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Enhanced Multi-objective Evolutionary Algorithms Using Local Dominance

Hiroyuki Sato, Hernán E. Aguirre and Kiyoshi Tanaka

Faculty of Engineering, Shinshu University, 4-17-1 Wakasato, Nagano, 380-8553 JAPAN
Email: {sato@iplab, ahernan@gipwc, ktanaka@gipwc}.shinshu-u.ac.jp

Abstract

In this paper, we propose a calculation method of local dominance and enhance multiobjective evolutionary algorithms by performing a distributed search based on local dominance. We divide the population into several sub-populations by using declination angles of polar coordinate vectors in the objective space. We calculate local dominance for individuals belonging to each sub-population based on the local search direction, and apply genetic operators to individuals within each sub-population. We verify the effectiveness of the proposed method by comparing the search performance between NSGA-II, SPEA2 and their enhanced versions.

1. Introduction

Recently, multiobjective evolutionary algorithms (MOEAs) [1], [2] have been increasingly investigated to solve multiobjective optimization problem (MOP). Two important goals of a MOEA are to achieve convergence to Pareto Optimal Solutions (POS) and keep a good distribution in objective space of the solutions found. Among various methods proposed so far [1], [2], approaches that use elitism based on dominance are becoming the state of the art [3], [4]. In general, these algorithms are quite effective obtaining POS when the search space is relatively small. However, when the search space becomes large and/or the number of objectives increase, it becomes gradually difficult for them to obtain POS with sufficient diversity in the objective space.

In order to solve this problem and obtain fully spread POS satisfying diversity conditions, we propose a calculation method of local dominance and enhance MOEAs by performing a concurrent distributed search based on local dominance. In this method, we first transform all fitness vectors of individuals to polar coordinate vectors in the objective function space. Then we divide the population into several sub-populations by using declination angles. We calculate local dominance for individuals belonging to each sub-population, and apply selection, recombination, and mutation to individuals within each sub-population.

In this paper, we compare the search performance between the well-known NSGA-II [3] and SPEA2 [4] and their enhanced versions implemented with our method to verify the effectiveness of the proposed method obtaining POS satisfying diversity conditions. Benchmark problems with two and three objectives ($m = 2, 3$) are used.

2. Multi-Objective Optimization Problem

A MOP including m kinds of objective functions is defined as follows:

$$\begin{cases} \text{Maximize} & \boldsymbol{f}(\boldsymbol{x}) = (f_1(\boldsymbol{x}), f_2(\boldsymbol{x}), \ldots, f_m(\boldsymbol{x})) \\ \text{subject to} & \boldsymbol{x} \in \mathcal{F} \end{cases} \tag{1}$$

where, $\boldsymbol{x} \in \mathcal{F}$ is a feasible solution vector in the solution space $\mathcal{S}$ ($\mathcal{F} \subseteq \mathcal{S}$), and f_i ($i = 1, 2, \cdots, m$) are the m objectives to be maximized. That is, we try to find a feasible solution vector $\boldsymbol{x} \in \mathcal{F}$ in the solution space maximizing each objective function f_i ($i = 1, 2, \ldots, m$) in a vector fitness function $\boldsymbol{f}$. Important concepts used in determining a set of solutions for MOP are dominance, Pareto optimality, Pareto set and Pareto front. Next we define *dominance* between solutions $\boldsymbol{x}, \boldsymbol{y} \in \mathcal{F}$ as follows: If

$$\begin{array}{l} \forall i \in \{1, 2, \ldots, m\} : f_i(\boldsymbol{x}) \geq f_i(\boldsymbol{y}) \quad \wedge \\ \exists i \in \{1, 2, \ldots, m\} : f_i(\boldsymbol{x}) > f_i(\boldsymbol{y}). \end{array} \tag{2}$$

