Enhancing ε-Sampling in the AεSεH Evolutionary Multi-Objective Optimization Algorithm

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Abstract: AεSεH is one of the evolutionary algorithms used for many-objective optimization. It uses ε-dominance during survival selection to sample from a large set of non-dominated solutions to reduce it to the required population size. The sampling mechanism works to suggest a subset of well distributed solutions, which boost the performance of the algorithm in many-objective problems compared to Pareto dominance based multi-objective algorithms. However, the sampling mechanism does not select exactly the target number of individuals given by the population size and includes a random selection component when the size of the sample needs to be adjusted. In this work, we propose a more elaborated method also based on ε-dominance to reduce randomness and obtain a better distributed sample in objective-space to further improve the performance of the algorithm. We use binary MNK-landscapes to study the proposed method and show that it significantly increases the performance of the algorithm on non-linear problems as we increase the dimensionality of the objective space and decision space.

1 INTRODUCTION

Many real-world problems require that multiple objective functions be optimized simultaneously. Multi-objective evolutionary algorithms (Deb, 2001; Coello et al., 2002) (MOEAs) are a class of algorithms to solve these problems. MOEAs' initial success brought new challenges as their use became widespread in numerous application domains.

There are several important areas of ongoing research. Among them, the design of MOEAs to search effectively and efficiently on problems with larger search spaces, many objective functions, and robustness to distinct shapes of the Pareto front and distinct geometries of the Pareto set. Performance scalability of the algorithm when facing increased complexity of the search space, defined in terms of interacting variables, is also a challenge to state-of-art MOEAs and an active research area.

This work deals mainly with many objective problems and increased complexity due to variable interactions. It's known that the performance of MOEAs decreases as the objective space dimensionality increases (von Lücken et al., 2019). Several research efforts based on different approaches aim to improve evolutionary algorithms for many-objective optimization. These include decomposition into several single objective problems, extensions of Pareto dominance, and incorporation of performance indicators. It's also known that MOEAs' performance drops when variable interactions increase.

In this work, we focus on an algorithm based on an extension of Pareto dominance, AεSεH (Aguirre et al., 2013; Aguirre et al., 2014), and investigate deeply its survival selection mechanism aiming to improve its performance on many-objective problems with varying degrees of variable interactions.

AεSεH includes ε-dominance(Laumanns et al., 2002) for survival selection and parent selection. During survival selection, the algorithm samples from a large set of non-dominated solutions to reduce it to the required population size. The sampling mechanism works to suggest a subset of solutions spaced according to the ε parameter of ε-dominance, which boost the performance of the algorithm in many-objective problems compared to Pareto dominance based multi-objective algorithms.

However, the sampling mechanism does not select exactly the target number of individuals given by the

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population size. In most cases there will be a surplus or shortage of non-dominated individuals and an adjustment to either cut-off or add non-dominated individuals is requiered. This adjustment process after sampling is done by random selection in the conventional algorithm. In this work, we improve the adjustment process by adding another step based on ε-dominance to reduce randomness and obtain a better distributed sample in objective-space to further improve the performance of the algorithm.

We use MNK-landscapes (Aguirre and Tanaka, 2007) as benchmark problems. MNK-landscapes are binary multi-objective maximization problems, which can be randomly generated by arbitrarily setting the number of objectives M, the number of design variables N, and the number of interacting variables K for each of the variables of the problem. We conduct experiments on landscapes with $M = \{4,5,6,7\}$ objectives, $N = \{100,300,500\}$ bits and $K = \{5,6,10,15,20\}$ epistatic bits. We use various metrics to evaluate the non-dominated solutions found and show that the proposed method significantly increases the performance of the AεSεH algorithm on non-linear problems with increased dimensionality of the objective space and decision space. Furthermore, an experimental comparison with MOEA/D (Zhang and Li, 2007), a well known MOEA, is included for reference.

2 ADAPTIVE ε-SAMPLING AND ε-HOOD (AεSεH)

AεSεH is a multi- and many-objective evolutionary algorithm that includes mechanisms based on ε-dominance for survival selection and parent selection. For survival selection, it uses adaptive ε-Sampling to expand the dominance region and sample the non-dominated solution set, which becomes larger as the number of objectives increases. On the other hand, Adaptive ε-Hood is used to create neighborhoods in objective space. When generating offspring, the parents are selected from the same neighborhood.

2.1 ε-Dominance

In AεSεH, the ε-transformation function is applied to the vector of evaluated values $\boldsymbol{f}(\boldsymbol{x})$ of a solution $\boldsymbol{x}$ to transform it into $\boldsymbol{f}'(\boldsymbol{x})$. Considering a maximization problem, we say $\boldsymbol{x}$ ε-dominates $\boldsymbol{y}$ when the vectors of transformed values $\boldsymbol{f}'(\boldsymbol{x})$ and evaluated values $\boldsymbol{f}(\boldsymbol{y})$ of another solution $\boldsymbol{y}$ satisfy the following conditions.

$$\begin{array}{ll} \boldsymbol{f}(\boldsymbol{x}) \mapsto^{\varepsilon} \boldsymbol{f}'(\boldsymbol{x}) & \\ \forall i \in \{1,\cdots,M\} \quad f_i'(\boldsymbol{x}) \geq f_i(\boldsymbol{y}) & \wedge \\ \exists i \in \{1,\cdots,M\} \quad f_i'(\boldsymbol{x}) > f_i(\boldsymbol{y}), & \end{array} \quad (1)$$

where $\boldsymbol{f}(\boldsymbol{x}) \mapsto^{\varepsilon} \boldsymbol{f}'(\boldsymbol{x})$ is a transformation function controlled by the parameter ε.

