# HEMO: A Sustainable Multi-Objective Evolutionary Optimization Framework

**Jianjun Hu[+§], Kisung Seo[+], Zhun Fan[+], Ronald C. Rosenberg[Ψ], Erik D. Goodman[+]**

[+]Genetic Algorithms Research and Applications Group (GARAGe)
[§]Department of Computer Science & Engineering
[Ψ]Department of Mechanical Engineering
Michigan State University, East Lansing, MI, 48824
{hujianju, ksseo, fanzhun, rosenber, goodman}@egr.msu.edu

**Abstract.** The capability of multi-objective evolutionary algorithms (MOEAs) to handle premature convergence is critically important when applied to real-world problems. Their highly multi-modal and discrete search space often makes the required performance out of reach to current MOEAs. Examining the fundamental cause of premature convergence in evolutionary search has led to proposing of a generic framework, called HEMO, for evolutionary multi-objective optimization. HEMO is characterized by its simultaneous maintenance of individuals of all degrees of evolution in hierarchically organized repositories, by its continuous inflow of random individuals at the base repository, by its intrinsic hierarchical elitism and hyper-grid-based density estimation. Two experiments demonstrate its search robustness and its capability to provide sustainable evolutionary search for difficult multi-modal problems. HEMO makes it possible to do reliable multi-objective search without risk of premature convergence. The paradigmatic transition of HEMO to handle premature convergence is that instead of trying to escape local optima from converged high fitness populations, it tries to maintain the opportunity for new optima to emerge from the bottom up as enabled by its hierarchical organization of individuals of different fitnesses.

## 1 Introduction

After a decade of intensive study on evolutionary multi-objective optimization (EMO), extensive insight has been obtained regarding convergence and the diversity of the Pareto front. Several successful multi-objective EAs have emerged, such as PESA [1], NSGA-II [4], and SPEA2 [14]. However, the capability to handle premature convergence for difficult multi-modal optimization problems has attracted insufficient attention. The performances of modern MOGAs are usually compared on some easy continuous test prob-

lems [5]. The scalability of MOEAs is focused on the scalability over the objective dimension rather than over the problem difficulty [11]. Unfortunately, many real-world problems are characterized as highly multi-modal in highly discrete search spaces. Without careful attention to the premature convergence issues, modern MOGAs will easily fail to find the true Pareto fronts for these problems [3] and the performance comparison results will be misleading for MOGA practitioners.

Based on the research on dealing with premature convergence of single-objective EA search [9], a sustainable multi-objective optimization framework called HEMO (Hierarchical Evolutionary Multi-objective Optimization) is proposed in this paper. In addition to the external Pareto archive commonly found in PESA and SPEA, HEMO features hierarchically organized archives of individuals with different fitness ranks, a "workshop" subpopulation associated with each archive, and a random individual generator that continually feeds raw genetic material into the lowest-level archive. By incorporating favorable features from PESA [1], SPEA [12], and HFC (Hierarchical Fair Competition) EA model [9, 10], and extending ideas from the improved NSGA-II [3], this framework promises to have strong capability to avoid premature convergence in EMO and thus to constitute a sustainable search procedure for solving difficult real-world problems.

## 2 Convergence, Diversity and Premature Convergence in EMO

From the first generation of modern MOGAs such as NSGA, SPEA, and PAES to the improved versions like NSGA-II, SPEA2 and PESA, much attention is allocated to diversity maintenance of the Pareto front by estimating the density of individuals along the Pareto front (SPEA2, NSGA-II, PESA), ensuring sufficient selection pressure in special cases (SPEA2), utilization of elitism (NSGA-II), and other efforts to obtain computational efficiency. However, the diversity along the Pareto front is different from the diversity required for avoiding premature convergence, which is labeled as lateral diversity in [3]. The capability to maintain lateral diversity varies widely among MOGAs, which contributes much to the performance differences for different test problems.

