Differential Evolution Enhanced with Evolution Path Vector

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ABSTRACT
In order to combine the advantages of distributed model (DM) and centralized model (CM) offspring generation models, this paper proposes to use the differential evolution (DE) algorithm as the base population reproduction method and enhance its DM scheme with one of the key CM features, which is the covariance matrix adaptation (CMA) used in CMA-ES. In this way, an enhanced DE population reproduction scheme with evolution path (DE/EP) is developed. The proposed DE/EP scheme is kept almost as simple as the original DE but works better due to the advantages of the CMA feature.

Categories and Subject Descriptors
B.2.4 [Arithmetic and Logic Structures]: High-Speed Arithmetic –Algorithms, Cost/performance.

General Terms
Algorithms.

Keywords
Differential evolution; CMA-ES; hybrid algorithm; parametric model; non-parametric model; estimated distribution algorithm.

1. INTRODUCTION
This paper is based on the study of [1] and tries to combine the distributed model used in [2] [5-7] and the centralized model used in [3] to make a new hybrid population generation model. In this paper, we propose to use the evolution path (EP) of the population (used in [3]) to modify the distribution shape of differential evolution (DE). In order to utilize the EP information, we add an additional differential vector to the original DE mutation vector. The added vector is generated by an asymmetric Gaussian model like the one used in [1] along the direction of the accumulated EP. Moreover, an adaptive method is used in the asymmetric Gaussian model to adjust the model center. The DE/EP scheme applied to one of the most efficient DE algorithm JADE [2] and is tested on the CEC05* test suite [4]. The experimental results show its promising performance improvement.

2. The DE/EP Scheme
The DE/EP tries to incorporate the EP vector as an additional mutation to the original DE algorithm. Thus the main frame of DE/EP remains unchanged as the DE algorithm. An additional \( p_c \) mutation will be added to the mutant vector \( v'_i \) generated by the DE mutation:

\[
v'_i = v_i + F'_i \cdot \omega_i \cdot \sigma \cdot \text{pc}
\]

where \( F \) is the scale vector adopted from the original DE mutation, \( \sigma \) is an additional scale factor in order to adjust the size of the mutation and \( \omega \) is a weight factor generated by an asymmetric Gaussian distribution like the one used in [1]. The \( p_c \) vector is generated as the migration vector of the mean point of the population from the last generation to this generation:

\[
p_c = 0.9 \cdot p_c + 0.1 \cdot (\text{mean}(P_g(i_{best,ls})) - \text{mean}(P_{g-1}(i_{best,ls})))
\]

where \( i_{best,ls} \) indicates the first \( sl \) best individuals in the population. The \( p_c \) vectors shows how the center of the population moves between generations in the search space roughly. The parameter \( F \) is adopted in \( p_c \) mutation in order to enjoy the adaptive mechanism if there is any in the original algorithm. The parameter \( \omega_i \) is generated as follows:

\[
\omega_i = \begin{cases} 2 \cdot x \cdot \mu, & \text{if } x < 0; \\ 2 \cdot x \cdot (1 - \mu), & \text{otherwise}. \end{cases}
\]

where \( \mu \) is the balance factor of the asymmetric Gaussian distribution and \( x \) is a random number generated by the standard Gaussian distribution \( N(0,1) \). The balance factor \( \mu \) is adaptively adjusted by the same way \( CR \) is adapted in JADE [2]: in every generation, each individual in the population will get a \( \mu \) from a Gaussian random generator \( N(\mu_0,0.05) \) and truncated into the range \([0.01, 0.5]\) as shown in (7).

\[
\mu = N(0.5,0.05) \text{if } \mu > 0.5; \quad \mu = 0.5; \quad \text{if } \mu < 0.01; \quad \mu = 0.01.
\]

After the evaluation of the population, those \( \mu \) generated better offspring will be used to adapt \( \mu \):

\[
\mu = 0.9 \cdot \mu + 0.1 \cdot \text{mean}(\mu_{good})
\]

where \( \text{mean}(\mu_{good}) \) indicates the mean value of these balance factors which generate better offspring than their parents. The adaptive adjustment of \( \mu \) can let the algorithm itself to find a better pattern of the distribution shape of the \( p_c \) mutation during the search process.

3. Experiments
The JADE [2] algorithm was taken as the base algorithm to test DE/EP. All algorithms were tested on the 30-dimensional CEC’05 benchmark [4]. The test results presented here show the mean final best solutions values and the standard variances every algorithm found with the termination condition set as the maximum function evaluations (FEs) 3E+5 (For functions 1 and 9, 5E+4 and 1E+5 respectively). All test results were based on 50 times of independent runs. The test results with better mean fitness values are shown by bold type, while the test results with significantly different mean fitness values determined by the Wilcoxon rank-sum test (significant level 5%) are shown by italic type.
4. Conclusion

In this paper we extend the work of [1] and propose to combine the advantage of the CM model to enhance the search efficiency of a DM algorithm. Instead of directly combining the two target algorithm DE and CMA-ES, we use the evolution path of CMA-ES as a CM feature to improve the performance of DE. The proposed DE enhanced by evolution path adaptation scheme shows certain performance advantage against the original DE algorithm.

On the future work, machine learning techniques can be used to help the combination of the two kinds of models [8]. Moreover, we will apply the EP scheme to other evolutionary evolutionary algorithms like particle swarm optimization [9]-[11], ant colony optimization [12], brain storm optimization [13][14], and recent enhanced DE variants [15].

5. ACKNOWLEDGMENTS

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6. REFERENCES


Table 1. Tests results of JADE/EP with different $\sigma$ and $\mu_{sig}$ settings compared with the original JADE algorithm

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