% of the population. That means the whole range will not be used effectively. Selecting z_{th}=±1.65, however, covers 90% of the population and upper and lower halves of the whole range covers 31% and 59% of the population. The remaining 10% is rounded to the upper boundary as the extreme values.

3.2.2.3. Foundation of Diversity Measures:

Genotypic or phenotypic diversity of a chromosome can be calculated as the sum of the distances between the genes of an individual and some reference points. If the desired diversity measure is individual based then calculations are carried out between two individuals. In this case the reference point, pointed out previously, is another chromosome. However if we want to measure an individual's diversity from the whole population, then the reference point is the mean traits of whole population.

Regardless of whether diversity measure is population or individual based, the basic statistical properties of the population have to be calculated. Mean and standard deviation of a certain gene can be calculated from Equation 3.1 and 3.2, respectively.

$$\mu(\gamma_k) = \frac{1}{N}\sum_{i=1}^{N} {}^{\gamma_k}C_i \qquad (3.1.)$$

$$\sigma(\gamma_k) = \sqrt{\frac{1}{N}\sum_{i=0}^{N}\left({}^{\gamma_k}C_i - \mu(\gamma_k)\right)^2} \qquad (3.2.)$$

where: $\mu(\gamma_k)$ and $\sigma(\gamma_k)$is population mean and standard deviation of gene γ_k, respectively. The letter γ is used for symbolizing gene and the letter k is used to indicate the index of a particular gene in a chromosome *C*. *N* is the population size.

In order to eliminate the chromosomes' range effect, discussed earlier, z scores should be used for calculations. Throughout the calculations we need to use absolute z scores that is given in Equation 3.3:

$$\dot{z}(Q,R,\sigma) = \frac{|Q-R|}{\sigma} \tag{3.3.}$$

where; R is a reference point (usually mean), σ is the standard deviation and Q is the data to be evaluated for diversity. As it can be expected, absolute z score ($\dot{\boldsymbol{z}}$) may have values in unlimited ranges. Since we are dealing with diversity, any $\dot{\boldsymbol{z}}$ value that is larger than a threshold value (z_{th}) can be confidently clipped off to an upper boundary. Any absolute z score ($\dot{\boldsymbol{z}}$) larger than this threshold z score will be evaluated highly differing from reference point. Normalized Absolute z Score ($\ddot{\boldsymbol{z}}$) will limit the scores to be in the range of 0 and 1, and given as

$$\ddot{z}(Q,R,\sigma) = \frac{\dot{z}(Q,R,\sigma)}{z_{th}} \tag{3.4.}$$

3.2.2.4. Genotypic Diversity

Genotypic diversity can be measured in two ways; between two chromosomes or between chromosome and population mean. In either case, Normalized Absolute z Score ($\ddot{z}$) (Equation 3.4) provides us the power of dimensionless and normalized difference measuring capability. Genotypic diversity between two chromosomes ($^{ind}_{g}\delta$) can be calculated from Equation 3.5.

$$ {}^{ind}_{g}\delta(C_a, C_b) = \frac{1}{2\gamma_c}\sum_{k=1}^{\gamma_c} \ddot{z}\left({}^{\gamma_k}C_a, {}^{\gamma_k}C_b, \sigma_k\right) \quad (3.5.)$$

where, ${}^{ind}_{g}\delta(C_a, C_b)$ is genetic individual diversity (${}^{ind}_{g}\delta$) between two chromosomes C_a and C_b , γ_c is the number of genes in a chromosome and $\ddot{z}\left({}^{\gamma_k}C_a, {}^{\gamma_k}C_b, \sigma_k\right)$ is Normalized Absolute z Score for k[th] gene of chromosomes C_a and C_b. σ_k is the population standard deviation of k[th] gene.

$$ {}^{pop}_{g}\delta\left(C_a, \mu(\gamma_k)\right) = \frac{1}{\gamma_c}\sum_{k=1}^{\gamma_c} \ddot{z}\left({}^{\gamma_k}C_a, \mu(\gamma_k), \sigma_k\right) \quad (3.6.)$$

Genotypic diversity between a chromosome and the population mean (${}^{pop}_{g}\delta$) can be calculated using Equation 3.6. It is measured in a similar fashion with Equation 3.5. The first difference is in the reference point for calculation of normalized absolute z score. It is, naturally, the population mean ($\mu(\gamma_k)$) rather than being another chromosome. Secondly, the absence of coefficient 2 at the denominator. The distance between two chromosomes that are located at the lower and upper ends of the range is double of the distance between a chromosome located at the lower or upper end of the range and the mean of the population. Therefore, while calculating individual diversity the range should be divided by two.

3.2.2.5. Phenotypic Diversity

Phenotypic diversity calculations, as in genotypic diversity calculations, are made between two chromosomes or chromosome and population mean. Phenotypic measure of a chromosome has been chosen as its fitness value. Even though, fitness of a chromosome is related to its genes, same fitness values can be obtained from different chromosome structures. Fitness of a chromosome can be thought as a measure of how wealthy, healthy, or handsome, is the individual.

Phenotypic diversity between a chromosome and the population mean (${}^{pop}_{ph}\delta$) is equal to normalized absolute z score ($\ddot{z}(f_{C_a}, \mu_f, \sigma_f)$) and given in Equation 3.7 as;

$${}^{pop}_{ph}\delta(f_{C_a}, \mu_f) = \ddot{z}(f_{C_a}, \mu_f, \sigma_f) \quad (3.7.)$$

where, f_{C_a}, μ_f and σ_f are fitness of chromosome 'a', mean fitness of whole population and standard deviation of population fitness, respectively.

Phenotypic diversity between two chromosomes (${}^{ind}_{ph}\delta$) is equal to half of normalized absolute z score ($\ddot{z}(f_{C_a}, f_{C_b}, \sigma_f)$) and given in Equation 3.8. as;

$${}^{ind}_{ph}\delta(f_{C_a}, f_{C_b}) = \frac{1}{2}\ddot{z}(f_{C_a}, f_{C_b}, \sigma_f) \quad (3.8.)$$

where, f_{C_a}, f_{C_b}, and σ_f are fitness of chromosomes 'a', 'b' and standard deviation of population fitness, respectively.

3.2.2.6. Selection Score Calculation

Traditional selection mechanisms are built on the principle of "survival of the fittest" to converge to optimum solution. Like the most of GAs, proposed selection mechanisms also, employ fitness value in conjunction with the ADM strategies for selection procedure. Each mechanism (Fitness + ADM) affects the mate selection strategy relatively through their selection scores; Fitness Score (FS) and ADM score.

3.2.2.6.(1). Fitness Score (S_f)

Each individual's Fitness Score (S_f) is directly linked to normalized absolute z score ($\ddot{z}(f_{C_a}, \mu_f, \sigma_f)$) of its fitness. If the objective is minimization, in order to assign greater probabilities to individuals having smaller fitness values, fitness scores are

assigned in inverse proportion to the original fitness. In order to assign greater probabilities to individuals with less fitness values, the fitness values are reversed as in Equation 3.9.:

$$S_f(C_a) = 1 - S_f(C_a) \tag{3.9.}$$

3.2.2.6.(2). ADM Scores

The ADM based mechanisms define a selection score of individuals depending on some measure of distance of the candidate solutions which are based on three subjects: similarity/dissimilarity, individual/population and phenotypic/genotypic. Depending on a selected strategy, it may favour the production of additional diversity (Dissortative Mating) or the refinement of the solutions (convergence, Assortative Mating). These strategies are: PPS, PPD, PIS, PID, GPS, GPD, GIS and GID. The first letters of each strategy indicates whether the strategy is based on (P)henotypic or (G)enotypic traits. The second letters indicate whether the reference point for the measurements is (P)opulation mean or another (I)ndividual. The third letter indicates the measurement type (S)imilarity or (D)issimilarity.

$$\text{PPS}(C_a, R) = 1 - {}^{pop}_{ph}\delta\left(f_{C_a}, f_R\right) \tag{3.10.}$$

$$\text{PPD}(C_a, R) = {}^{pop}_{ph}\delta\left(f_{C_a}, f_R\right) \tag{3.11.}$$

$$\text{PIS}(C_a, R) = 1 - {}^{ind}_{ph}\delta\left(f_{C_a}, f_R\right) \tag{3.12.}$$

$$\text{PID}(C_a, R) = {}^{ind}_{ph}\delta\left(f_{C_a}, f_R\right) \tag{3.13.}$$

$$\text{GPS}(C_a, R) = 1 - {}^{pop}_{g}\delta(C_a, R) \tag{3.14.}$$

$$\text{GPD}(C_a, R) = {}^{pop}_{g}\delta(C_a, R) \tag{3.15.}$$

$$\text{GIS}(C_a, R) = 1 - {}^{ind}_{g}\delta(C_a, R) \tag{3.16.}$$

$$\text{GID}(C_a, R) = {}^{ind}_{g}\delta(C_a, R) \tag{3.17.}$$

The ADM scores of a chromosome (C_a) are calculated from Equations 3.10.-3.17. However, a careful eye will easily spot that if any strategy pair that share same letters for the first two letters always result with a sub total score of 1 (the other terms will cancel out each other). In order to prevent this, only one score is calculated for the strategies that are complementary of each other (PPS-PPD for example). The joint strategies ADM score can be calculated from Equation 3.18.

$$\text{KLM}(C_a, R) = |1 - 2 * {}^{L}_{K}\delta(C_a, R)| \quad (3.18.)$$

where K, L and M are substitutes of the first, second and third letters of the ADM strategies, respectively. Figure 3.4 illustrates the Equation 3.18 in graphical terms. It has to stress out that only one joint score will be calculated rather than two separate scores. As it can be observed from the Figure 3.4, if diversity score of strategy KL(D) is ${}^{L}_{K}\delta(C_a, R) = 0.1$, it means chromosome C_a closely resembles to the reference point. In this case if KL(S) is also to be calculated then modified joint ADM score will be 0.8. For an individual that has ${}^{L}_{K}\delta(C_a, R) = 0.5$, that is neither so diverse, nor so similar, joint ADM score will be 0, as expected.

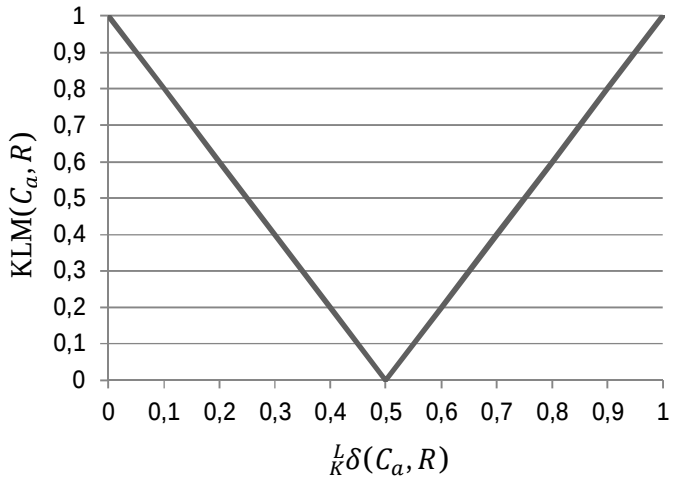


Figure 3.4. Joint ADM score.

