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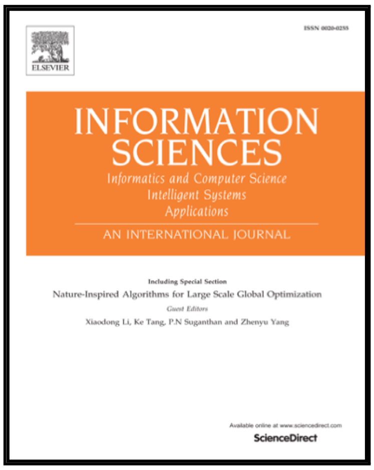

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Region-based Memetic Algorithm with Archive for multimodal optimisation

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Abstract

In this paper we propose a specially designed memetic algorithm for multimodal optimisation problems. The proposal uses a niching strategy, called region-based niching strategy, that divides the search space in predefined and indexable hypercubes with decreasing size, called regions. This niching technique allows our proposal to keep high diversity in the population, and to keep the most promising regions in an external archive. The most promising solutions are improved with a local search method and also stored in the archive. The archive is used as an index to effiently prevent further exploration of these areas with the evolutionary algorithm. The resulting algorithm, called Region-based Memetic Algorithm with Archive, is tested on the benchmark proposed in the special session and competition on niching methods for multimodal function optimisation of the Congress on Evolutionary Computation in 2013. The results obtained show that the region-based niching strategy is more efficient than the classical niching strategy called clearing and that the use of the archive as restrictive index significantly improves the exploration efficiency of the algorithm. The proposal achieves better exploration and accuracy than other existing techniques.

Keywords: Multimodal optimisation, memetic algorithm, niching strategy

1. Introduction

Many real world problems offer various solutions considered as global optima. The identification of multiple solution has thus gained popularity in the research community. It is referred to as multimodal optimisation as the objective is to retrieve more than one optima. While classical evolutionary algorithms

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(EA) were designed to identify a single optimum, some modifications have to be applied to identify multiple optima, preventing their premature convergence and maintaining the diversity in their population to ensure the exploration of distinct areas of the fitness landscape. Such techniques, known as niching strategies [6], are meant to stay in the population subgroups of individuals, or *niches*, in different parts of the search domain.

Most existing techniques' efficiency relies on two problem dependent parameters, the niche radius and the population size [7, 16, 42]. The first one should be defined according to the distance between optima in the fitness landscape and the second one according to the number of optima to locate. Both data are however usually unknown in real world problems. Nowadays, research interest focuses on designing EA which are less dependent on those parameters.

The main challenge when designing an EA for multimodal optimisation is to create an algorithm capable of approximating with the highest level of accuracy the different global optima.

Memetic algorithms (MA) [35] are the hybridisation between EA and local search methods (LS) combining in one model the exploration power of the former and the exploitation capacity of the latter. This hybridisation can achieve a good trade-off between the exploration of the domain search and the exploitation of found solutions, so it is important to obtain good results in EAs [59], and it also offers interesting properties when applying them to multimodal optimisation problems from the multimodal optimisation point of view. Indeed, as we said before, niching techniques used with classical EA forms sub-populations destined to explore and optimise different areas of the search space with the same mechanism. MA separate these efforts, leaving the exploration task to the EA and the refinement of the most promising regions identified by the EA to the LS method.

In a previous work [21], we designed a MA for global continuous optimisation problems called region based memetic algorithm with local search chaining (RMA-LSCh). It proposed a novel niching strategy, the originality of which lies in the definition of a niche. While traditionally the niche surrounding a solution is defined by the radius around it, the proposed niching technique partitions the search into equal hypercubes called regions. The dependency to the niche size (defined by the number of divisions of the search space) is reduced by increasing the number of divisions during the search. In this work we propose a new algorithm specially designed for continuous multimodal optimisation, Region-based Memetic Algorithm with Archive (RMAwA). Although RMAwA maintains the same definition of a niche and alternatively applies the EA and the LS, the memetic scheme is modified and a novel archive is implemented to match the requirements of multimodal optimisation. First, while RMA-LSCh uses LS Chaining [32, 33] and thus limites the number of fitness evaluation per LS application, RMAwA applies the LS until it has reached a local or global optimum. Most importantly, regions intensively explored by LS are discarded by the proposal from further exploration. RMAwA contains an indexed archive with these regions to reduce the search domain in a very efficient way. Also, because the identified optima are stored into the archive and not into the population, the number of optima that RMAwA can identify is not limited by the population size [12, 63, 64].

