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Biased Random Key Genetic Algorithm with Hybrid Decoding for Multi-objective Optimization

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Abstract—A biased random key genetic algorithm (BRKGA) is an efficient method for solving combinatorial optimization problems. It can be applied to solve both single-objective and multi-objective optimization problems. The BRKGA operates on a chromosome encoded as a key vector of real values between $[0, 1]$. Generally, the chromosome has to be decoded by using a single decoding method in order to obtain a feasible solution. This paper presents a hybrid decoding, which combines the operation of two single decoding methods. This hybrid decoding gives two feasible solutions from the decoding of one chromosome. Experiments are conducted on realistic instances, which concern acquisition scheduling of agile Earth observing satellites.

I. INTRODUCTION

THIS PAPER proposes a hybrid decoding to apply with a biased random key genetic algorithm (BRKGA) for solving multi-objective optimization problems. We experiment on instances of multi-user observation scheduling problem for agile Earth observing satellites (EOSs).

The biased random key genetic algorithm (BRKGA) was first presented in [1]. BRKGA combines the concept of random key and the principles of genetic algorithms. The random key vector represents one solution. In the process to apply BRKGA for solving combinatorial problems, there is a step, which depends on the considered problem. It is a decoding step, which is used to decode the random key chromosome to become a feasible solution. The efficient decoding method can obtain a good solution. Hence, the specification of the decoding step is an important issue for BRKGA.

BRKGA was used to solve combinatorial optimization problems in various domains (e.g. communication, transportation, scheduling) [3]. For example, BRKGA was applied to solve the fiber installation in an optical network optimization problem [4]. The objective function was to minimize the cost of the optical components necessary to operate the network. In [5], a resource-constrained project scheduling problem with makespan minimization was solved by BRKGA. Nevertheless, all these works address optimization problems involving a single objective function. This paper considers multi-objective optimization. Several real world problems, e.g., in the area of engineering research and design, can be modeled as multi-objective optimization problems. When many objectives are considered, the search will not give a unique solution but a

set of solutions. Hence, our idea for improving the efficiency of BRKGA for solving multi-objective optimization problems, is to combine the importance of its decoding step and the need of a non-unique solution of multi-objective optimization.

A hybrid decoding, which combines two single decoding methods, is proposed in this paper. A hybrid decoding can obtain more than one solution from the decoding of one chromosome. Two separate single-decoding and the hybrid decoding are experimented on the multi-user observation scheduling problem for agile Earth observing satellites.

The mission of Earth observing satellites (EOSs) is to obtain photographs of the Earth surface satisfying users' requirements. When the ground station center receives the requests from users, it has to manage the requirements by selecting and scheduling a subset of photographs and transmit the schedule, which consists of a sequence of selected photographs, to the satellites. We consider an agile satellite, which has only one on-board camera that can move around three axes: roll, pitch, and yaw. The starting time of each photograph is not fixed; it can slide within a given visible time interval. The problem description of agile EOSs scheduling problem is presented in the ROADEF 2003 challenge [10]. This challenge required the scheduling solutions that maximize total profit of the acquired photographs for a single user and have to satisfy all physical constraints of agile EOSs. Algorithms based on simulated annealing [11] and tabu search [12] were particularly proposed for this challenge. In [13], multiple users have been considered. However, a single objective is considered.

The originality of our work also lies in the consideration of multi-user requests, but we need to optimize two objectives. The ground station center should maximize the total profit of the acquired photographs and simultaneously share fairly the satellite resources for all users by minimizing the maximum profit difference between users. In [9], we proposed a biased random-key genetic algorithm (BRKGA) with a single decoding method to solve this multi-objective optimization problem. BRKGA with a single decoding succeeded to obtain quite good solutions. However, the average value of the obtained hypervolumes and the range of the solutions should be improved.

For our study, the ROADEF 2003 instances of the observa-

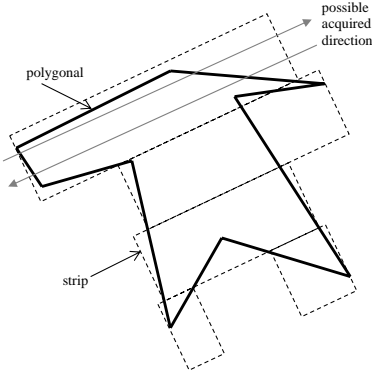


Fig. 1. A polygon is decomposed into several strips; one of two possible directions can be selected for the acquisition of each strip

tion scheduling problem for agile EOSs are modified in order to consider in case of multi-user requirements. Two possible shapes of area can be required: spot or polygon. The polygon is a big area that the camera cannot take instantaneously. Hence it has to be decomposed into several strips of rectangular shape with fixed width but variable length, as shown in Figure 1. Among two possible directions, one acquisition can be selected for each strip. Two types of photograph can be required: a mono photograph is taken only once, whereas a stereo photograph should be acquired twice in the same direction but from different angles.