### 2.1 Performance Comparison of Modern MOGAs

In terms of lateral diversity maintenance, PESA, NSGA-II, and SPEA2 have different strategies, which largely determine their advantages and disadvantages. Among the three, PESA is the greediest algorithm. By selecting the mating pool only from the currently discovered Pareto front, it is on one extreme of elitism and depends strongly on the mutation operator for exploration. As a result, PESA has the fastest convergence speed, but is only good for continuous, relatively simple problems. It is shown to be inferior on the T4 test function, for example, which is a continuous multi-modal problem [1]. It can be expected that the uncontrolled, extreme elitism of PESA will make PESA unusable for highly discrete multi-modal problems.

By maintaining a constant size of the archive (parent) population, SPEA2 and NSGA-II allow the persistence of dominated individuals in cases in which the non-dominated

individuals do not fill the archive population. So for some continuous multimodal test functions such as QV and KUR [14], SPEA2 and NSGA-II are shown to be able to achieve good performance. However, for other multimodal problems in which there are too many non-dominated individuals, SPEA2 and NSGA-II will always select mating individuals from the current Pareto front, in effect degrading to the extreme elitism case of PESA. This uncontrolled elitism makes NSGA-II without mutation perform poorly on difficult multimodal problems such as ZDT4, ZDT6, and Griewank [3]. As high mutation rate is not the solution to premature convergence, even with mutation, NSGA-II will fail on other difficult multimodal problems. To explicitly maintain the dominated individuals to promote lateral diversity, Deb and Goel [3] proposed the controlled elitism NSGA-II, which turns out to be very successful. The basic idea is to allocate a predefined distribution of individuals to each current Pareto front in NSGA-II. However, as the fronts in NSGA-II usually move in clusters to better regions of the objective space based on limited evaluations (for minimization problems), there is increasing risk that all fronts get trapped in local Pareto fronts, and gradually, the exploratory capability will be lost. This is attributable to the fitness assignment scheme of NSGA-II, which is based on the relative fronts, and on the convergent nature of conventional GAs.

### 2.2 Premature Convergence and the Issue of Exploitation vs. Exploration

To a large extent, the premature convergence problem in EMO is similar to of the situation in single-objective EAs. Most previous studies attributed the cause of premature convergence to the loss of diversity of the population and proposed various diversity-oriented approaches to increase the population diversity by "brute force." Representative methods include increasing the mutation rate; introducing random individuals into highly converged populations, and using diversity-detection and increasing techniques. All these methods are shown to ameliorate only partially the premature convergence problem. For example, in genetic programming, a high mutation rate usually destroys the good solutions evolved and, despite the diversity of the population, no progress can be made with this "brute-force" diversity maintenance.

Actually, the loss of diversity is only a symptom of premature convergence. The more fundamental reason is, instead, the loss of exploratory capability. In single-objective EAs, the absolute average fitness of the whole population is constantly increasing as the result of fitness-biased selection. The consequence is that "new explorer" individuals (i.e., early individuals in a new region of the search space), whether the offspring of mutation or crossover or randomly generated, find it increasingly hard to survive, since these explorer individuals usually have low fitness until sufficient exploration in the new search region is conducted. Rare high-fitness "explorer" individuals, due to their sparseness, will also have high risk of getting lost as the result of sampling bias in parent selection toward more crowded areas, similar to the analysis in [2]. To fight against this "unfair competition" among highly evolved individuals and new "explorers", there must be some mechanism to protect new explorers. This is achieved to some extent by widely used approaches such as fitness sharing and crowding. However, using horizontal expansion in the genetic space, these techniques usually suffer from the problem of balancing a

limited population size against a huge number of local optima in difficult multi-modal problems.

