Enhancing Differential Evolution Utilizing Proximity-based Mutation Operators

M.G. Epitropakis, Member, IEEE, D.K. Tasoulis, Member, IEEE, N.G. Pavlidis,
V.P. Plagianakos, and M.N. Vrahatis

Abstract—Differential Evolution is a very popular optimization algorithm and considerable research has been devoted to the development of efficient search operators. Motivated by the different manner in which various search operators behave, we propose a novel framework based on the proximity characteristics among the individual solutions as they evolve. Our framework incorporates information of neighboring individuals, in an attempt to efficiently guide the evolution of the population towards the global optimum, without sacrificing the search capabilities of the algorithm. More specifically, the random selection of parents during mutation is modified, by assigning to each individual a probability of selection that is inversely proportional to its distance from the mutated individual. The proposed framework can be applied to any mutation strategy with minimal changes. In this paper, we incorporate this framework in the original Differential Evolution algorithm, as well as other recently proposed Differential Evolution variants. Through an extensive experimental study, we show that the proposed framework results in enhanced performance for the majority of the benchmark problems studied.

Index Terms—Differential Evolution, Mutation Operator, Affinity Matrix, Nearest Neighbors

I. INTRODUCTION

EvoluTionary Algorithms (EAs) are stochastic search methods that mimic evolutionary processes encountered in nature. The common conceptual base of these methods is to evolve a population of candidate solutions by simulating the main processes involved in the evolution of genetic material of organism populations, such as natural selection and biological evolution. EAs can be characterized as global optimization algorithms. Their population-based nature, allows them to avoid getting trapped in a local optimum and consequently provides a great chance to find global optimal solutions. EAs have been successfully applied to a wide range of optimization problems, such as image processing, pattern recognition, scheduling, and engineering design [1], [2]. The most prominent EAs proposed in the literature are: Genetic Algorithms [1], Evolutionary Programming [3], Evolution Strategies [4], Genetic Programming [5], Particle Swarm Optimization (PSO) [6], and Differential Evolution [7], [8].

In general, every EA starts by initializing a population of candidate solutions (individuals). The quality of each solution is evaluated using a fitness function, which represents the problem at hand. A selection process is applied at each iteration of the EA to produce a new set of solutions (population). The selection process is biased toward the most promising traits of the current population of solutions to increase their chances of being included in the new population. At each iteration (generation), the individuals are evolved through a predefined set of operators, like mutation and recombination. This procedure is repeated until convergence is reached. The best solution found by this procedure is expected to be a near-optimum solution [2], [9].

Mutation and recombination are the two most frequently used operators and are referred to as evolutionary operators. The role of mutation is to modify an individual by small random changes to generate a new individual [2], [9]. Its main objective is to increase diversity by introducing new genetic material into the population, and thus avoid local optima. The recombination (or crossover) operator combines two, or more, individuals to generate new promising candidate solutions [2], [9]. The main objective of the recombination operator is to explore new areas of the search space [2], [10].

In this paper, we study the Differential Evolution (DE) algorithm, proposed by Storn and Price [7], [8]. This method has been successfully applied in a plethora of optimization problems [7], [11]–[19]. Without loss of generality, we only consider minimization problems. In this case, the objective is to locate a global minimizer of a function \( f \) (objective function).

Definition 1: A global minimizer \( x^* \in \mathbb{R}^D \) of the real-valued function \( f: \mathcal{E} \to \mathbb{R} \) is defined as:

\[
 f(x^*) \leq f(x), \quad \forall x \in \mathcal{E},
\]

where the compact set \( \mathcal{E} \subseteq \mathbb{R}^D \) is a \( D \)-dimensional scaled translation of the unit hypercube.

A main issue in the application of EAs to a given optimization problem, is to determine the values of the control parameters of the algorithm that will allow the efficient exploration of the search space, as well as its effective exploitation. Exploration enables the identification of regions of the search space in which good solutions are located. On the other hand, exploitation accelerates the convergence to the optimum solution. Inappropriate choice of the parameter values can cause the algorithm to become greedy or very explorative and
consequently the search of the optimum can be hindered. For example, a high mutation rate will result in much of the space being explored, but there is also a high probability of losing promising solutions; the algorithm has difficulty to converge to an optimum due to insufficient exploitation. Several Evolutionary Computation approaches have been proposed that try to give a satisfactory answer to this exploration/exploitation dilemma [20]–[27]. Recent studies of the exploration and exploitation capabilities of different mutation operators have shown that after a number of iterations of the DE algorithm the individuals exhibit the tendency to gather around optimizers of the objective function [21], [22].

Motivated by these findings, we propose an alternative to the uniform random selection of parents during mutation. We advocate a stochastic selection framework in which the probability of selecting an individual to become a parent is inversely proportional to its distance from the initial undergoing mutation. By favoring search in the vicinity of the mutated individual this framework promotes efficient exploitation, without substantially diminishing the exploration capabilities of the mutation operator. The proposed framework can be applied to any mutation strategy and, as shown through extensive experimental evaluation, produces remarkable improvement. We also incorporate this framework to a number of recently proposed DE variants and observe performance gains.

The rest of the paper is organized as follows: Section II describes the original Differential Evolution algorithm. In Section III, we include a short literature review. Section IV illustrates the behavior of different mutation operators, providing the motivation for the proposed framework, which is presented in Section V. Next, in Section VI we present the results of an extensive experimental analysis, and the paper concludes with a discussion in Section VII.

II. THE DIFFERENTIAL EVOLUTION ALGORITHM

Differential Evolution [7], [8] is a population–based stochastic parallel direct search method that utilizes concepts borrowed from the broad class of EAs. The method typically requires few control parameters and numerous studies have shown that it has good convergence properties. DE outperforms other well known EAs in a plethora of problems [7], [11]–[13], [15] and has attracted the interest of the research community. Consequently, several variations of the classical DE algorithm have been proposed in the literature [13], [14], [22], [23], [26]–[34]. A detailed description of the DE algorithm and experimental results on hard optimization problems can be found in [12]–[15], [18].

The DE algorithmic schemes can be classified using the notation DE/base/num/cross. The method of selecting the parent that constitutes the base individual is indicated by base. For example, DE/rand/num/cross selects the parent for the base individual randomly, while in DE/best/num/cross the parent for the base individual is the best individual of the population. The number of differences between individuals that are used to perturb the base individual is indicated by num. Finally, cross stands for the crossover type utilized by the mutation strategy, i.e. exp for exponential and bin for binomial. Exponential and binomial crossover will be discussed in subsection II-C. In this study, we always employ binomial crossover, and thus we exclude the cross part to simplify the notation.

In DE the central search operator is known as mutation strategy. Consequently, a substantial amount of research has been devoted to the development and the analysis of efficient mutation operators and their dynamics [12], [13], [15], [18], [35], [36]. In more detail, for each individual undergoing mutation (mutated individual) a set of individual solutions are uniformly selected across the population (parents). The parents and the mutated individual are subsequently mixed to construct a new candidate solution (mutant individual). The mutation operators prescribe the manner in which this mixing is performed, and the number of parents that will be used. The search operators efficiently shuffle information among the individuals, enabling the search for an optimum to focus on the most promising regions of the solution space. Next, we describe in detail the DE procedures.

A. Initialization

Following the general concept of EAs, the first step of DE is the initialization of a population of NP, D–dimensional potential solutions (individuals) over the optimization search space. We shall symbolize each individual by \( x^i_g = \{x^i_{g,1}, x^i_{g,2}, \ldots, x^i_{g,D}\} \), for \( i = 1, 2, \ldots, NP \), where \( g = 0, 1, \ldots, g_{\text{max}} \) is the current generation and \( g_{\text{max}} \) the maximum number of generations. At the first generation \( (g = 0) \) the population should be sufficiently scaled to cover as much as possible of the optimization search space. Initialization is implemented by using a random number distribution to generate the potential individuals in the optimization search space. The optimization search space can be defined by lower and upper bound values, i.e. \( L = [L_1, L_2, \ldots, L_D] \) and \( U = [U_1, U_2, \ldots, U_D] \). Hence, we can initialize the \( j \)-th dimension of the \( i \)-th individual according to:

\[
 x^i_{0,j} = L_j + \text{rand}_j(0,1) \cdot (U_j - L_j),
\]

where \( \text{rand}_j(0,1) \) is a uniformly distributed random number confined in the \([0,1]\) range.