2.2 ε-Sampling

In elitist multi-objective evolutionary algorithms survival selection is typically performed after joining the parent and offspring populations. The number of non-dominated solutions $|F_1|$ in this joined population rapidly surpasses the population size $|P|$, particularly when the number of objectives is larger than 3. When this occurs, the surviving population is a subset of the non-dominated set of solutions F_1. ε-Sampling is a method designed to obtain a well distributed sample of non-dominated solutions from F_1 for the next generation. In the following we explain the process with more detail.

1. The individuals in F_1 with the largest and smallest evaluation values in each objective are selected for survival, added to the ε-sampled front F_1^{ε} and deleted from F_1.
2. One individual $\boldsymbol{x}$ is randomly selected from F_1, and $\boldsymbol{f}(\boldsymbol{x})$ is transformed to $\boldsymbol{f}'(\boldsymbol{x})$ by the ε-transformation function using the parameter ε_s. We eliminate from F_1 the solutions that are ε-dominated by $\boldsymbol{x}$ and add them to a subpopulation of discarded solutions D. Move $\boldsymbol{x}$ to the first ε-front F_1^{ε}.
3. Step 2 is repeated until F_1 is exhausted.
4. If $|F_1^{\varepsilon}|$ is less than the population size $|P|$ then $|P| - |F_1^{\varepsilon}|$ individuals are randomly selected from the subpopulation of discarded solutions D and added to F_1^{ε}. On the other hand, if $|F_1^{\varepsilon}|$ is larger than $|P|$ then $|F_1^{\varepsilon}| - |P|$ individuals are randomly removed from F_1^{ε}.

The above operations are used to select parent individuals well distributed in objective space.

2.3 ε-Hood

In AεSεH, ε-Hood is used to divide the parent population P in neighborhoods in the objective space, and mating partners for recombination are determined within the neighborhoods (Aguirre et al., 2013; Aguirre et al., 2014). ε-Hood uses a different parameter ε_h than ε-Sampling to generate neighborhood populations based on ε-dominance.

2.4 ε-Transformation Function

In this paper, MaxMedian is used as the ε-transformation for each objective function as shown below.

$$f_i'(\boldsymbol{x}) = f_i(\boldsymbol{x}) + (\varepsilon \times (max\,\{f_i(\boldsymbol{x}) : \boldsymbol{x} \in P\} - median\,\{f_i(\boldsymbol{x}) : \boldsymbol{x} \in P\})) \quad (2)$$

Here, the ε-dominant region is determined by adding to the fitness value ε multiplied by the difference between the maximum and median values of the *i*-th function.

2.5 Adaptive Changes in ε

The parameters ε_s of ε-Sampling is changed adaptively at each generation depending on the size of the set of non-dominated solution sampled by ε-Sampling NS (before the adjustment) and the population size $|P|$.

$$\begin{aligned} &if\ \ NS > |P| \\ &\quad \Delta \leftarrow min(\Delta \times 2, \Delta max) \\ &\quad \varepsilon_s \leftarrow \varepsilon_s + \Delta \\ &if\ \ NS < |P| \\ &\quad \Delta \leftarrow max(\Delta \times 0.5, \Delta min) \\ &\quad \varepsilon_s \leftarrow max(\varepsilon_s - \Delta, 0.0) \end{aligned} \quad (3)$$

In this paper, the initial values of ε_s and Δ are set to $\varepsilon_{s0} = 0.0$, $\Delta_0 = 0.005$, Δ to $\Delta_{max} = 0.1$, $\Delta_{min} = 0.0000001$.

To adapt ε_h for ε-Hood we follow a similar procedure, comparing the created number of neighborhoods with a desired number specified by the user (Aguirre et al., 2013).

3 AεSεH SHORTCOMING

ε-Sampling does not select exactly the target number of individuals from the set of non-dominated solutions. In most cases there will be a surplus or shortage of individuals and an adjustment to either cut-off or add individuals will be done by random selection to achieve the target number of individuals (section 2.2, Step 4). To illustrate this, after ε-Sampling is performed, the degree of random selection is checked by actually solving MNK-landscapes test problem. The parameters given to the MNK-landscapes and evolutionary algorithm are shown in Table 1 and Table 2. For each value of M, the same MNK-landscape is solved 30 times from different random initial populations. Two-point crossover and bit-flip mutation are used as operators.

Table 1: Parameters of MNK-landscapes.

Parameters	Value
Number of Objectives M	4, 5, 6, 7
Number of Variables N	100
Number of Interacting Variables K	5
Variables Interaction	Random

Table 2: Parameters of EA.

Parameters	Value
Generations G	10,000
Population Size $|P|$	200
Mutation Ratio P_m	$1/N$

Figure 1 shows the number of non-dominated individuals before and after ε-Sampling, averaged over 30 trials for each generation. As expected, note that the number of pre-sampled non-dominated solutions increased with the dimensionality of the objective space. Looking at the difference between population size and the number of solutions after sampling, note that the application of ε-Sampling resulted in the random selection of less than 25 individuals for four objectives and approximately 50 individuals for five and more objectives. From the above, it can be seen that there is always a random part in the selection of surviving individuals by ε-Sampling, which increases with the number of objectives. In the problem set up for this experiment, this increase in random selection is particularly noticeable when the number of objectives increased from four to five.

