

Evolutionary Many-Objective Algorithm Using Decomposition-Based Dominance Relationship

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Abstract—Decomposition-based evolutionary algorithms have shown great potential in many-objective optimization. However, the lack of theoretical studies on decomposition methods has hindered their further development and application. In this paper, we first theoretically prove that weight sum, Tchebycheff, and penalty boundary intersection decomposition methods are essentially interconnected. Inspired by this, we further show that highly customized dominance relationship can be derived from decomposition for any given decomposition vector. A new evolutionary algorithm is then proposed by applying the customized dominance relationship with adaptive strategy to each subpopulation of multiobjective to multiobjective framework. Experiments are conducted to compare the proposed algorithm with five state-of-the-art decomposition-based evolutionary algorithms on a set of well-known scaled many-objective test problems with 5 to 15 objectives. Simulation results have shown that the proposed algorithm can make better use of the decomposition vectors to achieve better performance. Further investigations on unscaled many-objective test problems verify the robust and generality of the proposed algorithm.

Index Terms—Dominance relationship, evolutionary algorithm, many-objective, multiobjective to multiobjective (M2M) decomposition.

I. INTRODUCTION

E VOLUTIONARY algorithms have achieved great success in handling multiobjective optimization problems (MOPs) [1]–[3], but they encounter severe difficulties when the optimization problems have more than three

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objectives, i.e., many-objective optimization problems (MaOPs) [4]. Nowadays, the study of many-objective optimization has become a really hot issue due to its wide applications and great importance [5]. Recently, a lot of evolutionary multiobjective optimization (EMO) algorithms have been proposed for MaOPs [6], and roughly four categories can be seen.

The first category is to modify the Pareto dominance relationship. Pareto dominance-based EMO algorithms [7]–[9] use Pareto dominance and a diversity measure method as the selection criteria. With the increasing of the number of objectives, more and more solutions become incomparable. Under this situation, Pareto dominance-based selection mainly depends on the diversity measurement to differentiate solutions, and thus population will loss selection pressure. To keep selection pressure, great efforts have been made to modify the Pareto dominance [10]–[14]. The second category is to reduce the search dimension by dimension reduction methods. Many dimension reduction algorithms have already been used to identify the redundant objectives in many-objective optimization [15], [16]. The third category is to use indicators, such as hypervolume indicator [17]–[20], R^2 indicator [21], and $I_{\varepsilon+}$ indicator [22]. Hypervolume is one of the most popular indicators [17], [18], but its computational complexity increases exponentially with the number of objectives. The recent studies are almost all about how to fast calculate the hypervolume indicator [19], [20]. The fourth category is decomposition-based EMO algorithms, where a set of decomposition vectors is either used for objectives aggregation [23], [24] or diversity and convergence enhancement [26]–[31]. For example, multiobjective evolutionary algorithm based on decomposition (MOEA/D) [24], [25], decomposes an MaOP into a number of scalar optimization subproblems by weight vectors. MOEA/D-multiobjective to multiobjective (M2M) [26] is a new variant of MOEA/D for population decomposition, and it can decompose an MaOP into a number of many-objective optimization subproblems by direction vectors. Deb and Jain [27] suggested the third generation nondominated sorting genetic algorithm (NSGA-III) by using the reference points to enhance the convergence and maintain the diversity. Reference points are also used for decomposition in the following MOEA/DD [28] and θ -DEA [29]. Cheng *et al.* [30] proposed the reference vector-guided evolutionary algorithm (RVEA). Although descriptions for those vectors used in different algorithms may vary, we collectively call them decomposition vectors in this paper.

Because no matter how those vectors are used, they are all essentially based on the decomposition.

Decomposition-based EMO algorithms are very promising in many-objective optimization [31], [33], [34], and it is mainly for two reasons. The first is that decomposition methods do not encounter the difficulty of solutions indiscriminate in high-dimensional space, and the second is that its computational complexity is acceptable. The three basic decomposition methods: 1) weight sum [35]; 2) Tchebycheff [35]; and 3) penalty boundary intersection (PBI) [36] have been widely used in many-objective optimization. However, previous studies are mainly about the applications of the decomposition methods, and the lack of theoretical study has hindered their further development. Motivated by this, we first focus on the theoretical study of the decomposition methods in this paper. To be specific, we theoretically prove that the three decomposition methods are essentially the same idea with different pattern of manifestation. The theoretical study also indicates that PBI decomposition is more generalized than the two others. Based on this, we establish a new linkage between decomposition and dominance by deriving a novel dominance relationship called D-dominance from PBI decomposition. For any given decomposition vector and parameter $\beta \in (0, \pi/2]$, we can define a D-dominance based on the PBI decomposition. The evolutionary path of the defined D-dominance is determined by the decomposition vector, but its usage is totally different from that of traditional decomposition methods. In D-dominance, the decomposition vector is actually a decomposition free vector, and this kind of freedom can make each individual evolve centering itself instead of the decomposition vector. The dominance area and dominated area of D-dominance can be easily adjusted by the parameter $\beta \in (0, \pi/2]$. Thus, the proposed D-dominance inherits the inner parallelism of dominance and the directionality of decomposition.

Decomposition-based EMO algorithms use decomposition vectors to maintain the convergence and diversity, whereas how to balance diversity and convergence is not an easy task, especially in the high-dimensional space. Studies [13], [27], [29] have shown that a solution found by a decomposition method can actually be far away from its corresponding decomposition vector due to the curse of dimensionality. Recently, subregion strategy has been adopted by many researchers [28]–[30] to remedy this issue. Those methods are essentially based on PBI decomposition, and thus a parameter needs to be set to balance convergence and diversity. Nevertheless, whenever the parameter is set, there will be at least two problems: 1) the improvement area for each individual is fixed and confined by the subregion and 2) the evolutionary path of each individual is highly dependent on the associated decomposition vector. Consequently, it is highly possible that one decomposition vector needs to select more than one solutions to fill the next generation population slots in actual scenarios.

In this paper, we try to deal with the above two problems involved in traditional decomposition methods. We propose an adaptive D-dominance relationship-based evolutionary algorithm called DrEA by applying D-dominance to the MOEA/D-M2M framework [26]. In DrEA, each

decomposition vector can define a specific D-dominance, and those customized D-dominance relationships are then employed to each subpopulation independently. For the first problem, we propose an adaptive strategy to adjust the parameter β such that the improvement area of each individual varies with the evolution. For the second problem, the inherent parallelism of D-dominance makes the update process of each individual centered by itself instead of the decomposition vector. Besides, we also design a decomposition-based crowding measurement to further diversify each subpopulation. We summarize the main contributions of this paper as follows.