B. Mutation Operators

Following initialization, the evolution process begins with the application of the mutation operator. For each individual of the current population a new individual, called the mutant individual \( v^i_g \), is derived through the combination of randomly selected and pre-specified individuals. The originally proposed and most frequently used mutation strategies in the literature are:

1) “DE/best/1”

\[
 v^i_g = x^i_{\text{best}} + F(x^r_1 - x^r_2),
\]

2) “DE/rand/1”

\[
 v^i_g = x^r_1 + F(x^r_2 - x^r_3),
\]
3) “DE/current-to-best/1”
\[ v_i^g = x_i^g + F \cdot (x_{\text{best}}^g - x_i^g) + F \cdot (x_{g_j}^i - x_g^{g_j}) \] (4)

4) “DE/best/2”
\[ v_i^g = x_i^g + F \cdot (x_{\text{best}}^g - x_i^g) + F \cdot (x_{g_j}^i - x_{g_j}) \] (5)

5) “DE/rand/2”
\[ v_i^g = x_i^g + F \cdot (x_{g_j}^i - x_i^g) + F \cdot (x_{g_j}^i - x_{g_j}^i) \] (6)

6) “DE/current-to-best/2”
\[ v_i^g = x_i^g + F \cdot (x_{\text{best}}^g - x_i^g) + \frac{F \cdot (x_{g_j}^i - x_i^g) + F \cdot (x_{g_j}^i - x_{g_j}^i)}{2} \] (7)

where \( x_{\text{best}}^g \) denotes the best (fittest) individual of the current generation, the indices \( r_1, r_2, r_3, r_4, r_5 \in S_r = \{1, 2, \ldots, NP\} \setminus \{i\} \) are uniformly random integers mutually different and distinct from the running index \( i \), \( (x_{g_j}^i - x_g^{g_j}) \) is a difference vector that mutates the base vector, \( (r_x, r_y) \in S_r \), and \( F > 0 \) is a real positive parameter, called mutation or scaling factor. The mutation factor controls the amplification of the difference between two individuals and is used to prevent the stagnation of the search process. Large values of this parameter amplify the differences and hence promote exploration, while small values favor exploitation. The inappropriate choice of the mutation factor can therefore cause the deceleration of the algorithm and a reduction of population diversity [12], [15], [28]. In the original DE algorithm, the mutation factor \( F \) is a fixed and user defined parameter, while in many adaptive DE variants each individual is associated with a different adaptive mutation factor [23], [26]–[31], [33], [37], [38]. Several DE variants that either introduce new mutation strategies or new self-adaptive techniques to tune the control parameters have been recently proposed [12], [15], [18], [22], [25]–[27], [31], [34], [35], [39]–[44]. A detailed discussion about the current state-of-the-art of DE can be found in a recently published survey [13].

In an attempt to rationalize the mutation strategies, Eqs. (2)–(7), we observe that Eq. (3) is similar to the crossover operator employed by some Genetic Algorithms. Eq. (2) is derived from Eq. (3), by substituting the best member of the previous generation, \( x_{\text{best}}^g \), with a random individual \( x_{g_j}^i \). Eqs. (4), (5), (6) and (7) are modifications obtained by the combination of Eqs. (2) and (3). It is clear that new DE mutation operators can be generated using the above ones as building blocks. Such examples include the trigonometric mutation operator [39], the recently proposed genetically programmed mutation operators [45], or new classes of mutation operators that attempt to combine the explorative and exploitative capabilities of the original ones [21], [22].

C. Crossover or Recombination Operators

Following mutation, the crossover or recombination operator is applied to further increase the diversity of the population. It is important to note that without the crossover operator, the original DE algorithm performs poorly on multimodal functions [12]. In crossover, the mutant individuals are combined with other predetermined members of the population, called target individuals, to produce the trial individuals. The most well known and widely used variants of DE utilize two main crossover schemes; the exponential and the binomial or uniform crossover [7], [12], [13], [46]. The exponential crossover scheme was introduced in the original work of Storm and Price [8], but in the subsequent DE literature the binomial variant [7], [13] is mostly used.

The binomial or uniform crossover is performed on each component \( j (j = 1, 2, \ldots, D) \) of the mutant individual \( v_i^g \). In detail, for each component of the mutant vector a random real number \( r \) in the interval \([0, 1]\) is drawn and compared with the crossover rate or recombination factor, \( CR \in [0, 1] \), which is the second DE control parameter. If \( r \leq CR \), then we select, as the \( j \)-th component of the trial individual \( u_i^g \), the \( j \)-th component of the mutant individual \( v_i^g \). Otherwise, the \( j \)-th component of the target vector \( x_g^i \) becomes the \( j \)-th component of the trial vector. The aforementioned procedure can be outlined as:
\[ u_{g,j}^{i} = \begin{cases} v_{g,j}^{i}, & \text{if } (\text{rand}_{i,j}(0,1) \leq CR \text{ or } j = j_{\text{rand}}), \\ x_{g,j}^{i}, & \text{otherwise}, \end{cases} \] (8)

where the \( \text{rand}_{i,j}(0,1) \) is a uniformly distributed random number in \([0, 1]\), different for every \( j \)-th component of every individual, and \( j_{\text{rand}} \in \{1, 2, \ldots, D\} \) is a randomly chosen integer which ensures that at least one component of the mutant vector will be assigned to the target vector. It is evident that for values of the recombination factor close to zero the effect of the mutation operator is very small, since the target and the mutant vector become identical.

D. Selection

Finally, the selection operator is employed to maintain the most promising trial individuals in the next generation and to retain the population size constant over the evolution process [12]. The original DE adopts a simple monotone selection scheme. It compares the objective values of the target \( x_g^i \) and trial \( u_g^i \) individuals. If the trial individual reduces the value of the objective function then it is accepted for the next generation; otherwise the target individual is retained in the population. Thus, the selection operator can be defined as:
\[ x_{g+1}^{i} = \begin{cases} u_{g}^{i}, & \text{if } f(u_{g}^{i}) < f(x_{g}^{i}), \\ x_{g}^{i}, & \text{otherwise}. \end{cases} \] (9)

The original DE algorithm (DE/rand/1/bin) is illustrated in Algorithm 1.

III. Related work

Darwin was the first to realize that populations may exhibit a spatial structure which can influence the population’s dynamics. The Evolutionary Computing (EC) literature today utilizes spatial information in populations and the general concept of a neighborhood in several domains. In this section, we briefly discuss how the neighborhood concept has been utilized in the context of the Differential Evolution algorithm.
Algorithm 1 Algorithmic scheme for the original Differential Evolution algorithm (DE/rand/1/bin)

Set the generation counter \( g = 0 \)

/* Initialize the population of \( NP \) individuals: \( P_g = \{x^1_g, x^2_g, \ldots, x^NP_g\} \), with \( x^i_g = \{x^1_{i,g}, x^2_{i,g}, \ldots, x^D_{i,g}\} \) for \( i = 1, 2, \ldots, NP \) uniformly in the optimization search hyper-rectangle [\( L, U \)]. */

for \( i = 1 \) to \( NP \) do

for \( j = 1 \) to \( D \) do

\( x^0_{i,j} = L_j + \text{rand}(0, 1) \cdot (U_j - L_j) \)

end for

Evaluate individual \( x^i_0 \)

end for

while termination criteria are not satisfied do

Set the generation counter \( g = g + 1 \)

for \( i = 1 \) to \( NP \) do

/* Mutation step */

Select uniformly random integers \( r_1, r_2, r_3 \in S_r = \{1, 2, \ldots, NP\} \setminus \{i\}

/* For each target vector \( x^i_j \) generate the corresponding mutant vector \( v^i_g \) using Eq. (3) */

for \( j = 1 \) to \( D \) do

\( v^i_{j,g} = x^i_{j,g} + F(x^r_{j,g} - x^r_{j,g}) \)

end for

/* Crossover step: For each target vector \( x^i_g \) generate the corresponding trial vector \( u^i_g \) through the Binomial Crossover scheme. */

\( j_{\text{rand}} = \) a uniformly distributed random integer \( \in \{1, 2, \ldots, D\} \)

for \( j = 1 \) to \( D \) do

\( u^i_{g,j} = \begin{cases} u^i_{g,j}, & \text{if } \text{rand}(j, 0, 1) \leq CR \text{ or } j = j_{\text{rand}}, \\ x^i_{g,j}, & \text{otherwise,} \end{cases} \)

end for

/* Selection step */

if \( f(u^i_g) < f(x^i_g) \) then

\( x^i_{g+1} = u^i_g \)

else

if \( f(u^i_g) < f(x^\text{best} \_g) \) then

\( x^i_{g+1} = u^i_g \) and \( f(x^\text{best} \_g) = f(u^i_g) \)

else

\( x^i_{g+1} = x^i_g \)

end if

end if

end for

end while

A. Neighborhood concepts in structured EAs

In structured EAs the population is decentralized into sub-populations which can interact and may have different evolutionary roles. Two of the most prominent structured EAs are cellular Evolutionary Algorithms (cEAs) [47] and distributed Evolutionary Algorithms (dEAs) [48], [49]. A comprehensive classification and presentation can be found in [50], [51]. Generally, in cEAs, the sub-populations are created according to a neighborhood criterion and thus each sub-population has both an explorative and an exploitative role for a different region of the search space. On the other hand, in dEAs, distinct sub-populations (islands) explore in parallel the entire search space. In biological terms, dEAs resemble distinct semi-isolated populations in which evolution takes place independently. The migration operator in dEAs controls the exchange of individuals between subpopulations. This operator defines the topology, the migration rate, the migration frequency, and the migration policy [49], [52], [53]. These additional degrees of freedom make dEAs more flexible and capable of tackling harder optimization tasks.

