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On the equivalences and differences of evolutionary algorithms

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ABSTRACT

Evolutionary algorithms (EAs) are fast and robust computation methods for global optimization, and have been widely used in many real-world applications. We first conceptually discuss the equivalences of various popular EAs including genetic algorithm (GA), biogeography-based optimization (BBO), differential evolution (DE), evolution strategy (ES) and particle swarm optimization (PSO). We find that the basic versions of BBO, DE, ES and PSO are equal to the GA with global uniform recombination (GA/GUR) under certain conditions. Then we discuss their differences based on biological motivations and implementation details, and point out that their distinctions enhance the diversity of EA research and applications. To further study the characteristics of various EAs, we compare the basic versions and advanced versions of GA, BBO, DE, ES and PSO to explore their optimization ability on a set of real-world continuous optimization problems. Empirical results show that among the basic versions of the algorithms, BBO performs best on the benchmarks that we studied. Among the advanced versions of the algorithms, DE and ES perform best on the benchmarks that we studied. However, our main conclusion is that the conceptual equivalence of the algorithms is supported by the fact that algorithmic modifications result in very different performance levels.

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1. Introduction

Evolutionary algorithms (EAs) (Schwefel, 1995; Whitley, 2001; Yao et al., 1999) such as the genetic algorithm (GA) (Reeves and Rowe, 2003; Vose, 1999), biogeography-based optimization (BBO) (Ma, 2010; Simon, 2008), differential evolution (DE) (Das and Suganthan, 2011; Storn and Price, 1997), evolution strategy (ES) (Arnold and Beyer, 2001; Beyer, 1994) and particle swarm optimization (PSO) (Bratton and Kennedy, 2007; Kennedy and Eberhart, 1995; Kennedy, 1997) have received much attention regarding their potential as global optimization methods in real-world applications. Inspired by natural evolution and survival of the fittest in the biological world, EAs are search methods that are different from traditional optimization techniques, and are based on a collective learning process within a population of candidate solutions. In this paper we often use the shorthand term *solution* to refer to a candidate solution. The population in EAs is usually arbitrarily initialized, and each iteration (also called a generation) evolves toward better and better solution regions by means of randomized processes of selection (which is deterministic in some

algorithms), mutation, and recombination (which is omitted in some algorithms). The environment delivers quality information (fitness values for maximization problems, and cost values for minimization problems) about candidate solutions. The solutions with high fitness are selected to reproduce more often than those with lower fitness. All solutions have a small mutation chance to introduce innovation into the population. Each EA works on the principles of a different natural phenomena. GA uses survival of the fittest, BBO uses the migration behavior of species between islands, DE uses vector differences of candidate solutions, ES uses self-adaptive mutation rates, and PSO uses the foraging behavior of birds. But all of these EAs have certain features in common, and probabilistically share information between candidate solutions to improve the solution fitness. This makes them applicable to all kinds of optimization problems.

These EAs have been applied to many engineering optimization problems and have proven effective for solving some specific problems, including unimodal, multimodal, and deceptive optimization, constrained optimization, dynamic optimization, noisy optimization, multi-objective optimization, and so on (Ahn, 2006; Chiong et al., 2012; Oltean, 2007). So they are becoming increasingly popular tools to solve various hard optimization problems. Now many efforts have also been devoted to compare these algorithms to each other. Typically, such comparisons have been based on artificial numerical benchmark problems. Most

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studies are to verify that one algorithm outperforms another on a given set of benchmarks. However, there has not been much comparative study of various EAs and their principles of operation. Therefore, it is interesting to discuss and compare the characteristics of popular EAs from the conceptual and algorithmic aspects.

The aim of this paper is to show the equivalences and differences of various popular EAs, including GA, BBO, DE, ES and PSO in a notional as well as in an experimental way. Because these algorithms bear so many similarities due to their reliance on organic evolution, it is not a surprising fact that these algorithms have equivalences under certain conditions. In this study, we formalize a general description of these algorithms and provide detailed theoretical and empirical comparisons. This paper can provide an appropriate overview of the strong similarities of these algorithms to stimulate further discussions.

There has been much previous work comparing various EAs, including comparisons between genetic algorithms, memetic algorithms, particle swarm optimization, ant colony optimization, and shuffled frog leaping (Elbeltagi et al., 2005); comparisons between genetic algorithms and particle swarm optimization (Eberhart and Shi, 1998); comparisons between genetic algorithms and evolution strategies (Hoffmeister and Bäck, 1990); comparisons between memetic algorithms, tabu search, and ant colony optimization (Merz and Freisleben, 1999); and many others (Gao, 2004; Lai et al., 1998; Settles et al., 2003). Those papers focus mostly on the motivation behind the algorithms and differences in performance on benchmarks or specific applications. In this paper we add to the research literature by providing a more extensive comparison, by focusing on similarities and differences between algorithms, by including the recently developed BBO algorithm in our comparison, and by focusing on differences in performance on a larger and more recent set of benchmarks. The benchmarks we study in this paper are recently-proposed real-world continuous problems from the 2011 IEEE Congress on Evolutionary Computation (Das and Suganthan, 2010).