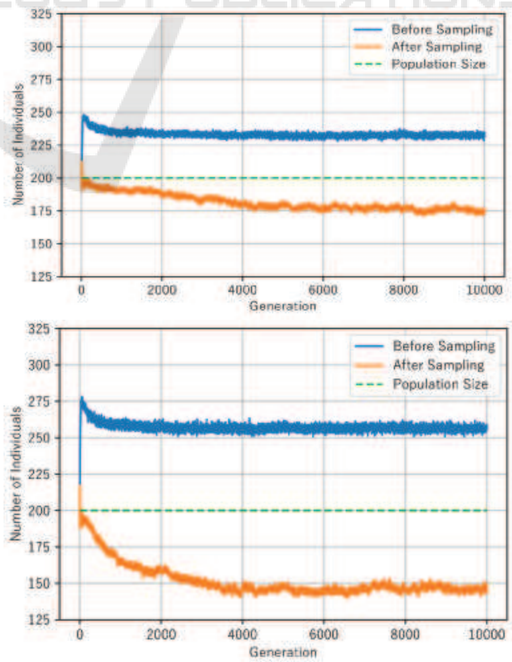


Figure 1: Average number of individuals before and after ε-Sampling. Top 4 objectives, bottom 5 objectives.

It is likely that the individuals randomly selected may disrupt the adequately spaced populations obtained by ε-Sampling. In the next section, we propose a method that aims to enhance ε-Sampling by selecting all individuals appropriately spaced.

4 PROPOSED METHOD

4.1 Reducing Randomness in Survival Selection

As a method to reduce the random selection in ε-Sampling, we consider applying ε-dominance again after ε-Sampling to a reference subpopulation of non-dominated solutions (explained with detail in section 4.2). In this case, a different ε-transformation function is used with a new ε, in addition to the expansion ratio ε_s adapted throughout all the generations in ε-Sampling. The new ε is computed by estimating the mean distance in objective space of the top-rating individuals. Several iterations of sampling over increasingly smaller reference subpopulations, resetting ε appropriately, are repeated until the target number of individuals is reached. This method is expected to achieve better uniformity in the selected sample than the conventional method.

In the following we deatil the main steps of the proposed method. The procedure receives a reference set of solutions R from which a target number N_S must be sampled, i.e. $|R| - N_S$ solutions must be deleted from R. It returns a sample $S \in R$ of size $|S| = N_S$.

1. Set the iteration counter $k \leftarrow 1$ and the maximum number of iterations T. Also, set the initial sampling population $R_k \leftarrow R$ and save its size for reference $N_R \leftarrow |R|$.
2. Set a base expansion value u_{ki} for each one of the M objective functions, $\boldsymbol{u}_k \leftarrow (u_{k1}, \cdots, u_{ki}, \cdots, u_{kM})$ according to the distribution of R_k. Set the sample to empty, $S_k \leftarrow \varnothing$. Set the set of discarded solutions to empty, $D_k \leftarrow \varnothing$.
3. Select one solutiom $\boldsymbol{x}$ randomly from R_k and transform its vector of fitness values $\boldsymbol{f}(\boldsymbol{x})$ to $\boldsymbol{f}^{'}(\boldsymbol{x})$ using $\boldsymbol{u}_k$ and ε_k. Use the $\boldsymbol{f}^{'}(\boldsymbol{x})$ vector to compute ε-dominance between $\boldsymbol{x}$ and the other solutions in R_k. Remove solutions in R_k that are ε-dominated by $\boldsymbol{x}$ and add them to the set D_k of discarded solutions. Remove $\boldsymbol{x}$ from R_k and add it to the set S_k of sampled solutions.
4. Repeat Step 3 if $R_k \neq \varnothing$ (not empty). Otherwise, continue with Step 5.
5. If $|S_k| > N_S$ and $k < T$ then resample from S_k; that is, increase the iteration counter $k \leftarrow k+1$, set the new current sampling population $R_k \leftarrow S_{k-1}$. Update the expansion rate $\varepsilon_k \leftarrow \varepsilon_{k-1} \times \Delta$ and repeat from Step 2. Otherwise, continue to Step 6.
6. If the sample size is not exactly equal to the number required then adjust the sample size randomly. That is, if $|S_k| > N_S$ eliminate randomly $|S_k| - N_S$ solutions from S_k. Otherwise, if $|S_k| < N_S$, select randomly $N_S - |S_k|$ solutions from the current set of discarded solutions D_k and add them to S_k.
7. Return S_k

The base expansion value u_{ki} at the k-th iteration of the procedure for the i-th fitness function is computed as shown in (4) below.

$$u_{ki} = (max\,\{f_i(\boldsymbol{x}) : \boldsymbol{x} \in R_k\} - median\,\{f_i(\boldsymbol{x}) : \boldsymbol{x} \in R_k\})/(\frac{n_k}{2}+1) \tag{4}$$

where n_k is the number of individuals in the sampling population R_k, max_k and $median_k$ are the maximum and median values in the i-th objective function computed from R_k. The ε-transformation function at the k-th iteration to expand the i-th fitness value of the solution is as shown in (5) below.

$$f_i'(\boldsymbol{x}) = f_i(\boldsymbol{x}) + u_{ki} \times \varepsilon_k, \tag{5}$$

where u_{ki} is the base expansion value and ε_k is the expansion rate.