One more point that has to be mentioned is, if the selection strategy is based on population, then both of the individuals are selected by the help of diversity

measurement. However if the selection strategy is based on individuals, then only selection of second person employs diversity measurement, since the reference point is the first individual. Finally total ADM score of an individual for selection is calculated from Equation 3.19;

$$\begin{aligned} &\text{ADMS}(C_a,\text{R})= \\ &\boldsymbol{\beta}[\ \text{PPS}(C_a,\text{R})+\text{PPD}(C_a,\text{R})+\text{PIS}(C_a,\text{R})+\text{PID}(C_a,\text{R})]+ \\ &\boldsymbol{\lambda}\ [\text{GPS}(C_a,\text{R})+\text{GPD}(C_a,\text{R})+\text{GIS}(C_a,\text{R})+\text{GID}(C_a,\text{R})] \end{aligned} \tag{3.19.}$$

where, coefficients, β and λ, are used as scaling factor to adjust the effects of phenotypic and genotypic features and $\text{ADMS}(C_a, R)$ is the Assortative/Dissortative Mating selection score of a chromosome C_a.

3.2.2.6.(3). Final Selection Score

In this thesis, two scoring mechanisms; Fitness Score (Equation 3.9) and ADM Score (Equation 3.19) have been discussed for mate selection. Equation 3.20 fuses these two scoring mechanisms together to obtain a total selection score of a candidate mate;

$$\text{SS}(C_a, R) = \alpha S_f(C_a, R) + \text{ADMS}(C_a, R) \tag{3.20.}$$

As shown in Figure 3.2, the mating scheme is divided into eight operation modes depending on the strategies to choose Parent A and Parent B. Then this operation mode is combined with traditional fitness based method. In addition to this combination, the scaling factors α, β and λ are added to equation to adjust the influence of each mechanism. The operation modes with α =1, β=0 and λ=0 is the same as the standard fitness-based tournament selection. Also the case α =0, β=1, λ=1 is also actually the opposite of the case of as α =1, β=0 and λ=0 is, because two candidates will be evaluated with only their similarity or dissimilarity. In those

studies, the values of α, β and λ were fixed throughout the 1. All the strategies are examined in section "Result and Discussions" while some of them are recommended.

4. RESULTS AND DISCUSSIONS

To investigate the performance of ADM strategies ten real valued, well known benchmark test functions were employed. These global optimization test problems consist of different levels of complexity and multimodality including unimodal and multimodal functions. Several quantities are used to measure and compare the performances of the suggested strategies. The primary ones are the average fitness, median fitness and best fitness.

4.1. Experimental Setup

In order to evaluate the performance of a suggested strategy, various parameters have to be taken into consideration. Population size, maximum number of generations, mutation and crossing over rates has to be tuned up for best performances. Ideally all of these parameters should be defined from an experimental setup that each parameter should gradually incremented or decremented from a base line with a predefined step size. For example, changing population size from 10 to 200 with step size 10 will result testing 20 different settings. Without giving too much detail let's say we test 10 different values for mutation rate, 50 different values for crossing over rate. May be, 10 different maximum numbers of generations settings, 5 different tournament size settings etc. should be tested for each one of 256 ADM strategies. Table 4.1 displays hypothetic setup possibilities for adjustable parameters;

Table 4.1. Adjustable parameters and their setting counts

Parameters	**Count**
Number of ADM Strategies	256
Number of test functions	10
Number of Population size settings	20
Number of mutation settings	10
Number of Cross over settings	50
Number of generation settings	10
Number of Tournament size setting	5
Number of Elitism settings	10
Number of child number settings	5

Such hypothetical setup requires 64 trillion combinations. In order to decrease the effect of randomness on the results (Hamzacebi, 2008), if we repeat the tests with 15 different random seed values, we will come across with 960 trillion settings. This value is just for experimental setups. In each experimental setup the algorithm needs to execute huge numbers of operations. Within the limited time of this study, it is almost impossible to complete the tests.

Table 4.2. Preliminary GA parameters used in determining GA strategies

GA Parameter	**Preliminary Value**
Population Size	30
Tournament Size	3
Maximum Number of Generations	200
Elitism	10(%)

Therefore we need to decide as much parameter as possible with commonly accepted practices without testing. Commonly it is accepted the population size to be at least 10 times greater than the variable number (Shopova and Vaklieva-Bancheva, 2006). Since the problem domain is in two dimension 30 will be sufficient enough

for population size. Similarly, 10% elitism is widely practiced value in the literature. We can confidently set the maximum number of generations to 200, since preliminary experiments showed that all the strategies have converged to a certain solution well before 200 generations. Tournament size is also can be set to 3, since it is the most common setting in the literature. All these parameters are listed in Table 4.2.

Having all these, crossover and mutation rates that produce the best optimization results individually for each test function have been determined by testing 500 different combinations for each benchmark test function. Deciding the remaining parameters beforehand, the number of tests required to set the optimum parameters was reduced to 7500. Table 4.3 lists optimum crossover and mutation rates for each benchmark functions after tuning up.

Table 4.3. Mutation and crossover parameters for benchmark functions

Function	Mutation Rate (%)	Crossover Rate (%)
Rosenbrock	0	75
Rastrigin	3	91
Schwefel	9	88
Ackley	8	94
Langerman	0	78
Fifth function of De Jong	4	71
Drop wave	3	93
Shekel	9	71
Griewangk	6	96
Deceptive	9	93

It has to be emphasized that mutation and crossover rates are optimized just and only for (RC)-SGA. The suggested ADM strategies have been thought as enhancer(s) of any GA type reported in the literature. So in order to increase

population diversity and enhance the searching capacity of a genetic algorithm, the suggested strateg(y)ies can be easily add on into the any existing algorithm.

Test results that include minimum, maximum, average, best and worst fitness values that are obtained from fifteen independent run for Rosenbrock function is given in Appendices. Also, the results for each test function can be found in http://bmb.cu.edu.tr/skartal/thesis/ GA_ADM_Selection.html.

4.2. Performance comparisons of ADM-RCGA

In GA literature, the performance of the GA is usually measured on two basic criteria; reliability and efficiency. Reliability evaluates how much of the search space is scanned, in other words, it measures level of dispersion. Efficiency, on the other hand, measures the rate of convergence. In the present study, standard deviation is employed to compare the reliability of algorithms. It points out the level of scattering in obtained solutions. Bigger standard deviation denotes more scattered and reliable solutions. However, smaller standard deviation means lower level dispersion which can cause to premature convergence. The average fitness of the population is used to present the efficiency of solutions.

4.3. Comparisons of ADM Strategies

In this thesis, 255 different ADM strategies examined to observe their effects on (RC)-SGA. It has been observed that while some of the strategies have positive effect on the performance of RC-SGA, a large portion of the devised strategies have negative impact. This may be the result of experimental setup. Because, in this study, we intended to suggest an enhancer add on to a standard GA. In order to observe the enhancer's performance, all the parameters are tuned up for the standard GA. This has been done just for research purposes. Of course, in practice we should tune up the whole algorithm (SGA+ADM) to obtain the best performance. It has to be pointed out that if we had enough time to tune up every strategy for every function

there may be a chance to improve the results. However as stated earlier on, time limits of this study prevents us to investigate further more.

Even though 255 ADM strategies are suggested, most of them are in the list just for the sake of completeness. Some of the ADM components, for example, promise to provide exploration (GPD, GID, etc.), some others hint to provide exploitation (GPS, GIS, etc.). Combination of different components will have varying effects on the algorithm. If there is enough time, one can always test all of ADM strategies, and identify the best one accordingly. However this may not be possible in every case. So, we feel obliged to suggest better performing components for any type of problem.

In order to identify the components that have strong positive or negative effect on overall performance of SGA, some numerical methods should be employed. In statistics, factor analysis or principal component analysis are such methods that can identify the major elements effecting the problem. However both of the methods rely on statistical measures like standard deviation and mean. In our case, however, an ADM strategy component (PPD, GIS, etc.) is either exist or not exist in a strategy. Therefore it is in binary form. Mean of any component in 255 strategies is 0.5 and standard deviation is also equal to 0.5. Therefore factor analysis and principal component analysis cannot be used since all the components have the same statistical measures. We need to devise a method to evaluate each components performance. Following sections are dedicated to introduce these methods.

4.4. The proposed Component Performance Evaluation Method

This section describes a method to identify the common components of ADM strategies that have strong positive or negative effect on overall performance of GA. In order to achieve this, for each benchmark function, average fitness values of 255 ADM strategies and (RC)-SGA are calculated and arranged in descending order from the best one to the worst. The best performing strategy has the rank score of 256 and the worst has 1. If a component is frequently exist/non-exist in the good/bad solutions, it is assumed that this component has positive/negative effect on the

performance. The simplest way to calculate the observation frequency of a component among the successful/failed strategies is to calculate its percentage in a certain portion of sorted list. That portion can be located in either sides of (successful or failed strategies) sorted list. However, to be more precise, we suggest the use of a total rank score gathered from the whole strategies for each component.

Total rank score of a component can be minimum =8,256 or maximum =24,640. According to the distribution of a component's existence in sorted list, its rank score will have a value within the range of [8,256-24,640]. If a component gathers 8,256 total rank score we can say that this component has 100% negative effect on the performance. If it scores 24,640 then we can claim that it has 100% positive effect.

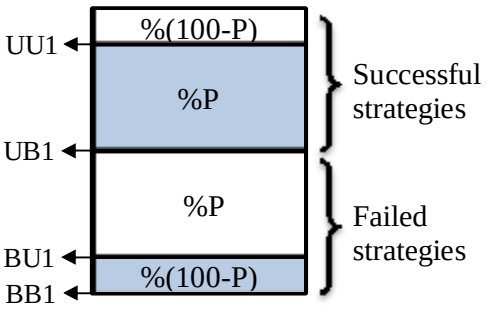


Figure 4.1.The worst possible distribution of %P successful component

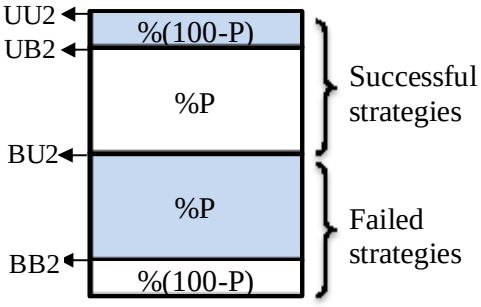


Figure 4.2. The best possible distribution of %P failed component

We have divided the sorted list in two halves. The strategies located at the upper half of this list are called *successful ADM strategies (Figure 4.1.)* and the ones at the lower half are called *failed ADM strategies (Figure 4.2.)*. Let's assume that component ***C*** is observed in ***P***% of the successful ADM strategies. The component ***C*** could be observed in any distribution as long as it satisfies P% of it, is in the upper half. Since, distribution can vary, a threshold value for being P% of the observations in the upper half ( ) has to be calculated (Equation 4.1). This can be achieved by considering P% of the observations are located at the bottom of upper half (as illustrated in Figure 4.1.) and the remaining (100-P)% of the observations are at the bottom of bottom half.

$$ {}^{S}_{P}R_{Th} = \frac{UU1*(UU1+1)}{2} - \frac{UB1*(UB1+1)}{2} + \frac{BU1*(BU1+1)}{2} - \frac{BB1*(BB1+1)}{2} \quad (4.1.) $$

$$ {}^{F}_{P}R_{Th} = \frac{UU2*(UU2+1)}{2} - \frac{UB2*(UB2+1)}{2} + \frac{BU2*(BU2+1)}{2} - \frac{BB2*(BB2+1)}{2} \quad (4.2.) $$

UU1, UB1, BU1, BB1, UU2, UB2, BU2 and, BB2 denote the top and bottom indexes used in calculation of success and failure limit values. Similarly, a threshold value for being P% of all observations in the bottom half (${}^{F}_{P}R_{Th}$) (in failed ADM strategies) can be calculated from Equation 4.2.