We note that there are many other popular EAs that we could include in our comparison, including ant colony optimization (ACO) (Dorigo et al., 2002; Dorigo and Gambardella, 1997), artificial immune systems (AIS) (Hofmeyr and Forrest, 2000), and artificial bee colony (ABC) optimization (Karaboga and Basturk, 2007). These algorithms may be similar to the five EAs that we examine in this paper, but their similarity has not yet been examined. We restrict our comparison to five algorithms due to space constraints, and we leave the comparison of other algorithms for future work. We chose the five algorithms that we did because GA and ES are two of the basic and foundational approaches to computer intelligence; DE is a mid-generation addition to the EA family that has proven very successful; PSO takes a fundamentally different approach as a swarm intelligence algorithm; and BBO is a typical late addition to the family of EAs. The five algorithms that we chose thus form a representative set rather than a complete set.

The rest of this paper is organized as follows. Section 2 first gives a brief overview of various basic EAs and analyzes their equivalences, and then discusses both their differences and their unique characteristics. Section 3 presents performance comparisons of the basic and advanced EAs on real-world application benchmarks, and Section 4 gives conclusions and directions for future research.

2. Equivalences and differences of EAs

This section first introduces various basic EAs, including GA, BBO, DE, ES and PSO, and then conceptually analyzes their equivalences under special conditions (Section 2.1). This section

then discusses their differences based on biologic motivations and algorithmic details (Section 2.2).

2.1. Equivalences of EAs

2.1.1. Genetic algorithms

GAs are popular evolutionary algorithms which were introduced as a computational analogy of adaptive biological systems. They are modeled on natural selection in evolution. GAs use a set of candidate solutions as a population, and use fitness functions to evaluate these candidate solutions. In the process of evolution, the candidate solutions are improved through selection, mutation and recombination (crossover) operators, and then pass on the candidate solutions with the best fitness to the next generation. A general description of one generation of a simple GA is given in Algorithm 1.

Algorithm 1. A general description of one generation of a simple GA, which is divided into four steps.

Select the best-fit solutions for reproduction
 Breed new solutions through recombination (crossover) and mutation operations
 Evaluate the fitness of the new solutions
 Retain the most fit solutions for the next generation

The simple GA described in Algorithm 1 is usually the one applied to most problems presented to a GA. The new solutions are obtained each generation by recombination and mutation. Prior to its mutation an offspring is produced by recombining parent solutions:

$$y_k(s) = \begin{cases} y_a(s) & \text{(A) no recombination} \\ y_a(s) \text{ or } y_b(s) & \text{(B) discrete} \\ y_a(s) + \alpha(y_b(s) - y_a(s)) & \text{(C) intermediate} \end{cases} \quad (1a)$$

$$y_k(s) = \begin{cases} y_{a(s)}(s) \text{ or } y_{b(s)}(s) & \text{(D) global, discrete} \\ y_{a(s)}(s) + \alpha(s)(y_{b(s)}(s) - y_{a(s)}(s)) & \text{(E) global, intermediate} \end{cases} \quad (1b)$$

where α and $\alpha(s)$ are contraction factors between 0 and 1, y is the entire population of candidate solutions, a , b , $a(s)$, and $b(s)$ are parent indices, k is the offspring index, and s is the decision variable index of a candidate solution. For example, y_k denotes the k th offspring, and $y_k(s)$ is the s th decision variable of y_k . For options (A), (B), and (C), parent indices a and b are two randomly-selected indices that are independent of decision variable index s , and contraction factor α is also independent of s . For options (D) and (E), $a(s)$ and $b(s)$ are randomly-selected indices that depend on decision variable index s , and $\alpha(s)$ is a contraction factor that depends on s .

By convention all parents in a population have the different mating probabilities, namely, all parents are determined by fitness-based selection, for example, roulette-wheel selection or tournament selection. In the case of discrete recombination option (B) in (1a), the s th decision variable of the offspring is chosen from either of two parents, which may be interpreted as crossover with a varying number of crossover points. In the case of intermediate recombination option (C) in (1a), the s th decision variable of the offspring is the weighted average of the two parents, and the weighting coefficient is α . In the case of the global recombination options (D) and (E) in (1b), $a(s)$ and $b(s)$ are chosen independently for each decision variable index s , which means that many parents can contribute to a single offspring. This results in a higher mixing of genetic information than in the case of options (B) and (C).

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