Proc. of the Intl. Conf. on Advances in Civil, Structural and Mechanical Engineering - ACSM 2015.

ISBN: 978-1-63248-039-2 doi: 10.15224/ 978-1-63248-039-2-30

An Improved Nondominated Sorting Multiobjective Genetic Algorithm and Its Application

Xiaoping Zhong, Yan Zhao and Qing Han

***Abstract*—The nondominated sorting genetic algorithm with elitism (NSGA-II) is widely used due to its good performance on solving multiobjective optimization problems. In each iteration of NSGA-II, truncation selection is performed based on the rank and crowding distance of each solution. There are, however, drawbacks in this process. These drawbacks to some extent cause overlapping solutions in the population and have an affection on the spread of nondominated solutions, which reduces the diversity of the obtained solution set. In this paper, 4 causes for generation of the overlapping solutions are investigated firstly. A new technique for alleviating this phenomenon is incorporated to enhance the capability of NSGA-II. The improved algorithm is referred to as NSGA-II+ in this paper. In NSGA-II+, overlapping solutions are removed during the truncation selection from the merged population (which is a combination of parent population and offspring population) after ranking in each iteration. The overlapping solutions and the ones with small crowding distance are removed one by one. The crowding distance is recalculated once a solution is removed. The performance of the improved algorithm is evaluated on four difficult test problems. Then NSGA-II+ is applied to the optimization of a composite wing structure with 2 objectives. Numerical results are reported which demonstrate the effectiveness of NSGA-II+.**

***Keywords*—nondominated sorting genetic algorithm, overlapping solutions, truncation selection, composite wing structure**

I. Introduction

Nondominated sorting genetic algorithm (NSGA) proposed by Srinivas and Deb[1] suffers from the computational complexity $O(MN^3)$ (where M is the number of objectives and N is the population size) and the difficult specifying of the share parameter σ_{sh}. The NSGA-II of Deb et al. [2,3] incorporates a fast nondominated sorting approach with $O(MN^2)$ computational complexity. And the crowding distance is introduced to identify better solutions with the same rank, which eliminates the specifying of the share parameter. These features make NSGA-II a well-known and frequently-used evolutionary multiobjective optimization (EMO) algorithm.

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There are drawbacks during the evaluation of crowding distance and truncation selection of NSGA-II. During the truncation selection those with lower rank and larger crowding distance are chosen as the next parent population. Instead, those with higher rank and smaller crowding distance should be removed. Once a solution is removed, the crowding distance of its neighbor should be reevaluated. And a large number of overlapping solutions are observed in the population at later iterations on many test problems. The crowding distance of an overlapping solution is not always zero. Its crowding distance is larger sometimes. Therefore, overlapping solutions with lower rank can survive and continue to recombine in the next iteration. Overlapping solutions, however, is adverse to the diversity preservation. An improved NSGA-II is proposed to overcome the above drawbacks.

II. NSGA-II

NSGA-II is a fast and elitist multiobjective genetic algorithm in discrete and continuous domain. Simulated binary crossover (SBX)[4,5] operator and polynomial mutation[6] are used for real-valued problems. Mating selection is performed on parent population by binary tournament scheme with replacement. The winners recombine to generate offspring with prescribed probabilities. Truncation selection is conducted to identify a set of solutions from the merged population comprised of parent and offspring population. The ranking and the crowding measure are embedded in the truncation selection. Those selected comprise the next parent population. The process continues until a terminated criterion is met. And a nondominated solution set is obtained. The Schematic of the NSGA-II procedure[7] is given in Fig. 1.

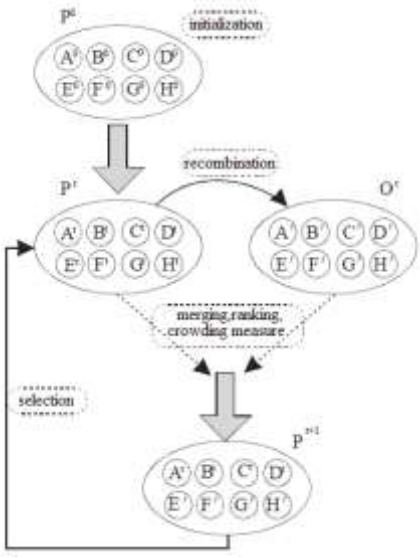

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Figure 1. Schematic of NSGA-II procedure.