In order to calculate whether component C is P% successful or not, an iterative process has been applied. P has been changed from 100 to 71* and ${}^{S}_{P}R_{Th}$ and ${}^{F}_{P}R_{Th}$ are calculated and checked for every component whether their total rank scores exceeds these threshold values. If a component's total rank score is higher than ${}^{S}_{P}R_{Th}$ it has been noted that this component has P% success rate (P_s=P and P_F=0) and it has P% positive effect on overall performance. If a component's total rank score is lower than ${}^{F}_{P}R_{Th}$ it has been noted that this component has P% failure (P_s=0 and P_F=P) and it has P% negative effect on overall performance. If neither of the cases are satisfied then P is reduced and the test is repeated with the new P value. P_S or P_F are nothing different than P value but has sub-indices stating whether this P value for (S)uccess or (F)ailure.

Once a component's effect is identified, it is excluded from the remaining tests. For example, let's assume that we identified component GPD has positive effect with P% success. All the strategies that do not include component GPD are removed from the sorted list and all the calculations for the remaining components restarted with the reduced list. Since the remaining components could not achieve more success than GPD, success rate P will not be reset. The remaining calculations are carried out with the reduced list, since the component's effect is known. If a component is identified as having negative effect on performance, removing any ADM strategy containing this component from the list will prevent its interference to the remaining components.

* ${}^{S}_{P}R_{Th}$ and ${}^{F}_{P}R_{Th}$ overlap when P value reaches 71.

Table 4.4 $P_{S/F}$ values of each component for each benchmark function.

Test functions	**Methods**															
	GPS		**GPD**		**GIS**		**GID**		**PPS**		**PPD**		**PIS**		**PID**	
	P_S	P_F	P_S	P_F	P_S	P_F	P_S	P_F	P_S	P_F	P_S	P_F	P_S	P_F	P_S	P_F
F1	-	89	94	-	-	81	74	-	71	71	74	-	-	72	71	71
F2	-	85	87	-	-	86	76	-	-	72	79	-	71	71	71	71
F3	-	88	95	-	-	76	72	-	-	75	78	-	71	71	71	71
F4	-	86	89	-	-	80	76	-	-	77	83	-	-	76	71	71
F5	-	88	89	-	-	81	73	-	-	79	82	-	-	75	73	-
F6	-	88	93	-	-	78	73	-	-	77	74	-	-	75	72	-
F7	-	87	89	-	-	83	76	-	-	76	79	-	71	71	72	-
F8	-	90	90	-	-	76	71	71	-	77	74	-	71	71	71	71
F9	-	90	90	-	-	82	74	-	-	78	78	-	71	71	72	-
F10	-	84	87	-	-	81	73	-	-	78	85	-	-	78	74	0
Average	0,00	87,50	90,30	0,00	0,00	80,40	73,80	7,10	7,10	76,00	78,60	0,00	28,40	73,10	71,80	35,50
Median	0,00	88	89,5	0,00	0,00	81	73,5	0	0	77	78,5	0,00	0	71,5	71,5	35,5
Status	OFF		ON		OFF		ON		OFF		ON		OFF		ON	
Confidence	Strong		Very Strong		Strong		Weak		Mild		Mild		Weak		-	

Table 4.4 shows the corresponding Success (P_S) or Failure (P_F) values, achieved by 8 different ADM methods for benchmark test functions. Recommendation confidence labels are arranged as in Table 4.5.

Table 4.5. Recommendation confidence labels.

Label	**Lower Boundary P%**	**Upper Boundary P%**
Very Strong	90	100
Strong	80	89.99
Mild	75	79.99
Weak	71.99	74.99
-	71	71

It shown in Table 4.4 that the GPD exhibits ***very strong*** relationship with average 90.30% and median 89.5% P_S value. We can confidently suggest that the ADM strategy you select for your problem should include GPD component. On the other hand, GPS and GIS have ***strong*** negative effect on the performance with average 87.50% - 80.40% and median 88% - 81% P_F values, respectively. Therefore it is strongly not recommended to use GPS and GIS components in any ADM strategy. Deciding on three components with high confidence, the number of appropriate ADM strategies for a problem decreases to 32. Furthermore, with ***milder*** confidence level, we can recommend to include PPD component and not to include PPS component in an ADM strategy.

If 'Status' row of Table 4.4 is closely inspected, we can clearly observe that any component that has similarity measure embodied into, has negative effect on the overall performance. Similarly, it can be seen that dissimilarity has the opposite effect. GID component, however, has weak positive effect among the dissimilarity based components. Since the bottom level for success rate P_S is 73.8%, 73.5% is slightly over the critical value.

As a result, we can conclude the ADM strategies that work on the concept of diversity, especially genetic-based approaches, provide higher efficiency when added on to SGA. The similarity based components cause SGA to demonstrate poor-performance. Also, the population based approaches provide higher efficiency than individual based methods.

4.5. Detailed Evaluation of Rosenbrock Valley (F_1)

Previous section was dedicated to identify performance effect of ADM strategy components. Can we rely on the proposed performance evaluation method? In this section we intend to evaluate the performance test results in another way. Figure 4.3 is arranged to display the relationship between the components and their performance visually. Each ADM strategy corresponds a column in the image. If a component is active (ON) in a strategy it is painted with a color rather than white. Because white means the component is not used (OFF) within the strategy. ADM strategies are sorted from the best (Left hand side) to the worst (Right hand side) performance.

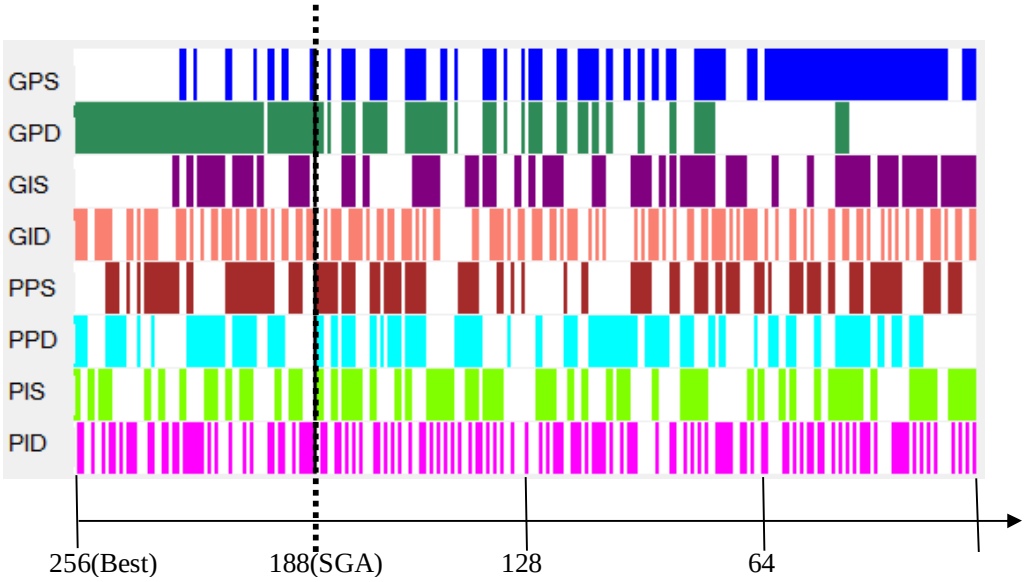


Figure 4.3. Existence of ADM components in strategies.

Visual inspection of Figure 4.3 strongly agrees with the findings of proposed performance evaluation method. Left hand side of GPD row is heavily painted with green, because the most successful strategies are those consist of GPD. Furthermore, we can easily observe that failed ADM strategies (located at right hand side) rarely employ GPD component.

The same discussion can be made for GPS, but in opposite way. GPS is heavily distributed in failed ADM strategies. It can be occasionally observed in successful ADM strategies too (at least more often than what GPD does in failed ADM strategies). This is also in agreement with the recommendation confidence levels for GPD (Very Strong) and GPS (Strong).

GIS component is also quite distinguishable, mostly distributed in failed ADM strategies region but it can be observed throughout the scale. If we recall its average 80.40% and median 81% P values, we should set a recommendation confidence level of 'Strong'.

It is quite obvious from the visual inspection of Figure 4.3, the status of three components GPS, GPD, GIS should be set as OFF, ON and OFF, respectively. This is in total agreement with the findings of Table 4.4.

Additional to above discussion, the components GID and PIS displays a behavior that evenly distributed throughout the scale. This can be interpreted as the components may have no direct effect on the performance. That is in agreement with Table 4.4 where they are labelled as 'Weak'. We should also consider the effect of components on each other. Rankings are made in the existence of all ADM strategies which most of them are there just for the sake of completeness of experiments. As soon as a component's effect on the performance is identified, it should be excluded from the following discussions, since it may affect the performance of the other components.

Figure 4.4. Existence of PID component in the ADM strategies which are located underneath the window.

In order to quantify the visual data presented in Figure 4.3, the following operations have been applied to each component. A sliding window with the size of 16 has been used to find the number of existence of a component in the ADM strategies which are located underneath the window (Figure 4.4.). The graphs that are obtained from sliding windows for each component are given in Figure 4.5. The effects of GPS and GPD components are clearly displayed. The slope of regression line fitted for the GPS count is 0.059 and positive. That means it has negative effect on the performance of ADM strategies. If we rescale GPS count axis to 256 rather than 16, the slope will be 16*0.059=0.94 which is almost 1. That shows strong negative correlation. If we look at the graph that is drawn for GPD component, the slope is 0.075 and negative (0.075*16=1.2). In this case we can say that GPD has very strong positive effect on the performance. We can conclude on GIS as it has milder negative effect than GPS and it should not be used on ADM strategies.

Remaining five components, on the other hand, have slopes that almost flat. This can be resulted from the oppressing effect of dominant component GPS and GIS that are already decided having strong negative effect on the performance. Keeping component GPD 'ON' and omitting the components GPS and GIS, we will have 32 different ADM strategies. In all of the remaining strategies, there will be GPD component but no GPS and GIS components. Table 4.6 documents the new ranks and old ranks of each ADM strategy. (Note that '1' means that component exists in the ADM strategy.)

SGA is located at the bottom third row in Table 4.6. The remaining ADM strategies are the ones with ranks 256 through 229 and 198,199,186,187. Average old rank scores is calculated as 236. That means discarding GIS and GPS components from the ADM strategies resulted with higher performing strategies.

