MAGNITUDE OF DIFFERENCE (MDV) BETWEEN TARGET VECTOR AND TRIAL VECTOR IN ANCDE AND STANDARD DIFFERENTIAL EVOLUTION

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Abstract

This paper describes an ancestral extension to the standard Differential Evolution algorithm called AncDE and attempts to explain why its ancestral cache helps improve performance. We compute the magnitude difference between the target vector and the trial vector for each generation for DE and AncDE. Results for 6 problems are used in this study. Our findings indicate that ancestors can help overcome some of the local variation in solutions quality and improve solution quality by improving population diversity.

Keywords: Ancestor template, Differential Evolution, magnitude difference vector.

I.   INTRODUCTION

Differential Evolution (DE) has become extremely popular because of its efficiency and simple implementation and has been shown to be one of the most reliable algorithms in dealing with optimization problems [1]. In standard DE, three distinct target vectors $r1$, $r2$, $r3$ are randomly selected from initial population G = {$x1$, $x2$,...,$x/G/$}. In mutation stage, F is a mutation factor in [0, 2] that controls the extension of differential variation $(X_{r2,G} - X_{r3,G})$ then added with the third target vector. Crossover phase produces a trial vector:

$$u_{j,i,G} = \begin{cases} u_{j,i,G}, & \text{if} \left(rand_j [0,1] \leq CR \right) or \left(j = j_{rand} \right) \\ x_{j,i,G}, & otherwise \end{cases} , j = 1,2\ldots D$$

CR is crossover constant in range [0,1] while j_{rand} in randomly chosen integer in range [1,D] to ensure the trial vector $U_{i,G}$ is differ from related target vector $X_{i,G}$ at least in one dimension. Last stage is selection phase, and all stage repeated until it reaches the stopping criteria [2]:

$$X_{i,G+1} = \begin{cases} U_{i,G}, & \text{if } f(U_{i,G}) \leq f(X_{i,G}) \\ x_{i,G}, & otherwise \end{cases}$$

One of the benefits of difference vectors is that the magnitude of moves decreases as the population converges to an optimum, allowing a more fine - grained search to occur [3]. Therefore by applying new regions of the solution space that associated with random mutations of difference vector, it will allow large jumps in the solution space to uncover a new path to the global optimum.

II.   ANCESTRAL DIFFERENTIAL EVOLUTION –ANCDE

AncDE has proposes the following extension to the standard Differential Evolution: first, a second shadow population of archived ancestor vectors, which are updated stochastically. Second, use this population of ancestor vectors when generating donor vectors. This property allows the use of current and ancestral population in difference vectors to broaden the search thus offer facilitating the exploration of the solution space. There are two parameters introduced in AncDE to control the ancestor influence upon the current population; ancestor usage probability (*aup*) and ancestor replacement probability (*arp*). Ancestor usage probability (*aup*) moderates the frequency that an ancestor is used to calculate the difference vector. The ancestor replacement probability (*arp*) controls the relative age of the ancestral population.

The version of AncDE in this paper is based on *DE/best/1/bin* but the techniques can be easily applied to most variants of DE. Similar to DE, AncDE initialize a population by random sample for each $\vec{X}_i$. However at mutation stage, AncDE is using ancestor usage probability (*aup*) to select $A(\vec{X}_i)$:

$$\vec{V}_{i,j} = \begin{cases} \vec{X}_1, \text{ if } rand(0,1) \leq aup \\ A(\vec{X}_1), otherwise \end{cases} - \begin{cases} \vec{X}_2, \text{ if } rand(0,1) \leq aup \\ A(\vec{X}_2), otherwise \end{cases}$$

In crossover stage, for *binomial* crossover we use the following formula with $p = Cr$ and each j is an element of a vector $\vec{X}_i$:

$$\vec{U}_{i,j} = \begin{cases} \vec{V}_{i,j} & \text{if } rand(0,1) \leq Cr \text{ or } \leq i = j \\ \vec{X}_{i,j} & otherwise \end{cases}$$

However, AncDE had added additional step at the end of the crossover of vector $\vec{X}_i$ and $\vec{V}_i$, the ancestor of the new trial vector $\vec{U}_i$ will be either the parent target vector $\vec{X}_i$ or the ancestor $\vec{X}_i, A(\vec{X}_i)$ using the ancestor replacement probability (*arp*):

$$A(\vec{U}) = \begin{cases} \vec{X}_i, & \text{if } rand(0,1) \leq arp \\ A(\vec{X}_i), & otherwise \end{cases}$$

AncDE uses the same selection and replacement process as standard DE and all stage repeated until it reaches the stopping criteria.

