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A Systematic Mapping Study on Diploid Genetic Algorithms

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Abstract: ***Diploid Genetic Algorithm is an approach for addressing performance and diversity issues in dynamic environments. Unlike the conventional implementation of genetic algorithm in various applications lacks in giving optimal performance as they deal with the static environment. There are problems where environment may change dynamically with time. In such cases, it becomes necessary to deal with this change. The paper defines and explains that diploid genetic algorithm increases diversity and adapts more quickly as the recessive genes become active whenever the environment changes dynamically. The paper investigates to present the diploidy representation by giving performance comparisons of some of the existing genotype to phenotype mapping. In the work explored, we take a systematic mapping study by presenting a broader survey of diploid genetic algorithms. The paper focuses to enable the academics and practitioners in order to examine the varied perspectives and applications where diploid genetic algorithms can give the direct efforts for future research.***

Keywords: Diploid Genetic Algorithm (DGA), Diploidy and Dominance, Dynamic Optimization Problem (DOPS), Genetic Algorithm (GA), Genotype to Phenotype Mapping.

1. Introduction

Genetic Algorithms (GAs) are often used to solve optimization problems i.e. it tries to find the optimal solution from a large set of problem or class of problems but these are limited in the scope of their adaptability to problems. However, there are problems where environment changes which are often known as dynamic optimization problems (DOPs) [1]. To overcome with this problem researcher's uses diploid GA that proves to be efficient in dynamic [2] environment. The basic difference between haploid genetic algorithm and diploid GA is:

- Diploid cells contain 2n number of chromosomes while haploid cells contains half the number as diploid.
- They have different representations and evaluation methodology.
- They have different reproduction operations like diploid cells are reproduced by mitosis while haploid cells are produced by the process of meiosis.
- All the cells in body like muscles, brain etc are diploid cells while germ cells, sperm are haploid.

Diploid genetic algorithm contains two alleles at each position of the chromosome where one allele is expressed as dominant (high fitness) and other is recessive (low fitness). Dominance allows the active harmful alleles to become inactive; thus providing as extra element of protection against excessive selection [3]. The basic factor which needs to be considered in diploid genetic algorithm is to determine the most optimal chromosome from the initial population which comes under the dominance probability vector in genotype to phenotype mapping. The main advantage of using diploid GA is they enhance the performance and efficiency while working in dynamic environment. The paper does not address the evolution of dominance but presents an intuitive way to represent dominance. Moreover, diploid GA adapts quickly to the sudden changes that leads to better fitness function and hence better solution.

The paper has been organized as follows. Section II presents an extensive literature review of the existing methodologies used in Diploid GA, section III discusses the diploid structure, section IV explains Genetic algorithm (GA) in detail, section V suggests how genotype to phenotype mapping is conducted and section VI concludes.

2. Literature Review

A. State of the Art

A systematic mapping involves going into the depth of the literature and examining the nature, content and quality of the published papers in this domain. The grouping of primary studies is done to produce a view of the specific research area by the systematic mapping of the related studies.

After following a keen analysis, Table I summarizes the selection process and presents the number of papers identified with respect to the keyword search from a list of scientific libraries.

Table 1: Relevant DGA Papers

Scientific Libraries	*Relevant Papers*	*Refined Papers*
ACM	9	7
Springer	7	4
Science Direct	3	1
IEEE	17	8

The systematic literature review process is necessary to ensure that the further innovative research can be carried out by the various researchers, practitioners and also to aim at gaining an overall idea of the distinct researchers in this field. In this respect, we intent to address the research questions which reflect our purpose as follows:

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RQ1: What types of studies are published by the abundant researchers?

RQ2: What is the end result produced by the study carried out in this domain?

RQ3: Who are the prominent researchers who have presented their contributions?

The various domination schemes are developed. Table II briefly presents the work done in this field by various researchers.

