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Experiment of Different Mutation Strategies in Differential Evolution Algorithm Employed for Calibration of a Lumped Water Balance Model

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Abstract – Differential evolution algorithm (DEA) is one featured kind of population based evolutionary algorithms. Although it is stated in previous studies that the algorithm is more sensitive to the crossover rate, it is tried out in this study whether DEA depends on mutation operation in which scaled differences of randomly chosen individuals existed in the population are used. Within this context, the presented study aims to carry out an empirical assessment regarding the comparison of DEA with the different mutation strategies for the calibration phase of a lumped water balance model. Both stable solution availabilities and convergence capabilities of DEA variants operated through five mutation approaches were performed on four parameter-Thorthwaite water balance model prepared for Gordes watershed. The findings derived from the model calibrations have indicated the usage of the fifth mutation strategy termed as current to best mutation strategy, which is more predominant in guaranteeing the achievement of stable solutions.

Keywords – Model Calibration, Differential Evolution Algorithm, Mutation Strategies, Gordes watershed.

I. Introduction

Conceptual water balance models (CWBMs) are typically used to interpret hydro-climatologic alterations influencing the watershed system. As the defined parameters in CWBMs are generally not directly observed, the modeling performances depend on how CWBMs are calibrated [1]. In the calibration concept, population-based evolutionary algorithms (PBEAs) have been proved to be robust to calibrate CWBMs [2]. PBEAs are found superior compared to conventional calibration techniques (manual approaches, Newtonian methods and Simplex variants) in two aspects. First, they need no derivative operation on the cost function in determining the search direction. Second, they carry out parallel searching due to defining a population matrix and thereby have much more chance to detect the global solution in the calibration of computationally intensive models [3, 4].

Although the Genetic Algorithms (GAs) were enormously employed in this concept, the relatively high number of variables controlling the crossover, mutation and selection operators may confuse the users in the decision-making phase. Besides, Differential Evolution Algorithm (DEA) proposed by Storn and Price [5] introduces one competitive kind of PBEAs. DEA modifies known mutation operations by using the difference vector(s) derived from randomly selected individuals existed in the population. Leon and Xiong [4] have stated that the mutation in DEA is rendered based upon the distribution of possible solutions in the population rather than a predetermined probability density function. It has been stated in the companion work prepared by Kirdemir and Okkan [6] that the DEA is more sensitive to the crossover phase operated through a constant crossover rate, it is also aimed in this study whether structure of DEA is sensitive to mutation operation. In the literature, several mutation strategies have been implemented to improve original version.

For example, in the study conducted by Leon and Xiong [4], several mutation variations were tested in a set of benchmark functions (various unimodal and multimodal functions) in terms of both the qualification of solutions and the computational cost. The results compiled from their experiments subjected to benchmark functions have led to the recommendation of a strategy termed as "*current to best mutation*". Leon and Xiong [4] also set an example for us, and the presented study aims to carry out an empirical assessment regarding the comparison of DEA with the different mutation strategies for the calibration phase of Thorthwaite water balance model (TWBM), which is lumped and parametric. Thus, it was provided to test the validity of the findings obtained from benchmark functions in the solution of an engineering problem. The remaining of the text is organized as follows. Section II outlines both conventional DEA and alternative sorts including different mutation strategies. Section III explains the TWBM model and data used. In Section IV, the results were interpreted. Lastly, Section V includes the concluding remarks.

II. DEA with Different Mutation Strategies

The DEA is a population-based algorithm introduced by Storn and Price [5], and involves similar operators with GAs. Contrary to GAs, the process of producing new individuals in DEA is performed with much less chromosomes, and the mutation operator is applied to the individuals prior to crossover operation. One individual (or chromosome) in the population is represented by vector $X_{i,t}$ with i=1,2,…,Np (population size) and t referring to the index of the generation (or iteration). Once the random initialization is made, aside from the i^{th} chromosome, three chromosomes with different row numbers (x_{r1}, x_{r2}, and x_{r3}) are randomly chosen from the available population to operate mutation process in each generation.