Another perspective on premature convergence can be obtained by examining building block concepts. The evolution process is widely seen as a process in which different building blocks become co-adapted to achieve higher and higher fitness by mixing and mutation. The higher the fitness of an individual, the stronger the coupling of its sub-components, and the more difficult to make large modification of the highly evolved individual without destroying the co-adaptation relationship. So the exploratory capability decreases with increasing fitness of the population. It is similar to the Cambrian explosion in the evolution of living organisms, during which most existing species (body plan innovations) were created. However, by allocating all the search effort to highly evolved individuals, without control, conventional EAs essentially discard the low-fitness evolution stages after limited mixing experiments, and thus are essentially convergent algorithms.

NSGA-II, with its controlled elitism [3], is one of the first algorithms that pays special attention to dominated inferior individuals. However, while derived from the conventional EA framework, the improved NSGA-II still suffers from the tendency that all individuals in the fronts are moving toward the best yet-discovered regions of the objective space, based on limited mixing experiments, and the components are increasingly co-adapted to each other (Fig. 1). As the result, the exploratory capability of the population is gradually lost and premature convergence occurs. The distribution of individuals to the relatively diverse fronts is insufficient to avoid this kind of premature convergence.

Based on the analysis above, it turns out to be important to maintain intermediate individuals and to make the building block mixing process occur at all fitness levels. This naturally provides a mechanism to ensure fair competition and protects "explorer" individuals. At the same time, to reduce the large population size requirement [7] for diffi-

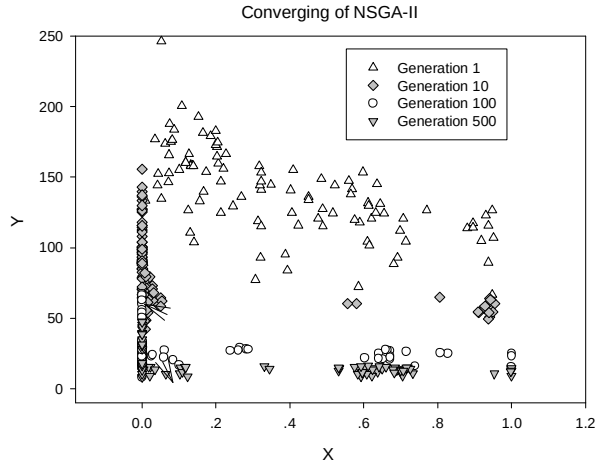


**Fig. 1.** The population of NSGA-II moves in clusters leaving the initial low objective value space and converging to the promising space. Even the maintenance of a predefined proportion of population into all fronts, but in the whole these fronts are converging to local areas, thus making it incapable to maintain the explorative capability in the long run.

cult problems, it is desirable to continuously introduce random individuals into the lowest fitness levels to provide the required building blocks, rather than depending on a large initial population to identify them, as is done in messy GA [8]. This suggests the assembly line structure of the subpopulations in the HFC framework proposed in [9]. The HEMO framework is thus an extension of HFC to multi-objective optimization, incorporating ideas from SPEA, PESA and the improved NSGA-II.

### 2.3 Combining Ideas in SPEA, PESA, and the Improved NSGA-II

The different performances of SPEA, PESA and NSGA-II over different test functions reflect the unique, positive features of each approach. HEMO will attempt to capture some features of each of these. Specifically, the maintenance of an external Pareto archive and the breeding population first proposed in SPEA [12] is employed in the HEMO framework, but extended so that both the Pareto archive and archives of intermediate individuals are maintained. The elitism in the Pareto front update is supported by low-level HFC archives, as explained in the next section. For density estimation, the grid-based methods in PESA [1] are used, which are naturally suited for the absolute division of the objective space as required by the HEMO framework. This grid-based method is also demonstrated to have excellent performance in maintaining Pareto front diversity [11]. The distribution of individuals into all fronts in the improved NSGA-II is extended to all fitness levels.