- 1) The theoretical studies in this paper have established the essential connection between weight sum, Tchebycheff, and PBI decomposition methods. Those mathematical proofs also show that PBI decomposition method is much more general than the two others.
- 2) The proposed D-dominance has blurred the line between dominance and decomposition. D-dominance combines the merits of dominance and decomposition such that better solutions discrimination and better balance between exploration and exploitation can be achieved in high-dimensional search space.
- 3) The proposed DrEA is an application of the D-dominance for MaOPs. In DrEA, a new adaptive strategy is utilized to automatically adjust the parameter for each customized D-dominance. We also develop a new decomposition-based method to evaluate the crowding degree of each solution in each subpopulation of DrEA.

To investigate the effectiveness of DrEA, a set of 32 benchmark problems from WFG family with 5-, 8-, 10-, and 15-objective are tested, and the proposed algorithm has been compared with five state-of-the-art decomposition-based EMO algorithms: MOEA/D [24], MOEA/DD [28], NSGA-III [27], θ -DEA [29], and RVEA [30]. The simulation results show that the proposed EMO algorithm can achieve comparable results. Further performance comparisons with NSGA-III on the popular unscaled DTLZ series test problems with 5-, 8-, 10-, and 15-objective also verify the robust and generality of the proposed DrEA.

This paper is organized as follows. Section II introduces MOPs (MaOPs) and MOEA/D-M2M [26] population decomposition. In Section III, we do theoretical study on the three popular decomposition methods. Section VI shows how we define the decomposition-based dominance and crowding measurement, and then presents the main framework of proposed algorithm. The simulation experiments to investigate the performance of DrEA are presented in Section V. Finally, we conclude this paper in Section VI.

II. PRELIMINARIES

In this section, we first define the MOP, and then briefly introduce MOEA/D-M2M framework [26].

A. Problem Definition

An MOP can be defined as

$$\begin{aligned} & \text{minimize } F(\mathbf{x}) = \{f_1(\mathbf{x}), \dots, f_m(\mathbf{x})\} \\ & \text{subject to } \mathbf{x} \in \mathbf{D} \end{aligned} \quad (1)$$

where \mathbf{D} is a feasible area of the decision (variable) space, $F : \mathbf{D} \rightarrow \mathbf{R}^m$ consists of m objective functions f_1, \dots, f_m . When $m > 3$, it is called an MaOP [4]. Let $\mathbf{u} = (u_1, \dots, u_m)$ and $\mathbf{v} = (v_1, \dots, v_m)$, \mathbf{u} is said to dominate \mathbf{v} if $u_i \leq v_i$ for all $i = 1, \dots, m$, and $\mathbf{u} \neq \mathbf{v}$. A point \mathbf{x}^* is called Pareto optimal if there is no $\mathbf{x} \in \mathbf{D}$ such that $F(\mathbf{x})$ dominates $F(\mathbf{x}^*)$. The set of all the Pareto optimal points is called the Pareto set (PS). PF = { $F(\mathbf{x}) \in \mathbf{R}^m | \mathbf{x} \in \text{PS}$ } is called the Pareto front (PF) [35]. $\mathbf{u}^* = (u_1^*, \dots, u_m^*)$ is called the ideal point if u_i^* is the minimal value of $f_i(\mathbf{x})$ over the decision space, and $\mathbf{z}^* = (z_1^*, \dots, z_m^*)$ is called the nadir point if z_i^* is the maximal value of $f_i(\mathbf{x})$ over the PS.

B. MOEA/D-M2M

In general, we can assume that all the objective functions to be optimized are nonnegative, i.e., $F(\mathbf{x}) \geq 0$. MOEA/D-M2M [26] population decomposition requires K unit direction (decomposition) vectors $\mathbf{v}^1, \dots, \mathbf{v}^K$ in \mathbf{R}_+^m . It divides \mathbf{R}_+^m into K subregions $\Omega_1, \dots, \Omega_K$, where Ω_k ($k = 1, \dots, K$) is defined as

$$\Omega_k = \left\{ \mathbf{u} \in \mathbf{R}_+^m \mid \langle \mathbf{u}, \mathbf{v}^k \rangle \leq \langle \mathbf{u}, \mathbf{v}^j \rangle \text{ for any } j = 1, \dots, K \right\} \quad (2)$$

where $\langle \mathbf{u}, \mathbf{v}^j \rangle$ is the acute angle between individual \mathbf{u} and decomposition vector \mathbf{v}^j . That is to say, \mathbf{u} belongs to Ω_k if and only if \mathbf{v}^k has the smallest angle to \mathbf{u} among all the K decomposition vectors. In this way, (1) can be transformed into K constrained multiobjective optimization subproblems. Subproblem k is

$$\begin{aligned} & \text{minimize } F(\mathbf{x}) = (f_1(\mathbf{x}), \dots, f_m(\mathbf{x})) \\ & \text{subject to } \mathbf{x} \in \Omega_k. \end{aligned} \quad (3)$$

MOEA/D-M2M optimizes these K subproblems in a collaborative way. During its evolutionary process, it will maintain and evolve K subpopulations: $\mathbf{P}_1, \dots, \mathbf{P}_K$, where \mathbf{P}_k ($k = 1, \dots, K$) is to approximate the PF of subproblem k .

III. THEORETICAL STUDY ON DECOMPOSITION METHODS

In this section, we first introduce the three decomposition methods, i.e., weighted sum [35], Tchebycheff [35], and PBI [36], and then prove their essential connection in theory.

A. Decomposition Method

Suppose that $\mathbf{v} = (v_1, \dots, v_m)$ is a unit vector (if not, we can replace it by $\mathbf{v}/\|\mathbf{v}\|$) in the first octant of the objective space, i.e., $v_i \geq 0$ for all $i = 1, \dots, m$ and $\sum_i v_i^2 = 1$. To facilitate the expression, all those decomposition methods are defined in the normalized objective space, and the three decomposition method can be expressed as follows.

1) *Weighted Sum Method*: Weighted sum method gives a convex aggregation of different objectives. For a given decomposition vector $\mathbf{v} = (v_1, \dots, v_m)$, MOP (1) can be converted to

$$\begin{aligned} & \text{minimize } g^{ws}(\mathbf{x}|\mathbf{v}) = \sum_{i=1}^m f_i(\mathbf{x})v_i \\ & \text{subject to } \mathbf{x} \in \mathbf{D} \end{aligned} \quad (4)$$

where decomposition vector \mathbf{v} works as the coefficient vector in the formation of aggregation function, and \mathbf{x} is the variables to be optimized.