Table 1. Mutated vectors in DEA variants ($V_{i,t}$ represents the mutant vector; r1, r2, r3, r4, and r5 ∈ {1,2,. . . ,*Np*} are randomly selected integers)

DEA variants	Formula	Equation number	Related Reference
DEA1	$V_{i,t} = x_{r3,t} + F(x_{r1,t} - x_{r2,t})$	(1)	Storn and Price [5]
DEA2	$V_{i,t} = x_{best,t} + F(x_{r1,t} - x_{r2,t})$	(2)	Xu and Wen [7]
DEA3	$V_{i,t} = x_{r5,t} + F1(x_{r1,t} - x_{r2,t}) + F2(x_{r3,t} - x_{r4,t})$	(3)	Gong and Cai [8]
DEA4	$V_{i,t} = x_{best,t} + F1(x_{r1,t} - x_{r2,t}) + F2(x_{r3,t} - x_{r4,t})$	(4)	Leon and Xiong [4]
DEA5	$V_{i,t} = x_{i,t} + F1(x_{best,t} - x_{i,t}) + F2(x_{r1,t} - x_{r2,t})$	(5)	Leon and Xiong [4]

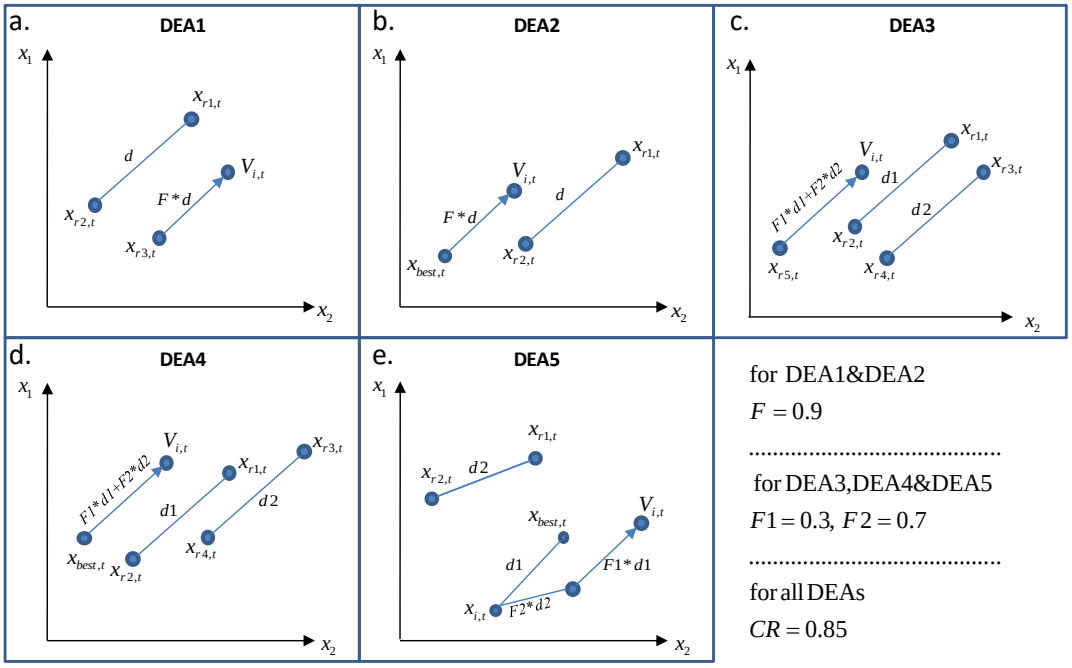


Figure 1. Depiction of mutation strategies used (compiled from Leon and Xiong [4])

In classic DEA (hereinafter referred to as DEA1), this procedure is operated with the help of one mutation (or scaling) factor *F (see first row of Table 1).* Besides, Figure 1a and Eq.(1) represent how this mutation strategy works in DEA1.

The effectiveness of the mutation is subsequently supported by a crossover stage. In the crossover, following the random number (*rand*) generation for each defined *j* gene in the present chromosomes, it is checked whether the $rand_j \leq CR$ is ensured (CR is crossover rate). In that case, the state of using the *j* gene of the vector (mutated vectors formulized in Table 1) occurs. Otherwise, the *j* gene of the corresponding chromosome is kept to be used in the next iteration. Finally, a greedy criterion is implemented by checking cost function (sum of square errors function was used here) to lay down the chromosomes that will be transmitted to the new generation. If the cost (fitness) function calculated from the candidate chromosome improves compared to that of old one, it is stored for the next generation, and the old solution is thrown down, or else the location of the old vector is preserved. The operations stated above continue until the maximum generation number ($iter_{max}$) is reached [4, 5, 6].