are satisfied, $\boldsymbol{x}$ dominates $\boldsymbol{y}$. In the following, $\boldsymbol{x}$ dominates $\boldsymbol{y}$ is denoted by $\boldsymbol{f}(\boldsymbol{x}) \succeq \boldsymbol{f}(\boldsymbol{y})$. A solution vector $\boldsymbol{x}$ is said to be *Pareto optimal* with respect to $\mathcal{F}$ if it is not dominated by other solution vectors in $\mathcal{F}$. The presence of multiple objective functions, usually conflicting among them, gives rise to a set of optimal solutions. The set of Pareto optimal solutions (POS) is defined as

$$\mathcal{P} = \{\boldsymbol{x} \in \mathcal{F} \mid \neg\exists \boldsymbol{y} \in \mathcal{F} : \boldsymbol{f}(\boldsymbol{y}) \succeq \boldsymbol{f}(\boldsymbol{x})\}, \tag{3}$$

and the Pareto front is defined as

$$\mathcal{PF} = \{f_1(\boldsymbol{x}), f_2(\boldsymbol{x}), \ldots, f_m(\boldsymbol{x}) \mid \boldsymbol{x} \in \mathcal{P}\}. \tag{4}$$

MOEAs evolve a population to obtain $\mathcal{P}$ for a given MOP in a single run.

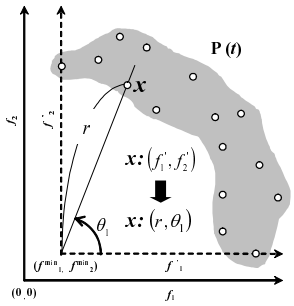


Fig.1 Solution expression with polar coordinate vector $(m = 2)$

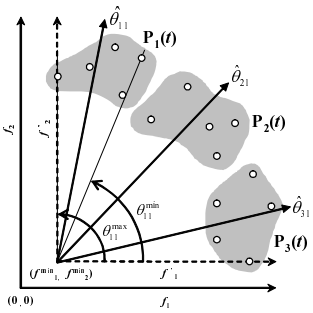


Fig.2 Determination of principle search direction for each sub-population $(m = 2, d = 3)$

3. Proposed Method

3.1. Population Division in Objective Function Space

In order to introduce necessary diversity and accomplish efficient search for POS, we divide the entire population into several sub-populations generation by generation. Each sub-population consists of individuals having similar search directions, and genetic operators are applied to them within each sub-population. We show the algorithm focusing population division with a parameter d in the following.

step1: Create a minimum fitness vector $(f_1^{\min}, f_2^{\min}, \cdots, f_m^{\min})$ consisting of the minimum fitness values in each objective function f_i $(i = 1, 2, \ldots, m)$ in the population, and calculate temporal fitness vectors for all individuals as

$$\boldsymbol{f}^{'}(\boldsymbol{x}) = (f_1^{'}(\boldsymbol{x}), f_2^{'}(\boldsymbol{x}), \ldots, f_m^{'}(\boldsymbol{x})) \tag{5}$$

$$= (f_1(\boldsymbol{x}) - f_1^{\min}, f_2(\boldsymbol{x}) - f_2^{\min}, \ldots, f_m(\boldsymbol{x}) - f_m^{\min}). \tag{6}$$

step2: Transform all temporal fitness vectors $\boldsymbol{f}^{'}(\boldsymbol{x})$ to polar coordinate vectors $\boldsymbol{p}(\boldsymbol{x})$, which components are a norm r and $m-1$ declination angles θ_j $(j = 1, 2, \ldots, m-1)$, as shown in **Fig.1**, i.e.

$$\boldsymbol{f}^{'}(\boldsymbol{x}) = (f_1^{'}(\boldsymbol{x}), f_2^{'}(\boldsymbol{x}), \ldots, f_m^{'}(\boldsymbol{x})) \rightarrow \boldsymbol{p}(\boldsymbol{x}) = (r(\boldsymbol{x}), \theta_1(\boldsymbol{x}), \theta_2(\boldsymbol{x}), \cdots, \theta_{m-1}(\boldsymbol{x})). \tag{7}$$

step3: Divide the entire population $P(t)$ at t-th generation into d^{m-1} sub-populations $P_k(t)$ $(k = 1, 2, \cdots, d^{m-1})$ with the following procedure.