RMAwA is tested using a specific benchmark for multimodal optimisation. The experiments carried out show that the use of the region based niching strategy coupled with an archive provides interesting improvements to the memetic framework, and that the RMAwA is a very competitive algorithm against existing ones.

This paper is organised as follows. In Section 2, we present a quick introduction on methods previously proposed to tackle multimodal problem optimisation. In Section 3, we present the RMAwA and detail each component. In Section 4, we explain the experimental framework used and the parameter setting of the algorithm. In Section 5, several comparisons are carried out to study the influence of the different components of the algorithm and our proposal is compared with other algorithms in the literature. Finally, In Section 6 some concluding remarks are pointed out.

2. Background

In order to identify multiple optima of a fitness landscape several techniques have been proposed. In this section, we give a brief overview of techniques that have been proposed to maintain the diversity in the population in order to prevent its convergence towards a single optimum. Such techniques are commonly called niching strategies and refer to the technique used for the discovery and preservation of distinct niches. This term is a reference to the ecological concept of niches referring to the formation of distinct species exploiting different niches (resources) in an ecosystem.

The main challenge in multimodal optimisation is the unknown nature and characteristics of the objective function, specifically the number of global optima and their repartition on the search domain. The main goal of the proposals presented in this section is to tackle these issues. Alternatively, [55] proposes a preprocessing tool to estimate the number of basins of attraction in the fitness landscape.

We have classified the methods proposed to tackle multimodal optimisation into two categories. The first one lists the classical niching strategies which mainly affect the replacement criterion of the EA they are applied to. The second one works with the idea of creating subgroups of solutions in different area of the search space by limiting the cooperation of each individual to its nearest neighbours. We refer to them as neighbourhood based techniques.

In this section, we first describe the different elements composing those two categories by giving a general overview of the proposal making use of such techniques. In a third section, we briefly introduce proposals combining those techniques with MA which demonstrate that the use of a refinement method improves the performance of EAs for multimodal optimisation.

2.1. Classical niching techniques

The first niching techniques consist in limiting the presence of multiple solutions within the same niche in order to keep the population highly diverse. When included in a classical EA, those mechanisms are mainly replacement strategies designed to remove solutions present in the same vicinity. We describe here the four main methods to achieve this objective: crowding, clearing, fitness sharing, and speciation.

2.1.1. Crowding

Crowding is one of the first techniques proposed to tackle multimodal optimisation problems [7]. After the generation of a new solution, a random sample of CF solutions is selected in the population. Each new solution competes with the closest solution of the sample to stay in the population. This technique's main drawback is the definition of the crowding factor parameter (CF). A small value can lead to the replacement of a distant solution to the offspring and thus a loss of information, and a very large value has a high computational cost. The efficiency of this technique has proven to be limited [30] and advanced versions have been proposed:

- *Deterministic crowding* proposed by [30] tries to limit the problem of replacement errors induced by the crowding technique by eliminating the need of defining the CF parameter. To do so, an offspring competes with its own parents to stay in the population.

- *Probabilistic crowding* [31] on the other hand modifies the replacement strategy of the original technique. In this scheme, the offspring and its most similar individual in the crowding sample compete in a probabilistic tournament where the probabilities of winning for each individual X, $p(X)$, is calculated according to their fitness:

$$p(X) = \frac{f(X)}{f(X) + f(Y)} \tag{1}$$

  where $f(X)$ is the fitness of the same solution X and $f(Y)$ is the fitness of the other solution. The idea is not to always show preference to solutions with higher fitnesses which may lead to the loss of niches.

In [57], Thomsen proposed the popular crowding differential evolution (CDE) applying a classical crowding strategy on a differential evolution (DE) where a new solution is created by means of classical DE mutation and crossover scheme comparing with its closest solution in the whole population for replacement.

CDE was then extended to multi-population crowding DE (MCDE) in [63] where multiple sub-population evolve in parallel using CDE. When all the sub-populations have converged, the optima identified by each of them are stored in an archive and the sub-populations are reinitialised.

More recently, Qu et al. proposed the dynamic grouping of CDE (DGCDE) [45] with ensemble of parameters. The population is divided into three sub-population to which a set of control parameters is assigned.

In [44], Qing et al. proposed a Crowding Clustering Genetic Algorithm (CCGA) using a clustering technique to eliminate the genetic drift introduced by the crowding strategy.

2.1.2. Clearing

Clearing techniques [42] lie in the principle of dedicating the limited resources of a niche to its best individuals. The population is sorted according to the individual fitness values. The solutions are then selected one after the other and the solutions with worse fitness falling within their niche radius σ_{clear} are removed. Clearing has a low complexity and shows the best performances amongst the classical techniques but is highly sensitive to the niche radius [51].