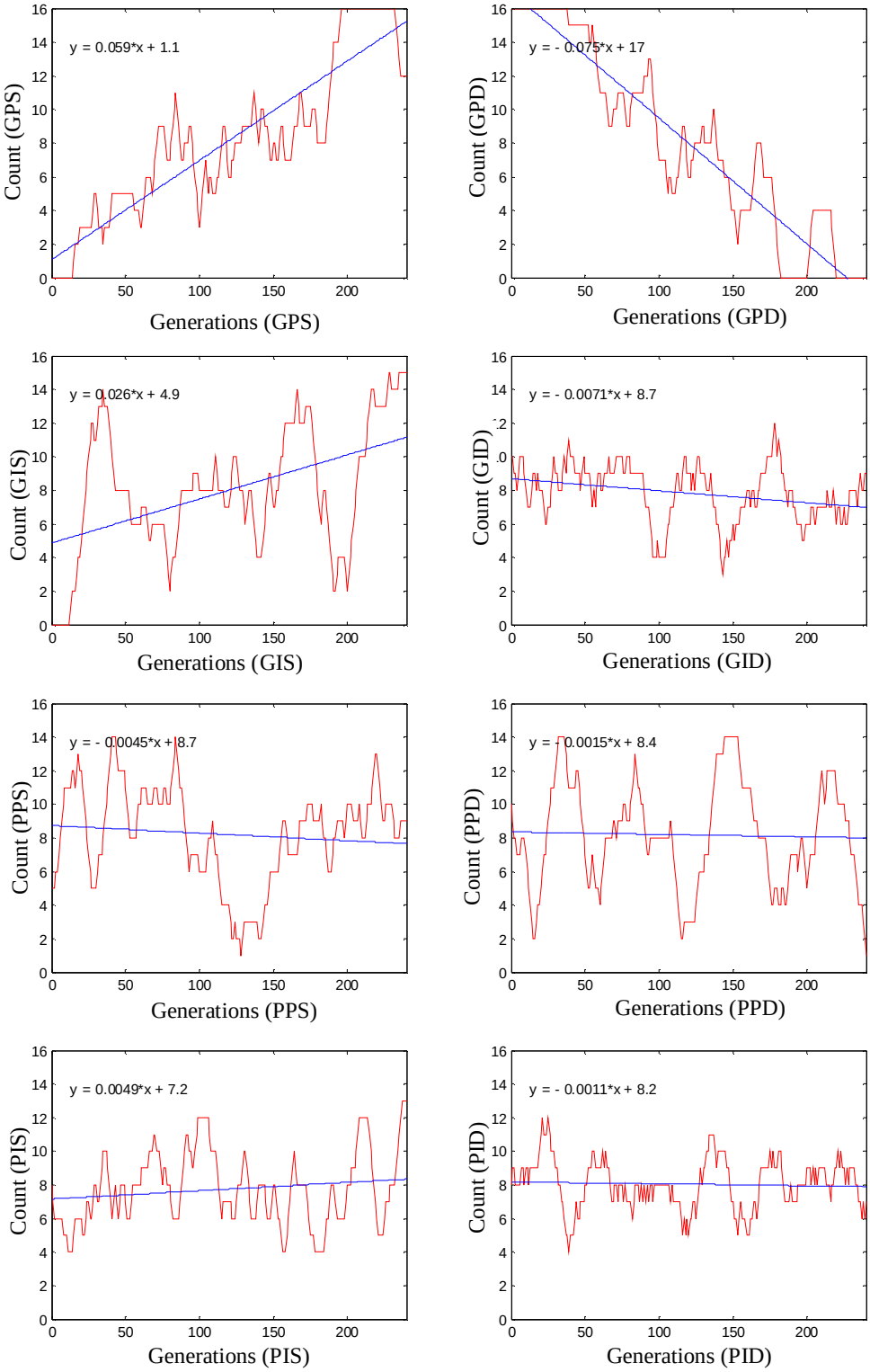


Figure 4.5. Sliding window figures for ADMS components.

Table 4.6. New and old ranks of remaining 32 strategies and SGA.

GPS	GPD	GIS	GID	PPS	PPD	PIS	PID	Avg. Fitness	Rank Score	General Rank Score
0	1	0	1	0	1	1	0	0,000222349	33	256
0	1	0	1	0	1	1	1	0,000222349	32	255
0	1	0	1	0	1	0	1	0,000256406	31	254
0	1	0	1	0	1	0	0	0,00032208	30	253
0	1	0	0	0	0	1	0	0,000360695	29	252
0	1	0	0	0	0	1	1	0,000360695	28	251
0	1	0	1	0	0	0	0	0,000399104	27	250
0	1	0	1	0	0	1	0	0,00042613	26	249
0	1	0	1	0	0	1	1	0,00042613	25	248
0	1	0	1	1	1	1	0	0,000457137	24	247
0	1	0	1	1	1	1	1	0,000457137	23	246
0	1	0	0	1	1	0	1	0,000556395	22	245
0	1	0	0	1	1	0	0	0,000732431	21	244
0	1	0	0	0	1	0	1	0,000755561	20	243
0	1	0	0	0	1	0	0	0,000793567	19	242
0	1	0	1	1	0	0	1	0,000908037	18	241
0	1	0	1	0	0	0	1	0,001009142	17	240
0	1	0	0	0	0	0	1	0,001069168	16	239
0	1	0	1	1	1	0	0	0,001072654	15	238
0	1	0	0	0	0	0	0	0,0011572	14	237
0	1	0	1	1	0	1	0	0,001918676	13	236
0	1	0	1	1	0	1	1	0,001918676	12	235
0	1	0	1	1	1	0	1	0,002889884	11	234
0	1	0	1	1	0	0	0	0,003093539	10	233
0	1	0	0	1	0	1	0	0,003378354	9	232
0	1	0	0	1	0	1	1	0,003378354	8	231
0	1	0	0	1	0	0	1	0,004089242	7	230
0	1	0	0	1	0	0	0	0,005081286	6	229
0	1	0	0	0	1	1	0	0,032119402	5	199
0	1	0	0	0	1	1	1	0,032119402	4	198
0	0	0	0	0	0	0	0	0,042001999	3	188
0	1	0	0	1	1	1	0	0,048009078	2	187
0	1	0	0	1	1	1	1	0,048009078	1	186

If we carry out sliding window process with undecided components, the graphs in Figure 4.6 will be obtained. However, sliding window size has been chosen as 8, since the number of ADM strategies is reduced to 32. The slope of regression line for PPS is quite steep. PPS can be confidently considered as having negative effect on performance. Therefore it should not be used as ADM strategy component. Contrary to PPD, GID has positive effect on performance and a successful ADM strategy should employ GID and PPD as components.

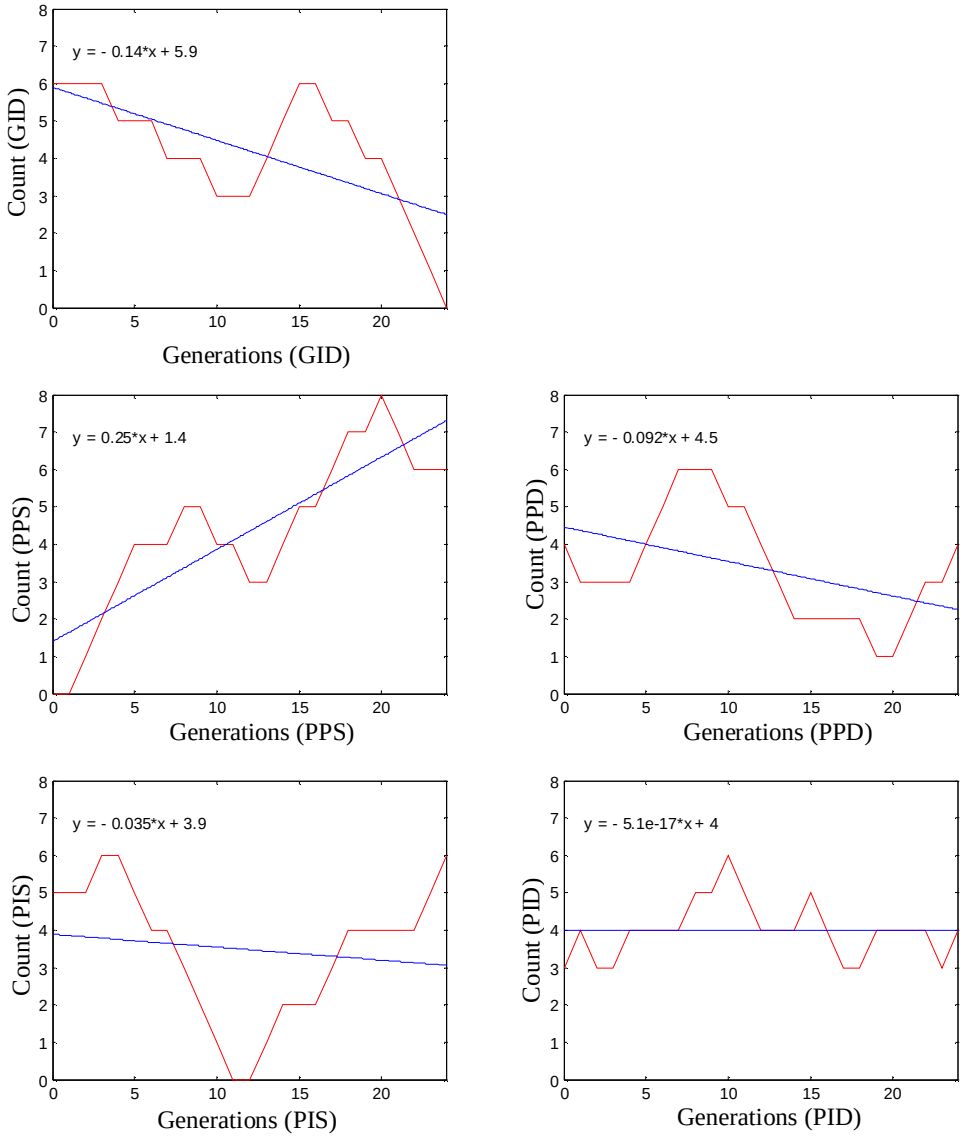


Figure 4.6. Sliding window figures for remaining ADMS components.

The effect of undecided two components; PID, and PIS can be observed from Table 4.7. The average old rank score is calculated as 254.5. Finally, it is recommended that an ADM strategy performs well if it contains GPD, GID and PPD components and does not contain GPS, GIS and PPS components. The common characteristic of the components that have positive effect on performance is all of them are based on dissimilarity. Contrary to this, all the components that have negative effect on performance are based on similarity.

Table 4.7. New and old ranks of remaining 4 strategies and SGA.

GPS	GPD	GIS	GID	PPS	PPD	PIS	PID	Avg. Fitness	Rank Score	General Rank Score
0	1	0	1	0	1	1	0	0,000222349	5	256
0	1	0	1	0	1	1	1	0,000222349	4	255
0	1	0	1	0	1	0	1	0,000256406	3	254
0	1	0	1	0	1	0	0	0,00032208	2	253
0	0	0	0	0	0	0	0	0,042001999	1	188

4.6. Suggested ADM Strategy and Its Evaluation

Previous sections are dedicated to identify the effects of ADM strategy components on performance. The components GPD, GID and PPD are identified as those causing positive effect, and GPS, GIS and PPS are identified as those causing negative effect. The effect of components PID and PIS could not be decided. Even though, one is free to employ any component in his/her ADM strategy, a generalization has been made and the ADM strategy (RC)-SGA+***GPD***+***GID***+***PPD*** has been suggested in this study.

In this section, the effect of suggested ADM strategy on performance will be examined for Rosenbrock function. Similar discussion methodology can be extended to the remaining nine benchmark functions. Figure 4.7a-d displays the performance results of four different optimization attempt with (RC)-SGA. In the first attempt (A1), (RC)-SGA has been used for optimization. The parameters crossover and

mutation rate have been set to 0.75 and 0.01, respectively, as suggested in the literature (Shopova and Vaklieva-Bancheva, 2006). In the second attempt (A2), the parameters for RC-SGA have been tuned up for the best performance. Crossover rate is determined as 0.75 and mutation rate is, surprisingly, set to 0. In the third attempt (A3) the suggested ADM strategy (RC)-SGA+***GPD***+***GID***+***PPD*** has been used. The parameters were exactly the same of A2. As suggested earlier, ADM strategy is an add-on to SGA. By using the same parameters, it is intended to show direct effect on the standard algorithm. Fourth, and the last, attempt (A4) has been made to display full performance of suggested ADM strategy on (RC)-SGA by tuning up the strategy for best performance. In this case, crossover and mutation rate are set to 0.98 and 0.09, respectively.