As mentioned above, the expansion rate ε_k is updated at each iteration k of the procedure as shown in (6) below.

$$\begin{aligned} \varepsilon_k &= \varepsilon_{k-1} \times \Delta \\ \varepsilon_0 &= 1 \\ \Delta &= 1.05, \end{aligned} \tag{6}$$

where the constat $\Delta > 0$ works to increase ε_k at each iteration to prevent the number of iterations from becoming too large.

Note that for the base expansion u_{ki} in (4) we use a value slightly smaller than the average distance between the top-rating individuals in the i-th objective. This means that the individuals eliminated by ε-dominance when $\varepsilon_k = 1$ are those whose inter-individual distance in objective space is closer than the mean of the top-rating individuals.

In this paper, experiments are conducted with the maximum number of iterations $T = 100$. Regarding the time complexity of the proposed method, the lower bound is 0 (when the sample size given by ε-Sampling equals the population size) and the upper bound is given by $|R|^2 \times T$. Box plots of the actual number of iterations $k < T$ required by the

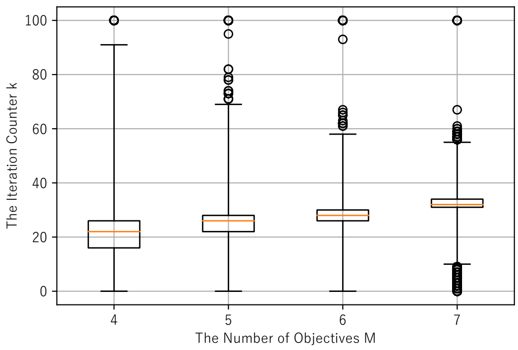
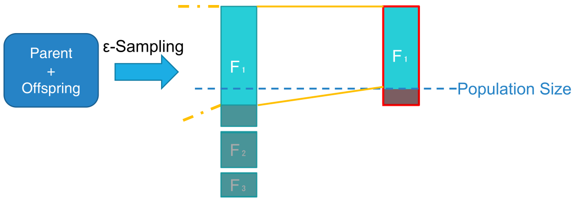
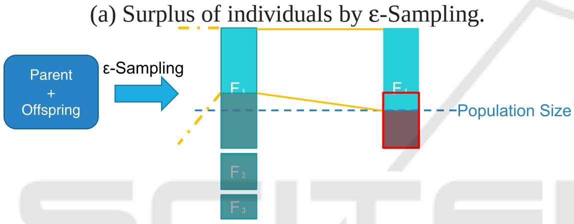


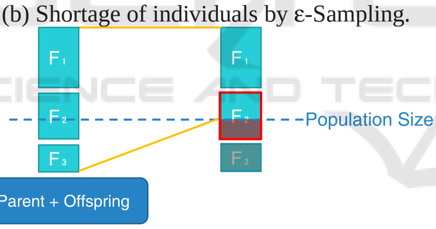
Figure 2: The iteration counter k for each objectives.



(a) Surplus of individuals by ε-Sampling.



(b) Shortage of individuals by ε-Sampling.



(c) Application to lower front.

Figure 3: Cases where the proposed method will be used.

proposed method are shown in Figure 2 for $M = \{4, 5, 6, 7\}, N = 100$ and $K = 5$ computed over 10,000 generations and 30 runs of the algorithm. Note that the median k falls between 20 and 30 iterations.

4.2 Cases in Which the Proposed Method Will be Used

Depending on the number of individuals after ε-Sampling is performed, the proposed method can be applied to the three different cases illustrated in Figure 3 and listed below.

4.2.1 Selection in Case of Surplus

If the number of individuals sampled by ε-Sampling exceeds the target population size, the proposed method is performed on the sample provided by ε-Sampling as shown in Figure 3a. Then, the sample returned by the proposed method becomes the population for the next generation.

4.2.2 Selection in Case of Shortage

If the number of individuals sampled by ε-Sampling is less than the target number, the proposed method is performed on the sub-population of non-dominated individuals initially discarded by ε-Sampling as shown in Figure 3b. Then the sample provided by ε-Sampling and the one returned by the proposed method are joined to form the population for the next generation.

4.2.3 Selection in Lower Front

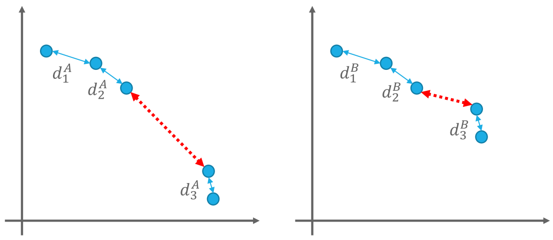
If the number of individuals in the top front is less than the target number, ε-Sampling is not performed. In this case, the top fronts are allowed to survive, and the proposed method is performed on the last front that overflowed the size of the surviving population as shown in Figure 3c. The sample returned by the proposed method is joined to the top fronts to form the population for the next generation.

5 EXPERIMENTAL METHOD AND EVALUATION INDICATORS

5.1 Experimental Method

To examine in detail the effects on solution search by the proposed method, we first solve MNK-landscapes (Aguirre and Tanaka, 2007) varying M from 4 to 7 fixing $N = 100$ and $K = 5$ and starting from 30 initial populations generated with different seeds. The parameters and other conditions used in the experiments are the same as those used in Table 1 and Table 2. Next, we perform experiments varying $N = \{100, 300, 500\}$ and $K = \{5, 6, 10, 15, 20\}$.

