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# Distributed Estimation of Distribution Algorithms for continuous optimization: How does the exchanged information influence their behavior?



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## ABSTRACT

One of the most promising areas in which probabilistic graphical models have shown an incipient activity is the field of heuristic optimization and, in particular, in Estimation of Distribution Algorithms. Due to their inherent parallelism, different research lines have been studied trying to improve Estimation of Distribution Algorithms from the point of view of execution time and/or accuracy. Among these proposals, we focus on the so-called distributed or island-based models. This approach defines several islands (algorithms instances) running independently and exchanging information with a given frequency. The information sent by the islands can be either a set of individuals or a probabilistic model. This paper presents a comparative study for a distributed univariate Estimation of Distribution Algorithm and a multivariate version, paying special attention to the comparison of two alternative methods for exchanging information, over a wide set of parameters and problems – the standard benchmark developed for the IEEE Workshop on *Evolutionary Algorithms and other Metaheuristics for Continuous Optimization Problems* of the ISDA 2009 Conference. Several analyses from different points of view have been conducted to analyze both the influence of the parameters and the relationships between them including a characterization of the configurations according to their behavior on the proposed benchmark.

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## 1. Introduction

Estimation of Distribution Algorithms (EDAs) are a set of techniques that belong to the field of Evolutionary Computation. Since they were introduced in the 90s [32,43], the research community has put a lot of effort in their development, providing powerful algorithms which have been successfully applied to both artificial and real-world problems. In general terms, EDAs are similar to Genetic Algorithms (GAs), but their main characteristic is the use of probabilistic models to extract information from the most promising individuals of the current population (instead of using crossover or mutation operators) in order to create a new and presumably better population. The complexity of the different EDAs approaches is usually related to the probabilistic model used, and the ability of that model to identify and represent the (in) dependencies among the variables.

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Detailed information about the main characteristics of EDAs, as well as the different algorithms that belong to this family can be found in [25,27,35,36].

The main drawback of the most complex EDAs –those that try to consider all the possible (in) dependencies among the variables– is their high computational cost. Due to this, and thanks to the modularity of EDAs, several parallel approaches have been proposed. These proposals can be divided into two groups:

- Direct parallelization or parallel EDAs (pEDAs): Those whose behavior is exactly the same of the corresponding sequential version. Their main goal is the reduction of the execution time by the parallelization of the computation of the fitness function or the construction of the graphical models [27,29,38].
- Island-based approach or distributed EDAs (dEDAs): Those that create different subpopulations and exchange information among them, trying to improve the quality of the solutions of the sequential algorithm.

In this work, we pay attention to the second approach. In this scheme, an EDA instance is executed in each island, and some information is exchanged among the islands during the execution. This information can be made up of individuals (as done in other EAs), or probabilistic models (following the rationale that EDAs use them to extract and gather information about the population). Migration of individuals is a classic approach and has proven to obtain successful results in these and other Evolutionary Algorithms [2,4,9,28]. In addition, migration of models was explicitly developed for the distributed Estimation of Distribution Algorithms [1,11,12,19,20].

Until now, most of the previous work in dEDAs has been conducted in the discrete domain, and little research has been done in comparing both migration methods (individuals versus models). In particular, in continuous optimization, as far as the authors are aware, only two studies have been carried out [10,11]. Although these papers concluded that the migration of models obtains significantly better results than the migration of individuals, the experimental scenario was restricted to (a) a limited number of problems with small dimensions and (b) a small number of parameters. In this paper, a thorough study has been conducted to analyze the behavior of the distributed approaches in the context of EDAs. This study has demonstrated that the statement of the previous studies is not correct, at least not in the field of continuous optimization, using, for this task, a standard benchmark, formal methods for conducting the analysis of the influence of the parameters, and validating the results with formal statistical procedures. Briefly, the precise objectives pursued in this work are the following:

- Conduct an extensive study of different distributed EDAs configurations over several functions and dimensions.
- Identify the parameters that have a greater influence on the final behavior and the relationships between them.
- Analyze the relationship of the parameter values of both the best and the worst configurations.
- Compare the performance of the distributed configurations against their equivalent sequential configurations.
- Compare the performance of both methods for exchanging information: individuals vs models.
- Characterize the distributed configurations according to their behavior on the proposed benchmark.

The rest of the paper is organized as follows: Section 2 presents an overview of the previous studies on EDAs and dEDAs. Section 3 describes the proposed experimental scenario. Section 4 presents and comments the results obtained and lists the most relevant facts extracted from this analysis. Finally, Section 5 contains the concluding remarks derived from this study.

## 2. Preliminaries

In this section the main characteristics of EDAs and dEDAs are briefly reviewed.

### 2.1. Estimation of Distribution Algorithms: EDAs

EDAs are stochastic heuristic search strategies that are part of the Evolutionary Computation paradigm. In EDAs, multiple solutions or individuals are created at every generation, evolving successively until a satisfactory solution is achieved. In brief, the characteristic that clearly differentiates EDAs from other evolutionary search strategies, such as GAs, is that the evolution from one generation to the next is achieved by estimating the probability distribution of a set of individuals, sampling later the induced model. This avoids the use of crossing or mutation operators, and the number of parameters required by EDAs is considerably reduced. Based on the probabilistic model considered, three main groups of EDAs can be distinguished: univariate models, which assume that variables are marginally independent; bivariate models, which accept dependencies between pairs of variables; and multivariate models, in which there is no assumption about independences.

The univariate model is the simplest model, in which independence among variables is assumed. Therefore, the joint probability distribution is defined as the product of the marginal probability of each variable. The main advantage of this model is its low computational cost, although the assumption of independence among all the variables could lead to a very simplistic approach for some problems. Some representative algorithms of this model are: the Population-Based Incremental Learning algorithm (PBIL) [5], the compact Genetic Algorithm (cGA) [18] and the most extended heuristic within this model, the Univariate Marginal Distribution Algorithm UMDA [26,31] and its continuous version, the Univariate Marginal Distribution Algorithm for Gaussian Models (UMDA<sub>g</sub>) [21,23].

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