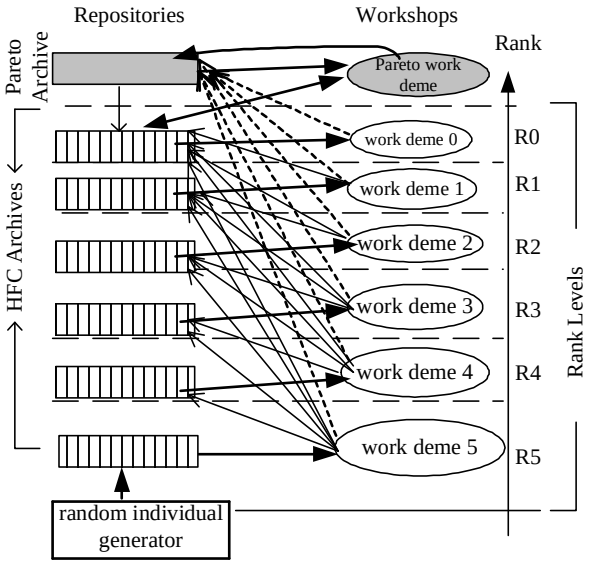


**Fig. 2.** The assembly line structure of the HEMO Framework. In HEMO, repositories are organized in a hierarchy with ascending fitness level (or rank level in the objective space as employed in this paper). Each level accommodates individuals within a certain fitness range (or belonging to a given rank level) as determined by the admission criteria.

## 3 HEMO: Hierarchical Evolutionary Multiobjective Optimization

Based on the analysis of the fundamental cause of premature convergence and drawing ingenious ideas from previous successful MOGAs, we propose the HEMO framework for difficult multi-objective problems in which the avoidance of premature convergence is of great concern. Essentially, it is an extension of PESA enhanced with the continuing search capability of HFC. In addition to the Pareto archive and the Pareto workshop population, a succession of archives for maintaining individuals of different fitness levels is added to allow mixing of lower- and intermediate-level building blocks. A random individual generator is located at the bottom to feed raw genetic material into this building block mixing machine continually. The structure of HEMO is illustrated in Fig. 2:

The HEMO algorithm proceeds as follows:

1) Initialization

- Determine the number of levels (*nLevel*) into which to divide the objective space for each objective dimension. Determine the grid divisions (*nGrid*) as in PESA. Note that nLevel is different from *nGrid*. The first one is used to organize intermediate individuals into the hierarchical archives, while the latter is used to estimate the density of individuals.
- Determine the population sizes of the Pareto archive, HFC archive and corresponding workshop demes. The distribution of population sizes among archives (workshop demes) can be determined separately or using some special distribution scheme like the geometric distribution in (Deb and Goel, 2000).
- Initialize the workshop demes with random individuals. The archives are empty at the beginning.
- Evaluate all individuals and calculate the crowding factor of each individual according to the hyper-grid approach in PESA.
- Calculate the fitness range of each objective dimension for all individuals in the whole population:
  $[f^i_{\min}, f^i_{\max}]$ where $i = 0,...,ObjDim-1$
- Divide the fitness range into *nLevel* Levels. For all individuals, calculate the objective ranks for each objective dimension, $r_i, i = 0,...,ObjDim-1$, $r_i \in [0, nLevel-1]$;
- For each individual, calculate its fitness rank = the average rank over all objective dimensions of each individual. $r^f = \frac{1}{ObjDim} \sum_{i}^{ObjDim-1} r_i$
- Migrate (move out) individuals in the workshop demes to the corresponding HFC archives according to their fitness ranks $r^f$. Then add all non-dominated individuals of each workshop deme to the Pareto archive. There are two cases possible during these migrations. If the target archive is full, we will replace a selected individual according to the Pareto archive and HFC archive update procedures described below; else, we simply add the migrating individual into the target repository.

2) Loop until meeting stopping criterion

A steady state evolutionary model is used in the HEMO framework. First,

- Compute the breeding probability of each workshop deme of the HFC rank levels. This is calculated as follows:

$$pBreed^{l} = \frac{Popsize\,of\ workshop\,deme\,of\ level\,l}{\sum_{k=1}^{nLevel-1} Popsize\,of\ workshop\,deme\,of\ level\,k}$$

  These probabilities can instead be dynamically adjusted irrespective of the workshop deme sizes. These probabilities determine the allocation of search effort to each level, thus determining the greediness of the algorithm.
- Decide whether to do Pareto workshop breeding or HFC workshop deme breeding by probability *pParetoBreed* . If setting *pParetoBreed* =1, then HEMO reduces to an algorithm similar to PESA. This parameter is used to control the greediness of the Pareto search.