The concept of structured populations has been incorporated in DE. In [23] and [54], distributed DE variants were presented which control adaptively the migration and the DE control parameters according to a genotype diversity criterion. In [55], a distributed DE algorithm is proposed that preserves diversity in the niches in order to solve multimodal optimization problems. In [56] a ring topology distributed DE was proposed with a migration operator that exchanges best performing individuals and replaces random individuals among neighboring subpopulations. In [57], Apolloni et al. proposed a modified version of [56], in which migration is performed through a probabilistic criterion. Modifications of [56] presented in [58]–[60] utilize a locally connected topology, where each node is connected to \( l \) other nodes. The recently proposed Distributed Differential Evolution with Explorative—Exploitative Population Families (DDE-EEPF) [24] employs sub-populations which are grouped into two families: explorative and exploitative. Explorative subpopulations have constant size, are arranged according to a ring topology and employ a migration of best performing individuals. On the other hand, exploitative subpopulations have dynamic size, are highly exploitative, and aim to quickly detect fittest solutions. Numerical results show that DDE-EEPF is an efficient and promising distributed DE variant. The Distributed Differential Evolution with Scale factor inheritance mechanism (FACPDE) [61] implements sub-populations arranged in a ring topology. Each sub-population is characterized by its own scale factor and migrates the best individual with its associated scale factor to its neighbors. The distribution of the successful scale factors and the fittest individuals among the subpopulations, enhances the scheme, and its performance substantially.

B. Index neighborhood concepts in Differential Evolution

A popular neighborhood structure in EC is the index-based neighborhood concept, introduced in the PSO algorithm. PSO incorporates an index-based neighborhood structure in its population and not real topological-based neighborhoods. Thus, the neighbors of each potential solution do not necessary lie in the vicinity of its topological region in the search space. Recently, the index neighborhood structures of PSO have also been considered in DE. The Differential Evolution with Global and Local Neighborhoods (DEGL) [13], [25], [42] incorporates concepts of the UPSO algorithm [62], such as the index neighborhoods of each individual, a local and a global scheme to facilitate the exploration and the exploitation of the search space, and a convex combination of these schemes to balance their effect. The Self-adaptive DE (SDE) [63], has been modified by using a ring neighborhood topology.
in [64]. The same authors introduced the Barebones Differential Evolution [65] (BBDE). BBDE employs the concept of index neighborhoods in DE and enhances the DE mutation scheme by utilizing as a base vector either a randomly chosen personal best position or a stochastic weighted average of the individual’s attractors (e.g., its personal and neighborhood best positions). This mutation scheme tends to explore the search space around the corresponding base vector and thus to exploit the vicinity of the current position.

C. Neighborhood concepts in mutation strategies

Numerous DE variants utilize specialized mutation strategies to exploit population structure. In [66], five mutation strategies have been proposed that produce new vectors in the vicinity of the corresponding base vector. To this end, the weighted difference between two individuals is used in conjunction with an adaptive scaling factor. DE with Parent Centric Crossover (DEPCX) and DE with Probabilistic Parent Centric Crossover (Pro. DEPCX) [67] are inspired by the parent centric crossover operator (PCX) used in GAs [68]. DEPCX utilizes the parent centric approach in the mutation strategy to generate new solution vectors, while Pro. DEPCX stochastically utilizes the parent centric mutation operator along with the basic DE mutation operation. The PCX procedure increases the probability of producing new candidate solution vectors in the vicinity of the parent vectors and thus exploits the neighborhood of parent vectors. In [44] and [69], two modified DE variants called DE with Random Localization (DERL) and DE with Localization using the best vector (DELB) were proposed. Both variants incorporate simple techniques to produce solutions that exhibit a local search effect around the base vector, with global exploration characteristics at the early stages of the algorithm and a local effect in terms of convergence at later stages of the algorithm.

D. Neighborhood concepts through local search

Various DE variants attempt to exploit and refine the position of the best individuals, by incorporating a list of local search procedures. MDE [70] makes use of the Hooke-Jeeves algorithm and a Stochastic Local Searcher adaptively coordinated by a fitness diversity-based measure. The EMDE [16], [17] combines the powerful explorative features of DE with the exploitative features of three local search algorithms employing different pivot rules and neighborhood generating functions, e.g., Hooke Jeeves Algorithm, a Stochastic Local Search, and Simulated Annealing. The Super-Fit Memetic Differential Evolution (SFMDE) [71] employs PSO, the Nelder-Mead algorithm and the Rosenbrock algorithm. SFMDE coordinates the local search algorithms by means of an index that measures the quality of the super-fit individual with respect to the remaining individuals in the population and a probabilistic scheme based on the generalized beta distribution. Noman and Iba [72] recently proposed a Fittest Individual Refinement (FIR), a crossover-based local search DE variant to tackle high dimensional problems. In [73], FIR is enhanced through a local search technique which adaptively adjusts the length of the search, utilizing a hill-climbing heuristic. This approach accelerates DE by enhancing the search capability in the neighborhood of the best solution in successive generations. Additionally, the Scale Factor Local Search Differential Evolution (SFLSDE) [74] is based on the DE/rand/1 mutation strategy and incorporates, within a self-adaptive scheme, two local search algorithms to efficiently adapt the mutation factor during the evolution. The local searchers aim to detect a value of the scale factor that corresponds to a refined offspring and thus tend to correct “weak” individuals.

IV. THE DYNAMICS OF DE MUTATION STRATEGIES

In this section, we investigate the impact of DE dynamics, i.e., the exploration/exploitation capabilities of the different DE mutation strategies. Our findings suggest that the individuals evolved through some of the original DE mutation strategies sometimes tend to gather around minimizers of the objective function. This motivates our approach, which aims to appropriately select neighboring individuals for incorporation in each mutation strategy. The goal is to efficiently guide the evolution of the population towards a global optimum, without sacrificing the search capabilities of the DE algorithm. The exploration and exploitation capabilities of different DE mutation strategies were studied in [21], [22], where it was shown that not all DE search operators have the same impact on the exploration/exploitation of the search space. Thus, the choice of the most efficient mutation operator can be cumbersome and problem dependent.

In general, we can distinguish between mutation operators that promote exploration and operators that promote exploitation. An observation of the equations of the mutation operators (Eqs. (2)–(7)), reveals that operators that incorporate the best individual (e.g., DE/best/1, DE/best/2, and DE/current-to-best/1) favor exploitation, since the mutant individuals are strongly attracted around the current best individual. Note that DE/best/2 usually exhibits better exploration than DE/best/1, because it includes one more difference of randomly selected individuals, which adds one more component of random variation in each mutation. In contrast, mutation operators that incorporate either randomly chosen individuals or many differences of randomly chosen individuals (e.g., DE/rand/1 and DE/rand/2) enhance the exploration of the search space, since a high degree of random variability affects each mutation. Again, although DE/current-to-best/2 is based on DE/current-to-best/1 the utilization of a second difference vector further promotes the exploration of the search space [12], [13], [15].

Next, we investigate the impact of the dynamics of different DE mutation strategies on the population. Experimental simulations indicate that DE mutation strategies tend to distribute the individuals of the population in the vicinity of the objective function’s minima. Exploitative strategies rapidly gather all the individuals to the basin of attraction of a single minimum, whereas explorative strategies tend to spread the individuals around many minima. To demonstrate this we employ as a case study the two-dimensional Shekel’s Foxholes benchmark function, illustrated in Fig. 1. This function has twenty four distinct local minima and one global minimum $f(-32, 32) = 0.998004$, in the range $[-65.536, 65.536]^2$ [75].
We utilize two DE variants with different dynamics: the explorative DE/rand/1 and the exploitative DE/best/1. Contour plots of the Shekel’s Foxholes function and the positions of a population of 100 individuals after 1, 5, 10, 20 generations of DE/best/1 and DE/rand/1 are depicted in Figs. 2 and 3, respectively. The two figures show that both DE/best/1 and DE/rand/1 first explore the search space around their initial population positions. The exploitative character of DE/best/1 causes the individuals to gather rapidly around the basin of attraction of the global minimum, (see Fig. 2). On the other hand, DE/rand/1, Fig. 3, spreads the individuals over many minima locations, before gathering them around the global minimum.