2) *Tchebycheff Method*: For a given decomposition vector $\mathbf{v} = (v_1, \dots, v_m)$, Tchebycheff decomposition method converts MOP (1) to

$$\begin{aligned} & \text{minimize } g^{te}(\mathbf{x}|\mathbf{v}) = \max_{1 \leq i \leq m} \{f_i(\mathbf{x})/v_i\} \\ & \text{subject to } \mathbf{x} \in \mathbf{D}. \end{aligned} \quad (5)$$

Notice that if any of the $v_i = 0$ ($i = 1, \dots, m$), we will replace it with a number close to zero such as 10^{-6} in the practical applications. In our theoretical analysis, we just assume that $v_i > 0$ for all $i = 1, \dots, m$.

3) *Penalty Boundary Intersection Method*: For a given decomposition vector $\mathbf{v} = (v_1, \dots, v_m)$, PBI method decomposes MOP (1) to

$$\begin{aligned} & \text{minimize } g^{pbi}(\mathbf{x}|\mathbf{v}) = d_1(F(\mathbf{x})) + \theta d_2(F(\mathbf{x})) \\ & \text{subject to } \mathbf{x} \in \mathbf{D} \end{aligned} \quad (6)$$

where $\theta \geq 0$ is a preset penalty parameter, $d_1(F(\mathbf{x})) = F(\mathbf{x})^T \mathbf{v}$ is the projection distance of $F(\mathbf{x})$ to the decomposition vector \mathbf{v} , and $d_2(F(\mathbf{x})) = \|F(\mathbf{x}) - d_1(F(\mathbf{x}))\mathbf{v}\|$ is the perpendicular distance of $F(\mathbf{x})$ to decomposition vector \mathbf{v} . $d_2(F(\mathbf{x}))$ has many good properties, and for any two given solutions \mathbf{x} and \mathbf{y} , we have the following.

- 1) *Non-Negativity*: $d_2(F(\mathbf{x})) \geq 0$, $d_2(F(\mathbf{y})) \geq 0$.
- 2) *Symmetry*: $d_2(F(\mathbf{x}) - F(\mathbf{y})) = d_2(F(\mathbf{y}) - F(\mathbf{x}))$.
- 3) *Triangle Inequality*: $d_2(F(\mathbf{x}) + F(\mathbf{y})) \leq d_2(F(\mathbf{x})) + d_2(F(\mathbf{y}))$.

The three properties can be easily derived from its definition, and we will use them in the following theoretical studies.

B. Theoretical Study

The three decomposition methods are actually relevant, and we will reveal it by mathematical proof.

Theorem 1: For any given vector, its weight sum decomposition and Tchebycheff decomposition can be explicitly represented by the PBI decomposition with specific settings of parameter θ .

Proof: The claim that weight sum decomposition can be represented by PBI decomposition is obvious. Let $\theta = 0$ for PBI decomposition, we can have $g^{pbi}(\mathbf{x}|\mathbf{v}) = d_1(F(\mathbf{x})) = \sum_{i=1}^m f_i(\mathbf{x})v_i = g^{ws}(\mathbf{x}|\mathbf{v})$, and that is exactly weight sum decomposition. For clarity, we only use the function name in our following theoretical analysis. We now prove that Tchebycheff decomposition can also be represented by PBI decomposition. For 2-D situation, we have $d_1 = v_1 f_1 + v_2 f_2$ and $d_2 = \sqrt{(f_1^2 + f_2^2 - d_1^2)} = |v_2 f_1 - v_1 f_2|$. If $v_2 f_1 \geq v_1 f_2$, we can get $g^{te} = \max\{f_1/v_1, f_2/v_2\} = f_1/v_1$. By setting $\theta = v_1/v_2$, we can get $g^{pbi} = d_1 + v_2/v_1 d_2 = v_1 f_1 + v_2^2/v_1 f_1 = ((v_1^2 + v_2^2)/v_1) f_1$. Since $v_1^2 + v_2^2 = 1$, it can be deduced that $g^{te} = f_1/v_1 = g^{pbi}$. Similarly, if $v_2 f_1 < v_1 f_2$, $g^{te} = f_2/v_2 = g^{pbi}$ can also be deduced in this way.

For readability, the rest of the proof is presented in the supplementary material. ■

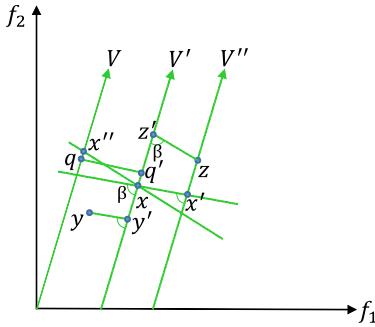


Fig. 1. Illustration of D-dominance in the 2-D objective space.

Therefore, we have proved that PBI decomposition can represent weight sum decomposition and Tchebycheff decomposition.

IV. MAIN IDEA OF PROPOSED ALGORITHM

In this section, we first show how the decomposition-based dominance relationship and crowding measurement are defined, and then discuss their properties. At last, we present the main framework of the proposed algorithm.

A. Decomposition-Based Dominance Relationship

As we have discussed, the three popular decomposition methods actually share some similarities in essential, where PBI decomposition is most generalized among the three decomposition methods. Inspired by this, we propose a decomposition-based dominance relationship, called D-dominance according to the definition of projection distance d_1 and perpendicular distance d_2 in PBI decomposition. For MaOP or MOP to be minimized, the D-dominance is defined as follows.

Definition 1 (D-Dominance): Given two solutions \mathbf{x} and \mathbf{y} , a parameter $\beta \in (0, \pi/2]$, and a unit decomposition vector \mathbf{v} in the objective space.

If $d_1(F(\mathbf{x})) + d_2(F(\mathbf{x}) - F(\mathbf{y})) \cot(\beta) < d_1(F(\mathbf{y}))$, $F(\mathbf{x})$ is said to D-dominate $F(\mathbf{y})$, denoted by $F(\mathbf{x}) \prec_D F(\mathbf{y})$.

Else if $d_1(F(\mathbf{y})) + d_2(F(\mathbf{y}) - F(\mathbf{x})) \cot(\beta) < d_1(F(\mathbf{x}))$, $F(\mathbf{x})$ is said to be D-dominated by $F(\mathbf{y})$, denoted by $F(\mathbf{y}) \prec_D F(\mathbf{x})$.

Otherwise, $F(\mathbf{x})$ and $F(\mathbf{y})$ is called mutually non-D-dominated.