step3-1: Set $l = 1$ and $P_1 = P(t)$.

step3-2: Sort all individuals in P_k $(k = 1, 2, \cdots, d^{l-1})$ with l-th angle information θ_l.

step3-3: Divide each P_k $(k = 1, 2, \cdots, d^{l-1})$ into d sub-populations with the results of *step3-2*.

step3-4: Increment l. If $l \leq m - 1$, repeat *step3-2* $\sim$ *step3-3* for sub-populations already obtained. Otherwise go to *step4*.

step4: Calculate local dominance for all individuals in each sub-population $P_k(t)$ $(k = 1, 2, \cdots, d^{m-1})$ with the procedure described in 3.2, and then apply selection and genetic operations within each sub-population by using the conventional MOEAs [3], [4].

3.2. Calculation of Local Dominance in Sub-population

Local dominance among individuals in each sub-population P_k $(k = 1, 2, \cdots, d^{m-1})$ is calculated after rotating each principle search direction with the following procedure.

step4-1: Find minimum and maximum declination angles, $\theta_{kj}^{\max}$ and $\theta_{kj}^{\min}$ $(j = 1, 2, \cdots, m-1)$, in $P_k(t)$, and determine the principle search direction as shown in **Fig.2** by

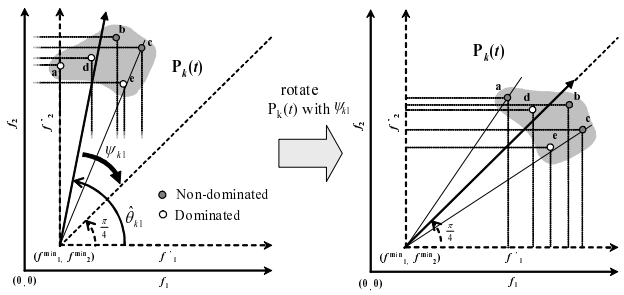
$$\hat{\theta}_{kj} = \frac{\theta_{kj}^{\max} - \theta_{kj}^{\min}}{2} + \theta_{kj}^{\min} \quad (j = 1, 2, \cdots, m-1). \tag{8}$$

step4-2: Calculate $m - 1$ rotating angles

$$\psi_{kj} = \hat{\theta}_{kj} - \frac{\pi}{4} \qquad (j = 1, 2, \cdots, m-1). \tag{9}$$

step4-3: Change all polar coordinate vectors of individuals in $P_k(t)$ as shown in **Fig.3** by

$$\boldsymbol{p}^{'}(\boldsymbol{x}) = (r_k(\boldsymbol{x}), \theta_{k1}^{'}(\boldsymbol{x}), \theta_{k2}^{'}(\boldsymbol{x}), \cdots, \theta_{km-1}^{'}(\boldsymbol{x})) = (r_k(\boldsymbol{x}), \theta_{k1}(\boldsymbol{x}) - \psi_{k1}, \theta_{k2}(\boldsymbol{x}) - \psi_{k2}, \cdots, \theta_{km-1}(\boldsymbol{x}) - \psi_{km-1}). \tag{10}$$



(a) before circulation (b) after circulation

Fig.3 Rotation of sub-population $P_k(t)$ and its affection to dominance among solutions

step4-4: Transform all polar coordinates vectors changed in $P_k(t)$ to modified temporal fitness vectors as

$$\boldsymbol{p}^{'}(\boldsymbol{x}) = (r(\boldsymbol{x}), \theta^{'}_{k1}(\boldsymbol{x}), \theta^{'}_{k2}(\boldsymbol{x}), \cdots, \theta^{'}_{km-1}(\boldsymbol{x})) \rightarrow \boldsymbol{f}^{''}(\boldsymbol{x}) = (f^{''}_{k1}(\boldsymbol{x}), f^{''}_{k2}(\boldsymbol{x}), \ldots, f^{''}_{km}(\boldsymbol{x})). \quad (11)$$

We calculate local dominance in *step4* in 3.1 for all modified temporal fitness vectors in $P_k(t)$ obtained by Eqs.(10) $\sim$ (11).