Table 2: Related Work

Shengxiang Yang [1]	This paper focuses on dynamic optimization problems and discusses the efficiency and performance of dominance schemes by comparing with DGA. It also presents the test results that were carried out on a series of DOP's constructed which validate the efficiency of dominance schemes.
Bara's Ali Atter [4]	The paper discusses the behaviour and analyzes the results produced by comparing the real values with binary coded operations in GA. It stresses on the DGA operators like recombination and mutation and concludes that real valued operators are more effective than bit coded operators in achieving the global minimum values in numerical optimization problems.
Rakesh Kumar [5]	This paper discusses the haploid, diploid and multiploid nature of organisms and compares the dynamic programming problem of TSP in terms of cost and time using haploid and diploid GA.
E.H J. Lewis [6]	The paper develops test cases on various diploid algorithms and analyzes their robustness, adaptability and better responsiveness over traditional GA. It also discusses the reduction in fitness observed in haploid GA by experimentation and test results.
KP. Wong & KC. Wong [7]	This paper presents new dominance schemes with four genotype alleles; two for dominant alleles, other two for recessive alleles. The fitness value increased due to change in dominance scheme.
Conor Ryan [8]	The paper introduces the new schemes of additive and polygenic inheritance diploid which can be applied to non standard GA. The paper showed that these two new schemes have superior gene effects over conventional dominance based schemes.
A. Sima Uyar [9]	The paper explores novel approach that manages distinct changes in non order based problems by using a multi-allelic representation. The parameters like pattern, frequency of changes are evaluated to determine the aspects of changes which impacted GA by performing various test cases.
A. Sima Uyar and A. Emre Harmanci [10]	The paper focuses on the factor of choosing the right genotype to phenotype mapping. It also presents a new methodology of adaptation by forming a feedback mechanism from the previously generate population. It compares the performance issues in the existing NG-Wong and other diploidy approaches and rectifies them which prove to be more effective in dynamic environments by generating test results.
	The paper presents the creation of complex systems in dynamic environment in which
Robert Shafer [11]	individuals go through atmosphere/ metabolism problem but diploid population results in creating fit solutions.
Anthony M.L. Liekens [12]	This paper discusses the detailed algorithmic structure and implementation of diploid GA. It also discusses the behavior of transforming a diploid into haploid GA by reusing the conventional GA operators and constructing the diploid GA operators. It presents a Markov model by discussing the simulations of the above two.
Dr. Mayada F. Abdul- Halim, Dr. Abbas F. Abdul-Kader [13]	The paper introduces a scheme called exogenous recombination that improves performance on both stationary and non stationary functions.
Greene F [14]	This paper presents a method for implementing diploid GA in genetic search and evaluates the intermediate phenotype which gives optimal result.
Sheingxiang Yang [15]	This paper presents a method based on key factors of diploid GA i.e. cardinality of genotypic alleles and uncertainty in dominance schemes. These methods increase the efficiency and performance in dynamic environment.
Omidpour, Amineh [16]	The paper proposes a new real valued diploid genetic algorithm, some of which are tested using Moving Peak Benchmark (MPB).
Yoshida Yukiko [17]	The paper discusses that the pseudo-Meiosis Genetic Algorithm (PSM GA) and applying it on Travelling salesman Problem.
Beilin liu [18]	The paper discusses the feasibility a n d Effectiveness of Diploid GA by presenting a simulation model to solve the Flexible Job Scheduling Problem.

3. Diploid Structure and Domination

In diploid structures, all living organisms consist of cells and each cell has same set of one or more chromosomes and a chromosome can be divided into genes. Genes which are considered as the fundamental building blocks of GA are the smallest units having genetic information. A sequence of genes makes a chromosome. It may describe a possible solution to a problem, without actually being the solution. Overall genetic package or overall genetic representation that may contain multiple chromosomes is known as genome. The term genotype refers to the particular set of genes contained in a genome. Two individuals that have identical genomes are said to have the same genotype. Genotype of an individual contains genes that are represented in the form of phenotypes i.e. the structure of every gene is defined in a record of phenotyping parameters [4]. These parameters are instructions for mapping between genotype and phenotype. In a chromosome, the genes are represented as:

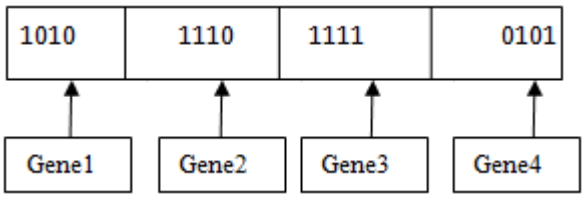


Figure 1: Representation of a gene

Each individual set of genotype consist of chromosomes having genes which contains some value called alleles [5]. Simplest genotype is called haploid which consist of

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single chromosomes. Diploid cells consist of two chromosomes, one set from each parent. Each gene is located at a particular locus (position) on the chromosome. In other words, diploid GAs (double stranded chromosomes) has two alleles (bits) at each locus (position) of the chromosome having distinct phenotype characteristics.