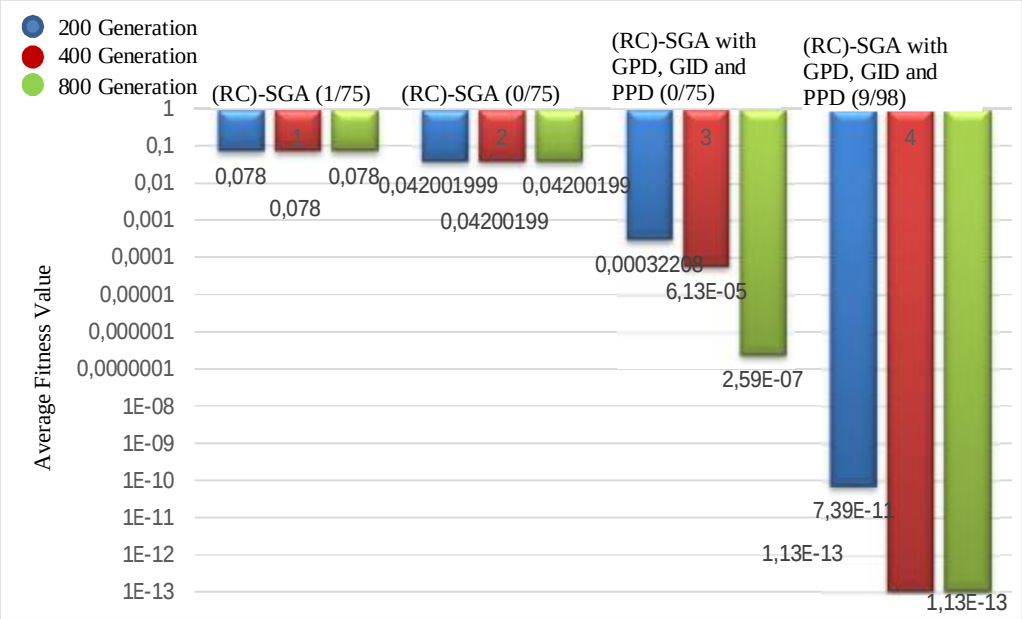


Figure 4.7a. Average fitness values of four different optimization attempt with three different maximum number of generations; 200, 400 and 800.

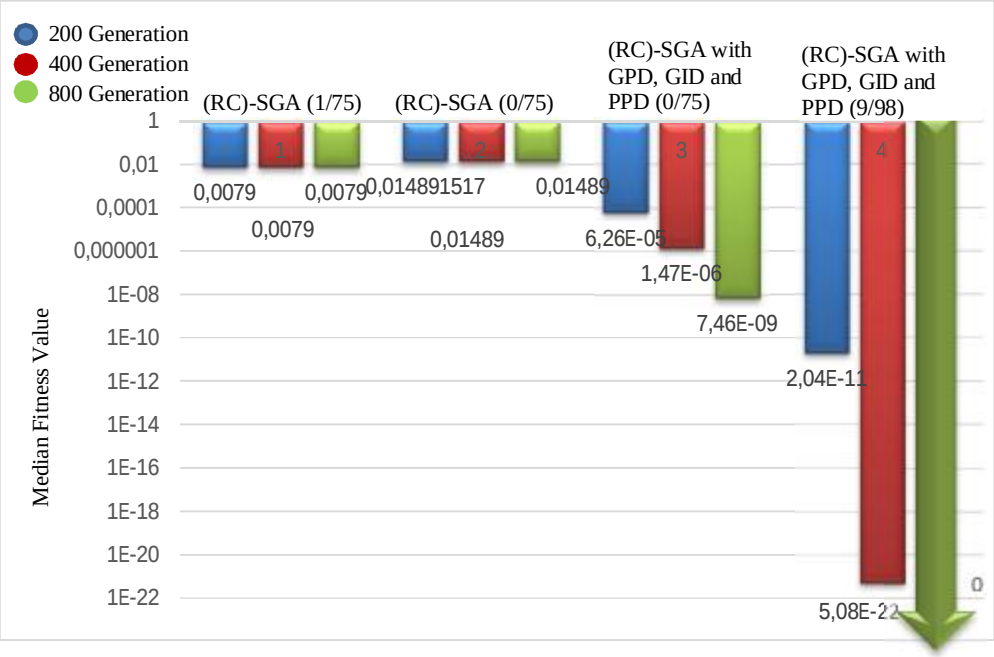


Figure 4.7b. Median fitness values of four different optimization attempt with three different maximum number of generations; 200, 400 and 800.

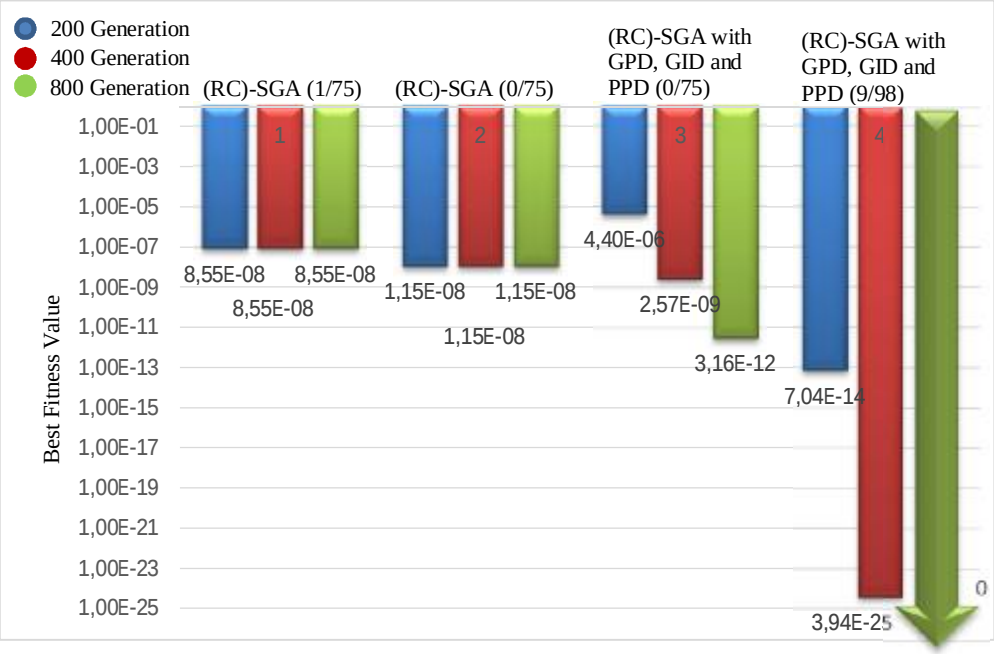


Figure 4.7c. Best fitness values of four different optimization attempt with three different maximum number of generations; 200, 400 and 800.

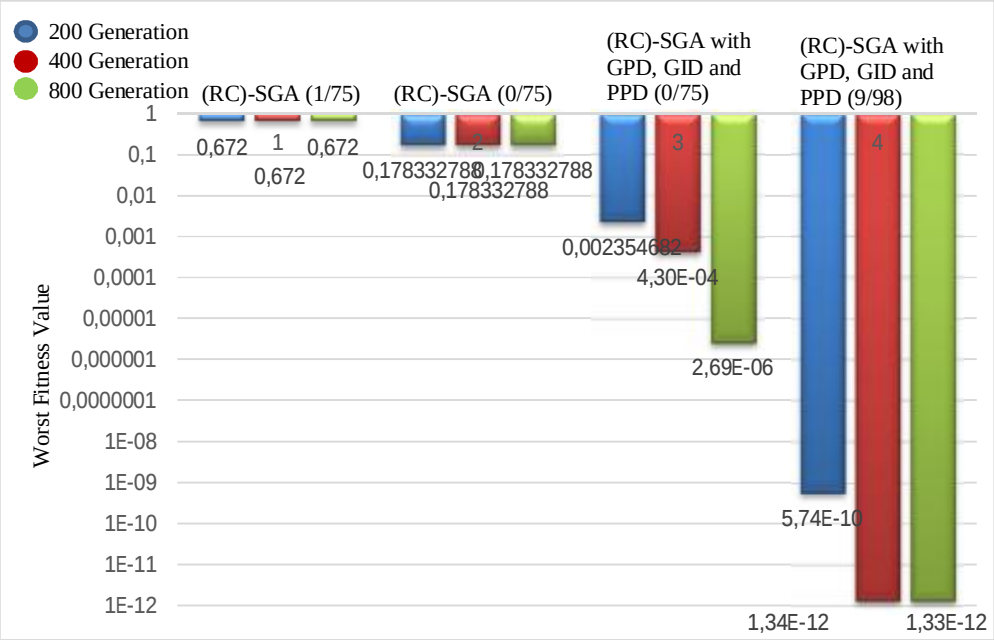


Figure 4.7d. Worst fitness values of four different optimization attempt with three different maximum number of generations; 200, 400 and 800.

The results that are displayed in Figure 4.7a-d are obtained from three different maximum number of generations; 200, 400 and 800. If we recall, in the previous sections, all the discussions were made on the results obtained from the tests in which maximum number of generations were set to 200. By selecting it as 400 and 800, we had a chance to investigate the algorithms' behaviors further more.

A1, (RC)-SGA with general parameters, converges to a solution earlier than 150 generations. Therefore all the results of A1, displayed in Figure 4.7a-d, are same for the selected maximum number of generations. The algorithm's early convergence can be seen from Figure 4.9a-d, also. The best and the worst fitness values of A1 are $8.55*10^{-8}$ and $6.72*10^{-1}$, respectively, for all generations. Average and Median fitness values are $7.8*10^{-2}$ and $7.9*10^{-3}$, respectively. Median fitness values are more reliable than average fitness values, since extreme large or small values do not affect median of values.

The discussion made for A1 holds for A2 too. Furthermore, even though A2 is improvised version of A1, the increase in performance is not so significant.

Significant performance increase in A3 displays the effectiveness of the suggested ADM strategy (RC)-SGA+***GPD***+***GID***+***PPD***. Considering vertical axis is in logarithmic scale, the improvement is overwhelmingly high. Furthermore, as the number of generations are increased, the suggested ADM strategy maintains its diversity and keep searching for better solution (Figure 4.8). On the other hand, (RC)-SGA quickly loses diversity after 200 generations.

Not surprisingly, the performance of A4 is tremendously better than those of A1 and A2, even A3. When the maximum number of generations are extended to 800, A3 converges to 0 which is the optimum point for Rosenbrock function. It should be noted that a double variable has a precision of 10^{-324}. When the optimum point found as 0, it means, the precision barrier has been reached and the result is rounded to 0. While, median fitness vale of A1 for 800 generations is calculated as $7.9*10^{-3}$, It has been calculated as $<10^{-324}$ for A4.

Also, the obtained results for A1, A2, A3 and A4 with 200 generations are given for each test function in Table 4.8. The results are in total agreement for all test functions.