Fig. 1 gives a visible illustration of how the proposed D-dominance works in the 2-D objective space. To identify if \mathbf{x} is D-dominated by \mathbf{y} , the decomposition vector \mathbf{V} should be moved to \mathbf{V}' as a free vector to intersect with \mathbf{x} . Then, we get \mathbf{y}' , the β projection of \mathbf{y} to the moved decomposition vector \mathbf{V}' , which is actually the PBI- β decomposition value of \mathbf{y} with regard to \mathbf{V}' . Since the projection \mathbf{y}' is intuitively lower than \mathbf{x} along \mathbf{V}' , we can conclude that \mathbf{x} is D-dominated by \mathbf{y} . In Fig. 1, the projection of solution \mathbf{q} to \mathbf{V}' , denoted as \mathbf{q}' is intuitively bigger than \mathbf{x} , but we cannot say \mathbf{q} is D-dominated by \mathbf{x} . In fact, we can only conclude that \mathbf{x} is not dominated by \mathbf{q} . To check if \mathbf{q} is D-dominated by \mathbf{x} , we need to find the β projection of \mathbf{x} to a moved decomposition vector intersecting with \mathbf{q} , which happens to be \mathbf{V} in this case. The β projection of \mathbf{x} to the decomposition vector \mathbf{V} , i.e., \mathbf{x}'' , is not better than

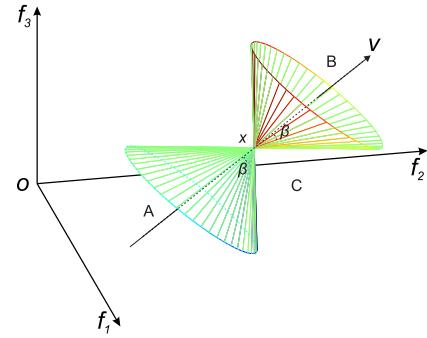


Fig. 2. Dominant and dominated areas of D-dominance in the 3-D objective space.

\mathbf{q} , and thus \mathbf{q} is not D-dominated by \mathbf{x} . That is to say, \mathbf{q} and \mathbf{x} are non-D-dominated. In another case, we can identify \mathbf{x} dominates \mathbf{z} . When we β project \mathbf{x} to the moved decomposition vector \mathbf{V}'' , we can conclude \mathbf{z} is D-dominated by \mathbf{x} by comparing the β projection \mathbf{x}' with \mathbf{z} . In short, whenever we want to see if a given solution is D-dominated by a specific solution, we need to β project this specific solution to the moved decomposition vector intersecting with the given solution, and then compare the β projection of the specific solution to the give solution.

Fig. 2 shows the dominance area (denoted as A), dominated area (denoted as B) and non-D-dominated area (denoted as C) of \mathbf{x} in 3-D objective space. Similar to Pareto dominance, a point \mathbf{x}^* is called D-optimal if there is no $\mathbf{x} \in \Omega$ such that $F(\mathbf{x})$ D-dominates $F(\mathbf{x}^*)$. The set of all the D-optimal points is called the D-optimal set (DS). The set of all the DS objective vectors is called the D-optimal front. Since the proposed D-dominance has adjustable dominant and dominated areas, its DS can be a subset of PS, or includes PS.

B. Properties Analysis

In fact, the proposed D-dominance relationship is asymmetric, transitive, and irreflexive, and the theoretical proofs of the three properties can be found in the supplementary material. The theoretical study has shown that the proposed D-dominance is well defined, and we have the following comments.

- 1) For any given decomposition vector and parameter $\beta \in (0, \pi/2]$, we can define a D-dominance relationship and this relationship represents a strictly partial order.
- 2) The area dominated by a solution in the objective space is an adjustable hypercone (cone in 3-D objective space and triangle in 2-D objective space), and the cone angle can be adjusted by the parameter β .
- 3) The dominated and the dominance area of a solution are symmetric with respect to a hyperplane (plane in 2-D objective space) through the solution and perpendicular to the decomposition vector.

Fig. 3 shows how the dominated and dominance area of solution \mathbf{x} are adjusted by the parameter β in the 2-D objective space. From this figure, we can see that when adjusting β_1 to β_2 , the dominated area and the dominance area are both enlarged. The adjustment is only controlled by a

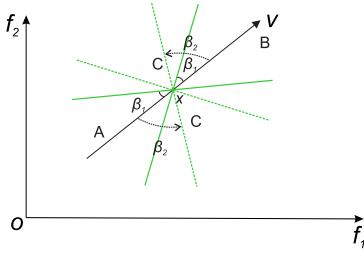


Fig. 3. Adjustment of D-dominance in the 2-D objective space.

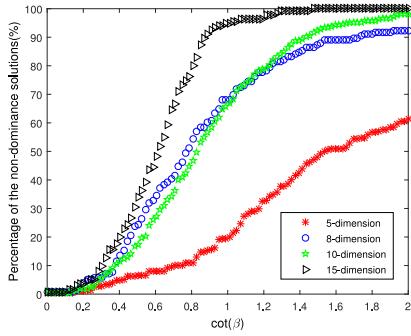


Fig. 4. Percentage of non-D-dominance solutions varies with the different setting of β .

parameter, which makes the D-dominance easy to be adjusted for many-objective optimization.

C. Adaptive Setting of Parameter β

In order to properly set this parameter, we propose an adaptive strategy to automatically adjust the parameter as follows:

$$\beta = \pi * \left(1 - \frac{1}{1 + \exp(-3 * \frac{\text{currentgen}}{\text{maxgen}})} \right) / 1.5 \quad (7)$$

where, currentgen is the current generation and maxgen represents the maximal generation for evaluation. β is maximal in the beginning and it will monotonically decrease with currentgen. The basic idea of this setting is that more selection pressure should be imposed on the population in the early stage of evolution to quickly approach the PF, and then selection pressure should be gradually decrease to make the population have better expansion along the PF. To understand how this adaptive strategy works for this purpose, we randomly generate 210, 156, 275, and 135 samples from the k -dimensional hypercube $[0, 1]^k$ for $k = 5, 8, 10, 15$, and show the percentage of non-D-dominance solutions with different setting of β in Fig. 4. In this figure, we can see that the percentage of non-D-dominance solutions is very small when β is around $\pi/2$, which means we will have the maximal selection pressure. The selection pressure of D-dominance will gradually decrease with the decreasing of β value for the percentage of non-D-dominance solutions increase gradually.

D. Novelty of D-Dominance

1) *Novelty Over Dominance and Decomposition*: As we have emphasized, D-dominance is derived from PBI decomposition, and it inherits both the metrics of dominance and decomposition. Comparing with Pareto dominance, D-dominance has adjustable dominant and dominated areas, which means D-dominance can be more flexible in dealing with many-objective optimization. Comparing with decomposition, each solution can evolve centered itself in D-dominance-based selection instead of the decomposition vector in decomposition-based selection. It can help diversify the population and reduce the possibility that one decomposition vector has two more associated solutions.