A. *Investigate the Generation of Overlapping Solutions*

On many test problems, a lot of overlapping solutions are observed in the population at later iterations. The redundant solutions are adverse to the diversity preservation and the exploration of the design space.

Since the initial population is often generated randomly, the overlapping solutions do rarely emerge at that time and are mainly produced in the recombination and selection phase. Offspring are generated by crossover and mutation of the parent mates with probabilities less than 1.0, say 0.9 for crossover and 1/*n* (*n* is the number of design variables) for mutation. With above crossover probability some offspring come directly from parents without crossover. And mutation maybe skipped on them due to the lower mutation probability. Thus, some offspring are identical to their parents, and overlapping solutions may emerge.

In effect, elitism operator combines the old population with the newly created one and chooses to keep better solutions from the combined population. In other words elitism helps preserve promising building blocks. Each parent should participate in recombination in order to generate new solutions as many as possible. And the crossover probability can reach to 1.0. Even so, some overlapping solutions still exist on experiment. One reason lies in the binary tournament selection with replacement during mating. That mating strategy cause some parent to breed more than once, and some have no chance to breed. To some extent the overlapping solutions can not be avoided.

Another two reasons may lead to overlapping solutions in NSGA-II. The first is SBX and the second truncation selection. Promising solutions can be effectively generated by SBX and polynomial mutation operation for real-valued problems. In case of a single design variable, SBX is a simulation of single point crossover of binary string. In case of more than one design variable, SBX is a simulation of uniform crossover of binary string. A random number belonging to [0,1] is generated in the later case. If the number is less than 0.5, SBX is performed on this design variable. Otherwise, SBX is skipped for this design variable. This process can also lead to overlapping solutions. The less, the number of design variables are, the larger the chance of generating overlapping solutions is. This phenomenon is observed in [7] on test of SCH1. The above 0.5 can be increased to 1.0 to eliminate this chance. But another problem occurs. The SBX mechanism is destroyed. We do test on ZDT4[2,3,8], the experimental results show that the performance of NSGA-II deteriorates when above 0.5 is change to 1.0.

B. *Problems with Truncation Selection*

Truncation selection is performed on the merged population in NSGA-II. Promising solutions are selected into a mating pool to breed. If the number of solutions in the mating pool exceeds the population size, and no overlapping solutions exist, the most crowded solutions should be removed. This kind of removal rule is applicable to solutions of all ranks. And we take the solutions on the nondominated rank (the first rank) as an example to illustrate the detail process.

Nondominated solutions of a two-objective minimization problem are shown in Fig 2. Eight circles denote eight nondominated solutions, and are labeled as A_1, A_2…A_8. Six solutions are to be selected. The crowding distance of A_2 is 2.0, A_6 1.77, and A_7 1.58 following the density estimation of NSGA-II. Only six solutions with larger crowding distance are chosen when truncation selection is performed in NSGA-II. They are A_1, A_2…A_5, A_8.

On the other hand, if the most crowded solution is removed, A_7 is the one because of its smallest crowding distance 1.58. After A_7 is deleted, the crowding distance of A_5 and A_6 should be recalculated. the crowding distance of A_6 is updated to 2.50 that is larger than its old value 1.77. Thus, the next removed solution is A_2 which is now the most crowded one. The left six solutions are A_1, A_3…A_6, A_8 that is different from those selected by NSGA-II.