To study the clustering tendency of different DE mutation strategies we utilize a statistical test called the Hopkins test [76]. Clustering tendency is a well known concept in the cluster analysis literature that deals with the problem of determining the presence or absence of a clustering structure in a data set [77]. The Hopkins test relies on the distances between a number of vectors which are randomly placed in the search space, and the vectors of a data set, \( X = \{x_i, i = 1, 2, \ldots, NP\} \), which in our case correspond to the individuals of the population. More specifically, let \( Y = \{y_i, i = 1, 2, \ldots, M\}, M \ll NP \), be a set of vectors that are uniformly distributed in the search space. In addition, let \( X_1 \subset X \) be a set of \( M \) randomly chosen vectors from \( X \). Let \( d_j \) be the distance of \( y_j \in Y \) to its closest vector in \( X_1 \), denoted by \( x_j \), and \( \delta_j \) be the distance between \( x_j \) and its nearest neighbor in \( X_1 \setminus \{x_j\} \). The Hopkins statistic involves the \( l \)-th powers of \( d_j \) and \( \delta_j \) and is defined as [77]:

\[
h = \frac{\sum_{j=1}^{M} d_j^l}{\sum_{j=1}^{M} d_j^l + \sum_{j=1}^{M} \delta_j^l}.
\]

This statistic compares the nearest neighbor distribution of the points in \( X_1 \) with that from the points in \( Y \). When the dataset \( X \) contains clusters, the distances between nearest neighbors in \( X_1 \) are expected to be small on average, and \( h \) assumes relatively large values. Therefore, large values of \( h \) indicate the presence of a clustering structure in the dataset, while small values of \( h \) indicate the presence of regularly spaced points. A value around 0.5 indicates that the vectors of the dataset \( X \) are randomly distributed over the search space. Due to the stochastic nature of H-measure, for every generation in every simulation we calculate the H-measure value 100 times, by considering different random solutions. Thus, in Fig. 4, we illustrate the mean value of the H-measure at each generation, obtained from 100 independent simulations for the 30-dimensional versions of the Shifted Sphere and Shifted Griewank functions [78]. Error bars around the mean depict the standard deviation of the H-measure. The Shifted Sphere is a simple unimodal function, while the Shifted Griewank is highly multimodal. These benchmarks were chosen to investigate the behavior of the DE mutation operators in two qualitatively different problems.

As shown, all mutation strategies exhibit large H-measure values within the first 100 generations, indicative of a strong clustering structure, even from these initial stages of the evolution. Also, the relative values of the H-measure for the different strategies indicate an ordering with respect to their exploitation tendency. DE/best/1 appears to be the most exploitative operator, and DE/current-to-best/1 behaves similarly. The least exploitative operator is DE/rand/2.
In this work, we attempt to take advantage of this clustering behavior. To this end, we modify the way that DE mutation strategies choose individuals to form the difference vectors, which are employed to mutate the base vector. More specifically, to generate a mutant individual, we propose to use individuals in the vicinity of the parent vector that probably reside in the same cluster, instead of uniformly random individuals. This has the potential to rapidly exploit the regions of minima, and thus accelerate convergence.

To illustrate this concept, Figs. 5 and 6 show the 5-nearest neighbors graphs for the DE/best/1 and DE/rand/1 populations of the two-dimensional Shekel’s Foxholes function, after 1, 5, 10, and 20 generations, respectively. As shown, selecting individuals amongst the 5-nearest neighbors to produce mutant individuals will achieve our goal of exploiting local information. The occasional connections between individuals clustered around different local minima, suggest that the exploration abilities of the algorithm will not be severely hindered. We further promote exploration by introducing stochasticity into the selection mechanism, instead of just using a prespecified number of nearest neighbors. In particular, we assign a probability of selection to each individual which is inversely proportional to its distance to the parent individual. In the next section, we describe in detail the proposed method.

V. THE PROPOSED PROXIMITY-BASED MUTATION FRAMEWORK

As shown in the previous section, it is possible to guide the evolution towards a global optimum without compromising the algorithm’s search capabilities by incorporating information from neighboring individuals. In this section, we discuss the main concepts behind a Proximity-based Differential Evolution framework (Pro DE). The easiest way to implement the proposed approach would be to select the indices \( r_1, r_2, r_3 \) of the individuals involved in mutation, to correspond to the 3-nearest neighbors of the parent individual, rather than being random. However, such an approach could result in an exceedingly exploitative (greedy) algorithm, especially during the first steps of the evolution where such a behavior can be detrimental. Instead, we propose a stochastic selection of \( r_i, i \in \{1, 2, 3\} \) in the mutation procedure.

Let us consider a population of \( NP, D \)-dimensional individuals \( P_g = [x^1_g, x^2_g, \ldots, x^{NP}_g] \). We calculate the affinity matrix, \( R_d \), based on real distances between individuals. Thus, the
Algorithm 2 Pro DE/rand/1: proximity-based mutation algorithmic scheme for DE/rand/1

/* Mutation step */
Calculate the probability matrix \( R_p \) based on Eq. (10)
Utilize a roulette wheel to select indices \( r_{1}^i, r_{2}^i, r_{3}^i \in S_r = \{1, 2, \ldots, NP\} \setminus \{i\} \) based on probability matrix \( R_p \)
/* For each target vector \( x_g^i \) generate the corresponding mutant vector \( v_g^i \) using Eq. (3) */
for \( j = 1 \) to \( D \) do
\[
v_{j,g}^i = x_{j,g}^i + F(x_{j,g}^r - x_{j,g}^r)
\]
end for

\[ R_d(i,j) \] element of the matrix corresponds to the distance between the \( i \)-th and the \( j \)-th individuals:

\[
R_d = \begin{bmatrix}
0 & \|x_{1,g}^i - x_{1,g}^j\| & \cdots & \|x_{NP}^i - x_{NP}^j\|
\|x_{2,g}^i - x_{2,g}^j\| & 0 & \cdots & \|x_{NP}^i - x_{NP}^j\|
\|x_{3,g}^i - x_{3,g}^j\| & \|x_{3,g}^i - x_{3,g}^j\| & 0 & \|x_{NP}^i - x_{NP}^j\|
\vdots & \vdots & \ddots & \vdots
\|x_{NP}^i - x_{NP}^j\| & \|x_{NP}^i - x_{NP}^j\| & \cdots & 0
\end{bmatrix},
\]

where \( \|x; y\| \) is a distance measure between the \( x \) and \( y \) individuals. In the case of decision variables with different search ranges, a scale-invariant distance measure (e.g. the Mahalanobis distance [77]) needs to be avoided to avoid any dependence on the scale of the variables. It has been shown that a fixed number of points becomes increasingly “sparse” as the dimensionality increases [79]. Therefore, in very high dimensional problems \( p \)-norms, with \( p \leq 1 \) can be used [80]. In this paper we use Euclidean distances, since in all the considered problems all the variables have equal ranges.

The affinity matrix is symmetric, due to the symmetric property of the distance. Thus, only the upper triangular part of \( R_d \) needs to be calculated. Based on the \( R_d \) matrix, we calculate a probability matrix \( R_p \), in which each element \( R_p(i,j) \) represents a probability between the \( i \)-th and \( j \)-th individual with respect to the \( i \)-th row. The probability of the \( i \)-th individual is inversely proportional to the distance of the \( j \)-th individual, i.e. the individual of the row with the minimum distance has the maximum probability:

\[
R_p(i,j) = 1 - \frac{R_d(i,j)}{\sum_i R_d(i,j)}, \quad (10)
\]

where \( i, j = 1, 2, \ldots, NP \). Thus, we incorporate a stochastic selection procedure, in the form of a simple roulette wheel selection without replacement [2], to obtain the indices \( r_{1}^i, r_{2}^i, r_{3}^i \in S_r = \{1, 2, \ldots, NP\} \setminus \{i\} \).

A notable observation is that it is not necessary to repeatedly calculate the probability matrix in every generation. As it is previously described, the key role of the proximity framework is to exploit possible clustering structure of the population over the problem’s minima and subsequently incorporate that information in the evolution phase of the algorithm. To this end, whenever an individual passes the selection operator its position is altered and the affinity matrix should be updated. Depending either on the computational cost we are willing to pay, or on the characteristics of the DE variant and the considered problem, the \( R_p \) matrix can be calculated in every or every few generations. It is evident that when the affinity matrix is not calculated in every generation, it contains errors. Inaccurate information in the affinity matrix may not significantly affect the algorithm’s dynamics, due to the desired randomness of indices \( r_1 \). In this paper, we propose to update the affinity matrix after each change of an individual’s position, which is in essence at every generation.

Some DE variants incorporate operators that rapidly change the position of many individuals either by the greediness of the evolution operator, e.g. the mutation strategies DE/best/1, DE/current-to-best/1, DE/best/2, or due to an extra operator that influences the evolution dynamics, e.g. the population of opposition-based DE [40], [41]. In these cases, we must immediately transfer this information to the proximity framework, and thus update the affinity matrix in every generation.

The proposed proximity-based framework affects only the mutation step, hence it could be directly applied to any DE mutation strategy. The application of this framework for DE/rand/1 is demonstrated in Algorithm 2. We use the notation Pro DE/rand/1 to designate that the proposed proximity-based framework is used.