The possible starting time interval for taking each acquisition is calculated, depending on the acquired direction, its earliest/latest visible time of the two extremities and the taking duration time of the strip. Moreover, adjacent selected acquisitions must also respect a sufficient transition time. It is a necessary time in order to move the camera from the ending point of the previous acquisition to the beginning point of the next acquisition. These imperative constraints have to be satisfied for finding the feasible solutions, which are the sequences of the selected acquisitions for being transmitted to the satellite. For each solution, the two objective function values can be calculated by using a piecewise linear function of gain. This function is associated with a partial acquisition of the acquired request, as illustrated in Figure 2.

The article is organized as follows. Section II explains the BRKGA for solving multi-objective optimization problems. The proposed hybrid decoding is presented in Section III. Section IV reports the computational results. Finally, conclusions are discussed in Section V.

II. BIASED RANDOM KEY GENETIC ALGORITHM FOR MULTI-OBJECTIVE OPTIMIZATION PROBLEMS

A genetic algorithm is a metaheuristic method, which operates on several individuals in a population. Individuals should spread through the search space. The genetic algorithm uses the concept of survival of the fittest to find the optimal solutions. Each individual consists of a chromosome, which represents a solution. The process of genetic algorithm is started by generating an initial population with its size equal

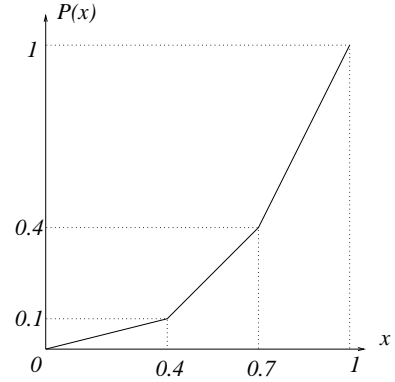


Fig. 2. Piecewise linear function of gain $P(x)$ depending on the effective ratio x of acquired area [10]

to p . For generating the next generations, selection, crossover, and mutation operators are applied. The iterations are repeated until a stopping criterion is satisfied.

A biased random key genetic algorithm (BRKGA) was first presented in [1]. The BRKGA has different ways to select two parents for the crossover operation, compared with the original of random key genetic algorithm (RKGA) [2]. For BRKGA, the random key chromosome is formed by several genes, which are encoded by real values in the interval $[0, 1]$. Then, the chromosome is decoded in order to obtain the solution. The decoding strategy is problem dependent. The fitness value of solution is computed in this decoding step. The current population is divided into two groups by using the selection mechanism. Selections are applied to choose p_e preferred chromosomes from the current population to become the elite set. The remaining chromosomes will be stored in the other group of non-elite chromosomes. Then, the process to generate the population in the next generation begins.

The standard procedure for BRKGA can be found in [3]. We will now explain how BRKGA was adapted for multi-objective optimization [9]. We will focus on the selection phase, fitness computation, and population recombination.

A. Population generation for the next iteration

The population of the new generation is generated from three parts, as in Figure 3. The first part is an elite set, which contains p_e preferred chromosomes. The second part is a set of p_m chromosomes, which are generated to avoid the entrapment in a local optimum. These chromosomes are called mutant. They are randomly generated by the same methods, which is used to generate the initial population. The last part is filled by generating offspring from the crossover operation of the elite set and another solution from the current population. Each element in the offspring is obtained from the element of elite parent with the probability p_e . Otherwise, the element of offspring is copied from the non-elite parent. Hence, the size of crossover offspring set is equal to $p - p_e - p_m$. The recommended parameter value setting is displayed in Table I.

In [3], BRKGA is applied to solve optimization problems arising in several applications. However, all problems consider

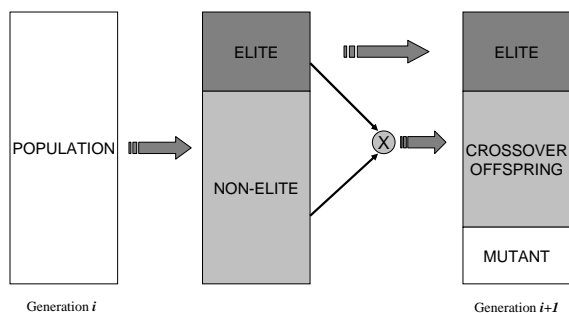


Fig. 3. The population of the new generation by using BRKGA

TABLE I
RECOMMENDED PARAMETER VALUES OF BRKGA [3]

Parameter	Recommended value
p	$p = a.n$, where $1 \leq a \in \mathbb{R}$ is a constant and n is the length of the chromosome
p_e	$0.10p \leq p_e \leq 0.25p$
p_m	$0.10p \leq p_m \leq 0.30p$
ρ_e	$0.5 \leq \rho_e \leq 0.8$

only one objective. In this work, we study BRKGA for solving a multi-objective optimization problem. The fitness of each chromosome must be taken into account for all objective functions. Algorithms for selecting the preferred chromosomes are needed.

