



Epistatic arithmetic crossover based on Cartesian graph product in ensemble differential evolution



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ABSTRACT

Epistasis in genetics denotes an impact of one gene on the expression of the another genes. This means that so called epistatic gene influences the characteristics of the so called hypostatic genes. As a matter of fact, there is no one-to-one correspondence between genes and traits in nature. On the other hand, values of offspring genes are inherited from the parents genes. In this paper, the impact of epistatic genes in evolutionary computation is studied, where each epistatic gene in offspring depends on the corresponding hypostatic genes of its parents by an epistatic arithmetic crossover used in differential evolution. Thus, epistatic genes are determined by the Cartesian graph product of both parents presented as linear graphs. The epistatic arithmetic crossover is applied as a mutation strategy to the ensemble differential evolution. The results of extensive experiments conducted on CEC-14 function benchmark suite showed a great potential of the proposed algorithm and encouraged us to start to experiment with other graph products as well.

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1. Introduction

Evolutionary algorithms (EAs) represents nowadays a powerful tool for solving the hardest problems with which humans are confronted today. They found an inspiration for their operation in Darwinian evolution [15], where the fittest individuals in a population have more chances for surviving and transferring the best characteristics on their offspring. Modern biochemistry and genetics have extended this Darwinian macroscopic view on evolution by microscopic view concerning the mechanisms of heredity [16].

In genetics, a genotype determines a characteristics (traits) of each individuals (i.e., its phenotype) and represents a blueprint or set of instructions for building and maintaining a living cell. Thus, all information are written in genes that represent transfer units of heredity. A sequence of genes is combined into a linear order known as chromosome. Each gene is positioned at the specific chromosomal position (also loci). Interestingly, a mapping of genes to traits is not one-to-one (not injective). Although one gene can determine one traits, in common, more genes in chromosome specify one trait. In line with this, the fitness of individual trait depends on contribution that one gene has on the value of another gene. This dependence is also known under the name epistasis, where the more epistatic genes influence the expression of one hypostatic gene.

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The phenomenon of epistasis in the genetic algorithms was the first considered by Davidor in [3,4] that connected each problem with its so called epistatic level. This level corresponds to the maximal number of dependent variables k of n representing a solution of some sub-problems into which the problem is decomposed. For instance, the problem with epistatic level zero cannot be decomposed into sub-problems, because all n variables in the solution are independent. In general, these k variables represent a block that can be overlapped with another block by sharing some variables. The classical problem of size n and epistatic level k with overlapping blocks is the NK -landscape [6]. The more complete survey of this domain can be found in Gras [5].

Mathematically, a set of epistatic genes can be determined in different ways. In our study, we use a tool from graph theory, more specifically, the Cartesian product of graphs. It turns out that many real-world problems can conveniently be described by means of a graph consisting of a set of nodes (vertices) together with lines (edges) joining certain pairs of these nodes [38–40,51]. Graphs represent invaluable models for better understanding of biological systems. Nodes in biological networks can represent biomolecules such as genes, proteins or metabolites, and edges connecting these nodes indicate functional, physical or chemical interactions between the corresponding biomolecules. The Cartesian product is a binary operation which creates a new graph from two initial ones, and in many cases properties of a Cartesian product graph can be derived from the properties of its factors. Cartesian products of graphs have applications in many branches, like coding theory, network designs, chemical graph theory, telecommunications, and others [41–43,50]. In this study the Cartesian product is used to determine epistatic genes, where the factors of this product are paths (linear graphs) representing both parents.

Differential evolution (DE) developed by Storn and Price in 1995 [7] has become one of the most prominent EAs for solving real-world optimization problems. Like other standard EAs, i.e., genetic algorithms (GA) [17], genetic programming (GP) [18], Evolution Strategies (ES) [16] and Evolutionary Programming (EP) [19], the DE is also population-based algorithm, where each individual in the population represents a solution of the problem to be solved in a form of real-vectors. These vectors (also parents) are subject of operators crossover and mutation. As a result, trial vectors (also offspring) are produced that compete with their parents for a place in the next generation. In this competition for surviving, the better among parent and a trial vector according to the fitness value is placed at the parent's position in the population.

In order to improve the algorithm, a lot of modifications have been applied to the original DE. Mainly, modifications concerned setting DE algorithm parameters and changing DE mutation strategies. Algorithm parameters control the evolutionary search process, because the parameters valid at the beginning become inappropriate at the end of the optimization and vice versa. Therefore, the DE parameters need to be adapted and self-adapted. The more successful algorithms of this kind are jDE [8] and SaDE [10]. The DE mutation strategies determine a way in which the search space is explored. As it is known, some DE mutations are more explorative, while the others are more exploitative. As a result, the mutation strategies need to be changed during a discovering of the search space. This kind of adaptation has previously been addressed in [11] and widened with so called arithmetic recombination as a mutation strategy in ensemble DE strategies in [20] based on linear arithmetic crossover as developed for GAs in [21]. Finally, some kind of DE algorithms try to improve the results of the original DE algorithm by using ensembles of parameters and mutation DE strategies [12,13]. A complete survey of DE methods can be found in [1,14].

In this study, the epistatic differential crossover based on Cartesian graph product in ensemble DE (eXEDE) is proposed, where the epistatic arithmetic crossover is used as a strategy in ensemble DE strategies that beside the ordinary arithmetic crossover [2] takes into account also interactions with epistatic genes. While the original linear crossover calculates three possible values for two parameters laying at the same positions in parent vectors, the epistatic arithmetic crossover selects one of these three values randomly and to this value adds contributions of the epistatic genes determined by Cartesian graph products. As a result, one offspring is generated. Let us notice that these contributions consist of two parts, i.e., dependence contribution of epistatic genes of the first as well as the dependence contribution of the second parent. However, the magnitude of both contributions that have an impact on the final value of a specific parameter can be regulated by weights. The corresponding eXEDE was applied to the CEC-14 function benchmark suite. The results of the optimization showed that the proposed eXEDE improved the results of the original DE, both self-adaptive DEs (i.e., jDE and SaDE), ensemble DE (EDE) as well as the ensemble DE with arithmetic crossover (XEDE).

The structure of the remainder of the paper is as follows. Section 2 discusses background information about foundations of Cartesian graph products and differential evolution. In Section 3, an evolution of arithmetic crossover strategies in differential evolution is given. The experiments and results are subjects of Section 4. Section 5 concludes the paper with summarizing of the performed work and the possible directions for further development are outlined.

2. Background information

2.1. Cartesian graph products

The Cartesian product $G \square H$ of graphs G and H is the graph with the vertex set $V(G) \times V(H)$ in which vertices (g, h) and (g', h') are adjacent whenever $gg' \in E(G)$ and $h = h'$, or $g = g'$ and $hh' \in E(H)$. Thus, $V(G)$ and $V(H)$ denote the vertex sets of graphs G and H , respectively, while the $E(G)$ and $E(H)$ their corresponding edge sets.

According to Imrich and Klavžar [25], Cartesian products of graphs were defined in 1912 by Whitehead and Russell. Later they were repeatedly rediscovered and studied extensively since the 1960s. Due to their nice metric properties, they have

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