2) *Novelty Over α -Dominance*: The α -domination [10] was first proposed to cope with the so-called dominance resistant problems by considering the weak tradeoff among objectives. It was later found that as a relaxation of the Pareto dominance, α -domination can also be used to deal with MaOPs. The proposed D-dominance shares some similarities with α -dominance, but D-dominance differentiate itself from the previous α -dominance mainly for three aspects.

- 1) *Calculation*: The decomposition-based D-dominance aggregates objectives to differentiate solutions, while α -domination relaxes objectives tradeoff to differentiate solutions. Comparing with α -domination, the proposed D-dominance is more flexible and easy to implement for many-objective optimization.
- 2) *Dominant and Dominated Areas*: In 2-D space, α -dominance is literally a specialized form of D-dominance. However, when it comes to two and more dimensional objective space, the situation is totally different. For instance, α -dominance has a pyramidal dominant and dominated areas in 3-D objective space, which is different from the proposed D-dominance.
- 3) *Customization*: D-dominance is defined by the decomposition vector, and thus it can be highly customized for any given decomposition vector. This unique characteristic of D-dominance makes it possible to adaptively use D-dominance for all the decomposition vectors simultaneously in an evolutionary algorithm.

E. Decomposition-Based Crowding Measurement

In this section, we design a new crowding measurement by utilizing sharing function, and the sharing function of solutions \mathbf{x} and \mathbf{y} is

$$sh(\mathbf{x}, \mathbf{y}) = \begin{cases} \frac{1}{1+d_2(F(\mathbf{x})-F(\mathbf{y}))} & \text{if } d_2(F(\mathbf{x})-F(\mathbf{y})) < r \\ 0 & \text{else} \end{cases} \quad (8)$$

where parameter r defines the radius of a niche, and it is actually set adaptively according to the distribution of a subpopulation. Suppose num solutions need to be selected from a total n ($num \leq n$) solutions in a subpopulation. We first calculate the perpendicular distance d_2 of the n solutions, find the maximum and minimum d_2 as \max_d_2 and \min_d_2 , and then r is set as $r = [(max_d_2 - min_d_2)/num]$. The crowding

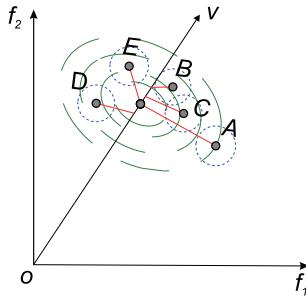


Fig. 5. Illustration of the decomposition-based crowding measurement.

degree of individual p in a subpopulation \mathbf{P} (denoted as DC) can be measured as

$$\text{DC}(\mathbf{p}) = \sum_{\mathbf{q} \in \mathbf{P}, \mathbf{q} \neq \mathbf{p}} \frac{sh(\mathbf{p}, \mathbf{q})}{d_2(\mathbf{p})}. \quad (9)$$

To emphasize the solution with the minimum d_2 , we reset its DC value as $-\infty$. An illustration of the measurement can be found in Fig. 5, and it shows the niche of five solutions in a subpopulation to the decomposition vector \mathbf{v} . The DC value of solution B is reset as $-\infty$ for it has the minimum d_2 , and that of the rest can be directly calculated by (9). They are then sorted by the DC values, and the solutions with smaller DC values are more likely to be selected.

F. Main Framework of Proposed Algorithm

This section shows how the proposed D-dominance and decomposition-based crowding measurement work in MOEA/D-M2M framework. DrEA is first initialized with N randomly generated individuals, and then the population is decomposed by the N predefined decomposition vectors. Unlike the original MOEA/D-M2M, the population decomposition of DrEA integrates a normalization procedure to deal with scaled MaOPs. The objectives $f_i(\mathbf{x})$ ($i = 1, 2, \dots, m$) of a solution \mathbf{x} can be normalized by: $f_i(\mathbf{x}) = ([f_i(\mathbf{x}) - z_i^{\text{ideal}}]/[z_i^{\text{nadir}} - z_i^{\text{ideal}}])$, where z_i^{ideal} is the minimum value of f_i found so far, and z_i^{nadir} is an approximation of the true nadir point [27]. The main framework of DrEA is presented by Algorithm 1.

Subpopulations $\mathbf{P}_1, \dots, \mathbf{P}_K$ are initially set in line 1 and reset in line 18 of Algorithm 1. To do it, we first determine the number of solutions S_k to be selected in subregion Ω_k ($k = 1, \dots, K$) as follows.

- 1) Set $\tilde{\mathbf{P}}_k = \{\mathbf{x} \in \Omega_k | \mathbf{x} \in \mathbf{Q}\}$, $k = 1, \dots, K$.
- 2) Set $S_k = 0$ and $R_k = |\tilde{\mathbf{P}}_k|$.
- 3) Sort R_k ($k = 1, \dots, K$) such that $R_{k_1} = R_{k_2} = \dots = R_{k_{t-1}} = 0 < R_{k_t} \leq R_{k_{t+1}} \dots \leq R_{k_K}$. Do: $i = t$;

repeat

$$\begin{aligned} S_{k_i} &= S_{k_i} + 1; \\ R_{k_i} &= R_{k_i} - 1; \\ i &= i + 1. \end{aligned}$$

until $\sum_{k=1}^K S_k = |\mathbf{P}|$.

Stop and return S_k ($k = 1, \dots, K$).

Algorithm 1: DrEA

Input :

- N : the population size;
- K : the number of the subproblems;
- MaxGen : maximum number of generations.

Output: A set of solutions.

- 1 **Initialization:** Uniformly initialize K unit direction vectors and population \mathbf{Q} , and normalize the population to set subpopulation \mathbf{P}_k ($k = 1, \dots, K$);
- 2 **while** the stopping criterion is not met **do**
- 3 **Generation of New Solutions:**
- 4 Set $\mathbf{R} = \emptyset$;
- 5 **for** $k \leftarrow 1$ to K **do**
- 6 **foreach** $\mathbf{x} \in \mathbf{P}_k$ **do**
- 7 Generate a random number rnd ;
- 8 **if** $rnd < 0.7$ **then**
- 9 Randomly choose \mathbf{y} from \mathbf{P}_k ;
- 10 **else**
- 11 Randomly choose \mathbf{y} from Ω/\mathbf{P}_k ;
- 12 **end**
- 13 Apply genetic operators on \mathbf{x} and \mathbf{y} to generate a new solution \mathbf{z} ;
- 14 Compute $F(\mathbf{z})$;
- 15 $\mathbf{R} := \mathbf{R} \cup \{\mathbf{z}\}$;
- 16 **end**
- 17 $\mathbf{Q} := \mathbf{R} \cup (\cup_{k=1}^K \mathbf{P}_k)$;
- 18 use \mathbf{Q} to set $\mathbf{P}_1, \dots, \mathbf{P}_K$.
- 19 **end**
- 20 Output $\cup_{k=1}^K \mathbf{P}_k$.
- 21 **end**

Algorithm 2: Subpopulations Updating

Input : \mathbf{Q} : a set of solutions and their F -values.