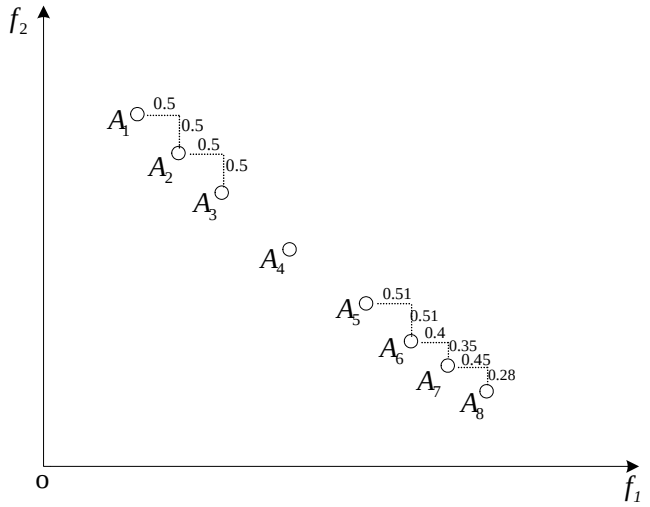

Figure 2. An illustration of truncation selection

A further investigation shows that the distance between A_5 and A_8 is larger than that between A_1 and A_3, which justifies the remaining of A_6 rather than A_2. The selection of A_1, A_3…A_6, A_8 into mating pool will help to increase the chance to generate new solutions at sparse space. And a uniformly spread solutions set could be obtained finally. The above simple illustration demonstrates that the solutions with larger crowding distance may not be correctly identified during the truncation selection in NSGA-II. By removing the most crowded solution one by one instead, this problem can be overcome. And the appropriate solutions can be identified.

III. NSGA-II+

A. *Removal of Overlapping Solutions*

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As stated above, crossover probability can be set to a higher level if elitism is adopted in the algorithm. Thus, the crossover probability is set to 1.0 in the paper..

If truncation selection is directly performed according to the rank and crowding distance of each solution in the merged population as does in NSGA-II, some overlapping solutions will survive to the next iteration. Instead some copies of overlapping solutions should be removed firstly to preserve diversity of the population. We assign rank 1 to solutions in the first front, rank 2 to those in the second front, and so on. The lower front a solution belongs to, the better it is. After identifying all the nondominated solutions (those in the first front) in the merged population, they are copied to a mating pool. And crowding distance of each solution in the mating pool is estimated in objective space.

In case of nondominated solutions exceeds the population size in the mating pool, some overlapping solutions with the smaller values of crowding distance are removed. In this context, only the most crowded overlapping solution is removed. This process continues until the number of left solutions is equal to the population size or no overlapping solutions are remained in the mating pool. Note that the crowding distance of the adjoining solutions should be re-estimated each time a solution is left out. For simplicity it can be reestimated for all the remained solutions of this rank in the mating pool in the implementation.

If the number of nondominated solutions is less than the population size in the mating pool, it is necessary to pick up all the dominated solutions in the second front. And they are copied to the mating pool. If it is not enough yet, those in the following front (the third front) are identified and added to the mating pool, too. This procedure is repeated until the number of solutions in mating pool is not less than the population size. Then the above overlapping solutions' elimination procedure is performed on the solutions in the highest front in the mating pool.

The truncation selection in the following subsection will start if the number of solutions in the mating pool is still more than the population size after removal of the overlapping solutions.

B. *Truncation Selection*

After removal of the overlapping solution, the truncation selection is performed on those in the highest front in the mating pool. The most crowded solutions are removed one by one. Once a solution is left out, the crowding distance of the adjoining solutions should be reestimated. This process continues until the appropriate number of solutions is left. This selection procedure will help to increase the chance to generate new solutions at sparse space.

IV. Structure of NSGA-II+

The flow of NSGA-II+ is described as follows:

(1) Set population size N_{pop}, the crossover probability P_c, the mutation probability P_m, the distribution index η_c for crossover operator, the distribution index η_m for mutation operator, the maximum iteration number t_{max}, and generate the initial population P(0) randomly, set t=0;

(2) Perform mating selection on $P(t)$ with binary tournament scheme. Generate offspring population $O(t)$ by crossover operators with probability P_c;

(3) Perform polynomial mutation on solutions in $O(t)$ with probability P_m;

(4) Create a mixed population $M(t)$ by merging $P(t)$ and $O(t)$. After ranking $M(t)$, start the removal of overlapping solutions as described in subsection 2.1. Then start the truncation selection as described in subsection 2.1 if needed;

(5) If the termination criteria are not met, let $t = t$+1 and go to step (2), otherwise output the obtained solution set.