Table 4.8 Ten benchmark test functions performance results for four different optimization attempt; A1, A2, A3, A4

Test functions	**Function Name**	**(RC)-SGA (A1)**		**(RC)-SGA with Tuned Mut. And Cross (A2)**		**(RC)-SGA + General Suggested Method (A3)**		**(RC)-SGA + General Suggested Method with Tuned Mut. And Cross (A4)**	
		Rank	Fitness	Rank	Fitness	Rank	Fitness	Rank	Fitness
F1	Rosenbrock	167	0,0781693	188	0,04200199	253	0,00032208		7,39319E-11
F2	Rastrigin	120	0,604595	240	0,06633061	241	0,06633060		0
F3	Schwefel	155	-761,43114	193	-790,5904403	195	-790,5904406		-837,96577
F4	Ackley	153	0,395249	235	1,42745 E-11	248	7,10542E-16		0
F5	Langerman	218	-3,990318	246	-4,13027155	229	-4,0438597		-4,153862
F6	Fifth function of De Jong	125	5,3205804	208	3,88914502	246	2,385704		1,3945621
F7	Drop wave	65	-0,930452	212	-0,9744981	253	-0,9957496		-0,99999
F8	Shekel	222	-3,16158241	239	-3,3069223	220	-3,1851846		-3,433239
F9	Griewangk	148	0,0503483	188	0,00772519	256	0,0019723		0,000642
F10	Deceptive	120	0,0534443	246	0,0046974	241	0,0052295		3,973642E-09

In addition to this, Figure 4.9a-d display the relationships between the maximum number of generations and fitness values of A2 and A3. It can be observed from Figure 4.8 that A2 quickly loses its diversity and converges to some point in early generations (as early as 100 generations). However A3 maintain the diversity for a long time and this pay off as better searching capacity.

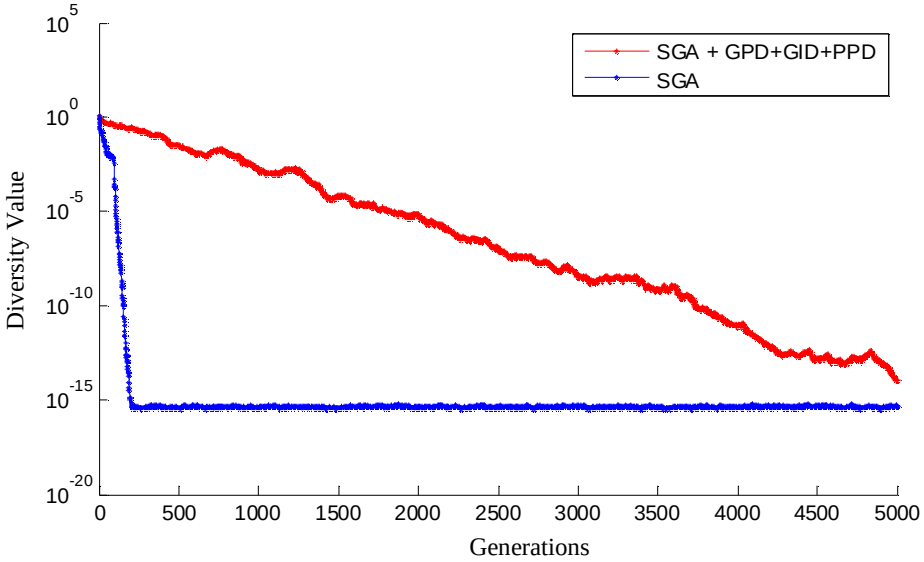


Figure 4.8. Diversity values over the generations.

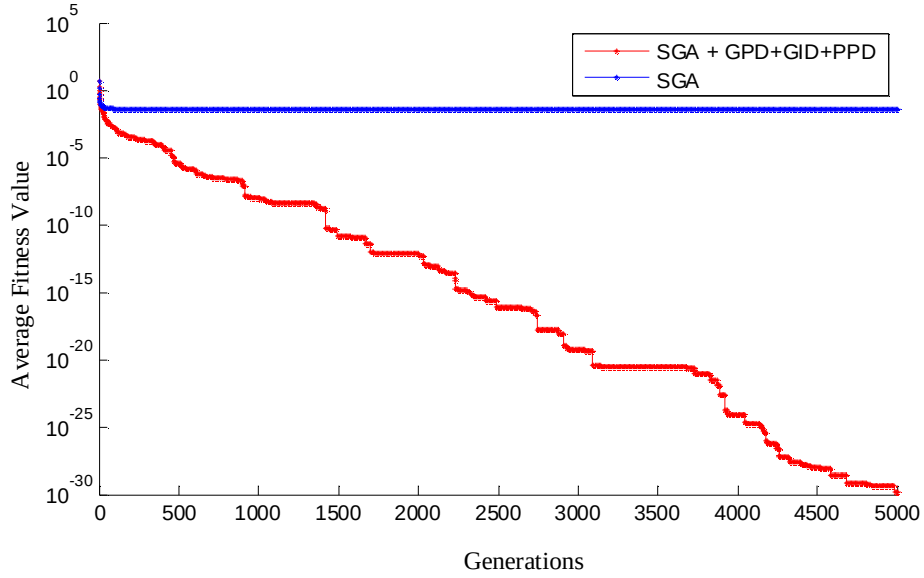


Figure 4.9a. Average fitness values over the generations.

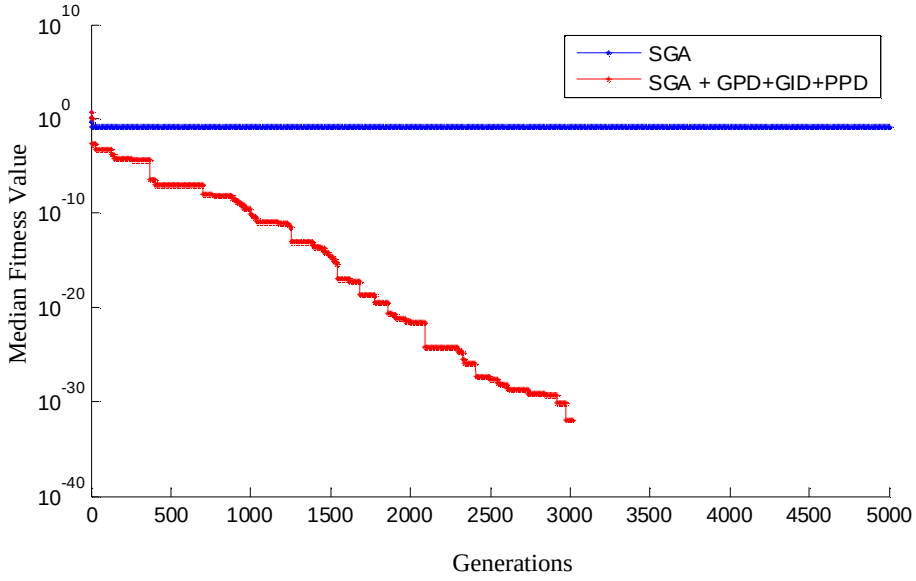


Figure 4.9b. Median fitness values over the generations.

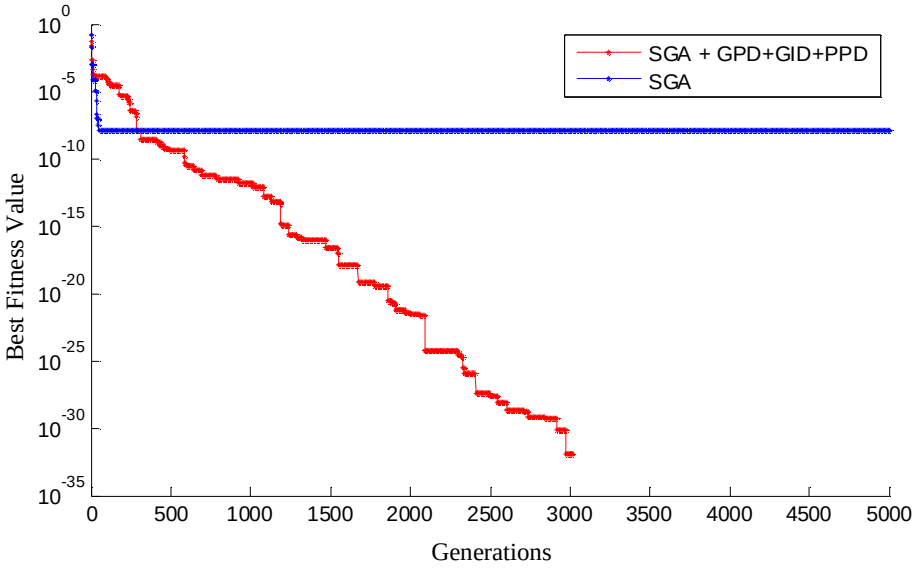


Figure 4.9c. Best fitness values over the generations.

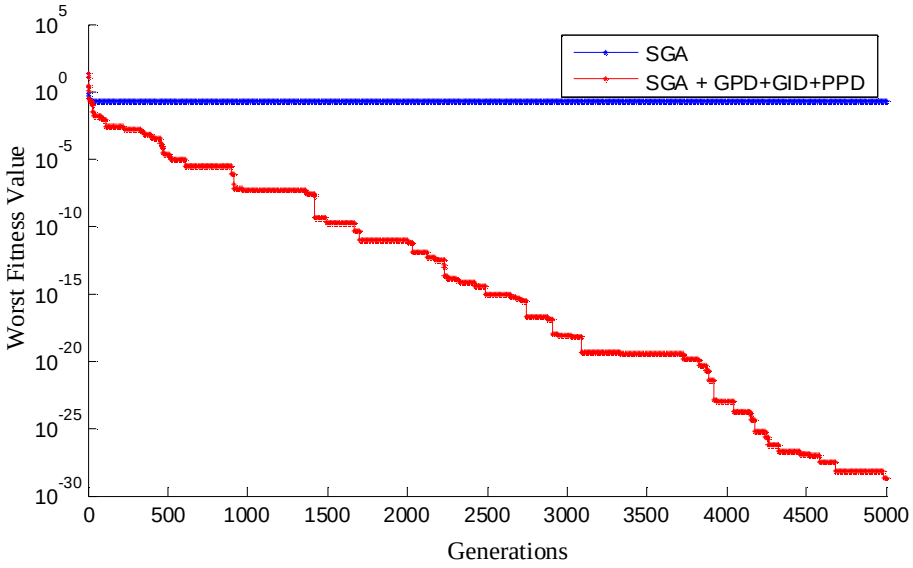


Figure 4.9d. Worsts fitness values over the generations.

5. CONCLUSIONS AND FUTURE WORKS

The current study has presented new strategies to selection process that focuses on reliability and efficiency within the context of RCGAs. 255 unique selection strategies that differs from choosing individuals randomly, have been proposed. The criteria of selecting mating pairs is based either on their genotypic similarity/dissimilarity or on their phenotypic similarity/dissimilarity. The similarity based strategies enable individuals to exploit the current search region extensively before exploring new ones. On the other hand, dissimilarity based strategies provide more reliable and efficient search mechanism and prevent the GA from being trapped in local optima.

To evaluate the performance of the proposed algorithm, a series of experiments are conducted on a set of 10 well known real-valued benchmark global optimization test functions. When compared with (RC)-SGA, the proposed ADM strategies, show a significant improvements in the quality of the global optimum solution found under the same simulation conditions.