B. Algorithm to select the preferred chromosomes in the context of a multi-objective optimization problem

Three strategies are proposed to select individuals.

1) *Fast nondominated sorting and crowding distance assignment*: Fast nondominated sorting and crowding distance assignment methods were proposed in the Nondominated Sorting Genetic Algorithm II (NSGA-II) [6]. In our work, the fast nondominated sorting method is used to find the nondominated solutions. If the number of nondominated solutions is more than the parameter setting value of maximum size of elite set, the crowding distance assignment method is applied to select some solutions from the nondominated set to become the elite set. Otherwise all nondominated solutions will become the elite set.

2) *\mathcal{S} metric selection evolutionary multi-objective optimization algorithm*: \mathcal{S} metric selection evolutionary multi-objective optimization algorithm (SMS-EMOA), which was proposed in [7], is applied to select some solutions in the current population to become the elite set. In our work, we use SMS-EMOA combining with the fast nondominated sorting from NSGA-II. The fast nondominated sorting is applied in order to find the nondominated solutions and SMS-EMOA compute the hypervolume as selection criterion for limiting the size of elite set. The hypervolume selection discards the solution, which obtains the least hypervolume in the set of nondominated solutions and the remaining solutions will

become the elite set.

3) *Indicator-based evolutionary algorithm based on the hypervolume concept*: The use of an indicator based on the hypervolume concept was proposed in the Indicator-Based Evolutionary Algorithm (IBEA) [8]. The indicator based method is used to assign fitness values based on the hypervolume concept to the population members. Then, some solutions in the current population are selected to become elite set for the next population. The indicator based method performs binary tournaments for all solutions in the current population. The selection is implemented environmentally by removing the worst solution from the population and updating the fitness values of the remaining solutions. The worst solution is removed repeatedly until the number of remaining solutions satisfies the recommended size of elite set for BRKGA.

III. DECODING METHODS

In this section, the decoding methods, which are used for obtaining the solutions from the random key chromosomes, are described. A chromosome consists of several genes. Each gene represents one job, which needs to be scheduled. When the processes of genetic algorithm finish, the chromosome is decoded in order to obtain a sequence of jobs, which become the solution of the problem. In this decoding step, the sequence of jobs will be generated. The order to consider each job depends on the priority, which is computed from its associated gene value. The job, which has the highest priority, will be firstly considered to be assigned in a sequence. Then, the next jobs are considered according to the priority order. The considered job can be scheduled in the sequence, only if all constraints are satisfied. Three decoding methods for assigning the priority are studied in this paper. The three methods are:

A. Basic decoding (D1)

The first decoding method is a basic decoding: the priority is assigned by using directly the gene value:

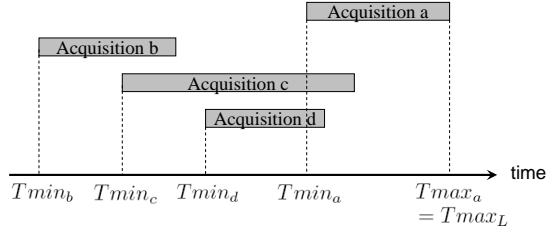
$$Priority_j = gene_j \quad (1)$$

This decoding method was implemented in the context of multi-objective optimization in [9]. Albeit it gave quite good results, we are convinced that the results regarding average values and standard deviations of hypervolumes can be yet improved. Thus, we searched for an idea to apply some useful data of the problem for assisting the basic decoding.