V. Examples

The performance of NSAG-II+ is evaluate and compared to NSAG-II on two unconstrained and two constrained test problems using the coverage metric C and spacing metric Δ [9,10]. The coverage metric, C, maps the ordered pair (A, B) to the interval [0,1]. The value C(A, B) =1 means that all solutions in B are dominated by A. The opposite, C(A, B) = 0, represents the situation when none of the solutions in B are covered by the set A. Note that always both directions have to be considered, since C(A, B) is not necessarily equal to 1 – C(B, A). In the case that 0 < C(A, B) < 1 and 0 < C(B, A) < 1, we say that neither A dominates B nor B dominates A. The spacing metric, Δ, gauges how evenly the solutions in the obtained nondominated set are distributed in the objective space. The smaller the spacing metric value is, the more evenly distributed the nondominated solutions are. The desired value for this metric is zero, which means that the elements of the set of nondominated solutions are equidistantly spaced.

The running parameters of the two algorithms are as follows: the crossover probability is 1.0, the mutation probability is 1/n (n is the number of design variables), the distribution index η_c=15 for crossover operator, the distribution index η_m = 20 for mutation operator.

A. *Test problems*

Four benchmark problems ZDT4, ZDT6, OSY and TNK from [2,3,8] are used to test the performance of multiobjective optimization algorithm. Among the four, two unconstrained problems are ZDT4 and ZDT6. The other two are constrained problems.

B. *Simulation Results and Discussion*

The results are from 50 independent runs of the two algorithms. Each experiment starts from a randomly generated population. Table 1 shows the mean of the coverage metric C obtained by NSGA-II+ and NSGA-II on the four test problems. For brevity, C(II+, II) is used to denote the coverage metric that nondominated sets obtained by NSGA-II+ dominates those of NSGA-II, C(II, II+) denotes the coverage metric that nondominated sets obtained by NSGA-II

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dominates those of NSGA-II+. And Δ(II+) stands for the spacing metric of nondominated sets obtained by NSGA-II+, Δ(II) denotes that of NSGA-II.

TABLE I. MEAN OF THE COVERAGE METRIC *C*

	ZDT4	***ZDT6***	***OSY***	***TNK***
C(II+, II)	0.342000	0.483800	0.222800	0.160800
C(II, II+)	0.204000	0.037800	0.139400	0.117000

TABLE II. MEAN OF THE SPACING METRIC Δ

	ZDT4	***ZDT6***	***OSY***	***TNK***
Δ(II+)	0.004807	0.004905	0.966510	0.004958
Δ(II)	0.010031	0.002980	1.235110	0.008280

From table 1 and table 2, we can see that NSGA-II+ performs better on ZDT4, ZDT6, OSY and TNK in terms of coverage metric. As for spacing metric, NSGA-II+ gets better spread of nondominated solutions on the four problems, too. We show the nondominated solutions obtained by a certain run on ZDT4, ZDT6, OSY and TNK in fig. 3, fig. 4, fig. 5 and fig. 6.