Variations have then been proposed to limit influence of the σ_{clear} parameter. For instance, in [47], similarly to the previously cited DGCDE, the authors propose an ensemble of clearing DE (ECLDE) in which the population was equally divided into 3 sub-populations each evolving in parallel using a clearing DE with different values of σ_{clear}.

Some techniques use a redefinition of the niche in order to remove the use of the parameter σ_{clear}. In [11], the niches are defined through a hill-valley detection mechanism instead of using a niche radius. In [50], the niches are defined by fuzzy clustering of the solutions of the populations.

2.1.3. Fitness sharing

Contrarily to the clearing technique which consist in dedicating niche resources to a single solution, fitness sharing [16] consists in reducing the fitness of individuals present in densely populated regions. The fitness used of the *ith* individual, $f_{shared}(i)$, is calculated by:

$$f_{shared}(i) = \frac{f_{original}(i)}{\sum_{j=1}^{NP} sh(d_{ij})} \tag{2}$$

where $f_{original}$ is the original fitness function, NP is the population size, and sh function is calculated by:

$$sh(d_{ij}) = \begin{cases} 1 - \left(\frac{d_{ij}}{\sigma_{share}}\right)^{\alpha}, & \text{if } d_{ij} < \sigma_{share} \\ 0, & \text{otherwise} \end{cases} \tag{3}$$

where d_{ij} is the distance between individual i and j, σ_{share} is the sharing radius and α is a constant called sharing level.

In [57], Thomasen also proposed an DE using sharing where, after each generation, the new shared fitnesses are calculated over the population individuals and the trial vectors, the best half being kept in the population.

2.1.4. Speciation

Proposed in [22], speciation or species conservation introduces the notion of species by separating the population into several groups (species) according to their similarity. Those species are identified by a dominating individual called the species seed and a species distance $\sigma_{species}$ defining the maximum distance between two individual of the same species. The set of species seed is build at each generation by iteratively adding individuals from the population that are further from any species seed than $\sigma_{species}/2$. The individuals are kept from one generation to another until a better solution is identified within their species while the classical recombination operators are applied.

In [23], this concept is applied to a speciation-based PSO (SPSO). In SPSO, the particles are gathered into species to form sub-populations. This proposal was later extended to reduce its dependency to the species distance parameter by using population statistics [3] and a time-based convergence measure [49].

2.2. Neighborhood based technique

Another class of niching strategies can be referred to as neighbourhood-based. Contrarily to the previous section where the niching strategy could be seen as replacement strategy, these methods use the geographical information of the solutions in a population to modify the recombination scheme of a given EA. The main idea is to make solutions by only considering their neighbours in order to emphasize the speciation.

Originally named spatially-structured EAs (SSEA) [58], these algorithms form sub-populations of individuals (called deme) based on their similarity and perform genetic operations within each deme.

This idea has then been extended and two kinds of neighbourhoods can be identified in the literature:

- *Index-based neighbourhood* [24] uses the indices in the population of a PSO to identify the neighbourhood of a solution. The velocity of a particle is thus influenced by the local best solution instead of the global best.
- *Distance-based neighbourhood* uses the euclidean distance between individuals. In [26], the author proposed the FER-PSO algorithm where particles are attracted towards the "fittest-and-closest" neighbours. Similarly, the notion of neighbourhood is applied for DE in [13]. A new mutation strategy, DE/nrand/x is proposed. It uses as a base vector the nearest neighbour of each individual. This mutation strategy has then been used for more advanced models like in [12]. In [4] a neighbourhood mutation is proposed that considers normalized distance. Another option is to use the distance to create a clustering partition of the population to maintain diversity [15].

Neighbourhood-based strategies have often been coupled with classical niching strategies. For instance in [10], the authors propose including in a SSEA a fitness sharing and a clearing strategy.

In [48], the authors use the DE/nrand/x operator with crowding, sharing and species-based niching strategies and obtain better results than the original algorithms.

2.3. Memetic algorithms for multimodal optimisation

As stated in the introduction, MA are the hybridisation of an EA and a LS method. This model is part of the more general Memetic computing (MC) family of algorithms which combine various optimisers (memes). The efficiency of these models have helped them gain popularity over the past decade [5, 37].

The coordination of the memes is the main research topic in MC. Ong et al. [40] proposed a classification which was later updated by Neri et al. [37]:

- Adaptive Hyper-heuristic [19]: the memes are coordinated by means of heuristic rules.
- Meta-Lamarckian learning [39]: the probabilities of using the memes are based on their success, providing an online adaptability.
- Self-Adaptive and Co-Evolutionary [20, 54]: the memes are encoded with the candidate solutions and evolve in parallel so the most appropriate can be selected.
- Fitness Diversity-Adaptive [38]: the selection of the memes to be operated is based on the diversity measure of the population.