B. Decoding of gene value and ideal priority combination (D2)

This decoding is presented in [5]. It considers the priority depending on the gene value, and also an ideal priority. For the concept of the ideal priority, the job, which has the earliest possible starting time, should be selected firstly and be scheduled at the beginning of the sequence. Hence the ideal priority gives a higher priority to select and schedule the job which has the earlier possible starting time. This ideal priority is the real value in the interval $[0, 1]$ which is given by

$$\frac{LLP_j}{LCP}, \quad (2)$$



Acquisition	a	b	c	d
Ideal priority	$\frac{T_{max_L} - T_{min_a}}{T_{max_L}}$	$\frac{T_{max_L} - T_{min_b}}{T_{max_L}}$	$\frac{T_{max_L} - T_{min_c}}{T_{max_L}}$	$\frac{T_{max_L} - T_{min_d}}{T_{max_L}}$

Fig. 4. Example of ideal priority calculation

where LLP_j is the longest length path from the beginning of job j to the end of the project and LCP is the length along the critical path of the project.

The factor that adjusts the priority to account for the gene values of the random key chromosome is given by $(1 + gene_j)/2$. Thus, the second decoding expression of each job j is

$$Priority_j = \frac{LLP_j}{LCP} \times \left[\frac{1 + gene_j}{2} \right] \quad (3)$$

This second decoding method was applied to solve the resource-constrained project scheduling problem with makespan minimization in [5]. In our paper, the second decoding will be implemented to the considered multi-objective optimization problem, which is the multi-user observation scheduling problem for agile Earth observing satellites. Hence, the second decoding expression of each acquisition j becomes:

$$Priority_j = \frac{T_{max_L} - T_{min_j}}{T_{max_L}} \times \left[\frac{1 + gene_j}{2} \right] \quad (4)$$

where T_{max_L} is the latest starting time of the last possible acquisition and T_{min_j} is the earliest starting time of acquisition j .

The example of the ideal priority calculation of the second decoding method is shown in Figure 4. It is applied to the multi-user observation scheduling problem for agile Earth observing satellites, which needs to select and schedule four acquisitions, which are acquisitions a, b, c, and d. For this example, the sequence of the acquisitions according to the ideal priority, is b, c, d, and a.

C. Hybrid decoding (HD)

Finally, we propose the third decoding method which is the hybrid method. It combines together the first and the second decoding methods. This hybrid method obtains two solutions from one chromosome. When applying the hybrid decoding, the methods to manage the elite set, must be defined. Three methods are tested for selecting the elite set.

1) *Elite set management - Method 1 (M1)*: Both solutions, obtained by the two decodings, are compared by using the dominance relation in the Pareto sense. If a solution can dominate the other one, the dominant solution is selected to be stored in the set of solutions. Otherwise, one of the

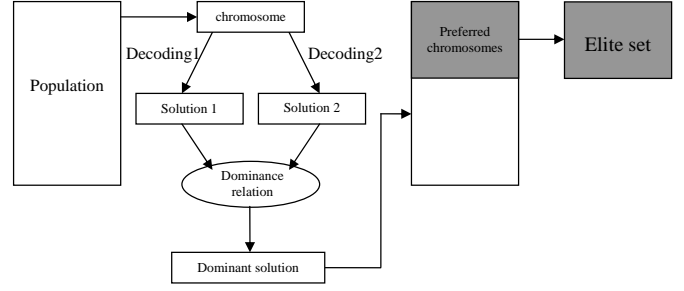


Fig. 5. Elite set management for hybrid decoding - method 1

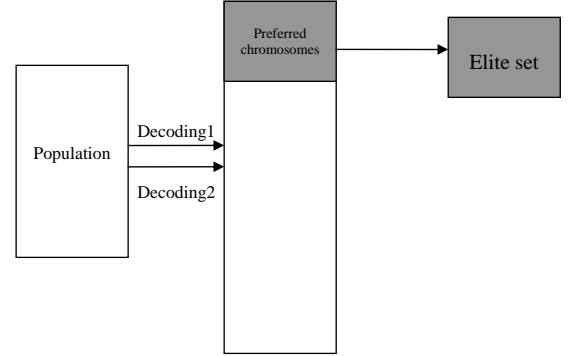


Fig. 6. Elite set management for hybrid decoding - method 2

two solutions is selected randomly. The decoding process is repeated until all chromosomes in the population are decoded. When it finishes, the size of the solution set is equal to p . Then, the p_e solutions are selected to become the elite set by using the same methods with only one decoding. The principle of elite set management - method 1 is shown in Figure 5.

2) *Elite set management - Method 2 (M2)*: All chromosomes in the population are decoded by using the two decoding methods. Two solutions are obtained from the decoding of one chromosome. Both of them are stored in the solution set. Hence, the size of the solution set is equal to $2p$, when all chromosomes from the current population are decoded. Then, the p_e solutions are selected from the solution set to become the elite set. The principle of elite set management - method 2 is shown in Figure 6.