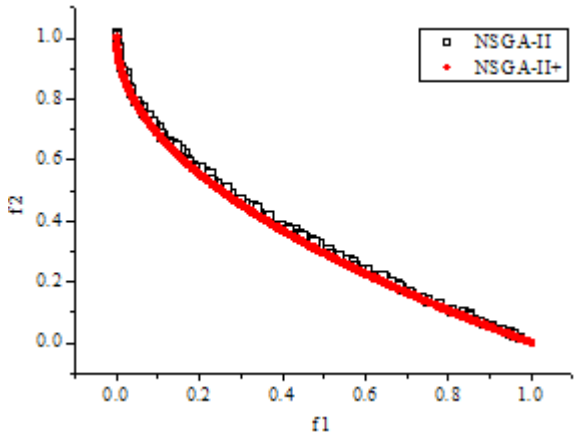

Figure 3. Nondominated solutions on ZDT4

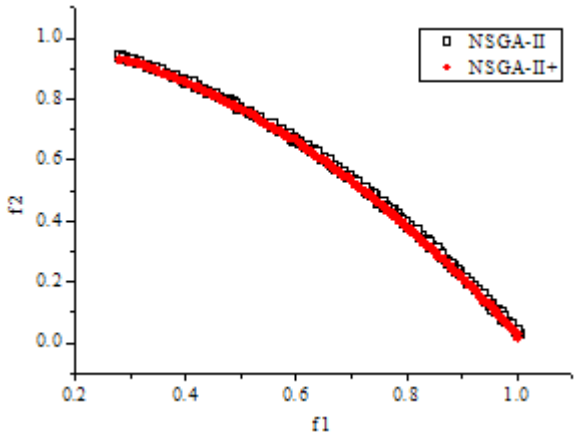

Figure 4. Nondominated solutions on ZDT6

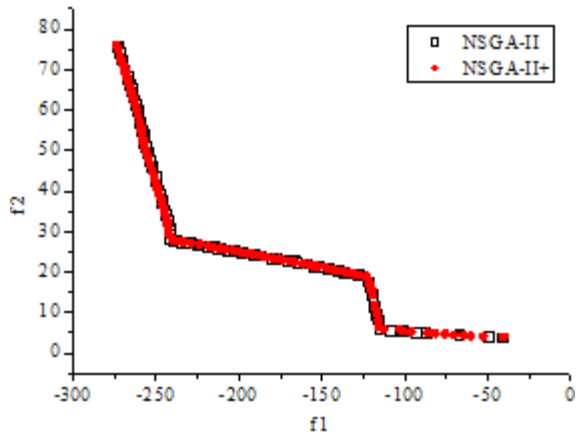

Figure 5. Nondominated solutions on OSY

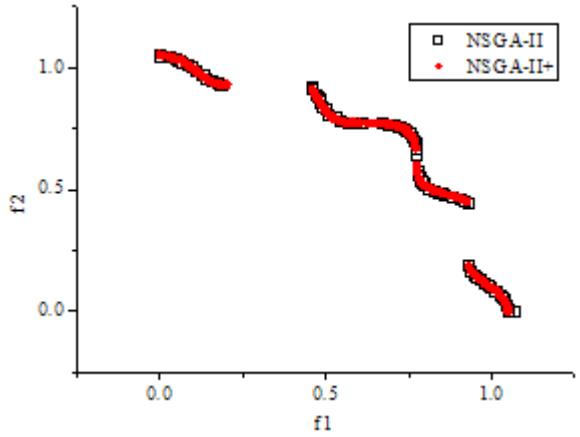

Figure 6. Nondominated solutions on TNK

We perform additional experiments by increasing the number of maximum generation to 500 with other parameters fixed. Table 3 and table 4 show the coverage metric and spacing metric respectively.

TABLE III. MEAN OF THE COVERAGE METRIC *C*

	ZDT4	***ZDT6***	***OSY***	***TNK***
C(II+, II)	0.062000	0.019600	0.235400	0.175600
C(II, II+)	0.053600	0.009600	0.088600	0.059200

TABLE IV. MEAN OF THE SPACING METRIC Δ

	ZDT4	***ZDT6***	***OSY***	***TNK***
Δ(II+)	0.002392	0.002246	1.179084	0.003653
Δ(II)	0.006868	0.008206	1.354876	0.008232

After 500 generations, NSGA-II+ outperforms NSGA-II on OSY, TNK and ZDT6, and is competitive with NSGA-II on ZDT4 in terms of coverage metric. And NSGA-II+ gets better spread of nondominated solutions on 4 test problems. The nondominated solutions of ZDT4 and ZDT6 on a certain run

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are shown in Fig. 7 and Fig. 8 respectively. There are axial translations for clarity in these two figures. It can be seen that the nondominated solutions set obtained by NSGA-II+ are more evenly spread than those of NSGA-II.