Output: $\mathbf{P}_1, \dots, \mathbf{P}_K$.

- 1 Non-dominated sort \mathbf{Q} to get \mathbf{Q}' ;
- 2 Update ideal point and nadir point for normalization;
- 3 **for** $k \leftarrow 1$ to K **do**
- 4 Initialize \mathbf{P}_k as the solutions in \mathbf{Q}' whose F -values are in Ω_k ;
- 5 Rank the solutions in \mathbf{P}_k using the non-D-dominated sorting and crowding sorting, and then remove from \mathbf{P}_k the $S_k - |\mathbf{P}_k|$ lowest ranked solutions.
- 6 **end**

Then, the proposed D-dominance and crowding measurement are utilized to select the S_k solutions for subpopulation \mathbf{P}_k , ($k = 1, 2, \dots, K$). Algorithm 2 shows how we proceed it.

V. EXPERIMENTAL STUDY

In this section, we first briefly introduce the five representative decomposition-based EMO algorithms, and then compare DrEA with them on a number of WFG [38] and DTLZ [39] test problems. The reason why only decomposition-based algorithms are compared is that their superiorities over other kinds

of EMO algorithms for MaOPs have been confirmed by many researches [31], [32].

A. EMO Algorithms in Comparison

The following five EMO algorithms are for comparison.

- 1) *MOEA/D-SBX* [24]: MOEA/D-SBX is an efficient version of MOEA/D with SBX and polynomial mutation [37]. A niching parameter T is used to define the neighboring decomposition vectors, and n_r defines the maximal number of solutions replaced by each child solution.
- 2) *NSGA-III* [27]: In NSGA-III, the nondominated sorting-based selection is first executed, and the selected solutions are then normalized. After normalization, the decomposition-based niching selection works on the last selected nondomination level to fill the slots of the next generation population.
- 3) *MOEA/DD* [28]: MOEA/DD decomposes the objective space into several subregions, and each vector will define a subproblem. A steady-state updating method is proposed, and the solution with the worst scalarization function value in the last nondomination level will be eliminated.
- 4) *θ -DEA* [29]: In θ -DEA, a dominance relation called θ -dominance is utilized to rank solutions in each subregion for environmental selection. θ -DEA can also enhance the convergence ability by utilizing the decomposition-based fitness evaluation scheme.
- 5) *RVEA* [30]: RVEA uses a set of reference vectors for decomposition and representing the user preferences. A new scalarization approach, called angle-penalized distance, is proposed for selection. RVEA adaptively adjusts the distribution of the reference vectors based on the scales of the objective functions.

B. Test Problems

Two kinds of scalable MaOP test problems from the WFG family [38] and DTLZ family [39] are used for experimental studies. WFG problems are characterized by scaled objectives and various complexities of PFs. In this paper, WFG2-WFG9 with the number of objectives $m = 5, 8, 10$, and 15 are tested for performance investigation. The number of decision variables is set as $n = m - 1 + l$, where $l = 20$ is the distance related variable [38]. The PFs of the unscaled DTLZ problems are featured with linearity, concave, and multimodality. DTLZ1–DTLZ4 problems with the number of objectives $m = 5, 8, 10$, and 15 are tested. The number of variables are set as $n = m - 1 + l$, where m is the number of objectives, and $l = 5$ for DTLZ1, and $l = 10$ for DTLZ2–DTLZ4 [27].

C. Performance Metrics

HV-metric [40] and IGD-metric [41] are used to measure the performance of those experimental algorithms.

- 1) *HV-Metric*: The HV value of an obtained set \mathbf{P} with the reference point $\mathbf{r}^* = (r_1^*, \dots, r_m^*)$ is the volume of the region which is dominated by \mathbf{P} and dominates \mathbf{r}^* in the objective

TABLE I
SETTING OF POPULATION SIZE, DIVISIONS, AND NUMBER OF GENERATIONS FOR TEST PROBLEMS WITH DIFFERENT NUMBER OF OBJECTIVES

# of objectives	Divisions	Population size	# of generations
5	6	210	750
8	3,2	156	1500
10	3,2	275	2000
15	2,1	135	3000

space, and it can be calculated by

$$\text{HV}(\mathbf{P}, \mathbf{r}^*) = L\left(\bigcup_{\mathbf{x} \in \mathbf{P}} [f_1(\mathbf{x}), r_1] \times \dots \times [f_m(\mathbf{x}), r_m]\right) \quad (10)$$

where $L(\cdot)$ denotes Lebesgue measure. Larger HV-metric value means better approximation to the true PF. The reference point is set as $\mathbf{r}^* = \text{nadir point} + 0.1$ in this paper. It is worth noting Monte Carlo sampling [17] is applied when calculating the HV values of 15-objective problems, and the HV values presented in this paper are all normalized to $[0, 1]$ by dividing $\prod_{i=1}^m r_i$.

- 2) *IGD-Metric*: The IGD-metric between the set of reference points \mathbf{P}^* and the obtained \mathbf{P} can be defined as

$$\text{IGD}(\mathbf{P}^*, \mathbf{P}) = \frac{\sum_{\mathbf{v} \in \mathbf{P}^*} d(\mathbf{v}, \mathbf{P})}{|\mathbf{P}^*|} \quad (11)$$

where $d(\mathbf{v}, \mathbf{P})$ is the minimum Euclidean distance from the point \mathbf{v} to \mathbf{P} . Intuitively, the smaller the value of IGD-metric is, the better the algorithm is.

D. General Parameter Settings

The general settings of DrEA, MOEA/D-SBX, MOEA/DD, NSGA-III, θ -DEA, and RVEA are as follows.

- 1) Population size N and divisions H for generating initial decomposition vectors (weight vectors in MOEA/D, reference points in MOEA/DD, NSGA-III, θ -DEA, and reference vector in RVEA) are shown in Table I.
- 2) Parameter θ is set as 5 in all PBI decomposition.
- 3) SBX crossover with $p_c = 1$ and $\eta_c = 30$, and polynomial mutation with $p_m = 1/n$ and $\eta_m = 20$ are used in all the experimental algorithms.
- 4) In MOEA/D-SBX: $T = 20$, $\delta = 0.9$, and $n_r = 2$, which is kept the same as in [24].
- 5) A set of 10 000 points is used in Monte Carlo sampling for HV-metric approximation in 15-D space following [17].