VI. EXPERIMENTAL RESULTS

In this section, we perform an extensive experimental evaluation of the proposed framework. We employ the CEC 2005 benchmark suite which consists of 25 scalable benchmark functions [78]. Based on their characteristics, the functions of the CEC 2005 benchmark set can be divided into the following four classes. Functions \( cf_1 \) - \( cf_5 \) are unimodal; \( cf_6 \) - \( cf_{12} \) are basic multimodal functions; \( cf_{13} \) and \( cf_{14} \) are expanded multimodal functions, and \( cf_{15} \) - \( cf_{25} \) are hybrid compositions of functions with a huge number of local minima. A thorough description of this test set is provided in [78].

To perform a comprehensive evaluation and highlight the different aspects of the proposed framework, we divide the presentation of the experimental results into four subsections. We first incorporate the proposed proximity framework into the original DE mutation strategies and compare the performance of each strategy with its “Pro DE” variant (Subsection VI-A). Subsequently, we discuss the suitability of the proximity framework for other well-known DE variants (Subsection VI-B). In Subsection VI-C the computational cost of the proposed framework is discussed. Finally, an overall performance comparison among all the considered approaches is provided in Subsection VI-D.

A. The Proximity-based Framework in DE

In this section we incorporate the proposed proximity-based framework in each of the six original DE mutation strategies. To maintain a reliable and fair comparison we employ parameter settings that are extensively used in the literature. In more detail, the parameter settings used are:

(a) Population size, \( NP = 100 \) [15], [31], [75].
(b) Mutation factor \( F = 0.5 \) [7], [15], [29], [31].
(c) Recombination factor \( CR = 0.9 \) [7], [15], [29], [31].
The population for all DE variants, over all the benchmark functions, was initialized using a uniform random number distribution with the same random seeds.

To evaluate the performance of the algorithms, we will use the solution error measure, defined as \( f(x') - f(x^*) \), where \( x^* \) is the global optimum of the benchmark function and \( x' \) is the best solution achieved after \( 10^4 \) function evaluations [78], where \( D \) is the dimensionality of the problem at hand. Each algorithm was executed independently 100 times, to obtain an estimate of the mean solution error and its standard deviation. For each pair of original mutation strategy and its proximity-based variant, we use boldface to indicate the best performance in terms of mean solution error. To evaluate the statistical significance of the observed performance differences we apply a two-sided Wilcoxon rank sum test between the original mutation strategies and their proximity-based variants. The null hypothesis in each test is that the samples compared are independent samples from identical continuous distributions with equal medians. We mark with "+" the cases where the null hypothesis is rejected at the 5% significance level and the proximity-based variant exhibits superior performance, with "−" the cases where the null hypothesis is rejected at the same level of significance and the proximity-based variant exhibits inferior performance and with "\( =\)" when the performance difference is not statistically significant. At the bottom of each table, for each pair, we also show the total number of the aforementioned statistical significant cases (+/−/+).

### Table 1: Error values of the original DE mutation strategies and their corresponding proximity-based variants over the 30-dimensional CEC 2005 benchmark set

<table>
<thead>
<tr>
<th>c/f</th>
<th>Mean St.D.</th>
<th>Mean St.D.</th>
<th>Mean St.D.</th>
<th>Mean St.D.</th>
<th>Mean St.D.</th>
</tr>
</thead>
<tbody>
<tr>
<td>DE/best/1</td>
<td>0.000e+00</td>
<td>9.787e-01</td>
<td>0.000e+00</td>
<td>3.579e-01</td>
<td>8.718e-01</td>
</tr>
<tr>
<td>DE/rand/1</td>
<td>0.000e+00</td>
<td>7.092e+04</td>
<td>0.000e+00</td>
<td>9.669e+02</td>
<td>6.623e+02</td>
</tr>
<tr>
<td>DE/best/2</td>
<td>5.893e+05</td>
<td>2.770e+05</td>
<td>5.893e+05</td>
<td>2.770e+05</td>
<td>5.893e+05</td>
</tr>
<tr>
<td>DE/rand/2</td>
<td>0.000e+00</td>
<td>1.234e+00</td>
<td>0.000e+00</td>
<td>1.234e+00</td>
<td>0.000e+00</td>
</tr>
</tbody>
</table>

Where \( D \) is the dimensionality of the problem.
Table II

Error values of the original DE mutation strategies and their corresponding proximity-based variants over the 50-dimensional CEC 2005 benchmark set.

<table>
<thead>
<tr>
<th>c_f</th>
<th>Mean</th>
<th>Std. D.</th>
<th>Mean</th>
<th>Std. D.</th>
<th>Mean</th>
<th>Std. D.</th>
<th>Mean</th>
<th>Std. D.</th>
<th>Mean</th>
<th>Std. D.</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0.000e+00 0.000e+00</td>
<td>0.000e+00 0.000e+00</td>
<td>1.000e+00 0.000e+00</td>
<td>1.000e+00 0.000e+00</td>
<td>2.198e+02 2.198e+02</td>
<td>5.241e+02 5.241e+02</td>
<td>2.305e+02 2.305e+02</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>6.700e+02 6.700e+02</td>
<td>2.378e+02 2.378e+02</td>
<td>1.041e+03 1.041e+03</td>
<td>1.041e+03 1.041e+03</td>
<td>2.590e+02 2.590e+02</td>
<td>6.597e+02 6.597e+02</td>
<td>2.019e+02 2.019e+02</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>9.218e+02 9.218e+02</td>
<td>3.292e+02 3.292e+02</td>
<td>1.155e+03 1.155e+03</td>
<td>1.155e+03 1.155e+03</td>
<td>2.905e+02 2.905e+02</td>
<td>6.914e+02 6.914e+02</td>
<td>2.286e+02 2.286e+02</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>8.919e+02 8.919e+02</td>
<td>2.708e+02 2.708e+02</td>
<td>1.049e+02 1.049e+02</td>
<td>1.049e+02 1.049e+02</td>
<td>2.857e+02 2.857e+02</td>
<td>6.295e+02 6.295e+02</td>
<td>2.223e+02 2.223e+02</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>6.590e+02 6.590e+02</td>
<td>1.449e+02 1.449e+02</td>
<td>9.914e+02 9.914e+02</td>
<td>9.914e+02 9.914e+02</td>
<td>2.076e+02 2.076e+02</td>
<td>5.069e+02 5.069e+02</td>
<td>2.179e+02 2.179e+02</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>6</td>
<td>3.049e+02 3.049e+02</td>
<td>4.590e+00 4.590e+00</td>
<td>1.180e+02 1.180e+02</td>
<td>1.180e+02 1.180e+02</td>
<td>2.047e+02 2.047e+02</td>
<td>5.046e+00 5.046e+00</td>
<td>2.123e+02 2.123e+02</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>7</td>
<td>7.105e+02 7.105e+02</td>
<td>1.876e+00 1.876e+00</td>
<td>1.217e+02 1.217e+02</td>
<td>1.217e+02 1.217e+02</td>
<td>2.076e+02 2.076e+02</td>
<td>4.590e+00 4.590e+00</td>
<td>2.123e+02 2.123e+02</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Table I reports the results on the 30-dimensional version of the CEC 2005 benchmark set. We observe that for the exploitative mutation strategies, DE/rand/1 and DE/rand/2, the incorporation of the proximity-based framework yields significant performance, with the best results obtained for DE/rand/1. For DE/rand/2, it exhibits substantial performance improvement in most of the unimodal functions (c_f1 – c_f6) with the exception of c_f5. Furthermore, there are 5 hybrid composition multimodal functions in which the proposed framework deteriorates performance slightly (c_f18 – c_f30, c_f32 and c_f25). The framework, however, yields a significant improvement in the other 5 hybrid functions (c_f11, c_f12, c_f13, c_f14 and c_f15). This implies that it does not hinder the algorithm's performance on the hybrid multimodal functions.

For the two exploitative strategies, DE/best/1, DE/current-best/1, the proximity-based framework does not yield similar performance improvement. DE/best/1 in most of the unimodal and multimodal functions exhibits either marginal improvement (c_f3, c_f7, c_f9, c_f12, c_f15 and c_f25) or an equal performance, while in five hybrid functions the proposed framework deteriorates performance slightly (c_f13 – c_f20, c_f22 and c_f25). DE/current-best/1 is not improved by the proximity-based framework. In general, this strategy produces the largest errors, which indicate its inability to locate global minimizers. This is more evident for the unimodal functions c_f1–c_f5. This behavior also explains the inability of the proposed approach to improve it. DE/current-best/1 is so exploitative that it has difficulty in locating the minimizers. This implies that it...
is highly unlikely for this strategy to produce a local structure that could be exploited from the proximity framework. Note also that this strategy utilizes only two random individuals to generate an offspring, whereas the similar and also exploitative DE/current-to-best/2 strategy uses four. Finally, despite the exploitative character of DE/best/2 the proximity framework enhances its performance in most multimodal and hybrid functions. The original DE/best/2 exhibits superior performance in five cases only ($c_{f3}$, $c_{f5}$, $c_{f14}$, $c_{f22}$ and $c_{f25}$). It must be noted that qualitatively similar results were also obtained for the YAO benchmark function set [75], but due to space limitations, we do not present them here.