3) *Elite set management - Method 3 (M3)*: Each chromosome in the population is firstly decoded by using the priority equation of basic decoding, and the obtained solution is stored in the first solution set. Similarly, the same chromosome is decoded by using the priority equation of the decoding of gene value with ideal priority combination. Then, the obtained solution from this decoding is stored in the second solution set. When all chromosomes in the population are decoded and the solutions are stored into two solution sets, the selection methods are applied to select p_e solutions for becoming the elite set. Hence, the $p_e/2$ preferred solutions must be chosen from each solution set, as shown in Figure 7.

In the decoding step for solving the multi-user observation scheduling problem for agile Earth observing satellites, the

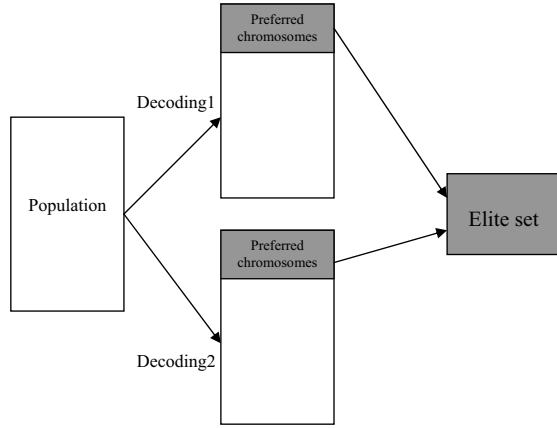


Fig. 7. Elite set management for hybrid decoding

priorities for selecting and scheduling each acquisition are computed depending on the decoding methods as previously presented. Then, the solution, which is the sequence of the selected acquisitions, can be generated. The imperative constraints are verified for each acquisition sequentially according to its priority. Each considered acquisition can be assigned in the sequence, only if the obtained sequence can satisfy all constraints. The flowchart of constraint verification and acquisition assignment is depicted in Figure 8. The example of one solution from the smallest size instance is shown in Figure 9. This instance consists of two strips. Hence the number of random key genes, which are associated with the acquisitions, equals to four. This example shows the solution, which is decoded from the basic decoding (the priority to select and schedule of each acquisition equals to its gene value). This decoding step is used to obtain the sequence of the selected acquisitions and the values of the two objective functions.

IV. COMPUTATIONAL RESULTS

The ROADEF 2003 challenge instances (Subset A) are modified for 4-user requirements. The format of instance names are changed to a_b_c , where a is the number of requests, b is the number of stereo requests, and c is the number of strips.

For the proposed biased random-key genetic algorithm (BRKGA), parameter values of the algorithm were experimentally tuned for our work. The population size of BRKGA is set equal to the length of the random-key chromosome or twice the number of strips. The sizes of the three parts, which are generated to become the population in the next generation, are set in accordance with the recommended values in Table I. The size of the elite set is equal to the number of non-repeating schedules from the nondominated solutions, but it is not over $0.15p$. The size of mutant set is equal to $0.3p$. The probability of elite element inheritance for crossover operation is set to 0.6. In each iteration, the nondominated solutions are stored in an archive. If there is at least one solution from the current population that can dominate some solutions in the archive, the archive will be updated. Therefore, we use the