*If Pareto workshop breeding is to be done:*

- Decide whether or not to do crossover according to its probability. Mutate each gene of the offspring with probability *pGeneMutate*.
- Select parents from the Pareto archive using tournament selection based on the crowding factors of individuals. The less crowded, the more chance an individual will get selected. When selecting parents for crossover or mutation, the probability to select only from the Pareto archive is *pSelectFromPareto*. The probability to select a second parent from the rank 0 HFC Archive is 1- *pSelectFromPareto*. When there is only one individual in the Pareto archive, the second parent for crossover is selected from the highest HFC archive.
- Create an offspring (two in crossover) and add it to the Pareto workshop deme. If the Pareto workshop deme is not full, simply add the new candidate to it; else, trigger the **Pareto Archive Update** Procedure. Then a migration process will move individuals of each HFC archive to their new qualified HFC archives because of the update of the objective ranges.

*If HFC workshop deme breeding is to be done:*

- Decide at which level (L) breeding will occur according to the probability $pBreed^{l}$
- Decide whether or not to do crossover according to its probability. Mutate each gene of the offspring with probability *pGeneMutate*.
- Select parents from the HFC archive of level L by tournament selection based on the crowding factors. The lower the crowding factor, the higher the probability to be selected. If there is only one parent in the current HFC archive, then the second parent will be selected from the next lower archive.
- Create an offspring (two in crossover) and add it to the workshop deme. If the workshop deme is not full, simply add to the end; else, trigger the **HFC Archive Update Procedure** and the **Pareto Archive Update Procedure**.

- With low probability *pRandomImport* , update *perRandomIn* percent of the individuals of the lowest HFC archive with random individuals.

**Pareto Archive Update Procedure ( )**

- Screen out the non-dominated individuals in the workshop deme.
- Update the objective ranges of the whole population with the non-dominated individuals.
- Recalculate the crowding factors of all individuals of the selected non-dominated individuals and the individuals in the Pareto archive.
- Update the Pareto archive with the selected non-dominated individuals. If the Pareto archive is full, truncate it by removing individuals with higher crowding factors.
- Empty the Pareto workshop deme.

**HFC Archive Update Procedure ( )**

- Update the objective ranges of the whole population and recalculate the fitness ranks of all individuals in the workshop demes.
- Migrate individuals in the current HFC archives into their corresponding new levels. If the target HFC archive is full, replace an individual selected by tournament selection. The more offspring an individual produces, the higher the probability it will be replaced.
- Update the HFC archives with the individuals in the workshop deme. If the target HFC archive is full, replace an individual selected by tournament selection. The bigger the crowding factor is, the higher probability it will have to be replaced. Note that only higher archives are updated with the current workshop deme (uni-directional migration policy)

## 4 Experiments and Results

In this section, two test functions are selected to demonstrate the exploratory capability of HEMO to avoid premature convergence. Here, HEMO is only compared to PESA, since HEMO is most closely derived from PESA.

1) Multi-objective Rastrigin's problem (ZDT4)

$$ZDT4: \begin{cases} Minimize\ f_1(x) = x_1 \\ Minimize\ f_2(x) = g(x)[1-\sqrt{x_1 / g(x)}] \\ g(x) = 91 + \sum_{i=2}^{10}[x_i^2 - 10\cos(4\pi x_i)] \\ x_1 \in [0,1],\ x_i \in [-5,5],\ i = 2,...,10. \end{cases}$$

2) Multiobjective Griewangk Problem (GWK)