In order to objectively evaluate the proposed method, we also compare the results with those obtained by MOEA/D (Zhang and Li, 2007), a representative decomposition based multi-objective evolutionary algorithm often applied for many-objective optimization. In this experiment, the scalarization function of MOEA/D is Tchebycheff, which is suitable for



(a) Population A (b) Population B

Figure 4: Example of populations with equal *SP*.

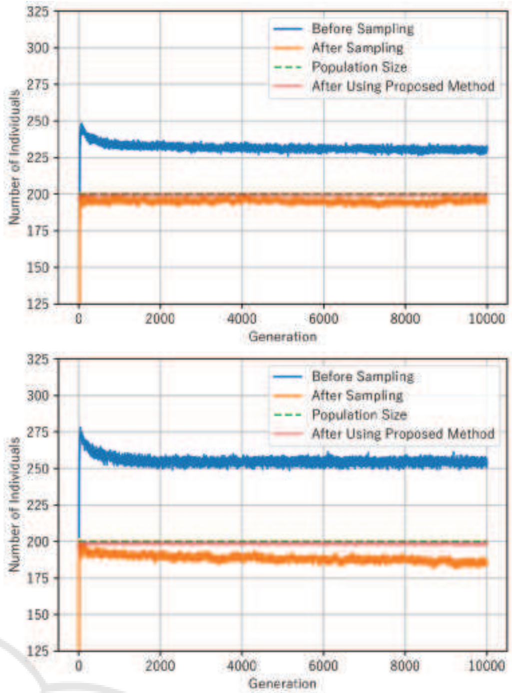


Figure 5: Population averages before and after ε-Sampling and after applying the proposed method. $N = 100, K = 5$, top 4 objectives, bottom 5 objectives.

nonlinear discrete problems, and the neighborhood size is set to the commonly used value of 20.

The evaluation indexes shown in the next section are used to evaluate the sets of solutions found by the algorithms.

5.2 POS Evaluation Indicators

In this study, to evaluate the Pareto optimal solutions set (POS) obtained by the optimization algorithm, we use the Hypervolume (*HV*) (Zitzler, 1999; Fonseca et al., 2006). To validate the features of the obtained POS, we also use the Coverage-metric (C-metric), Overall Pareto Spread (*OS*), Spacing (*SP*), and Distribution Metric (*DM*) (Audet et al., 2021; Zheng et al., 2017).

Note that the distribution of solutions may cause problems in the calculation of *SP*. Consider two populations that satisfy $(d_1^A, d_2^A, d_3^A) = (d_1^B, d_2^B, d_3^B)$ as shown in Figure 4. Note that these two populations clearly have different homogeneity, but when looking at the distance d_i to the nearest solution used to calculate *SP*, they have exactly the same value. That is, *SP* calculated from these values will be exactly the same. Thus, large distances between multiple neighborhood groups, such as in Figure 4a, cannot affect the value of *SP* and therefore it becomes an unreliable metric in these situations. *DM* is an indicator to measure diversity that does not suffer the problem observed in *SP* calculation.

6 RESULTS AND DISCUSSION

6.1 Changes in the Actual Number of Selected Individuals

First, we verify the number of individuals before sampling, after selection by ε-Sampling, and after applying the proposed method, averaged over 30 trials for each generation. Results are shown in Figure 5. It can be seen that the proposed method is able to select most of the individuals that were randomly selected by the conventional method i.e. pink line is similar to the population size shown in green. Comparing the number of individuals after sampling with that of the conventional method shown in Figure 1, it can be seen that when the proposed method is used ε-Sampling selects samples which size are closer to the target number for all numbers of objectives (orange line). In other words, ε-dominance performed after ε-Sampling, in addition to reducing randomness, helps improve ε-Sampling itself.

6.2 POS Evaluation

Next, we evaluate the POS using the indicators listed above and compare results by the conventional and proposed method every 1,000 generations using box-and-whisker diagrams. Welch's t-test is performed for the evaluation values of the last generation to determine if there is a significant difference between the results of the conventional and proposed methods based on the obtained *p*-values included in Table 3.

Figure 6 shows the *HV* over the generations by AεSεH and its improved version with the proposed method. These plots and the *p*-values of the *HV* row in Table 3 show that in terms of *HV* there is a significant difference in performance by both algorithms for five or more objectives, and that performance im-