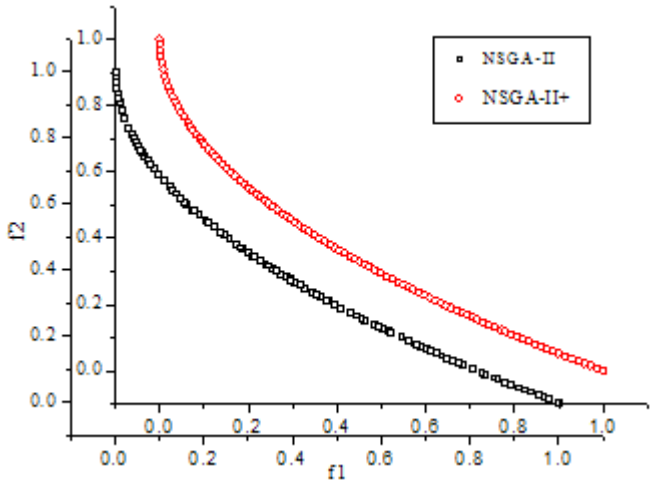

Figure 7. Nondominated solutions on ZDT4 after 500 generations

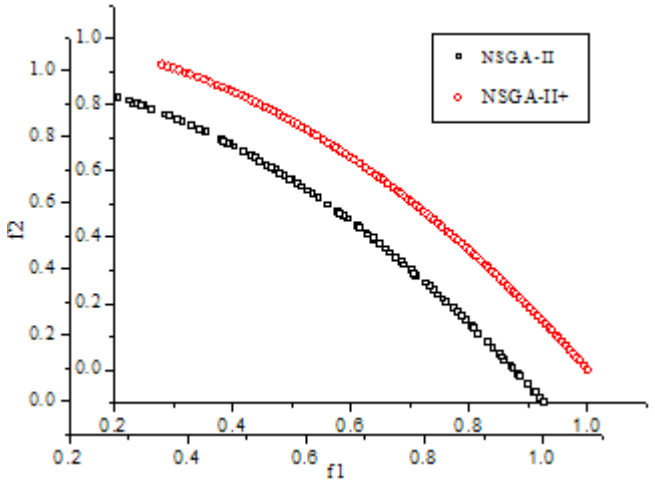

Figure 8. Nondominated solutions on ZDT6 after 500 generations

Further additional experiments are run by increasing the number of maximum generation to 800 with other parameters fixed. Table 5 and table 6 show the coverage metric and spacing metric respectively.

TABLE V. MEAN OF THE COVERAGE METRIC *C*

	ZDT4	***ZDT6***	***OSY***	***TNK***
C(II+, II)	0.031200	0.018800	0.218400	0.187400
C(II, II+)	0.028200	0.012800	0.078400	0.041600

TABLE VI. MEAN OF THE SPACING METRIC *Δ*

	ZDT4	***ZDT6***	***OSY***	***TNK***
Δ(II+)	0.002395	0.002203	1.210968	0.003227
Δ(II)	0.007111	0.008482	1.388401	0.008170

From table 5 and table 6, NSGA-II+ outperforms NSGA-II on the four test problems in terms of the two metrics after 800 generations.

NSGA-II+ needs more CPU-time cost than NSGA-II due to the removal of overlapping solutions and truncation selection scheme. For a single run on Intel Q6600 2.40GHz PC with 4G memories, the time cost is given in the following table.

TABLE VII. TIME COST OF THE TWO ALGORITHMS

		ZDT4	***ZDT6***	***OSY***	***TNK***
NSGA-II+	200	0.62	0.64	0.67	0.58
	500	1.76	2.11	1.77	1.45
	800	2.92	4.28	2.84	2.32
NSGA-II	200	0.56	0.58	0.57	0.53
	500	1.42	1.42	1.42	1.32
	800	2.23	2.23	2.21	2.08

In the above table, 200, 500 and 800 are the generations, and the other digits are the time cost in seconds. Although NSAG-II+ is more time consuming, the additional time costs can be negligible in engineering applications where the CPU time is mainly consumed by function evaluations (such as finite element analysis of a structure).

C. *Optimization of a Composite Wing Structure*

Fig. 9 shows the wing structure of a high altitude long endurance UAV. The root chord and tip chord are 1.372m and 0.494m respectively. The dual spars wing structure has a semi-span of 11.665m. The front and rear spars are located at 34 % and 67 % along the root chord respectively. There are 28 ribs and the spacing between every two adjacent ribs is about 700 mm. The top and bottom skins are made of carbon fiber. The fibers of composite material are oriented at 0°, - 45°, + 45°and 90° to reduce manufacturing costs. For simplicity the thickness of each orientation is identical. The material of the spars are 30CrMnSiA. The stringers are made of LY12.