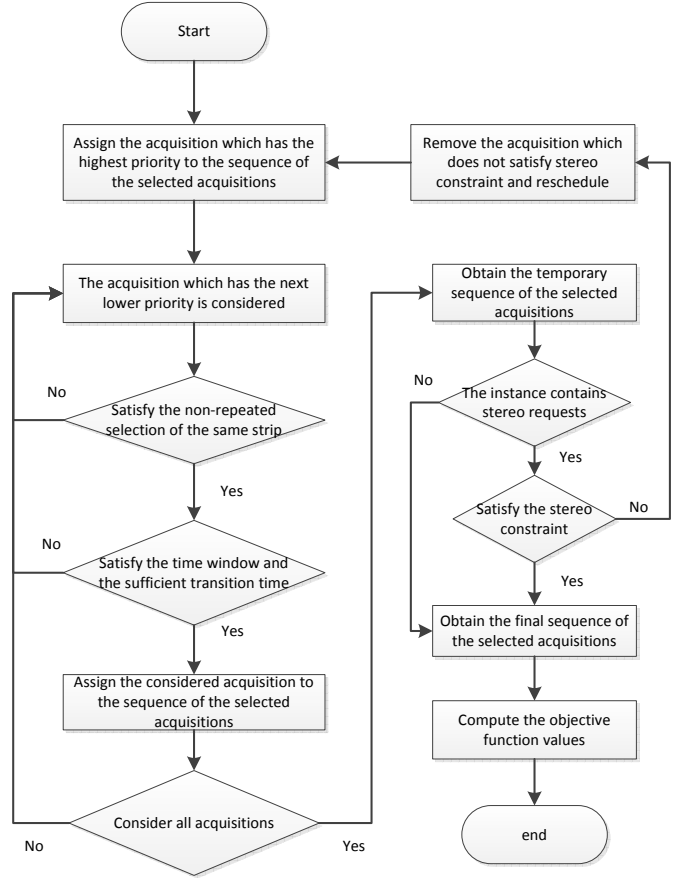


Fig. 8. Flowchart of constraint verification and acquisition assignment

Random-key chromosome	Acquisition0	Acquisition1	Acquisition2	Acquisition3
	0.6984	0.9939	0.6885	0.2509
Sequence of the selected acquisitions	1 2			
Total profit	1.04234e+007			
Maximum profit difference	0			

Fig. 9. Solution example from the modified instance, which needs to schedule two strips

number of iterations since the last archive improvement to be a stopping criterion. We opt for 50 iterations. Moreover, the computation time is used to be the second stopping criterion. It is adapted to the instance size. The iteration of BRKGA will be stopped, when one of the two stopping criteria is satisfied. The algorithm is implemented in C++ and ten runs per instance are tested. The hypervolumes of the approximate Pareto front are computed by using a reference point of 0 for the first objective (maximizing the total profit) and the maximum of the profit summations of each user for the second one (minimizing the profit difference between users). Three elite selecting methods from three efficient algorithms: NSGA-II, SMS-EMOA, and IBEA, are applied to select some solutions to become the elite set. The set of testing instances consists of ten instances. However, the results of the smallest instance (instance 2_0_2)

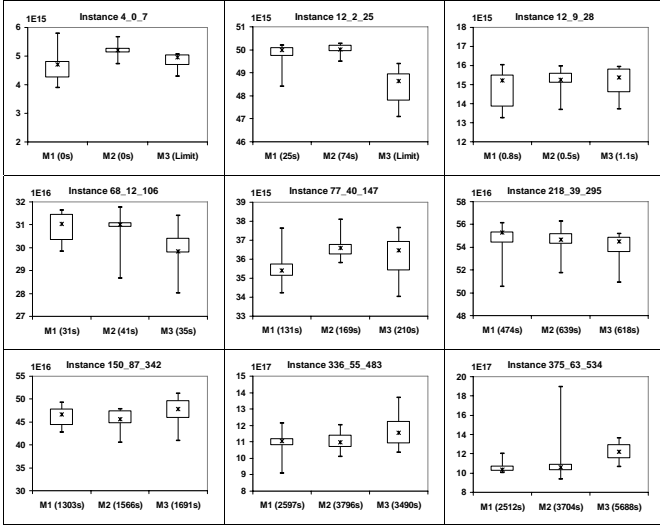


Fig. 10. Comparison of the results of the three methods for management of the elite set for hybrid decoding (M1, M2, and M3) by using the method for elite set selection borrowed from NSGA-II

cannot be reached, when using the population size equal to the length of the chromosome or twice of number of strips, because the population size is too small for generating the new population from the three sets of chromosomes in BRKGA process. Hence, the results of nine instances will be presented in the experimental results.

Firstly, the three methods of elite set management for hybrid decoding (M1–M3) are tested. The results, which are obtained from each method, are compared. The hypervolume values of the approximate Pareto front are computed. The maximum value, the median value, the minimum value, and the interquartile range are displayed in box plot. The box plots and the average computation times associated with the mechanisms of NSGA-II, SMS-EMOA, and IBEA are reported in Figures 10, 11, and 12, respectively.

The results show that the three methods obtain similar solutions regarding the hypervolume values. Each method has advantages in different instances. However, M2 spends more computation time for the large instances, especially, when using the elite set selection method borrowed from IBEA. Furthermore, M3 spends more computation time for the small instances, particularly when using the elite set selection method borrowed from NSGA-II or SMS-EMOA. Therefore, in the sequel only method M1 will be kept to compare the results between the hybrid decoding (HD-M1) and the two single ones (D1 and D2).

Secondly, the three decoding methods (D1, D2, and HD) are tested and the obtained results are compared. The box plots from the three elite set selection methods, which borrowed from NSGA-II, SMS-EMOA, and IBEA, are reported in Figures 13, 14, and 15, respectively. The graph illustrates the box plots of the hypervolume values, and the average computation times are presented.