III.   RESULT

This paper compares DE with AncDE by measuring the magnitude of *the difference vectors* (MDV) between the target vector and the trial vector for each generation. Where, n is number of population, X^{t+1} is the target vector; X^t is trial vector. This experiment focuses on the value of jump size between target vector and trial vector thus it represent distance between current solution and new solution.

$$\sum_{i=0}^{n} X^{t+1} - X^t$$

At the mean time, based on the magnitude difference, we would like to see the average between AncDE and standard DE. This paper set *aup* value to 0.25 and *arp* at 5×10^{-3} for AncDE to compare with standard DE over 6 different functions, listed in Table 1. The result in Table 1 shows that AncDE generally converges as well or better than standard DE and does so as fast as or faster than DE. This might be the result caused of its larger MDV; AncDE generated fewer distinct successive optima than DE for these 6 problems. In Table 2, 22 out 24 AncDE solution quality were smaller than DE, meanwhile 22 out of 24 MDV of AncDE were higher than DE, which is match with our hyphothesis.

Figure 1 and Figure 2, show the average graph between DE and AncDE for Rastrigin6 and Ackley. Both graphs shows that MDV average for AncDE is slighly higher than DE. Rastrigin6 did not reach 0 by 1500 generation due to function complexity.

TABLE I.   NUMBERS OF SOLUTIONS FOR SIX DIFFERENT FUNCTIONS

Functions	No. of Solution		Differences (%)	No. of Generation	No. of Runs
	DE	AncDE			
De Jong1	7001	4700	32.87	1000	30
De Jong2	15575	11624	25.37	1000	30
De Jong3	237	227	4.22	1000	30
Ackley	10910	9080	16.77	1000	30
PolyFitting	20520	12466	39.25	1000	30
Rastrigin6	804	656	18.41	1500	10

TABLE II.   MDV AND SOLUTION QUALITY FOR DE AND AncDE

| Functions	Formula	MDV		Solution Quality	
		DE	AncDE	DE	AncDE
De Jong1	min	2.2E-17	4.9E-15	4.0E-02	0.0E+00
	median	9.1E-03	5.4E-05	4.5E-01	2.3E-01
	max	3.1E-02	2.7E+02	3.7E+02	3.7E+02
	average	3.6E-05	2.6E+00	2.3E+01	2.5E+01
De Jong2	min	5.1E-13	3.8E-08	6.0E+01	4.5E+01
	median	1.4E-03	1.7E-02	1.1E+02	4.8E+01
	max	4.0E+04	3.3E+04	1.7E+04	1.7E+04
	average	1.8E+02	2.0E+03	4.2E+02	3.6E+02
De Jong3	min	0.0E+00	0.0E+00	0.0E+00	0.0E+00
	median	1.4E+01	1.5E+01	1.2E+02	1.2E+02
	max	1.0E+02	1.2E+02	2.4E+02	2.5E+02
	average	1.7E+01	1.8E+01	1.2E+02	1.2E+02
Rastrigin6	min	3.6E-05	2.3E-04	2.6E+02	2.0E+02
	median	8.1E+01	1.1E+02	7.1E+02	6.9E+02
	max	4.3E+02	6.2E+02	1.6E+03	1.6E+03
	average	8.4E+01	1.1E+02	7.8E+02	7.7E+02
Ackley	min	4.3E-14	5.3E-11	2.7E-02	4.6E-05
	median	3.3E-07	2.4E-04	1.9E-01	3.8E-02
	max	8.4E-03	1.7E+00	3.7E+00	3.6E+00
	average	6.3E-05	8.3E-03	9.5E-01	4.4E-01
Polynomial Fitting	min	0.0E+00	1.6E+13	7.7E+25	1.6E+18
	median	8.3E+15	5.8E+18	7.7E+25	7.7E+25
	max	2.3E+18	3.6E+25	7.7E+25	7.7E+25
	average	4.2E+16	1.8E+23	7.7E+25	6.8E+25
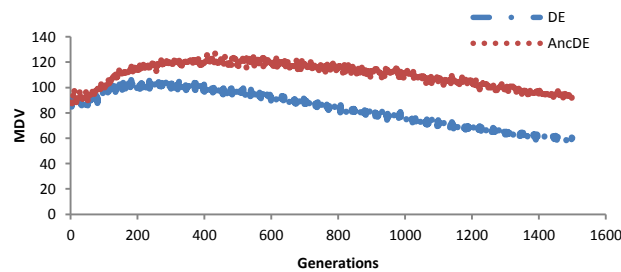
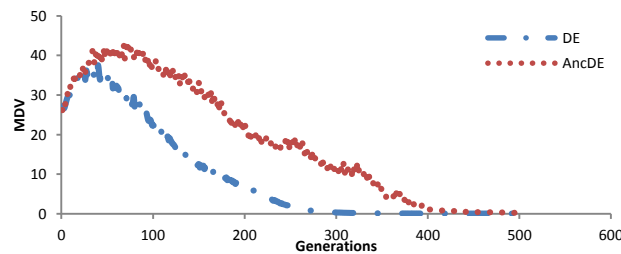Fig. 1.   Comparison of DE and AncDE on Rastrigin6

Fig. 2.   Comparison of DE and AncDE on Ackley

IV.   CONCLUSION

This study presented the computation of magnitude differences between target vector and trial vector for AncDE and standard DE. The purpose of computing magnitude difference vector to defined the jump size between the current solutions with new solution. From the result we may concluded that AncDE generate fewer distinct successive optima than DE might because of the bigger MDV between the target and trial vector.

ACKNOWLEDGMENT

References

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