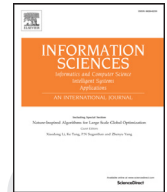




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Differential evolution with multi-population based ensemble of mutation strategies

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ABSTRACT

Differential evolution (DE) is among the most efficient evolutionary algorithms (EAs) for global optimization and now widely applied to solve diverse real-world applications. As the most appropriate configuration of DE to efficiently solve different optimization problems can be significantly different, an appropriate combination of multiple strategies into one DE variant attracts increasing attention recently. In this study, we propose a multi-population based approach to realize an ensemble of multiple strategies, thereby resulting in a new DE variant named multi-population ensemble DE (MPEDE) which simultaneously consists of three mutation strategies, i.e., “current-to-pbest/1” and “current-to-rand/1” and “rand/1”. There are three equally sized smaller indicator subpopulations and one much larger reward subpopulation. Each constituent mutation strategy has one indicator subpopulation. After every certain number of generations, the current best performing mutation strategy will be determined according to the ratios between fitness improvements and consumed function evaluations. Then the reward subpopulation will be allocated to the determined best performing mutation strategy dynamically. As a result, better mutation strategies obtain more computational resources in an adaptive manner during the evolution. The control parameters of each mutation strategy are adapted independently as well. Extensive experiments on the suit of CEC 2005 benchmark functions and comprehensive comparisons with several other efficient DE variants show the competitive performance of the proposed MPEDE.

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1. Introduction

Differential evolution (DE), first proposed by Storn and Price [47], is one of the most efficient evolutionary algorithms (EAs) currently in use. DE is a population-based stochastic search technique, in which mutation, crossover, and selection operators are utilized at each generation to move the population toward the global optimum [56]. Numerous studies have been done on DE with respect to the novel mutation strategy design [5,23,51,52], hybridization [37,43,72] and population diversity control

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[10,61,73]. DE has been now widely applied to solve various optimization problems from various fields, such as power systems optimization [7,60], time series prediction [15], and feature selection [2].

The performance of DE highly depends on the configuration of mutation strategy and control parameters, such as population size NP , scaling factor F and crossover rate C_r [33]. Generally, the most appropriate mutation and parameter settings required by DE to solve different optimization problems are different [56]. This is because some mutation strategies are effective for the global search [39] and some others are useful for rotated problems [12], and that some control parameter settings can promote the convergence [40] and some other settings are more efficient for solving separable functions [41]. In addition, evidences show that even for one specific optimization problem, the required best strategies and parameters may vary during the evolutionary process [39]. Moreover, as can be observed in literature, several claims and counter-claims were reported concerning the setting of the control parameters [14]. Nevertheless, traditional trial-and-error approaches for determining the best strategy and parameters are usually inefficient and time-consuming, especially when solving a variety of optimization problems.

As a result, methods for automated tuning or ensemble of mutation strategies and parameters naturally attract increasing attention [6,19,33,39,67]. Consequently, many enhanced DE variants such as SaDE (with adapted mutation strategies and parameters) [39], jDE (with self-adapted parameters) [6], CoDE (composition of multiple strategies and parameter settings) [56], JADE (with “current-to-pbest/1” mutation strategy and adaptive parameters) [67], DE-DPS [42] (with dynamic selection of the best performing combinations of parameters), self-CCDE and self-CSDE [17] (with cluster-based strategy and self-adaptive parameter control), ADE [63] (with two-level adaptive parameter control scheme), CoBiDE (with covariance matrix learning and bimodal distribution parameter setting) [57] and EPSDE (with ensemble of mutation strategies and parameters) [33], have been proposed.

In this study, we propose a novel DE variant (named MPEDE for short), in which a multi-population based approach is utilized to realize a dynamic ensemble of multiple mutation strategies. In addition, parameters such as scaling factor F and crossover rate C_r , associated with each mutation strategy are adapted based on the approach proposed in [67]. In MPEDE, mutation strategies “current-to-pbest/1”, “current-to-rand/1” and “rand/1” are taken as constituent mutation strategies. There are two types of subpopulations in MPEDE namely, three indicator subpopulations and one reward subpopulation. Initially, each mutation strategy obtains an indicator subpopulation and the reward subpopulation is randomly assigned to one of the three mutation strategies. Then during the evolutionary process, after every certain number of generations, the mutation strategy that performed the best during the previous generations is determined with respect to the ratios between the fitness improvements and consumed function evaluations. Subsequently, the reward subpopulation is assigned to the determined best performed mutation strategy as a reward. With the algorithm proceeding, the best mutation strategy determination and reward population assignment operations are executed periodically. By using these steps, we ensure that the recently best performing strategy will be given more computational resources. MPEDE is tested on the suit of CEC 2005 benchmark functions with 30 and 50 variables, respectively. The competitive performance of MPEDE is exhibited by extensive comparisons with several state-of-the-art DE variants.

Recently, population partitioning techniques for enhancing the performance of EAs and swarms, such as particle swarm optimization (PSO) and DE, attracted increasing attention [4,28,35,64,68,70]. Our work is different from previous studies in several aspects. First and foremost, the application of multi-population techniques in previous literature is aimed to maintain population diversities of EAs while our study is aimed to realize the ensemble of multiple mutation strategies as well as automated computational resource allocation among mutation strategies of DE. Second, all previous work partition the original population into multiple smaller ones that have the same sizes. By contrast, the sizes of subpopulations in this paper are not equal. Third, major former studies utilize the same mutation strategy in different subpopulations while in MPEDE three mutation strategies are employed and the best mutation strategy will dynamically be rewarded with larger population resources during the run of MPEDE. We believe that the proposed multi-population framework will be a new paradigm for effective ensemble of multiple strategies for DE.

The rest of the paper is structured as follows: Section 2 gives a brief introduction to canonical DE, including its typical mutation operators, crossover, and selection operators. Section 3 reviews the related works in literature. Section 4 introduces details of the implementation of MPEDE. Section 5 reports the experimental results. Section 6 applies MPEDE to solve a real-world problem. Section 7 concludes this paper.

51 2. Differential evolution

Differential evolution (DE) being a parallel direct search method utilizes NP , D -dimensional decision vectors called population that encodes the candidate solutions, i.e. $\mathbf{X}_{i,G} = \{x_{i,G}^1, \dots, x_{i,G}^D\}$, $i = 1, \dots, NP$. The initial value of the j th decision variable of the i th individual at generation $G = 0$ is generated within the search space constrained by the prescribed minimum and maximum decision variable's bounds $\mathbf{X}_{\min} = \{x_{\min}^1, \dots, x_{\min}^D\}$ and $\mathbf{X}_{\max} = \{x_{\max}^1, \dots, x_{\max}^D\}$ by:

$$x_{i,0}^j = x_{\min}^j + \text{rand}(0, 1) \cdot (x_{\max}^j - x_{\min}^j) \quad j = 1, 2, \dots, D \quad (1)$$

where $\text{rand}(0,1)$ represents a uniformly distributed random variable within the range $[0,1]$. In other words, the initial population is obtained by uniform random sampling of the search space.

After initialization, the population evolves over generations through operations such as mutation, crossover and selection. In every generation, corresponding to each individual in the current population, trial vectors are produced through mutation and crossover operations. Each trial vector competes to replace the corresponding parent in the population during the selection process.

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