Most of the results show that the hybrid decoding obtains

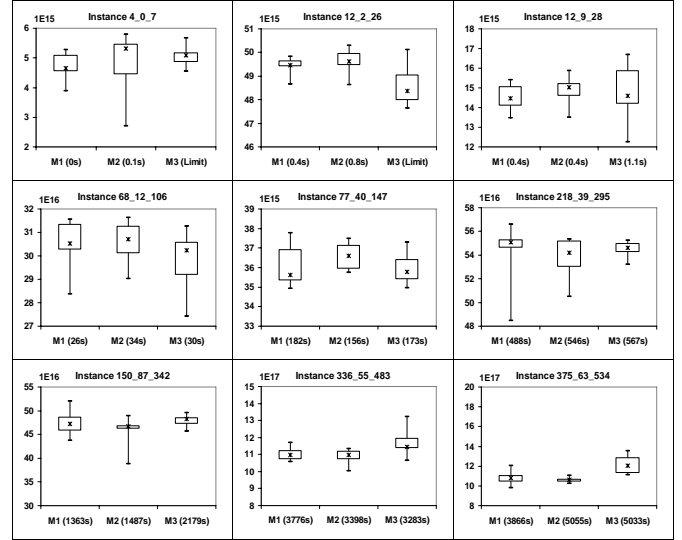


Fig. 11. Comparison of the results of the three methods for management of the elite set for hybrid decoding (M1, M2, and M3) by using the method for elite set selection borrowed from SMS-EMOA

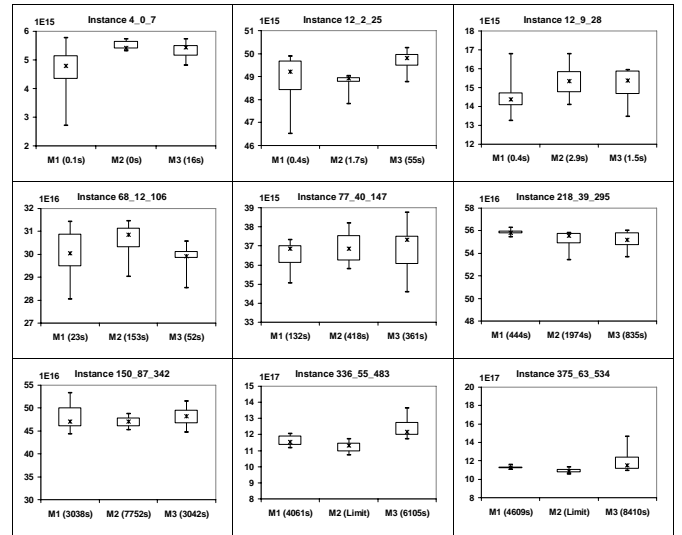


Fig. 12. Comparison of the results of the three methods for management of the elite set for hybrid decoding (M1, M2, and M3) by using the method for elite set selection borrowed from IBEA

the results close to the best ones, when comparing the two single decodings. Indeed, it can preserve the advantages of the two single decodings for all instances. For example, in instance 12_2_26, the first decoding method obtains better results than the second one, thus the hybrid decoding obtains results similar to the first one. For instance 77_40_147, the hybrid decoding obtains results similar to the second decoding, which obtains better results than the first one. Thus, the hybrid decoding method is efficient for solving most of the instances. Compared with D1, it can reduce the range of hypervolume values. This means that the hybrid decoding can provide results with better standard deviations. Moreover, for some

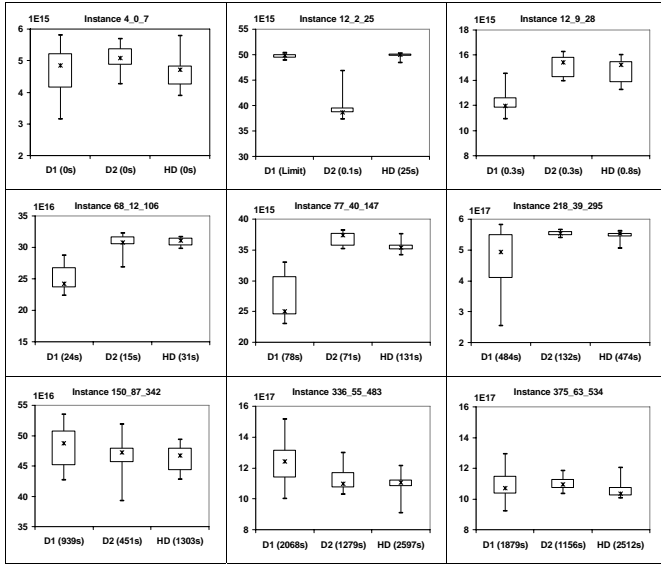


Fig. 13. Comparison of the results of the three decoding methods (D1, D2, and HD-M1) by using the method for elite set selection borrowed from NSGA-II