E. Experimental Studies on WFG Test Problems

In this section, we study the performance of the proposed DrEA on WFG test problems by comparing it with the five comparison algorithms described above.

- 1) *Experimental Results*: Table II shows the best (i.e., biggest), mean, and worst (i.e., smallest) of HV values of DrEA, MOEA/D, MOEA/DD, θ -DEA, NSGA-III, and RVEA for each WFG test instance with 5-, 8-, 10-, and 15-objective in 15 independent runs. The best HV values among the six comparison algorithms for each test instance are highlighted in bold face with gray background. By comparing the results,

TABLE II
BEST, MEAN, AND WORSE OF HV VALUES OF DREA, MOEA/D, MOEA/DD, θ -DEA, NSGA-III, AND RVEA IN 15 INDEPENDENT RUNS FOR EACH TEST INSTANCE WITH 5-, 8-, 10-, AND 15-OBJECTIVE. BEST PERFORMANCE IS HIGHLIGHTED IN BOLD

m			DrEA	MOEA/D	MOEA/DD	θ -DEA	NSGA-III	RVEA		DrEA	MOEA/D	MOEA/DD	θ -DEA	NSGA-III	RVEA
5	best	WFG2	0.992749	0.978277	0.967818	0.916029	0.992466	0.987814	WFG3	0.582305	0.498127	0.549289	0.569230	0.578884	0.570252
	mean		0.991281	0.957996	0.961720	0.911736	0.990770	0.984039		0.571472	0.463602	0.538601	0.562958	0.571372	0.554873
	worst		0.989211	0.905082	0.954400	0.906139	0.988252	0.978683		0.556833	0.425374	0.524566	0.551971	0.551163	0.543590
8	best	WFG3	0.997458	0.939588	0.960274	0.994339	0.996405	0.987986		0.540247	0.342622	0.463104	0.472043	0.569497	0.364376
	mean		0.995194	0.667804	0.950581	0.985459	0.994556	0.981266		0.528298	0.339179	0.455858	0.427735	0.534412	0.296209
	worst		0.993698	0.485531	0.944947	0.978172	0.991626	0.972906		0.521365	0.337657	0.449738	0.336876	0.469346	0.235546
10	best	WFG4	0.997452	0.952541	0.958525	0.997879	0.997616	0.992700	WFG5	0.539361	0.338455	0.465689	0.568577	0.600800	0.367550
	mean		0.996363	0.943463	0.953645	0.991560	0.996622	0.986641		0.532985	0.334822	0.444598	0.529218	0.572268	0.264374
	worst		0.995459	0.938476	0.943374	0.985979	0.995689	0.981514		0.526573	0.332404	0.426023	0.481300	0.467513	0.220226
15	best	WFG5	0.998442	0.636978	0.964604	0.792152	0.997248	0.974696		0.594837	0.347136	0.308194	0.566139	0.592064	0.586839
	mean		0.996701	0.458835	0.950321	0.786421	0.995737	0.921296		0.5031937	0.315798	0.282823	0.526086	0.559867	0.453784
	worst		0.995145	0.092902	0.938057	0.782232	0.991472	0.901396		0.4386881	0.297071	0.260347	0.490084	0.512561	0.398224
5	best	WFG6	0.718378	0.404753	0.692694	0.454703	0.715727	0.681988	WFG7	0.674865	0.514359	0.646058	0.419198	0.673896	0.665606
	mean		0.715443	0.296440	0.690145	0.452600	0.713165	0.674973		0.673304	0.458517	0.643990	0.418109	0.672487	0.662593
	worst		0.712617	0.191135	0.686283	0.449214	0.707166	0.669055		0.671133	0.370442	0.642118	0.416728	0.670974	0.659435
8	best	WFG7	0.849076	0.848834	0.759489	0.848835	0.848835	0.824943		0.792663	0.522349	0.689296	0.792841	0.792881	0.787404
	mean		0.845874	0.845199	0.740103	0.845881	0.845881	0.814122		0.791911	0.487248	0.672946	0.792237	0.791999	0.785650
	worst		0.843222	0.839999	0.712034	0.841735	0.841735	0.804384		0.790833	0.441577	0.647713	0.790737	0.790824	0.781632
10	best	WFG8	0.925223	0.701063	0.769664	0.925216	0.924457	0.904143		0.862502	0.585084	0.688904	0.862347	0.862369	0.857731
	mean		0.922143	0.557430	0.735590	0.923186	0.922834	0.898028		0.861938	0.546285	0.675817	0.861720	0.861829	0.856035
	worst		0.918433	0.170741	0.709400	0.919955	0.919660	0.889392		0.860905	0.515730	0.653381	0.860825	0.860893	0.854343
15	best	WFG9	0.964644	0.273533	0.565948	0.566139	0.925579	0.396296		0.890433	0.124124	0.465256	0.890072	0.863058	0.517904
	mean		0.963190	0.186326	0.527070	0.526086	0.922586	0.305596		0.888514	0.091343	0.424885	0.888197	0.861656	0.477991
	worst		0.961877	0.100424	0.442150	0.490084	0.919498	0.175662		0.886780	0.068169	0.360973	0.886640	0.859869	0.434695

we can observe that the performance of the proposed DrEA is very competitive among those experimental algorithms. To be specific, DrEA has the best overall performance on most of these test instances. Some exceptions can be found that the performance of DrEA is not the best, but it is still very competitive. The better performance of DrEA in terms of the mean HV-metric value also indicates its robust which is very crucial in practical use. To intuitively observe the performance of those algorithms, we plot the parallel coordinates of the obtained solutions with median HV values found by the six experimental algorithms on WFG9 test problems in the supplementary material. Those figures clearly show that DrEA has a good ability to find well distributed representative solutions among PFs.

2) *Results Analysis:* MOEA/D-SBX without normalization procedure does not perform very well on those WFG benchmark problems [28], [29]. To be fair, the normalization procedure used by DrEA is similarly applied to MOEA/D considering that WFG series test instances have scaled objectives. Despite all this, we still observe that MOEA/D-SBX does not perform very well in contrast to other experimental algorithms.