As shown in **Fig.3(a)**, if we calculate dominance among solutions with a conventional scheme, say NSGA-II [3], individuals $\boldsymbol{a}$, $\boldsymbol{d}$ and $\boldsymbol{e}$ would be dismissed with high probability in parent selection process since they are dominated by $\boldsymbol{b}$ and $\boldsymbol{c}$. On the other hand, if we take into account local search direction and properly rotate declination angle as shown in **Fig.3(b)**, the individual $\boldsymbol{a}$ becomes a non-dominated solution, which is expected to make the entire population spread.

3.3. Gap Suppression by Varying Sub-population Size

If we evolve the entire population with a fixed number of individuals in each sub-population, the search tends to produce gaps among sub-populations in the objective space. In order to suppress this phenomenon, we incorporate a particular population dividing scheme, which slightly fluctuates regions covered with sub-populations in the objective space. Suppose that a population P is divided into d sub-populations P_k $(k = 1, 2, \cdots, d)$. In this process, we describe the total population size in P as

$$|P| = \sum_{k=1}^{d} |P_k + C_k| \quad (12)$$

where $|\cdot|$ means number of individuals in the population. $|P_k|$ $(k = 1, 2, \cdots, d)$ includes an equivalent number of individuals but additional reserve individuals C_k are randomly given to sub-populations. We prepare a reserve individual vector $\boldsymbol{C} = (C_1, C_2, \cdots, C_k)$ in advance, and all elements are randomly permuted at every generation. This slight fluctuation of the solution coverage with sub-populations works to suppress (disappear) gaps in the objective space effectively.

4. Experimental Results and Discussion

4.1. Preparation

In this paper we use multiobjective 0/1 knapsack problems (KPn-m) [5] as benchmark problems to verify the search performance of the proposed method, where n and m denote item and knapsack (objective) numbers, respectively. Only in case of two objectives $(m = 2)$ we know the true POS for the problems downloaded from [6].

As genetic parameters, we adopt two-point crossover with a crossover probability $p_c = 1.0$ for recombination, and apply bit-flipping mutation with a mutation probability $p_m = 1/n$. In the following experiments, we show the average performance with 30 runs, each of which spent 2,000 generations. Population sizes are set to $|P| = \{200, 600\}$ for $m = \{2, 3\}$ objectives, respectively.

As metrics for performance evaluation, we use several metrics to evaluate POS obtained by the MOEAs compared in this work. Hyper-volume (HV) [7], GD proposed by Veldhuizen [8], inverse GD defined in this paper, and Spread (SP) proposed by Deb et al. [1] are used. IGD is the average distance for all members in the true POS to their nearest solutions in the obtained POS.

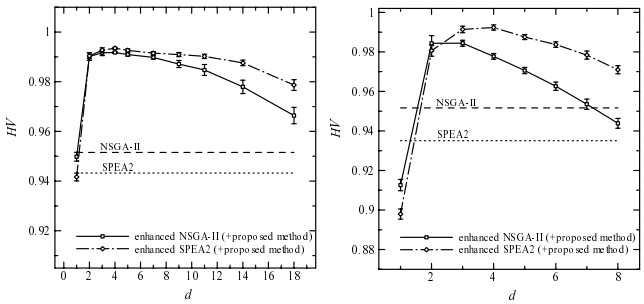
4.2. Results and Discussion

In our experiments, we compare the search performance achieved by four MOEAs, conventional NSGA-II, SPEA2, and their enhanced versions incorporating the proposed method considering local dominance.