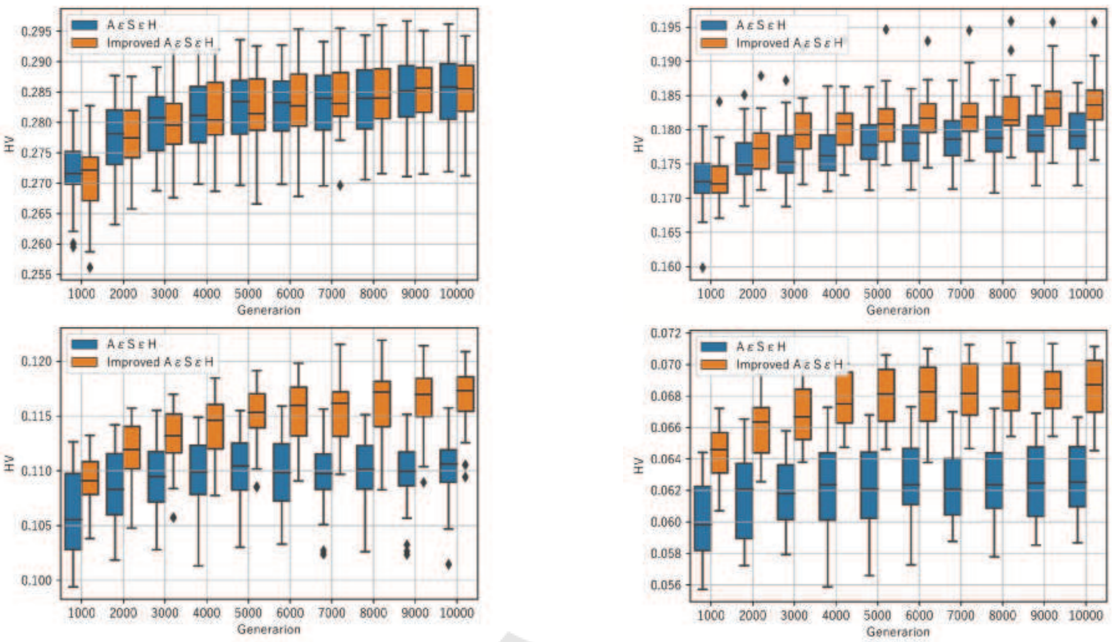


Figure 6: HV obtained in 30 runs. $N = 100, K = 5$, left to right, top 4, 5 objectives and bottom 6, 7 objectives.

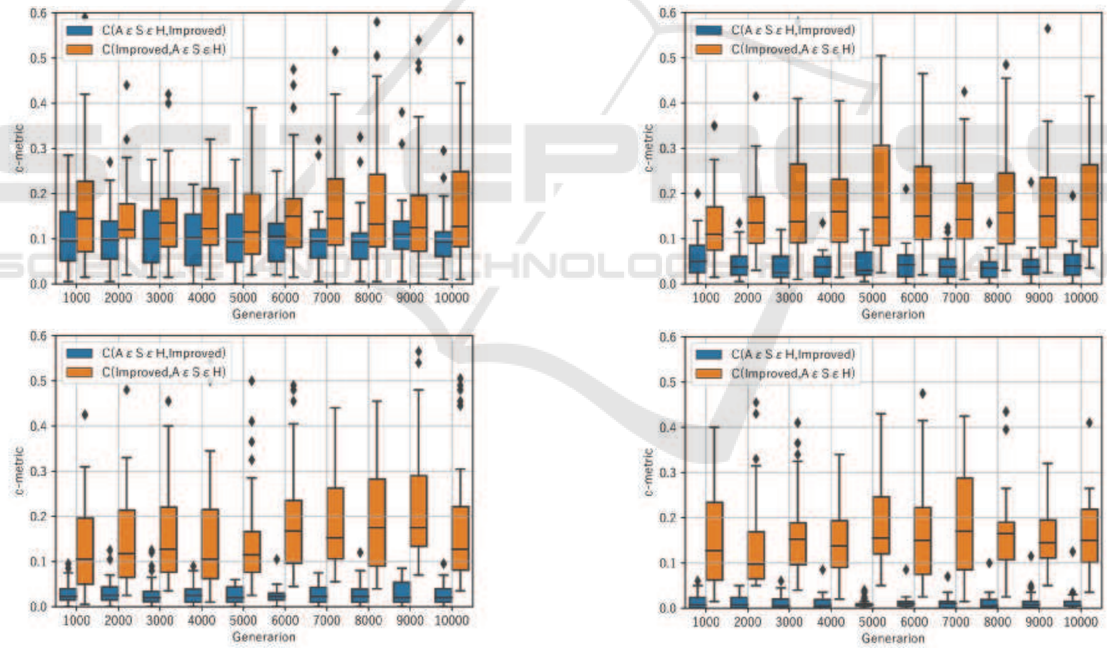


Figure 7: C-metric meassured in 30 runs. $N = 100, K = 5$, left to right, top 4, 5 objectives and bottom 6, 7 objectives.

Table 3: p-value in the last generation.

Ind.	Number of Objectives M			
	4	5	6	7
HV	8.62e-01	**2.18e-04**	**1.41e-11**	**1.81e-14**
C	**6.80e-03**	**4.53e-07**	**1.05e-06**	**4.07e-11**
OS	6.53e-01	6.44e-01	4.40e-01	1.94e-01
SP	**1.56e-04**	**2.64e-06**	**2.94e-06**	9.91e-02
DM	3.85e-01	**1.19e-02**	2.42e-01	2.25e-01

proves as the number of objectives increases.

Figure 7 shows results by the C-metric. $C(A\varepsilon S\varepsilon H, Improved)$ represents the proportion of the POS found by the proposed method that is dominated by the POS found by the conventional method, and $C(Improved, A\varepsilon S\varepsilon H)$ represents the opposite. The results show that convergence improved for all objectives tested, and this difference becomes more significant as the number of objectives