We further evaluate the proposed framework on the 50–dimensional version of the CEC 2005 set of benchmark functions. Higher dimensional problems are typically harder to solve and a common practice is to employ a larger population size. At present we increased the population size to 200, but we did not attempt to fine tune this parameter to obtain optimal performance. In this set of experiments algorithms terminated after performing 500,000 function evaluations [78]. The results summarized in Table II indicate that the behavior on the 50–dimensional benchmark function set is very similar to that on the 30–dimensional benchmark. The main difference is that the improvement of using the proximity–based approach is now statistically significant in the majority of the test functions. Despite the exploitative character of the DE/current-to-best/2 strategy its proximity-based modification is superior in most of the unimodal, multimodal and hybrid composition functions in this benchmark function set. On the other hand, the proximity framework does not improve the exploitative operator DE/current-to-best/1 strategy, while there is a marginal improvement for DE/best/1 in two unimodal and six multimodal functions.

Overall the comparison of each of the original DE mutation strategies with its proximity-based variant indicates that the proposed framework significantly improves the explorative strategies. Exploitative strategies are not improved when the original strategy is already too greedy and on some hard highly multimodal functions. Note however that in relatively few of the latter cases the proximity-based framework deteriorates performance significantly.

### B. Comparison Against Other DE Variants

In this subsection we apply the proximity-based framework on eight well known and widely used DE variants. Specifically, we implement the proximity framework on: i) the Trigonometric Differential Evolution (TDE) [39], ii) the Opposition based Differential Evolution (ODE) [40], [41], iii) the Differential Evolution with Global and Local Neighborhoods (DEGL) [25], [42], iv) the Balanced Differential Evolution (BDE) [22], v) the Self-Adaptive Control Parameters in DE algorithm (jDE) [31], vi) the Adaptive Differential Evolution with optional external archive algorithm (JADE) [18], [26], vii) the Differential Evolution algorithm with Strategy Adaptation (SaDE) [27], [43], and viii) the Differential Evolution Algorithm with Random Localization (DERL) [44].

We evaluate the performance of the eight DE variants and their corresponding proximity-based modifications over the 30–dimensional version of the CEC 2005 function set. Table III reports the experimental results for the first six DE variants, TDE, ODE, BDE, jDE JADE and SaDE. The results show that the proximity framework influences substantially the performance of TDE, JDE and ODE. Specifically, in nine functions the performance of TDE is not significantly different from that of Pro TDE. In 11 of the 25 functions Pro TDE achieves a significantly better performance. The benefit from the proximity framework is evident in the unimodal function $c_{f5}$, most of the basic multimodal functions, the two expanded functions ($c_{f13}$ and $c_{f14}$), and in most of the hybrid composition functions ($c_{f16} - c_{f20}$ and $c_{f24}$). TDE is significantly better than Pro TDE in only four functions ($c_{f4}$, $c_{f15}$, $c_{f22}$, and $c_{f25}$). Overall therefore, TDE is substantially enhanced through the proximity framework. Note that TDE is based on DE/rand/1 and the proximity-based framework has been shown to substantially improve this strategy.

For the Opposition-based DE, we observe that the proximity framework efficiently exploits the population structure and guides the evolution towards more promising solutions. As Table III indicates, Pro ODE outperforms ODE in fourteen cases and exhibits similar performance in seven functions. Particularly, in four out of five unimodal functions Pro ODE produces lower mean error values. The performance difference is statistically significant in $c_{f1}$ and $c_{f5}$, while in $c_{f2}$ and $c_{f4}$ it is not. Moreover, in basic multimodal and expanded functions Pro ODE performs either as well as ODE ($c_{f7}$, $c_{f8}$, $c_{f10}$ and $c_{f13}$) or significantly better ($c_{f6}$, $c_{f9}$, $c_{f11}$, $c_{f12}$ and $c_{f14}$). On the other hand, ODE is significantly superior only in four test functions ($c_{f3}$, $c_{f15}$, $c_{f22}$, and $c_{f25}$). Furthermore, the proximity framework produces substantial improvement in the optimization of hybrid composition functions which are characterized by a huge number of local minima. Pro ODE significantly outperforms ODE in seven out of eleven hybrid composition functions, ($c_{f16}$, $c_{f17}$, $c_{f19} - c_{f21}$, $c_{f23}$, and $c_{f24}$). Note that although the population in ODE changes rapidly, due to the opposition mechanism, the proximity approach efficiently exploits the population structure and guides the evolution process successfully towards more promising solutions.

Pro BDE either enhances BDE or performs equally well. In more detail, BDE is enhanced by the proximity framework in nine functions (three unimodal and six multimodal), while the performance of the two is not statistically different in the majority of functions (thirty of the twenty five functions). The impact of the proximity framework is evident in the expanded and hybrid composition functions ($c_{f13}$, $c_{f15}$, $c_{f18} - c_{f20}$ and $c_{f22}$). Moreover, BDE significantly outperforms Pro BDE only in three functions ($c_{f3}$, $c_{f14}$ and $c_{f25}$).

jDE is substantially enhanced by the proximity framework. Pro jDE exhibits either significantly better or similar performance in 23 of the 25 functions. Only in $c_{f3}$ and $c_{f25}$ jDE significantly outperforms Pro jDE. More specifically, in the unimodal functions Pro jDE is significantly better in $c_{f3}$ and $c_{f4}$ and exhibits similar performance in $c_{f1}$ and $c_{f2}$. In the basic multimodal functions, Pro jDE generally produces smaller or equal mean error to jDE ($c_{f6} - c_{f12}$ except for $c_{f5}$) and a significant enhancement in $c_{f6}$, $c_{f10}$, and $c_{f11}$. In

---

**Table III**

<table>
<thead>
<tr>
<th>Function</th>
<th>Pro TDE Performance</th>
<th>ODE Performance</th>
</tr>
</thead>
<tbody>
<tr>
<td>$c_{f1}$</td>
<td>Superior</td>
<td>Equivalent</td>
</tr>
<tr>
<td>$c_{f5}$</td>
<td>Superior</td>
<td>Equivalent</td>
</tr>
<tr>
<td>$c_{f2}$</td>
<td>Equivalent</td>
<td>Equivalent</td>
</tr>
<tr>
<td>$c_{f4}$</td>
<td>Equivalent</td>
<td>Equivalent</td>
</tr>
<tr>
<td>$c_{f13}$</td>
<td>Superior</td>
<td>Equivalent</td>
</tr>
<tr>
<td>$c_{f14}$</td>
<td>Superior</td>
<td>Equivalent</td>
</tr>
<tr>
<td>$c_{f15}$</td>
<td>Superior</td>
<td>Equivalent</td>
</tr>
<tr>
<td>$c_{f16}$</td>
<td>Superior</td>
<td>Equivalent</td>
</tr>
<tr>
<td>$c_{f17}$</td>
<td>Superior</td>
<td>Equivalent</td>
</tr>
<tr>
<td>$c_{f18}$</td>
<td>Superior</td>
<td>Equivalent</td>
</tr>
<tr>
<td>$c_{f19}$</td>
<td>Superior</td>
<td>Equivalent</td>
</tr>
<tr>
<td>$c_{f20}$</td>
<td>Superior</td>
<td>Equivalent</td>
</tr>
<tr>
<td>$c_{f21}$</td>
<td>Superior</td>
<td>Equivalent</td>
</tr>
<tr>
<td>$c_{f22}$</td>
<td>Superior</td>
<td>Equivalent</td>
</tr>
<tr>
<td>$c_{f23}$</td>
<td>Superior</td>
<td>Equivalent</td>
</tr>
<tr>
<td>$c_{f24}$</td>
<td>Superior</td>
<td>Equivalent</td>
</tr>
<tr>
<td>$c_{f25}$</td>
<td>Superior</td>
<td>Equivalent</td>
</tr>
</tbody>
</table>

**Footnotes:**
- cf7, cf8, cf10 and cf13 are significantly better.
- cf6, cf9, cf11, cf12 and cf14 are statistically significant.
- cf5, cf24, and cf25 are significantly superior.
- cf16, cf17, cf19 - cf21, cf23, and cf24 are significantly outperformed.
- cf3, cf15, cf22, and cf25 are not.
| Algorithm | CF1 | CF2 | CF3 | CF4 | CF5 | CF6 | CF7 | CF8 | CF9 | CF10 | CF11 | CF12 | CF13 | CF14 | CF15 | CF16 | CF17 | CF18 | CF19 | CF20 | CF21 | CF22 | CF23 | CF24 |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| Pro TDE  |     |     |     |     |     |     |     |     |     |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| Pro SaDE |     |     |     |     |     |     |     |     |     |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| Pro JADE |     |     |     |     |     |     |     |     |     |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| Pro BDE  |     |     |     |     |     |     |     |     |     |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |

Note: The table above represents the performance data of different algorithms on various functions. Each row corresponds to a different algorithm, and each column represents a specific function. The values indicate the performance metrics (mean, standard deviation, etc.). The algorithms compared are Pro TDE, Pro SaDE, Pro JADE, and Pro BDE.
of index neighborhoods [25], [42]. The DEGL algorithm combines a local and a global mutation model to produce the mutant individual. In the local model, which promotes exploration, a neighborhood based on indices is implemented to select individuals. In the global model, individuals from the entire population can be selected. Therefore, the proximity framework, and thus the concept of “real” neighborhoods, can be incorporated in more than one ways. We denote by Pro DEGL1 the variant of DEGL in which Pro DE is incorporated only in the global model. In this case the global model uses as parents the two individuals closer to the current one, as given by the proximity framework. A second DEGL variant (Pro DEGL2) is considered in which the proximity framework is incorporated in both the local and global models. In this variant, four individuals are selected through the proximity framework. To retain the intuition of DEGL, the two individuals closer to the current one are used in the global model, to promote exploitation, while the other two are utilized in the local model, to promote exploration.