First of all, we show the normalized HV with 95% confidence intervals obtained by our method as we vary the parameter d regarding population division in **Fig.4**, where two dashed lines are the results by conventional NSGA-II and SPEA2. The main conclusions from **Fig.4** are as follows: (i) As a general tendency, the superiority of the proposed method becomes remarkably large as we increase the solution space by increasing objective (knapsack) numbers m and/or item numbers n in the problem. (ii) There is an optimum parameter d^* to maximize HV depending on benchmark problem and algorithm to be used. (iii) Larger improvement by our method can be observed in case of SPEA2 rather than NSGA-II, while conventional NSGA-II always outperforms SPEA2 in this particular problem.

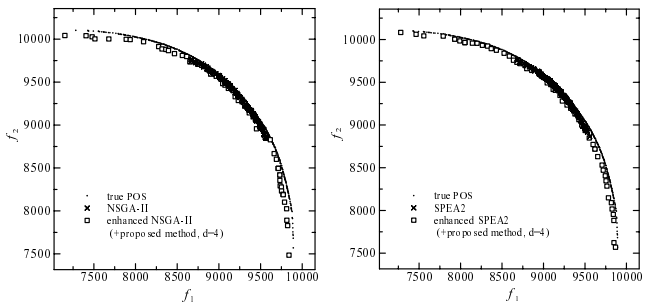
Next, we show the obtained POS in **Fig.5**. As the solution space increases, both enhanced NSGA-II and SPEA2 implementing our method achieve robust performance obtaining fully dispersed POS close to the true POS.

In **Fig.6**, we show the transition of GD and IGD over generation as indicators on convergence of POS. Conventional NSGA-II and SPEA2 achieve smaller GD than the enhanced ones, but the enhanced NSGA-II and SPEA2 achieve clearly smaller IGD than conventional ones.



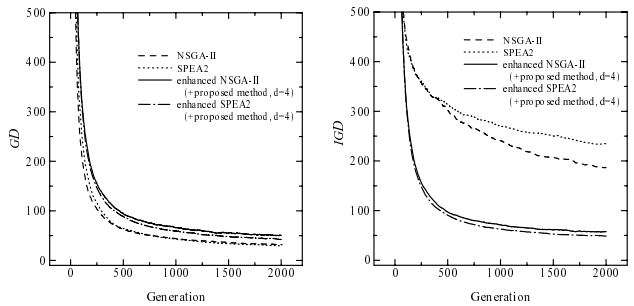
(a) KP250-2 (b) KP250-3

Fig.4 Performance comparison on hyper-volume (HV) for KP250-2,3



(a) NSGA-II (b) SPEA2

Fig.5 Obtained POS for KP250-2



(a) GD (a) IGD

Fig.6 Transition of GD and IGD over generations for KP250-2

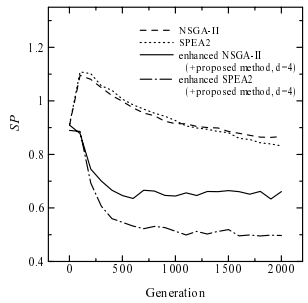


Fig.7 Transition of SP over generations for KP250-2

Furthermore, we show the transition of SP over generations as an indicator on diversity of POS in **Fig.7**. From this figure we can see that conventional NSGA-II and SPEA2 remarkably lose diversity in early stage of evolution, while enhanced methods continuously induce diversity into the entire population from the beginning of evolution. Precisely, enhanced SPEA2 always achieved smaller SP than enhanced NSGA-II, which could support the result that the former algorithm shows larger improvement on HV in **Fig.4**.

These results could be an evidence to show not only the difficulty for a single population to cover widely spread POS in the objective space but also the effectiveness of the proposed method based on local dominance.

5. Conclusions

In this paper, we have proposed a calculation method of local dominance and enhanced MOEAs by performing a distributed search based on local dominance. We have verified that the enhanced NSGA-II and SPEA2, implemented with our method, showed better search performance to obtain fully spread POS than their conventional versions. The difference in performance increased with the number of objective and/or size of the search space.

As future works, we should improve this method to achieve higher convergence of POS while keeping diversity as it is. Also, we should verify the performance of this method for the problems including more than three objectives and for other kinds of problems.

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