The main reason is that the decomposition-based selection in MOEA/D may select solutions with good decomposition function values but poor convergence to the decomposition vector in high-dimensional objective space. In that case, some of those decomposition vectors may not have optimal solution to associate with, which may lead to the loss of population diversity. This phenomenon can be clearly observed in the plot of the solutions obtained by MOEA/D-SBX shown in the supplementary material, and it also shows that MOEA/D's performance in population diversity drastically decreases with the increase of the number of objectives. MOEA/DD emphasizes the balance between the population convergence and diversity, and therefore can, to some extent, avoid the shortcoming of decomposition-based selection in MOEA/D. The simulation results show that performance of MOEA/DD is much better than MOEA/D-SBX. However, the fixed parameter $\theta = 5$ may have some bad effect on the balance between convergence and diversity. It happens that some decomposition vectors may have trouble to find associated solutions during the evolutionary process, and thus better performance can not be achieved. In θ -DEA, θ -dominance is utilized to

avoid the possible loss of population diversity by strengthening d_2 . Therefore, parameter θ plays an important role in balancing the convergence and diversity. As shown in Table II, the performance of θ -DEA is very promising to those WFG problems. The simulation results manifest that θ -DEA can effectively maintain the population diversity comparing with MOEA/D-SBX. However, θ -dominance is essentially the PBI decomposition, and thus it also has the similar shortcomings to MOEA/D-SBX and MOEA/DD. NSGA-III actually uses PBI decomposition with $\theta = 0$ to enhance the population diversity. The embedded decomposition makes NSGA-III very competitive among those experimental EMO algorithms, and the performance of NSGA-III is significantly better than MOEA/D-SBX. It can even be seen that NSGA-III is slightly better than DrEA for certain WFG test problems. Similarly, we can also observe reference vector-based RVEA has also achieved much better results than MOEA/D-SBX. In fact, the performance of MOEA/DD, θ -DEA, NSGA-III, and RVEA is very close to each other on those WFG test problems.

Benefiting from the newly developed D-dominance, DrEA can make better use of the decomposition vectors for subpopulation search. In MOEA/D-SBX, MOEA/DD, θ -DEA, NSGA-III, and RVEA, the evolutionary path in each subregion is explicitly defined by the decomposition vector. This kind of explicitness is beneficial for population exploitation in some way, but it also can inevitably damage the population's ability to explore more areas for it always limits the population's search in a certain direction. In DrEA, the decomposition vectors are free vectors, and thus subpopulations can make fully use those decomposition vectors to guide their search. The inherent parallelism of D-dominance-based selection strategy makes each individual search by centering itself instead of the decomposition vector, which means more explorations to be conducted. In this way, each individual in a subpopulation can get guidance from the decomposition vector, but the subpopulation search is not restricted by this decomposition vector. More importantly, the exploration and exploitation of each subpopulation will vary with the evolutionary process because of the adaptive strategy. There will be more explorations at the beginning of evolution, and gradually more exploitations will be involved in each subpopulation search. The proposed decomposition-based crowding measurement can help further diversify the subpopulations. This is where the advantages of DrEA lies comparing with the other five representative decomposition-based algorithms.

F. Experimental Studies on DTLZ Test Problems

In this section, we do further testing on the unscaled DTLZ1–DTLZ4 with 5-, 8-, 10-, and 15-objective, and compare DrEA with the most commonly used comparison algorithm for DTLZ test Problems: NSGA-III. The performance comparisons of the two algorithms are based on IGD-metric. Since all the PFs of those DTLZ test problems are known *a priori*, we can easily generate the reference points on PF for IGD-metric calculation following the method in [28]. The maximal number of generations for each test problem is kept

TABLE III
NUMBER OF GENERATIONS FOR DTLZ TEST PROBLEMS

# of objectives	DTLZ1	DTLZ2	DTLZ3	DTLZ4
5	600	350	1000	1000
8	750	500	1000	1250
10	1000	750	1500	2000
15	1500	1000	2000	3000

TABLE IV
BEST, MEAN, AND WORSE OF IGD-METRIC VALUES OF DREA AND NSGA-III IN 15 INDEPENDENT RUNS FOR DTLZ1 WITH 5-, 8-, 10-, AND 15-OBJECTIVE. BEST PERFORMANCE IS HIGHLIGHTED IN BOLD

m			DrEA	NSGA-III
3	DTLZ1	best	0.000438	0.000794
		mean	0.004080	0.03911
		worst	0.048618	0.014188
		best	0.002199	0.003780
		mean	0.002712	0.008265
		worst	0.003458	0.027726
5	DTLZ1	best	0.002260	0.002899
		mean	0.002943	0.005190
		worst	0.006719	0.019052
		best	0.002646	0.002785
		mean	0.007538	0.006208
		worst	0.031351	0.013839

the same for the two comparison algorithms, which is shown in Table III.

The simulation results of DTLZ1 test problems are shown in Table IV, and that of the rests are shown in the supplementary material. By comparing, we can see that both DrEA and NSGA-III have achieved very promising results, but overall DrEA is the better one. For DTLZ1 test problem with 5-, 8-, 10-, and 15-objective, the superiority of DrEA over NSGA-III is not very significant. DTLZ1 test problem is relatively simple among those DTLZ series test problems and its PF is relatively easy to be approximated. For DTLZ2 test problem with 5-, 8-, 10-, and 15-objective, DrEA has achieved much better results than NSGA-III. Similar observations can also be made for the DTLZ3 and DTLZ4 test problems with 5-, 8-, 10-, and 15-objective. The simulation results verify the effectiveness of the proposed DrEA on MaOPs with same objective magnitude over the PF. The reason behind this experimental results is the stability of the normalization procedure and the effectiveness of the D-dominance-based selection conducted in DrEA.

VI. CONCLUSION

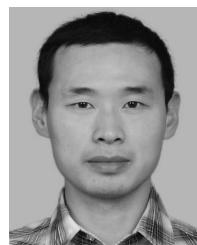
This paper theoretically shows that the three representative decomposition methods are actually based on the same principle. A new dominance relationship with adjustable dominant and dominated areas is derived from the PBI decomposition, and furthermore an adaptive D-dominance-based evolutionary algorithm called DrEA is then presented for many-objective optimization. DrEA decomposes an MaOP into a number of relatively simple subproblems, and each subproblem is independently evolved by its own customized D-dominance. A decomposition-based crowding measurement is employed in DrEA to further diversify those subpopulations. In such a way, better balance between population convergence and diversity

can be achieved. The performance of the suggested method is validated through a series comparative experiments.

Our future work will focus on the practical applications of the proposed D-dominance and the decomposition-based crowding measurement method.

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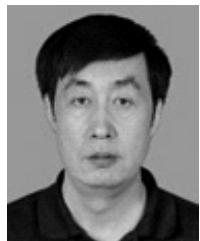
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