Table IV summarizes the experimental results for DEGL and DERL on the 30–dimensional version of the CEC 2005 benchmark set. But both Pro DEGL1 and Pro DEGL2 significantly outperform DEGL in thirteen and twelve cases, respectively. In more detail, Pro DEGL1 and Pro DEGL2 exhibit similar or significantly better performance in all unimodal functions (cfs1 – cfs5) and in most of the basic multimodal functions. In the expanded functions, DEGL outperforms the proximity variants in cfs4, while in cfs3 Pro DEGL1 is superior and Pro DEGL2 is not statistically different. The main effect of the proximity framework is once again observed in the hybrid composition functions. Pro DEGL1 and Pro DEGL2 exhibit better performance in seven hybrid composition functions, while their performance is not statistically different from DEGL in the remaining four. DERL is significantly better than Pro DERL in the unimodal functions cfs3 and cfs5. In the multimodal functions, Pro DERL significantly outperforms DERL in nine functions, while its performance is significantly worse than that of DERL in six functions. The DERL mutation operator is based on DE/rand/1 and utilizes as base vector the best of a set of randomly selected individuals. Thus, introducing the proximity framework could yield an overly exploitative approach. However, as the experimental results show, the proximity framework does not hinder the dynamics of DERL. On the contrary, Pro DERL in most of the functions either enhances DERL by exploiting the resulting population structure (as in DE/rand/1) or exhibits similar performance. In functions where there are no optimization bounds and the global optimum is located outside the initialization range (e.g. cfs7 and cfs25), the local characteristics of the proximity-based framework do not appear to enhance performance.

Tables V–VI summarize the experimental results of all the DE variants and their corresponding proximity-based modifications on the 50–dimensional versions of the CEC 2005 function set. As expected, almost all variants exhibit similar behavior with the 30–dimensional versions of the function set. The proximity-based framework clearly enhances TDE, ODE, jDE and DERL in the majority of functions. As previously, Pro BDE either enhances BDE or performs equally well, while Pro SaDE attains an equal performance in most of the functions and only in three cases exhibits a statistically significant performance improvement (cfs2, cfs9 and cfs12). On the other hand, JADE outperforms the proximity variant in nine functions, most of which are hybrid composition functions. Pro JADE on the other hand, demonstrates superior performance in three multimodal and two hybrid composition functions (cfs3, cfs11, cfs12, cfs14 and cfs15, cfs15, respectively). Pro DEGL1 exhibits a statistically significant better performance in three cases (cfs3, cfs4 and cfs25) and attains similar performance in the
rest of the function set. Finally, Pro DEGL2 exhibits improved performance in four functions (the unimodal $cf_3$, $cf_5$ and the hybrid compositions $cf_{10}$, $cf_{24}$), while DEGL outperforms the second proximity-based framework in four multimodal and two hybrid functions ($cf_{10}$, $cf_{11}$, $cf_{13}$, $cf_{14}$ and $cf_{16}$, $cf_{17}$ respectively).

Finally, in Fig. 7 we present convergence graphs for six of the 50–dimensional CEC 2005 benchmark functions, namely, $cf_3$, $cf_5$, $cf_{10}$, $cf_{11}$, $cf_{13}$ and $cf_{14}$. The graphs illustrate median solution error value curves for all DE variants considered in this section obtained from 100 independent simulations. As previously mentioned the graphs indicate that in most cases the proximity-based framework either enhances the convergence of a strategy or behaves similarly to it. There are relatively few cases where the proximity-based framework significantly deteriorates performance.

### TABLE V

<table>
<thead>
<tr>
<th>Function</th>
<th>Mean St.D.</th>
<th>Mean St.D.</th>
</tr>
</thead>
<tbody>
<tr>
<td>TDE</td>
<td>ODE</td>
<td>Pro TDE</td>
</tr>
<tr>
<td>$cf_1$</td>
<td>$0.000e+00$</td>
<td>$0.000e+00$</td>
</tr>
<tr>
<td></td>
<td>$5.506e-04$</td>
<td>$1.491e-03$</td>
</tr>
<tr>
<td></td>
<td>$2.935e+04$</td>
<td>$3.091e+04$</td>
</tr>
<tr>
<td></td>
<td>$2.000e+01$</td>
<td>$2.000e+01$</td>
</tr>
<tr>
<td></td>
<td>$2.000e+01$</td>
<td>$2.000e+01$</td>
</tr>
<tr>
<td>$cf_2$</td>
<td>$0.000e+00$</td>
<td>$0.000e+00$</td>
</tr>
<tr>
<td></td>
<td>$5.913e-04$</td>
<td>$1.520e-03$</td>
</tr>
<tr>
<td></td>
<td>$2.691e+04$</td>
<td>$2.691e+04$</td>
</tr>
<tr>
<td></td>
<td>$2.000e+01$</td>
<td>$2.000e+01$</td>
</tr>
<tr>
<td></td>
<td>$2.000e+01$</td>
<td>$2.000e+01$</td>
</tr>
</tbody>
</table>

### Computational Cost of the proposed framework

Several real-world problems implement computer based simulations that demand resource-intensive evaluations of the objective function, e.g. large-scale finite element analysis (FEA), computational fluid dynamics (CFD), engineering design problems, or demanding industrial applications [81]. Such simulations can be computationally expensive requiring minutes to hours to evaluate a candidate solution.

In the proposed framework, individuals are evolved using information contained in the Affinity Matrix. The computational complexity of the proximity framework depends on the update of this matrix. In the worst case where all individuals in the current population have been evolved, a situation that...
TABLE VI
ERROR VALUES OF THE ORIGINAL DEGL, DERL ALGORITHMS AND THEIR CORRESPONDING PROXIMITY-BASED VARIANTS OVER THE 50-DIMENSIONAL CEC 2005 BENCHMARK SET

<table>
<thead>
<tr>
<th>$c_f$</th>
<th>DEGL/1 Mean ± St.D.</th>
<th>Pro DEGL1 Mean ± St.D.</th>
<th>DEGL/2 Mean ± St.D.</th>
<th>Pro DEGL2 Mean ± St.D.</th>
<th>DERL Mean ± St.D.</th>
<th>Pro DERL Mean ± St.D.</th>
</tr>
</thead>
<tbody>
<tr>
<td>$c_{f1}$</td>
<td>0.000e+00 0.000e+00</td>
<td>0.000e+00 0.000e+00</td>
<td>0.000e+00 0.000e+00</td>
<td>0.000e+00 0.000e+00</td>
<td>0.000e+00 0.000e+00</td>
<td>0.000e+00 0.000e+00</td>
</tr>
<tr>
<td>$c_{f2}$</td>
<td>0.000e+00 0.000e+00</td>
<td>0.000e+00 0.000e+00</td>
<td>0.000e+00 0.000e+00</td>
<td>0.000e+00 0.000e+00</td>
<td>0.000e+00 0.000e+00</td>
<td>0.000e+00 0.000e+00</td>
</tr>
<tr>
<td>$c_{f3}$</td>
<td>2.000e-02 1.096e+03</td>
<td>4.822e+02 9.278e+02</td>
<td>9.662e+00 1.271e+02</td>
<td>9.229e+02 9.216e+02</td>
<td>6.195e+03 4.594e-12</td>
<td></td>
</tr>
<tr>
<td>$c_{f4}$</td>
<td>2.000e-02 1.096e+03</td>
<td>4.822e+02 9.278e+02</td>
<td>9.662e+00 1.271e+02</td>
<td>9.229e+02 9.216e+02</td>
<td>6.195e+03 4.594e-12</td>
<td></td>
</tr>
<tr>
<td>$c_{f5}$</td>
<td>2.000e-02 1.096e+03</td>
<td>4.822e+02 9.278e+02</td>
<td>9.662e+00 1.271e+02</td>
<td>9.229e+02 9.216e+02</td>
<td>6.195e+03 4.594e-12</td>
<td></td>
</tr>
<tr>
<td>$c_{f6}$</td>
<td>2.000e-02 1.096e+03</td>
<td>4.822e+02 9.278e+02</td>
<td>9.662e+00 1.271e+02</td>
<td>9.229e+02 9.216e+02</td>
<td>6.195e+03 4.594e-12</td>
<td></td>
</tr>
<tr>
<td>$c_{f7}$</td>
<td>2.000e-02 1.096e+03</td>
<td>4.822e+02 9.278e+02</td>
<td>9.662e+00 1.271e+02</td>
<td>9.229e+02 9.216e+02</td>
<td>6.195e+03 4.594e-12</td>
<td></td>
</tr>
<tr>
<td>$c_{f8}$</td>
<td>2.000e-02 1.096e+03</td>
<td>4.822e+02 9.278e+02</td>
<td>9.662e+00 1.271e+02</td>
<td>9.229e+02 9.216e+02</td>
<td>6.195e+03 4.594e-12</td>
<td></td>
</tr>
<tr>
<td>$c_{f9}$</td>
<td>2.000e-02 1.096e+03</td>
<td>4.822e+02 9.278e+02</td>
<td>9.662e+00 1.271e+02</td>
<td>9.229e+02 9.216e+02</td>
<td>6.195e+03 4.594e-12</td>
<td></td>
</tr>
<tr>
<td>$c_{f10}$</td>
<td>2.000e-02 1.096e+03</td>
<td>4.822e+02 9.278e+02</td>
<td>9.662e+00 1.271e+02</td>
<td>9.229e+02 9.216e+02</td>
<td>6.195e+03 4.594e-12</td>
<td></td>
</tr>
</tbody>
</table>