GWK problem is constructed by replacing g (x) in 1) with Griewangk's function, where

$$g(x) = 2 + \sum_{i=2}^{10} x_i^2 / 4000 - \prod_{i=2}^{10} \cos(x_i / \sqrt{i}),\ x_1 \in [0,1],$$

$$where \quad x_i \in [-512,511]\ i = 2,...,10$$

Fig. 3 illustrates the distribution of individuals of HEMO during the evolutionary proc-

ess. It is clear that HEMO works by trying to expand the individuals in its repositories evenly across the objective space, rather than by converging to the early-discovered high-fitness areas. This provides the necessary fitness gradient for new optima to emerge in a

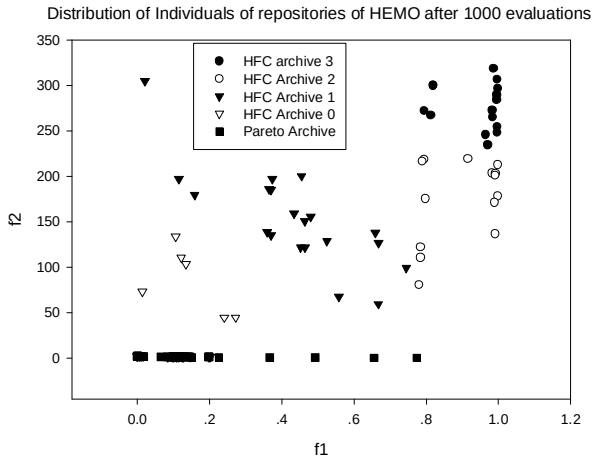


**Fig. 3.** Distribution of individuals over the objective space of GWK in HEMO after 1000 evaluations. Compared with Fig. 1. of NSGA-II, the difference is that the archive population of NSGA-II is drifting and has the risk of converging to a local area. HEMO has less tendency to converge, since it maintains representative individuals at many levels in the objective function space and continuously introduces new genetic material, thus providing the fitness gradient for new optima emerge in a bottom-up way.

bottom-up way, from the bottom level HFC archive and workshop subpopulations.

The robustness of PESA and that of HEMO are compared by examining the relationship of performance and the mutation rates applied to each *type double* gene after crossover. We use the statistical comparison method of [1] to compare the Pareto fronts obtained with different mutation rates by PESA and HEMO (Table 1). Cells in the upper right triangle of the table hold the comparison results of different mutation rates for HEMO, while the lower left (shaded cells) are for PESA. The first entry in each cell represents the percentage of Pareto front solutions obtained with the row's mutation rate that are non-dominated, with 95% confidence, by the solutions obtained with the column's mutation rate. The second entry in each cell, similarly, shows the percentage of Pareto front solutions obtained with the column's mutation rate that are non-dominated, with 95% confidence, by the solutions obtained with the row's mutation rate. From [3], we know that for test function ZDT4, NSGA-II fails to find the true Pareto front. This is also the case for PESA, as illustrated in the first column. PESA without mutation is worse than any PESA configuration with mutation. It is also suggestive that for PESA, the performance varies greatly with different mutation rates, achieving best performance here with a mutation rate of 0.12. In contrast, HEMO is more robust over mutation rates. The per-

formance difference with no mutation is not much different from that with mutation rate 0.16.

We also compared the best performance of PESA (mutation rate 0.12) with that of HEMO (mutation rate 0.16) for the same number (10,000) of evaluations (Table 2) . For ZDT4, the Pareto front found by HEMO was much better than PESA found. In the case of GWK, HEMO had limited advantage over PESA. The reason is that the statistical comparison procedure used here [6,1] compares the merged Pareto fronts found during 20 runs. PESA with different random seeds may converge to different points in the objec-

| Mutation Rate | 0.00 | 0.04 | 0.08 | 0.12 | 0.16 |
|---|---|---|---|---|---|
| 0.00 | | 99 100 | 99.5 100 | 99.7 100 | 97.5 100 |
| 0.04 | 100 50 | | 99.8 100 | 99.9 100 | 0.5 100 |
| 0.8 | 100 7.3 | 100 99.7 | | 100 100 | 2.4 99.7 |
| 0.12 | 100 3.2 | 100 50.0 | 100 70.6 | | 2.4 99.9 |
| 0.16 | 100 7.3 | 100 50.1 | 98.7 100 | 100 100 | |