Although several mutation approaches have been reviewed in the context of DEA [4, 7, 8], five well-known mutation strategies are treated here. Figure 1 denotes how mutant vectors are generated according to several strategies, where d, d1 and d2 are the difference vectors. For example, contrary to DEA1, best mutation approach with one difference vector termed as DEA2, which is formulated in Eq.(2), mutates the best individual (x_{best}) in the population using two random individual [7]. On the other part, Gong and Cai [8] have recommended another random mutation strategy (abbreviated as DEA3), which is actually similar to the DEA1, but includes two difference vectors controlled by two scaling factors that are namely F1 and F2 (see Eq.3). Similar to DEA2, the best mutation strategy with two difference vectors (DEA4), which were formulized in Eq.(4), also attempts to mutate x_{best}. The variant which is relatively different from the others is current to best mutation strategy termed as DEA5 [4, 8]. It moves the current individual ($X_{i,t}$) towards x_{best} before considering a scaled difference vector. With both components, the mutated vector in DEA5 is created by Eq.(5).

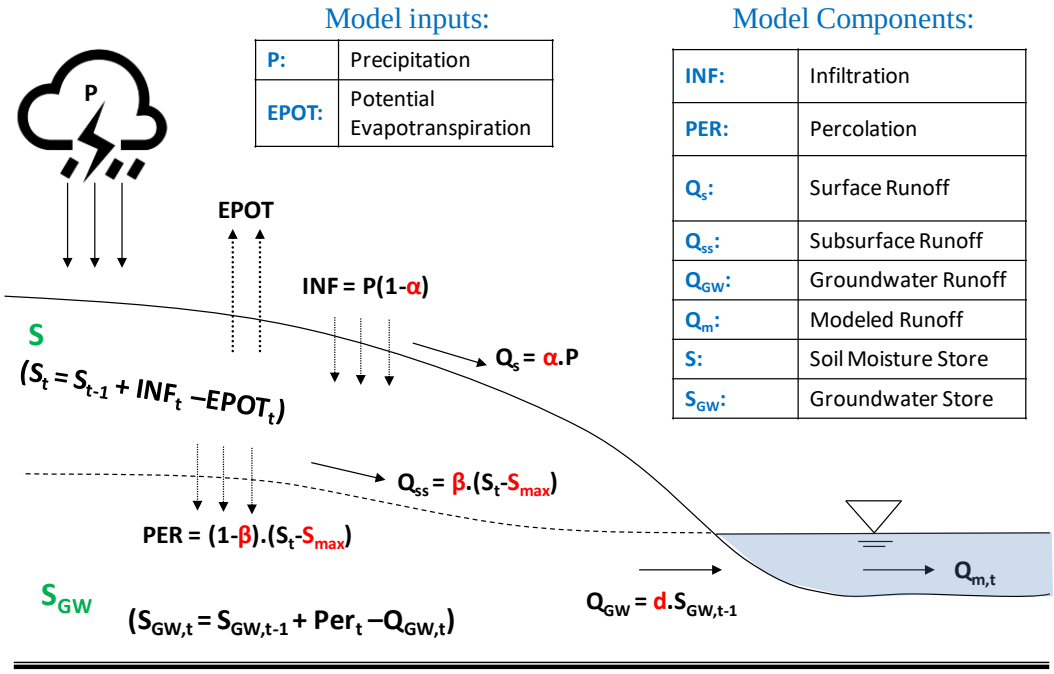


Figure 2. Conceptual scheme of TWBM including S_{max}, α, β and d parameters

III. TWBM AND STUDY AREA DESCRIPTION

Water balance models are generally assessed in three groups as physical-based, conceptual and empirical, and can also be implemented as distributed or lumped in terms of spatial resolution [2]. In this study, four-parameter version of TWBM, which was developed by Thornthwaite and Mather [9], was considered. The model, which requires only monthly total precipitation (*P*) and potential evapotranspiration (*EPOT*) as input, represent entire basin hydrology with a series of conceptual soil moisture and groundwater storage functions. In the model, the sum of three components obtained as surface runoff, subsurface runoff and groundwater flow provides the Q_m modeled runoff. Some definitions and calculation steps for the model are summarized in Figure 2.