The algorithm of the diploid algorithm is defined as:

For each generation do
1) Start with the initialization of the individual chromosomes and domination array.
2) Select the best individual using any selection method and the selected individuals are paired randomly.
3) Each parent performs meiosis operation which involves replication of chromosomes and goes through crossover operation to form offspring.
4) Each parent gives one chromosome to each offspring and at the end of reproduction, the size of the population becomes double which was single before this step.
5) Perform mutation operation on the genotype of each double individual.
6) For each dead parent, form new individuals.
7) Select next generation and calculate new domination array values and the population are calculated for the individual with the best fitness.

4. Genetic Algorithm

A GA is a search heuristic that mimics the process of natural evolution used to generate useful solutions to optimization and search problems [18] [19]. GA is guided by the principles of evolution and natural genetics [13]. In GAs, the parameters of the search space are represented in the form of strings. All such strings are collected to form a population. The algorithm for simple genetic algorithm can be defined as:

1. Start with a random population, which represents different solutions.
2. Next, fitness function is calculated of each chromosome.
3. Repeat the following steps until n offspring have been created:
   a. Perform selection i.e. Select a pair of parent chromosome from current population.
   b. Perform crossover between the pair to form two offspring.
   c. Perform mutation i.e. some bits are altered randomly in a chromosome.
4. Replace current population with new population.
5. Go to step 2.

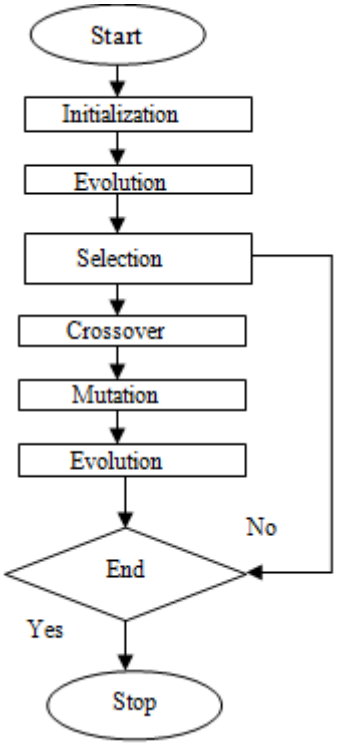


Figure 2 : Flow Chart of Genetic Algorithm

GA can be a powerful tool for solving problems and for simulating natural systems in a wide variety of scientific fields [16].

5. Genotype to Phenotype Mapping and Domination Schemes

The technique used to map the genotype onto the phenotype is called dominance. At each location of a gene on a chromosome, it determines the allele to be expressed where one allele takes a upper hand on the other alleles. The dominant alleles are represented by block and recessive ones by small letters in the phenotype Diploid representation increases diversity as the recessive genes become active whenever there is a change in environment [20] and improves performance when compared with conventional genetic algorithm. Dominance can be referred to as genotype to phenotype mapping or genotype reduction mapping [9].

In this a domination array is made up of real numbers in [0.0, 1.0] and length of array is same as the chromosomes length [6]. Each real number shows the dominance factor of allele 1 over allele 0 for the same location on chromosomes. The domination array is initialized to have the value 0.5 for all locations which means that either allele is equally likely to be expressed [10].

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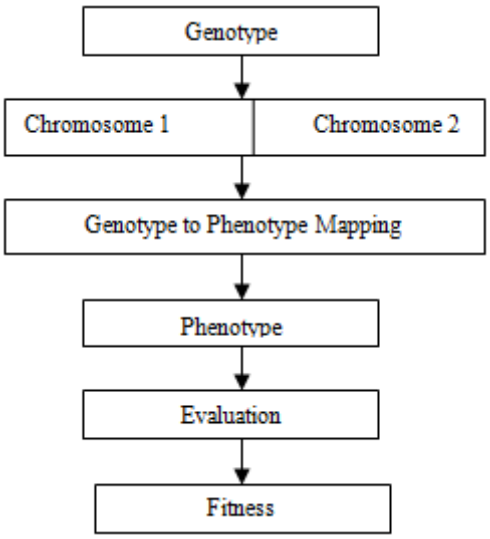


Figure 3 : Genotype to phenotype Mapping

6. Conclusion

In this paper, a systematic research has been done in the area of domination in diploid genetic algorithms. A survey has been done related to dominance schemes, diploid structure and algorithm for diploid representation in dynamic environment and also concludes that all methods have their own pros and cons when carried out in dynamic environments. So, on the basis of study and analysis confirm that diversity can be increased by Diploidy. Our future work could focus on developing a new algorithm that would satisfy all the requirements of diploid genetic algorithm and performing some mathematical analysis on fitness calculation methods to prove their advantage in different time varying problems by decreasing the computational effort.

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