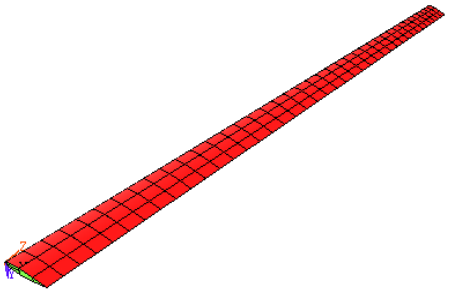

Figure 9. Shape of the wing structure

There are nine design variables x_1, x_2, …, x_9, among which x_1, x_2, …, x_6 are the thicknesses of the skin from root to tip and x_7, x_8 and x_9 are the thicknesses of the spar web from root to

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tip. The objectives of optimization design are to minimize the mass and the maximum vertical displacement of wing structure under a certain flight condition. The structural analyses of the wing structure are conducted by Aeronautic and Astronautics Structure Analysis (AASA) Software. The optimization formulation is written as:

$$\begin{aligned} \min \quad & f_1 = W(X) \\ & f_2 = \delta_{\max}(X) \\ \text{s.t.} \ & \sigma_i \le [\sigma_i] \qquad i=1,2,3,4 \\ & \delta_{\max} \le 1.5 \\ & x_{i+1} \le x_i \qquad i=1,\ldots,5 \\ & x_{i+1} \le x_i \qquad i=7,8 \\ & x_{i,\min} \le x_i \le x_{i,\max} \qquad i=1,\ldots,9 \end{aligned} \tag{1}$$

Here, $[\sigma_i]$ is the allowable stress for different elements, W represents the structure mass, $\delta_{\max}$ denotes the maximum vertical displacement of the wing structure, $x_{i,\max}$ and $x_{i,\min}$ are upper and lower bounds on each design variable. And $x_{i,\min}$ =1.2mm, $x_{i,\max}$=12mm, i=1,…, 9.

After running 150 generations with population size 100, the crossover probability 1.0, the mutation probability 1/9, the distribution index η_c=15 for crossover operator, the distribution index η_m = 20 for mutation operator, the obtained nondominated solutions set is shown in Fig. 10. it can be seen that a very evenly distributed set is found.

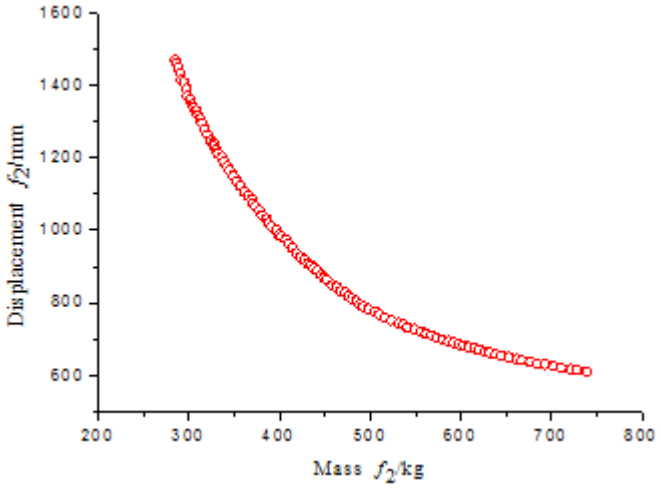

Figure 10. Nondominated solutions in objective space

VI. Conclusions

(1) 4 causes for the generation of overlapping solutions in NSGA-II are investigated.

(2) A technique for overcoming drawbacks during the evaluation of crowding distance and truncation selection and alleviating the problem of overlapping solutions is incorporated to improve NSGA-II.

(3) The performance of the improved algorithm NSGA-II+ is evaluated on four difficult test problems. The simulation results reveal that NSGA-II+ can approximate the true Pareto-optimal front closely and get a uniformly spread of nondominated solution set than NSGA-II.

(4) NSGA-II+ is applied to the optimization of a composite wing structure. A widely spread and uniformly distributed nondominated solution set is obtained.

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