For the functions in the YAO benchmark set [75]. The ratio is very high, with the median value approximately equal to 9.5351. In such cases, the proximity framework can only be justified if the improvement in the quality of the solutions is highly valued by the user.

D. Overall Performance

We conclude the presentation of the experimental results, by providing a summarizing comparison over all the benchmark functions. To this end, we utilize the Empirical Cumulative Probability Distribution Function (ECDF) of the Normalized Mean Error (NME).

The NME measure attempts to capture the relative performance of an algorithm against the best performing algorithm on a particular function. Specifically, for an algorithm $A$ on a function $f$ it is computed as the ratio of the Mean Error (ME) achieved by $A$ on function $f$, over the lowest $ME$ on $f$ achieved by any of the considered algorithms (denoted as $ME_{best}$):

$$NME_{A,f} = \frac{ME}{ME_{best} + \epsilon}$$

where $\epsilon = 1$ is a small real constant number used to avoid zero values in the denominator. Therefore, smaller values of $NME$ correspond to better performance.

The ECDF of NMEs for a number of algorithms $n_A$ and a number of functions $n_f$ is a cumulative probability distribution function defined as:

$$ECDF(x) = \frac{1}{n_f} \sum_{i=1}^{n_A} \sum_{j=1}^{n_f} I(NME_{i,j} \leq x)$$

where $I(\cdot)$ is the indicator function. In other words, the ECDF measure captures the empirical probability of observing an NME value smaller or equal to $x$. 

rarely occurs, the computational cost amounts to computing \(\left(\frac{NP^2 - 2NP}{2}\right)\) distances between individuals. This is due to the symmetric property of the distance measure.

Strictly speaking, in a pre-specified $D$-dimensional problem $f$, let the computational cost of a function evaluation be equal to $\epsilon$ units of real computation time, while the cost of computing a distance between two individuals be $d = \kappa - \epsilon$ units of real computational time. Thus, the computational cost per generation of an original DE strategy is: $\text{Cost}_{\text{DE}} = NP \cdot c_f$, while the worst case scenario for the computational cost of the corresponding proximity variant yields: $\text{Cost}_{\text{ProDE}} = NP \cdot c_f + \frac{NP^2 - 2NP}{2} \cdot c_f$. In a real case, the number of distances that have to be computed depends on the successful mutations of the algorithm (selection rate), which in turn depends on the phase of the evolution process and on the problem at hand. One can estimate the ratio $\text{Cost}_{\text{ProDE}} / \text{Cost}_{\text{DE}}$ to obtain an estimate of the computational overhead of the proximity framework.

In this study, we employed the CEC 2005 benchmark function set. To quantify the overhead of the proximity framework on these functions we compute $\text{Cost}_{\text{DE}}$ and $\text{Cost}_{\text{ProDE}}$ using the worst case scenario, in which each update of the affinity matrix involves the computation of all of its elements. The computed median value of the ratio for the CEC 2005 benchmarks is approximately 1.0834. The nature of the functions in the CEC 2005 benchmark set is such that the computational cost of DE algorithms is mostly determined by function evaluations. In such cases the implementation of the proximity framework is highly recommended, because it can yield significant improvements in the quality of the solutions, with a relatively small computational overhead. The overhead is reversed when the cost of a function evaluation is small relative to the cost of computing the affinity matrix.

To demonstrate this behavior, we have computed the ratio $\text{Cost}_{\text{ProDE}} / \text{Cost}_{\text{DE}}$ for the functions in the YAO benchmark set [75]. The ratio is very high, with the median value approximately equal to 9.5351. In such cases, the proximity framework can only be justified if the improvement in the quality of the solutions is highly valued by the user.
Fig. 7. Convergence graph (median curves) for the state-of-the-art DE variants over the 50–dimensional \( f_{3}, f_{4}, f_{9}, f_{11}, f_{12} \) and \( f_{13} \) CEC 2005 benchmark functions. The horizontal axis illustrates the number of generations, and the vertical axis illustrates the median of solution error values over 100 independent simulations.

First, we compute the NME for all considered algorithms over all the functions. We then separate the algorithms into two sets, the original DE algorithms and the Pro DE variants, and compute the ECDF for each set. This enables a summarizing comparison of the algorithms in the two sets, as larger values of ECDF for the same argument correspond to better performance.

Fig. 8 illustrates the ECDF of NMEs for all the original DE mutation operators versus their proximity-based variants for the CEC 2005 function set. The proximity framework exhibits a great potential on the CEC 2005 function set. The proximity DE mutation strategies significantly outperform the corresponding original DE mutation strategies in most cases. Despite the fact that the two very exploitative strategies, DE/current-to-best/1 and DE/best/2 and their Pro DE variants, yield high mean error values, the Pro DE ECDF curve is
almost always above that of the original DE strategies. In general, Pro DE mutation strategies produce two orders of magnitude less NME than the original DE mutation strategies, i.e. the Pro DE curve reaches unity at approximately NME ≈ 2,000 while the DE curve at NME ≈ 900,000.

Fig. 9 demonstrates the ECDF curves of NME for the considered state-of-the-art DE variants and their proximity-based modifications for the CEC 2005 function set. The ECDF curve of the proximity-based modifications of the state-of-the-art DE variants, during the initial stages, is below that of original algorithms’ ECDF curve. However, notice that the proximity-based ECDF curve reaches unity in two orders of magnitude less NME than the original state-of-the-art DE variants. Specifically, the proximity-based ECDF curve reaches unity at approximately NME ≈ 10^4, while the state-of-the-art DE variants curve at NME ≈ 10^6.

VII. CONCLUDING REMARKS

It has been recognized that during the evolutionary process of the Differential Evolution (DE) algorithm a clustering structure of the population of individuals can arise. In this work, we attempt to take advantage of this characteristic behavior to improve the performance of the algorithm. To this end, we substitute the uniformly random selection of parents during mutation. We propose a probabilistic selection scheme that assigns probabilities that are inversely proportional to the distance from the mutated individual. The proposed proximity-based scheme is generic, as it is independent of the mutation strategy. In this work we have applied it to the original DE mutation strategies and a number of state-of-the-art DE variants.

The experimental results show that the proposed framework improves significantly excessively exploratory mutation strategies since it promotes the exploitation of some areas of the search space. For exploitative mutation strategies the proximity scheme does not lead to great benefits. However, even for these strategies, the proximity-based framework very rarely deteriorates their performance. The incorporation of the framework in eight state-of-the-art DE variants with different dynamics exhibited either substantial performance gains, or statistically indistinguishable behavior. Moreover, the main impact of the proposed framework was observed in high dimensional multimodal functions like the hybrid composition functions of the CEC 2005 test set. Finally, the self-adaptive parameter mechanisms of state-of-the-art DE variants are not inhibited by the incorporation of the proximity framework.

This performance improvement comes at an additional computational cost due to the computation of pairwise distances between individuals. This cost can be substantial when the cost of the function evaluation is trivial. In such cases, the utilization of the proximity framework can only be justified, if the improvement in the quality of the obtained solutions is highly valued by the user. On the contrary, when a function evaluation is computationally or otherwise costly, the computational overhead is negligible.

The effect of dimensionality and different population sizes on the performance of the proposed framework is an important aspect which we intend to study further in future work. Another interesting aspect which will be considered is the effect of proximity on structured populations.

ACKNOWLEDGMENT

The authors would like to thank the Guest Editors, and the three anonymous reviewers for their valuable comments and suggestions that helped to improve the content as well as the clarity of the manuscript.

REFERENCES