To assess the performance of all DEA variants with different mutation strategies, a watershed at eastern region of Turkey was selected. It covers the Gordes watershed which is named by one of the prominent tributaries of Gediz River and it is located at Aegean Region of Turkey. The study region has typical Mediterranean climate characteristics. Gordes watershed has a drainage area of 1070 km^2 and annual mean runoff values obtained from Hacihidir flow gauging station is nearly 11 mm/month. Potential evapotranspiration values (*EPOT*) were estimated with Penman-Monteith equation. To achieve detailed information about the study area, readers can look through the work previously presented by Okkan and Kirdemir [10]. Further details about TWBM are available in [11] as well.

IV. EXPERIMENTS AND RESULTS

In this section, we tested the effectiveness of the five mutation strategies embedded into DEA on TWBM's calibration. The four control parameters for DEA are: population size (Np), generation number ($iter_{max}$), crossover rate (CR), and the scaling factors (*F* for DEA1 and DEA2, F1 and F2 for DEA3, DEA4, and DEA5).

In all algorithm experiments, which are run through a MATLAB code prepared by us, $iter_{max}$ was fixed to 500. Also two different population sizes were tried and Np was set to 30 and 60, respectively. Based on the study performed by Leon and Xiong [4], the main control parameters used in DEA experiments were specified as follows: CR = 0.85, and F=0.9 when only one difference vector is taken into account (as in DEA1 and DEA2), and F1=0.3 and F2=0.7 when two difference vectors are contained (as in DEA3, DEA4 and DEA5). A wide range of parameters has been defined for TWBM model to make algorithms further force in the process of finding the global solution. The range of parameters S_{max} is 10-1000 mm, while the range 0.001-0.999 is assigned for parameters α, β, d. In the study, the split-sample procedure, where the observed runoff series were divided into two equal parts for calibration and validation, was implemented [12]. According to this, the provided data covering the water period of 1981-1995 compiled for watershed were evaluated during the parameter calibration stage of the model, while data covering the water period of 1996-2010 were used in the validation.

In order to quantify the stability and convergence performance of DEA variants statistically, they were run 30 times. Following operation of them with multiple runs, stored fitness values at last iteration were primarily used to render mean fitness and standard deviation (Sd) statistics (see Table 2). Thereafter, geometric mean convergence rate (mean $Conv_{rate}$) formula recommended by He and Li [13] was utilized in the study. This index was also previously discussed in [6]. Sufficient number of iterations, where fitness is assumed to not be significantly changed after t^{th} iteration, for each run can also be determined here. All indices with mean *t* value obtained from all runs were specified in Table 2 for each population size.

Table 2. Performance indices compiled from 30 runs for DEA variants

Np size	DEA types	mean fitness (in mm^2)	Sd (in mm^2)	mean Conv$_{rate}$	mean *t*
Np=30	DEA1	10056.8511	90.8762	0.0044	156
	DEA2	10120.7839	120.8346	0.0084	82
	DEA3	10080.8259	107.8329	0.0057	130
	DEA4	10104.8007	117.5082	0.0114	60
	DEA5	10048.8595	82.8918	0.0059	128
Np=60	DEA1	10032.8763	60.8260	0.0030	163
	DEA2	10024.8848	43.7718	0.0056	85
	DEA3	10016.8932	2.27E-12	0.0035	140
	DEA4	10056.8511	90.8762	0.0082	59
	DEA5	10016.8932	2.08E-12	0.0038	126