The present study also compares the performance of the proposed strategies with tuned crossing over and mutation parameters, along with the conventional parameters. On the contrary to (RC)-SGA, the proposed GPD, PPD and GID combination shows superior performance. Furthermore, this combination also exhibits better performance with tuned parameters. Finally, we can conclude that the proposed ADM based strategies provide more accuracy, greater reliability, and higher efficiency than the other GAs considered in the present study.

The experiment outcome for the proposed strategies is excellent in most cases, but it still performed worse in some strategies due to the critical balance between exploitation of the best individuals and exploration of alternative regions of the search space and increasing the risks of local optima traps. As our future perspective, we plan to further improve the evolutionary efficiency by integrating the approach of design of experiment with the proposed ADM-RCGA algorithm.

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BIOGRAPHY

Serkan KARTAL was born in Adana, in 1986. He completed his elementary education at Meryem Abdurrahim Gizer Primary Education School, Adana in 2000. He went to high school at ÇEAŞ Anatolian High School. He completed university education at department of Computer Engineering of Çukurova University in 2010. Since 2011, he has been working as a research assistant at Computer Engineering Department of Çukurova University in Adana.

APPENDICES

Table 7.1. Test results for Rosenbrock Function with tuned crossover and mutation parameters

Function Number	GPS	GPD	GIS	GID	PPS	PPD	PIS	PID	Average Fitness	Median Fitness	Best Fitness	Worst Fitness	Standard Deviation	Rank Score
1	0	1	0	1	0	1	1	0	0,000222349	3,42887E-05	1,24757E-07	0,0022516	0,000575029	256
1	0	1	0	1	0	1	1	1	0,000222349	3,42887E-05	1,24757E-07	0,0022516	0,000575029	255
1	0	1	0	1	0	1	0	1	0,000256406	2,45975E-05	8,89603E-08	0,0017933	0,000475115	254
1	0	1	0	1	0	1	0	0	0,00032208	6,25775E-05	4,39959E-06	0,002354682	0,000665016	253
1	0	1	0	0	0	0	1	0	0,000360695	0,000100496	4,64627E-08	0,002097147	0,000625548	252
1	0	1	0	0	0	0	1	1	0,000360695	0,000100496	4,64627E-08	0,002097147	0,000625548	251
1	0	1	0	1	0	0	0	0	0,000399104	0,000145085	8,25246E-06	0,001483349	0,000458129	250
1	0	1	0	1	0	0	1	0	0,00042613	0,000112858	2,70513E-07	0,002906873	0,000779858	249
1	0	1	0	1	0	0	1	1	0,00042613	0,000112858	2,70513E-07	0,002906873	0,000779858	248
1	0	1	0	1	1	1	1	0	0,000457137	8,17928E-05	2,79477E-07	0,002510972	0,000748805	247
1	0	1	0	1	1	1	1	1	0,000457137	8,17928E-05	2,79477E-07	0,002510972	0,000748805	246
1	0	1	0	0	1	1	0	1	0,000556395	8,70235E-05	7,21577E-07	0,005106238	0,001298186	245
1	0	1	0	0	1	1	0	0	0,000732431	3,06366E-05	5,88328E-07	0,00665134	0,001760438	244
1	0	1	0	0	0	1	0	1	0,000755561	0,00052513	5,67031E-05	0,00453724	0,001107979	243
1	0	1	0	0	0	1	0	0	0,000793567	0,000122745	4,85116E-07	0,004220182	0,001245137	242
1	0	1	0	1	1	0	0	1	0,000908037	0,000190122	7,85652E-08	0,003720326	0,001165062	241
1	0	1	0	1	0	0	0	1	0,001009142	0,00048863	9,95755E-06	0,003718745	0,000983169	240
1	0	1	0	0	0	0	0	1	0,001069168	0,000561439	1,24556E-05	0,004696372	0,001493637	239
1	0	1	0	1	1	1	0	0	0,001072654	6,88421E-05	3,3439E-08	0,012243802	0,003139863	238
1	0	1	0	0	0	0	0	0	0,0011572	0,000415621	2,2834E-08	0,005070898	0,001500989	237
1	0	1	0	1	1	0	1	0	0,001918676	0,000220027	2,69019E-06	0,013950899	0,00397519	236
1	0	1	0	1	1	0	1	1	0,001918676	0,000220027	2,69019E-06	0,013950899	0,00397519	235
1	0	1	0	1	1	1	0	1	0,002889884	0,000110307	5,44272E-08	0,029672076	0,007988087	234
1	0	1	0	1	1	0	0	0	0,003093539	0,000303472	6,8552E-08	0,03191701	0,008383941	233
1	0	1	0	0	1	0	1	0	0,003378354	0,000283899	6,16438E-09	0,020576252	0,006224718	232
1	0	1	0	0	1	0	1	1	0,003378354	0,000283899	6,16438E-09	0,020576252	0,006224718	231
1	0	1	0	0	1	0	0	1	0,004089242	0,000886137	3,51132E-05	0,024974328	0,006912521	230
1	0	1	0	0	1	0	0	0	0,005081286	0,000260963	5,19296E-06	0,034131092	0,010083098	229

1	0	1	1	0	1	0	0	1	0,009238309	0,000784088	5,28968E-08	0,076723068	0,021095137	228
1	0	1	1	1	1	0	0	1	0,009238309	0,000784088	5,28968E-08	0,076723068	0,021095137	227
1	1	1	0	1	0	0	1	0	0,00984364	0,00069422	2,98059E-12	0,043055049	0,015077477	226
1	1	1	0	1	0	0	1	1	0,00984364	0,00069422	2,98059E-12	0,043055049	0,015077477	225
1	0	1	1	0	1	1	0	1	0,010571487	0,001931095	1,66153E-07	0,041622207	0,016074754	224
1	0	1	1	1	1	1	0	1	0,010571487	0,001931095	1,66153E-07	0,041622207	0,016074754	223
1	1	1	0	0	0	1	0	1	0,010689666	0,000224868	3,43373E-11	0,066788235	0,020422239	222
1	0	1	1	0	0	1	0	1	0,011434916	0,000239715	2,20141E-08	0,129686189	0,03313442	221
1	0	1	1	1	0	1	0	1	0,011434916	0,000239715	2,20141E-08	0,129686189	0,03313442	220
1	0	1	1	0	0	1	1	0	0,014461534	0,004200468	2,01669E-08	0,08039103	0,025849225	219
1	0	1	1	0	0	1	1	1	0,014461534	0,004200468	2,01669E-08	0,08039103	0,025849225	218
1	0	1	1	1	0	1	1	0	0,014461534	0,004200468	2,01669E-08	0,08039103	0,025849225	217
1	0	1	1	1	0	1	1	1	0,014461534	0,004200468	2,01669E-08	0,08039103	0,025849225	216
1	0	1	1	0	0	1	0	0	0,01496786	0,000950649	3,15252E-10	0,085902671	0,023653073	215
1	0	1	1	1	0	1	0	0	0,01496786	0,000950649	3,15252E-10	0,085902671	0,023653073	214
1	1	1	0	1	1	0	1	0	0,016373257	0,00060083	2,76255E-10	0,094455452	0,027954149	213
1	1	1	0	1	1	0	1	1	0,016373257	0,00060083	2,76255E-10	0,094455452	0,027954149	212
1	0	1	1	0	1	1	0	0	0,020731962	0,003095754	8,7761E-09	0,203498258	0,052276344	211
1	0	1	1	1	1	1	0	0	0,020731962	0,003095754	8,7761E-09	0,203498258	0,052276344	210
1	0	1	1	0	1	1	1	0	0,021995431	0,004643587	9,34976E-07	0,141387513	0,038385162	209
1	0	1	1	0	1	1	1	1	0,021995431	0,004643587	9,34976E-07	0,141387513	0,038385162	208
1	0	1	1	1	1	1	1	0	0,021995431	0,004643587	9,34976E-07	0,141387513	0,038385162	207
1	0	1	1	1	1	1	1	1	0,021995431	0,004643587	9,34976E-07	0,141387513	0,038385162	206
1	1	1	0	1	1	1	0	0	0,024222878	0,004179698	1,92488E-15	0,172610175	0,045646616	205
1	0	1	1	0	1	0	0	0	0,025246789	0,004982418	9,50574E-05	0,229032506	0,058101326	204
1	0	1	1	1	1	0	0	0	0,025246789	0,004982418	9,50574E-05	0,229032506	0,058101326	203
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1	1	1	0	0	1	1	0	1	0,027481135	2,90823E-06	2,37892E-14	0,299811874	0,077503824	201
1	1	1	0	1	1	1	0	1	0,028842099	0,004499299	3,92032E-11	0,136313795	0,046223826	200
1	0	1	0	0	0	1	1	0	0,032119402	2,28451E-05	1,77487E-07	0,374249421	0,098148681	199
1	0	1	0	0	0	1	1	1	0,032119402	2,28451E-05	1,77487E-07	0,374249421	0,098148681	198