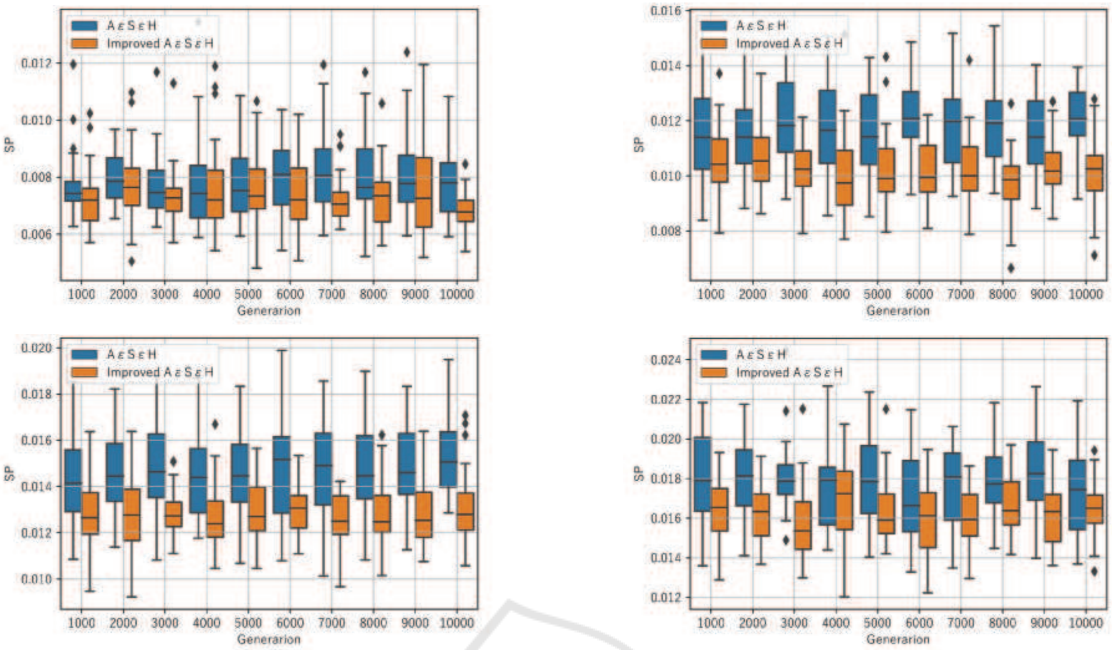


Figure 8: *SP* meassured in 30 runs. $N = 100, K = 5$, left to right, top 4, 5 objectives and bottom 6, 7 objectives.

increases. The *p*-values for the C-metric in Table 3 support this.

The *p*-values for the *OS* in Table 3 show that there is no statistical difference on spread by both methods. This is because the solutions with maximum and minimum evaluation values for each objective are kept, which is performed before applying ε-Sampling.

Figure 8 shows results on spacing computing *SP*. From Table 3, we can see that there is a significant difference in *SP* except for 7 objectives. In addition, the mean and variance are considerably smaller by the proposed method for all numbers of objectives as can be observed in Figure 8, which indicates that the uniformity is better in the proposed method.

The *p*-values for the *DM* in Table 3 show that no clear statistical differences between the two methods for *DM*.

6.3 Discussion

There is a statistically significant improvement in *HV* by the proposed method for many objective problems. To have a better understanding on the effects of the proposed method and determine whether the improvement is due to convergence or diversity we looked to other metrics.

First, C-metric shows that the convergence of POS improves regardless of the number of objectives. Also, the convergence difference between the conventional and proposed methods becomes larger as the number of objectives increases. Next, in terms of diversity, there was no difference in spread (*OS*), and while there was an improvement and stabilization in terms of uniformity (*SP*), there was no improvement in overall diversity (*DM*). This may be due to the aforementioned shortcomings of *SP*. While *SP* can only evaluate local uniformity, *DM* evaluates the diversity of the entire distribution of solutions. This indicates that the diversity has not improved when looking at the set of non-dominated solution as a whole, but it has improved locally. In other words, although uniformity is improved within groups of neighbor solutions, there is distance between the groups, and the distribution cannot be said to be uniform when viewed across the entire objective space.

From the above, it can be inferred that the solution search performance for each neighborhood improves as a result of better local uniformity, which improves the convergence of the solution group as a whole. Given that there is a correlation between the increase in the number of objectives and the improvement in convergence, uniform solution search becomes more important as the dimension of the objective space expands.

The fact that the proposed method also improves the accuracy of ε-Sampling as a side effect was revealed from the visualization of the actual selection of the proposed method. This is due to the improved uniformity of the solution distribution, which allows a more precise estimation of ε_s between generations.

Table 4: p-value in the last generation for each N.

N	M			
	4	5	6	7
100	8.62e-01	**2.18e-04**	**1.41e-11**	**1.81e-14**
300	**6.10e-06**	**8.16e-09**	**8.70e-12**	**9.63e-15**
500	**1.34e-06**	7.67e-08	**8.71e-12**	**1.88e-13**

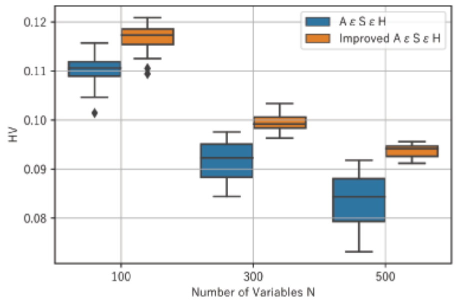


Figure 9: *HV* obtained at the last generation in 30 runs varying the number of variables N. $M = 6, N = \{100, 300, 500\}$ and $K = 5$.

6.4 Comparison Varying N and K

In this section we verify the performance of the proposed method increasing the complexity of the problem and the dimension of the search space.

Figure 9 shows results for $M = 6$ objectives and $K = 5$ bits, N from 100 to 500. Note that the proposed method performs significantly better than the conventional approach when we increase the size of the search space. In addition, note that the variance is smaller by the proposed method. This is corroborated by the p-values in Table 4, which also includes results for other values of M.