**Table 1.** Comparison of the robustness of PESA (in shaded cells) and HEMO with test function ZDT4. First entry in each cell is percentage of solutions obtained with row's mutation rate that are not dominated by those obtained with the column's mutation rate, and vice versa for the second entry. PESA can be seen to depend strongly on mutation to maintain its exploratory capability. It is very sensitive to the mutation rate, for which the optimal value is hard to know in advance. HEMO is much less sensitive to the mutation rate, since it doesn't depend on mutation to maintain the explorative

tive space, which on the whole comprise a good Pareto front. However, PESA is a poor opportunist in the sense that for both the ZDT4 and GWK functions, PESA converges to only one or two Pareto solutions in 6 or 7 runs of a total of 20. In contrast, HEMO always obtains diversified solutions in the Pareto archive.

| **Test Function** | **ZDT4** | | **GWK** | |
|---|---|---|---|---|
| | PESA | HEMO | PESA | HEMO |
| % Non-Dominated Pareto Solutions in 20-Run Ensemble | 0.3% by HEMO | 100% by PESA | 47.3% by HEMO | 53.7% by PESA |
| Premature Convergence Frequency | 6/20 | 0/20 | 7/20 | 0/20 |

**Table 2.** Opportunistic PESA and robust HEMO. HEMO obtains a much better Pareto front for ZDT4 and a small advantage for GWK. However, for each independent run, the frequency

## 5 Conclusions and Future Work

Current MOEAs still suffer from their convergent nature inherited from the conventional EA framework. The loss of population diversity turns out to be only a symptom of

the phenomenon of premature convergence. Maintenance of exploratory capability is central to ensuring sustainable evolutionary search. A new evolutionary multi-objective framework named HEMO is introduced, featuring: a hierarchical organization of repositories of individuals of different fitness levels (defined as the composite objective ranks in the divided objective space), the continual introduction of raw genetic material at the bottom evolutionary level, and hyper-grid-based density estimation. Two experiments are reported to show the sustainable search capability of HEMO, demonstrated along with its robustness over a variety of mutation rates, as compared to PESA. The paradigmatic transition in handling premature convergence from HEMO is: instead of trying to escape local optima from within converged, high-fitness populations, the continuing EA framework (as represented, for example, by HFC and HEMO here) ensure the opportunity for new optima to emerge from the bottom up, enabled by the hierarchical organization of individuals by fitness.

By combining features from PESA and SPEA and extending the ideas in the NSGA-II with controlled elitism, and including the HFC organization, HEMO is expected to be well suited for difficult multi-modal real-world problems in which premature convergence is of great concern. We also expect that HEMO will be especially advantageous in multi-objective genetic programming, where the highly multi-modal and discrete fitness landscape often makes modern MOEAs such as PESA fail by converging prematurely to a local Pareto front. It is interesting to sort the MOEAs by their capabilities to handle premature convergence. From the lowest to highest, we have PESA→SPEA2 → NSGA-II → NSGA-II with controlled elitism → HEMO, each improving the previous one by paying more attention to the non-inferior dominated individuals. However, HEMO differs from all the others in its continuing search nature without premature convergence, while the others are all based on the traditional, convergent EA framework.

As a generic framework, HEMO is easily applicable to other modern MOEAs such as SPEA-2 and NSGA-II. To improve running efficiency, a better density estimation method is needed. The scheme for organizing individuals by rank levels can also be improved. In addition, to distribute the individuals of the repositories more evenly in the objective space, the HFC archive update scheme needs further refinement. Especially, extensive comparative experiments with NSGA-II with controlled elitism and other MOEAs are required to fully demonstrate the potential of HEMO.

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