1	1	1	0	1	0	1	0	1	0,034164811	0,001989553	7,53067E-09	0,324040203	0,082145322	197
1	1	1	0	1	0	0	0	0	0,036639336	0,001453172	1,54599E-15	0,312053843	0,082989373	196
1	0	1	1	0	1	0	1	0	0,037850132	0,000473495	2,60912E-08	0,323632521	0,090374802	195
1	0	1	1	0	1	0	1	1	0,037850132	0,000473495	2,60912E-08	0,323632521	0,090374802	194
1	0	1	1	1	1	0	1	0	0,037850132	0,000473495	2,60912E-08	0,323632521	0,090374802	193
1	0	1	1	1	1	0	1	1	0,037850132	0,000473495	2,60912E-08	0,323632521	0,090374802	192
1	0	1	1	0	0	0	0	1	0,038962237	0,013909983	1,48871E-05	0,229384679	0,065781328	191
1	0	1	1	1	0	0	0	1	0,038962237	0,013909983	1,48871E-05	0,229384679	0,065781328	190
1	1	1	0	1	0	0	0	1	0,041368943	0,003551891	3,0295E-13	0,279169308	0,078388768	189
1	0	0	0	0	0	0	0	0	0,042001999	0,014891517	1,15106E-08	0,178332788	0,054896613	188
1	0	1	0	0	1	1	1	0	0,048009078	0,000250614	3,89849E-06	0,363159395	0,124011751	187
1	0	1	0	0	1	1	1	1	0,048009078	0,000250614	3,89849E-06	0,363159395	0,124011751	186
1	0	0	0	1	1	0	0	1	0,052981429	0,024576792	6,02671E-06	0,214157974	0,064853909	185
1	1	1	0	0	1	0	0	0	0,053148799	0,002424077	5,21708E-07	0,308230332	0,100681466	184
1	0	0	0	1	1	1	1	0	0,053693631	0,003669718	4,86276E-11	0,32283424	0,089912206	183
1	0	0	0	1	1	1	1	1	0,053693631	0,003669718	4,86276E-11	0,32283424	0,089912206	182
1	0	0	0	1	0	0	0	1	0,058487074	0,030072429	9,26626E-08	0,177745051	0,0651878	181
1	1	1	1	0	1	1	1	0	0,05915072	0,007890796	5,07218E-07	0,400807428	0,123129251	180
1	1	1	1	0	1	1	1	1	0,05915072	0,007890796	5,07218E-07	0,400807428	0,123129251	179
1	1	1	1	1	1	1	1	0	0,05915072	0,007890796	5,07218E-07	0,400807428	0,123129251	178
1	1	1	1	1	1	1	1	1	0,05915072	0,007890796	5,07218E-07	0,400807428	0,123129251	177
1	0	0	0	1	0	0	1	0	0,060581511	0,024849324	1,35926E-06	0,209780167	0,070971756	176
1	0	0	0	1	0	0	1	1	0,060581511	0,024849324	1,35926E-06	0,209780167	0,070971756	175
1	0	1	1	0	0	0	0	0	0,060915907	0,002478383	8,03887E-11	0,428163453	0,113446558	174
1	0	1	1	1	0	0	0	0	0,060915907	0,002478383	8,03887E-11	0,428163453	0,113446558	173
1	1	1	0	0	1	1	1	0	0,06448931	0,004038013	3,21263E-05	0,396366367	0,1185017	172
1	1	1	0	0	1	1	1	1	0,06448931	0,004038013	3,21263E-05	0,396366367	0,1185017	171
1	1	1	0	1	1	0	0	1	0,064898787	0,006842245	1,75072E-10	0,420993915	0,129331904	170
1	1	1	0	1	0	1	0	0	0,067610068	0,027055934	2,84104E-11	0,59153542	0,15151457	169
1	1	1	0	0	1	0	0	1	0,067614397	0,003983237	1,38126E-08	0,4672059	0,155487085	168
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1	0	0	0	1	1	1	0	1	0,073080737	0,047972307	3,87021E-07	0,24388114	0,080958282	166
1	0	0	0	0	1	1	1	0	0,079562165	0,019622884	6,59438E-08	0,596814451	0,156657396	165
1	0	0	0	0	1	1	1	1	0,079562165	0,019622884	6,59438E-08	0,596814451	0,156657396	164
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1	1	1	0	1	1	1	1	0	0,08331362	0,000523667	2,6233E-11	0,559114588	0,171068577	162
1	1	1	0	1	1	1	1	1	0,08331362	0,000523667	2,6233E-11	0,559114588	0,171068577	161
1	1	1	1	0	1	1	0	0	0,085530482	0,007035366	8,79765E-12	0,892596802	0,232841513	160
1	1	1	1	1	1	1	0	0	0,085530482	0,007035366	8,79765E-12	0,892596802	0,232841513	159
1	1	1	1	0	1	1	0	1	0,089296048	0,034452763	1,48706E-11	0,465416179	0,134582563	158
1	1	1	1	1	1	1	0	1	0,089296048	0,034452763	1,48706E-11	0,465416179	0,134582563	157
1	0	1	1	0	0	0	1	0	0,090731429	0,038569549	2,6297E-05	0,617194805	0,162398247	156
1	0	1	1	0	0	0	1	1	0,090731429	0,038569549	2,6297E-05	0,617194805	0,162398247	155
1	0	1	1	1	0	0	1	0	0,090731429	0,038569549	2,6297E-05	0,617194805	0,162398247	154
1	0	1	1	1	0	0	1	1	0,090731429	0,038569549	2,6297E-05	0,617194805	0,162398247	153
1	1	1	0	0	0	0	1	0	0,093409523	0,000671476	4,55714E-15	0,866229798	0,224306308	152
1	1	1	0	0	0	0	1	1	0,093409523	0,000671476	4,55714E-15	0,866229798	0,224306308	151
1	0	0	0	0	0	0	1	0	0,098517764	0,025920641	9,53842E-06	0,449648995	0,14235747	150
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1	0	0	0	0	1	1	0	1	0,102449989	0,041871541	0,000302257	0,776731388	0,196132062	147
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1	0	0	1	1	1	1	1	0	0,110124008	0,052188839	5,74405E-05	0,462625765	0,127656753	143
1	0	0	1	1	1	1	1	1	0,110124008	0,052188839	5,74405E-05	0,462625765	0,127656753	142
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1	0	0	1	1	0	0	0	0	0,136826478	0,011585711	0,002820215	0,720567013	0,243991152	130
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1	1	1	0	1	0	1	1	0	0,146404204	0,020791526	2,30668E-09	0,482252826	0,174534465	125
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1	0	0	0	1	0	1	1	0	0,156177122	0,077839722	4,58866E-05	1,125925913	0,277343051	116
1	0	0	0	1	0	1	1	1	0,156177122	0,077839722	4,58866E-05	1,125925913	0,277343051	115
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1	1	1	0	0	0	0	0	1	0,16894688	0,000553211	4,26502E-14	1,46408243	0,403179349	113
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1	1	1	0	0	0	1	1	1	0,196088761	0,003425925	5,56419E-10	1,379503525	0,39467255	104
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1	1	0	0	0	0	1	1	1	0,214745738	0,115635158	1,15745E-05	0,839265993	0,235944163	99
1	0	0	1	0	1	1	0	1	0,21495018	0,151922646	4,14446E-05	0,906812207	0,252297964	98
1	0	0	1	1	1	1	0	1	0,21495018	0,151922646	4,14446E-05	0,906812207	0,252297964	97
1	1	1	1	0	1	0	0	0	0,220040742	0,078304407	4,82374E-07	1,226743047	0,328735748	96
1	1	1	1	1	1	0	0	0	0,220040742	0,078304407	4,82374E-07	1,226743047	0,328735748	95
1	0	0	1	0	1	1	0	0	0,220329054	0,007809061	4,16508E-05	1,892878793	0,493743375	94
1	0	0	1	1	1	1	0	0	0,220329054	0,007809061	4,16508E-05	1,892878793	0,493743375	93
1	1	0	0	1	0	1	1	0	0,24568055	0,107680523	7,56726E-07	1,283934922	0,351530108	92
1	1	0	0	1	0	1	1	1	0,24568055	0,107680523	7,56726E-07	1,283934922	0,351530108	91
1	0	0	1	0	0	1	0	0	0,248130921	0,041511348	0,002181131	1,428879236	0,424649267	90
1	0	0	1	1	0	1	0	0	0,248130921	0,041511348	0,002181131	1,428879236	0,424649267	89
1	1	0	0	0	0	1	0	0	0,265504123	0,174093369	0,031628176	0,856247755	0,240837107	88
1	1	1	1	0	1	0	0	1	0,268501339	0,052805403	0,000151093	2,935332956	0,741917886	87
1	1	1	1	1	1	0	0	1	0,268501339	0,052805403	0,000151093	2,935332956	0,741917886	86
1	0	0	0	0	1	0	0	0	0,282844785	0,234487898	0,008505374	0,893815179	0,265506455	85
1	0	0	1	0	0	1	1	0	0,295135143	0,019055517	0,001846107	1,992304598	0,540836453	84
1	0	0	1	0	0	1	1	1	0,295135143	0,019055517	0,001846107	1,992304598	0,540836453	83
1	0	0	1	1	0	1	1	0	0,295135143	0,019055517	0,001846107	1,992304598	0,540836453	82
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1	1	1	1	0	1	0	1	0	0,297322175	0,095692861	0,000251564	1,463437315	0,429147038	80
1	1	1	1	0	1	0	1	1	0,297322175	0,095692861	0,000251564	1,463437315	0,429147038	79
1	1	1	1	1	1	0	1	0	0,297322175	0,095692861	0,000251564	1,463437315	0,429147038	78
1	1	1	1	1	1	0	1	1	0,297322175	0,095692861	0,000251564	1,463437315	0,429147038	77
1	1	1	1	0	0	1	0	0	0,297544214	0,04348226	1,44319E-08	1,937440731	0,500209778	76
1	1	1	1	1	0	1	0	0	0,297544214	0,04348226	1,44319E-08	1,937440731	0,500209778	75
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1	1	0	0	1	0	1	0	1	0,32064563	0,193554389	0,000703391	1,521805458	0,392982713	72
1	0	0	1	0	1	0	0	1	0,321331054	0,184855226	0,000895214	2,175652924	0,52837166	71
1	0	0	1	1	1	0	0	1	0,321331054	0,184855226	0,000895214	2,175652924	0,52837166	70
1	0	0	1	0	1	0	0	0	0,324797447	0,196676103	0,00016472	1,808153724	0,449016495	69
1	0	0	1	1	1	0	0	0	0,324797447	0,196676103	0,00016472	1,808153724	0,449016495	68
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1	0	0	1	1	0	0	0	1	0,327675081	0,017193935	0,00071536	2,792632714	0,780918394	66
1	1	0	0	1	0	0	1	0	0,382472417	0,333647622	0,04325442	0,822505748	0,256149315	65
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1	0	0	0	0	1	0	1	1	0,38939061	0,144088845	0,015804234	3,146989625	0,780532351	61
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1	1	0	1	1	0	1	0	0	0,406081668	0,400862197	0,0005169	1,475299783	0,410044862	57
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1	1	0	0	1	1	1	1	0	0,412159947	0,236813505	0,00504834	1,525506216	0,48890518	53
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1	1	0	0	0	1	0	0	0	0,413620832	0,277847983	0,081932633	0,928714375	0,276612923	51
1	1	0	0	0	1	0	0	1	0,423311931	0,329382099	0,063107167	0,911201941	0,295507812	50
1	1	0	0	1	0	0	0	0	0,427706046	0,429336179	0,000520843	0,928379924	0,310965477	49
1	1	0	1	0	1	0	0	1	0,440916046	0,384540133	0,005404768	1,467720267	0,360947568	48
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1	1	0	0	0	1	1	1	1	0,442351092	0,248064348	0,007541843	2,168496143	0,531714382	45
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1	1	1	1	0	0	1	1	0	0,474985444	0,311075604	7,81478E-08	2,556589592	0,676761584	40
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1	1	0	1	0	1	1	1	0	0,47505104	0,28345491	0,036811509	2,584795171	0,620819761	36
1	1	0	1	0	1	1	1	1	0,47505104	0,28345491	0,036811509	2,584795171	0,620819761	35
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1	1	0	1	1	1	1	1	1	0,47505104	0,28345491	0,036811509	2,584795171	0,620819761	33
1	1	0	1	0	0	1	0	1	0,481052731	0,213758532	0,010733632	2,190641271	0,576488902	32
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1	1	0	1	0	0	0	0	1	0,539203914	0,46350311	0,027789796	2,030738587	0,531984114	21
1	1	0	1	1	0	0	0	1	0,539203914	0,46350311	0,027789796	2,030738587	0,531984114	20
1	1	0	1	0	0	1	1	0	0,554524322	0,453336867	1,83253E-07	2,030804208	0,644342408	19
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1	1	0	1	1	0	1	1	0	0,554524322	0,453336867	1,83253E-07	2,030804208	0,644342408	17
1	1	0	1	1	0	1	1	1	0,554524322	0,453336867	1,83253E-07	2,030804208	0,644342408	16
1	1	0	1	0	1	0	1	0	0,554831804	0,421659992	0,081932633	1,548477464	0,438940267	15
1	1	0	1	0	1	0	1	1	0,554831804	0,421659992	0,081932633	1,548477464	0,438940267	14
1	1	0	1	1	1	0	1	0	0,554831804	0,421659992	0,081932633	1,548477464	0,438940267	13
1	1	0	1	1	1	0	1	1	0,554831804	0,421659992	0,081932633	1,548477464	0,438940267	12

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1	1	0	1	0	0	0	0	0	0,570498259	0,384540133	0,018388345	2,627143167	0,740459615	10
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1	0	0	1	0	1	0	1	0	0,583156343	0,34524205	0,025297008	2,486469142	0,648738428	8
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1	1	0	1	0	0	0	1	0	0,655274469	0,411547634	0,050518818	2,935382944	0,864725914	4
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1	1	0	1	1	0	0	1	1	0,655274469	0,411547634	0,050518818	2,935382944	0,864725914	1