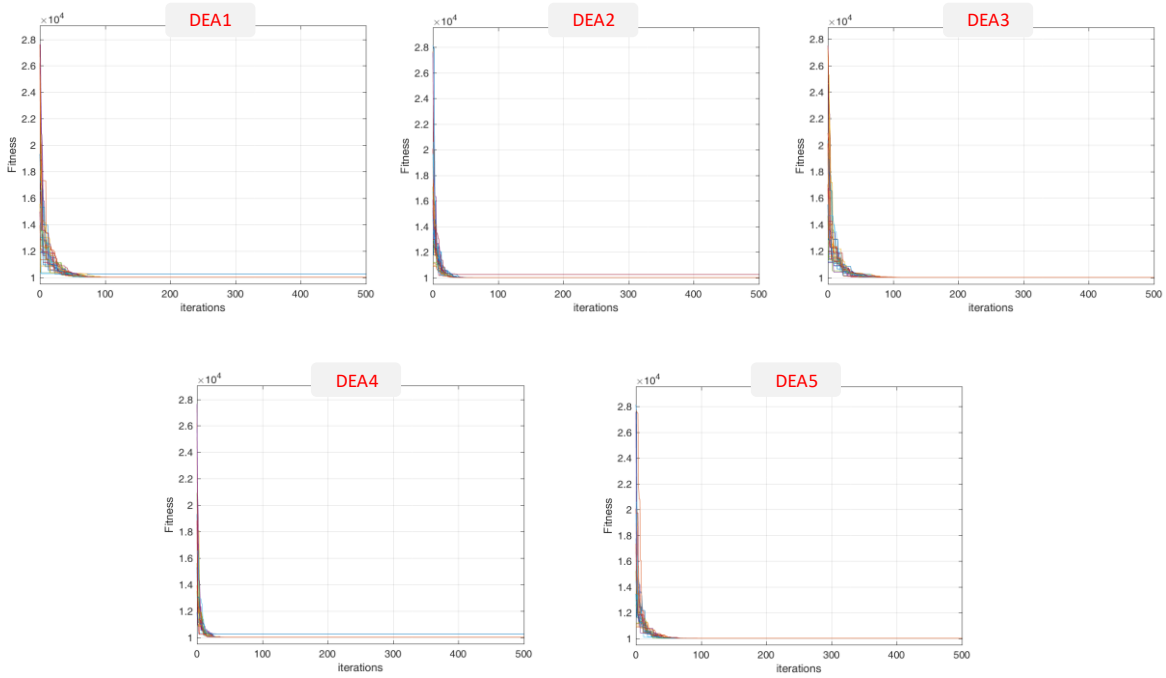


Figure 3. Convergence plots during generations for Np=60 (unit of fitness is mm^2)

In Table 2, the type of DEA which gives the best results in terms of the related index is indicated by underlined values for each population size. The increase in population size has certainly made it possible to obtain more reasonable results. Sd statistics for Np = 30 prove this remark. In this respect, it was more appropriate to compare the tried variants for size of Np = 60. The convergence results of experiments were also demonstrated in Figure 3. It can be seen from Table 2 that, under a small population size, DEA5 appeared as the strongest alternative since it provided the lowest standard deviation statistics. Besides, DEA5 and DEA3 also behaved very reasonable under a medium size of population (Np=60). Although DEA4 exhibited rapid convergence for each population size, it did not produce stable results in terms of mean fitness and Sd statistics. Conventional DEA1 was also attractive, as it responds as the second best approach by performance indices in a small population size. But it is not preferable for Np = 60, because other candidates including DEA3 and DEA5 variants acquired more optimal solutions.

Based on the above findings, we can point out that, for various population sizes, it is better to consider DEA5. These detections are in parallel with those done by Leon and Xiong [4].

V. CONCLUSIONS

The presented study tries to put across an empirical study to compare five particular mutation strategies in a water balance model's calibration stage. All the variants considered have been tested in Gordes watershed example in terms of the performance measures representing stability of solutions and the computational costs, i.e. the number of generations needed. The results derived from the experiments have pointed out the utilization of DEA5, which is more superior in guaranteeing the stable global solutions. Of course, these determinations obtained by a four parameter water balance model applied in a single study area cannot be generalizing.

So, in future works of ours, we would like to exploit the indication acquired in this study for more generic cases to get more generalized and reliable detections. Moreover, it would be useful to perform a dynamic sensitivity analysis over the scaling parameters.

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