Table 5: p-value in the last generation for each K.

K	M			
	4	5	6	7
5	8.62e-01	**2.18e-04**	**1.41e-11**	**1.81e-14**
6	9.77e-01	**1.35e-05**	**4.56e-14**	**8.58e-16**
10	1.57e-01	**6.78e-03**	**1.55e-10**	**1.28e-14**
15	3.57e-01	**3.41e-02**	**1.60e-05**	**4.05e-10**
20	4.23e-01	1.80e-01	**4.08e-03**	**3.88e-04**

Figure 10 shows results for $M = 6$ objectives and $N = 100$ bits, varying K from 6 to 20. Note that the proposed method performs significantly better in a broad range of K and that the advantage gradually decreases as K increases. The reason why the performance for $K = 20$ by both methods become similar is that the number of sampled solutions by ε-Sampling approaches the desired population size, as shown in Figure 11, leaving little room for the proposed method to improve the sample. Similar results in favor of the proposed method are observed with other values of M when we vary K, as corroborated by the p-values in Table 5.

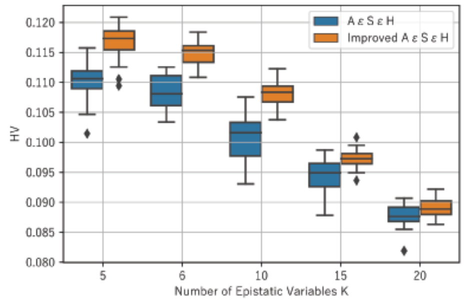


Figure 10: *HV* obtained at the last generation in 30 runs varying the number of interacting variables K. $M = 6, N = 100$ and $K = \{5, 6, 10, 20\}$.

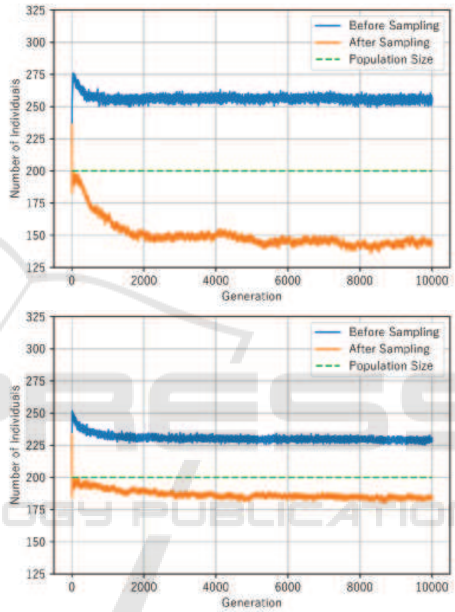


Figure 11: Average number of individuals before and after ε-Sampling. $M = 6, N = 100$, top $K = 10$, bottom $K = 20$.

6.5 Comparisson with Other MOEA

Decomposition based algorithms are being broadly used for many-objective optimization. To illustrate the relative performance of the improved AεSεH with respect to these kind of algorithms, we also conduct experiments with MOEA/D, a well known decomposition based algorithm. Figure 12 shows the transition of the *HV* over the generations by the improved AεSεH and MOEA/D on $M = 5, 6$ objectives, $N = 100$ bits and $K = 5$ epistatic interactions. From the figure we can see that the improved AεSεH achieves a significantly better *HV* than MOEA/D. Note that

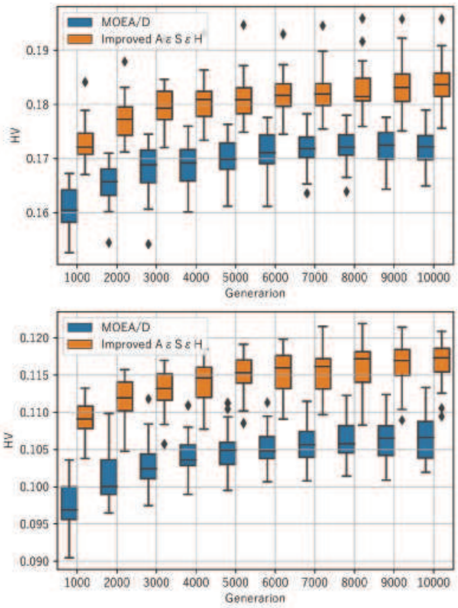


Figure 12: Comparisson with MOEA/D. $K = 5, N = 100$, top 5 objectives, bottom 6 objectives.

the performance of the proposed algorithm at the 2,000th generation is already better than MOEA/D at the 10,000th generation.

7 CONCLUSIONS

In this study, we focused on the ε-Sampling part of Adaptive ε-Sampling and ε-Hood (AεSεH) algorithm, and confirmed through experiments that AεSεH performs better solution search with the improved proposed method. This performance improvement was more pronounced as the number of objectives increased. This is attributed to the increased importance of a search process that emphasizes solution uniformity in response to the expansion of the objective space as the number of fitness functions increase. Since AεSεH is an algorithm developed for multi- and many-objective optimization, this improvement reinforces its many-objective characteristics. We also found that improving solution uniformity leads to the generation of solution distributions that are more prone to ε-Sampling with high accuracy. In addition, we showed that AεSεH scales up well with the dimension of the search space and complexity of the problem.

In the future, we would like to explore dynamic schedules for the amplification factor in the proposed scheme, reflecting, for example, the size of the target population and the number of target individuals, which would not only further reduce randomness but also reduce the number of calculations.

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