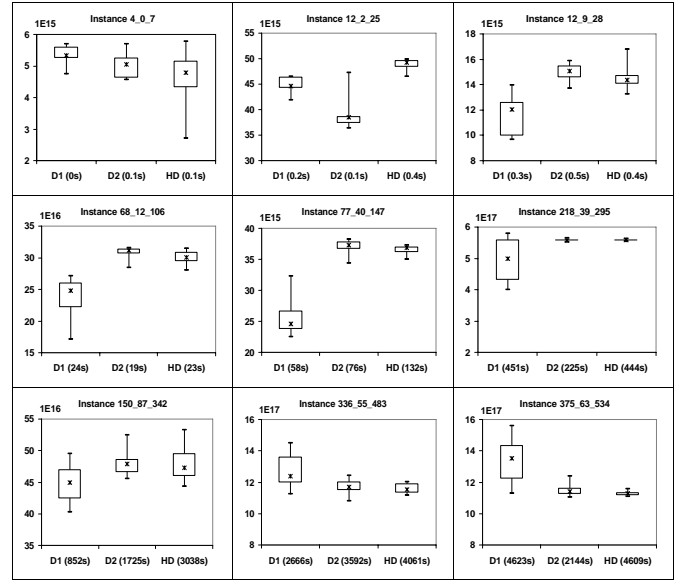


Fig. 15. Comparison of the results of the three decoding methods (D1, D2, and HD-M1) by using the method for elite set selection borrowed from IBEA

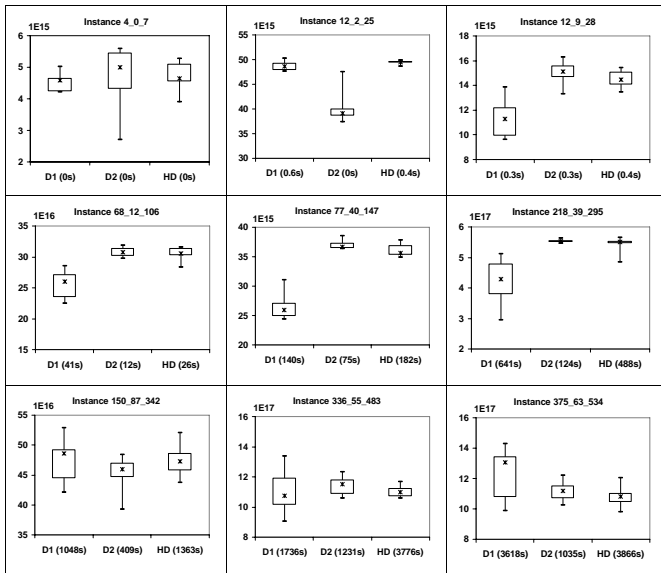


Fig. 14. Comparison of the results of the three decoding methods (D1, D2, and HD-M1) by using the method for elite set selection borrowed from SMS-EMOA

instances where the second decoding entraps in local optima, the hybrid decoding is able to reach the global optimum. Regarding the computation time, the hybrid decoding method spends longer time in each iteration, however it can obtain good solutions in a reasonable computation time, which is limited by the second stopping criterion of BRKGA process.

V. CONCLUSIONS

A biased random-key genetic algorithm or BRKGA is used for solving a multi-objective optimization problem. The BRKGA works on a chromosome encoded as a key vector. The chromosome consists of several genes, which are encoded

by the real values in the interval $[0, 1]$. During each iteration of BRKGA, the chromosomes are decoded to obtain the feasible solutions. A hybrid decoding, which combines two single decodings, is proposed in this paper. Two solutions are obtained from the decoding of one chromosome, when using the hybrid decoding. Thus, the methods for elite set management have to be defined and three methods are tested.

The experiments are conducted on the multi-user observation scheduling problem for agile Earth observing satellites. The requests are required from multiple users. The objectives of this problem are to maximize the total profit and simultaneously minimize the maximum profit difference between users for ensure the sharing fairness. Three elite selecting methods, which are borrowed from NSGA-II, SMS-EMOA, and IBEA, are used for selecting a set of preferred solutions to become the elite set of the population. For the three elite selecting methods, the hypervolume values, which are obtained from two single decodings and the hybrid decoding, are compared. The hybrid decoding can preserve the advantages of the two single decodings, since it obtains results close to the best results of the two single decodings in reasonable computation times. Moreover, it can improve the standard deviation of the hypervolume values and avoid to entrap in local optima. Finally, the hybrid decoding is proper to be applied in BRKGA process for solving multi-objective optimization problems, which need several feasible solutions on the Pareto front.

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