MA are particularly adapted to multimodal optimisation problems as, when applied to different solutions, an LS method can offer a strong refinement of the promising solutions discovered by the EA, providing great accuracy for the identification of multiple optima. The use of such model has raised interest in the research community.

For instance, the Sequential Niching Memetic Algorithm (SNMA) proposed by Vitela et al. in [60] and then extended in [61] is an MA which combines a genetic algorithm (GA) with a gradient-based LS method. Before each generation, the LS is applied to each solution of the population.

In [46], Qu et al. included an LS method to various previously cited PSO for multimodal optimisation (FER-PSO, SPSO, rPSO). The LS method used consisted in generating at each iteration new solutions in the neighbourhood of the personal best of each particle to explore its surrounding. They demonstrated that the resulting memetic PSO obtained better results than the original algorithms. Similarly, Wang et al. proposed a memetic SPSO [62] which adaptively uses two different LS methods and came to the same conclusions.

3. Region-based memetic algorithm with archive

In this section we present the region-based MA with archive (RMAwA), an algorithm designed for multimodal optimisation which uses a niching technique to obtain as much optima as possible.

RMAwA is a MA which alternatively applies an EA through a certain number of evaluations and a LS method to the best solution in the population until stagnation. It then considers that an optimum has been reached, thus it stores that solution in an external archive and the EA is carried on.

To maintain diversity during the search the algorithm divides each dimension in regions of same size, dividing the domain search in hypercubes. RMAwA uses these regions in two ways: First, only one solution is allowed in each region, thus when a solution generated by the EA falls in a region already occupied by a solution of the population the worst is removed. Second, regions in which one optimum has been found, by means of LS, are considered to be explored enough and discarded from the search space. The size of regions decreases during the run, by increasing the number of divisions per dimension.

In order to efficiently discard regions from further exploration, this model maintains an index of the regions represented by a solution in the archive. Also, it stores all the found optima to recalculate the regions when its number changes.

In the following subsections, we detail the algorithm. First, we briefly describe the concept of the region-based niching strategy. Then, we explain the general scheme of the algorithm along with how the different components are integrated. Finally, we explain how the archive works in detail: its structure, which solutions are stored, and how it is used.

3.1. Region-based niching strategy

In [21], a novel niching strategy was proposed that redefines the notion of niche from the area surrounding each solution in the population to a fixed division of the search space. Each dimension of the search space is divided into a certain number of divisions, ND, creating a predefined grid of equal hypercubes representing the niches.

In [56, 52], the authors use a similar partitioning of the search space to approximate the basin of attractions in multimodal fitness landscapes by means of clustered genetic search. In our algorithm, this fragmentation is used to define different niches in the search space. Ideally, regions contain a single basin of attraction but the unpredictability of the number of optima and their repartition in the search domain can not guarantee that. An illustration of the divisions of the search space can be seen in Figure 1. A solution $s_n \in \mathbb{R}^D$ is a real-parameter vector representing a solution to the problem at hand. It is associated with its region identified by its indices in each dimension, represented by a vector of integer values $r_n \in \mathbb{N}^D$. The advantage of such definition is to allow faster retrieval of the existing niches by avoiding the computationally expensive cost of calculating the euclidean distance between solutions.

In a region-based niching strategy, solutions generated in the evolutionary process compete with either the current solution present in the same region or the worst individual of the population. This technique can thus be assimilated to a clearing strategy in the sense that solutions compete to represent each niche in the population. The difference with classical niching strategy is the definition of the niche going from an euclidean distance-based representation to a region-based representation. In order to reduce the influence of the niche/region size, a

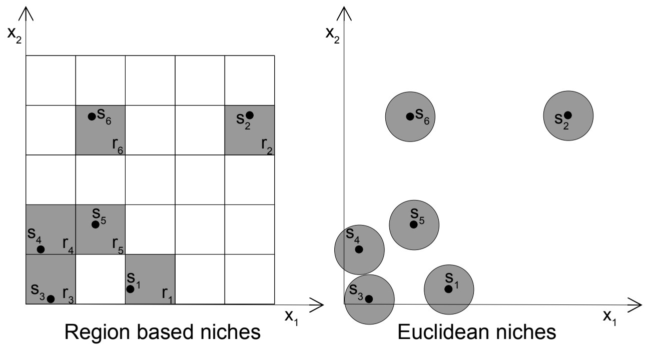

Figure 1: Example of region-based niches and distance-based niches

commonly critical parameter in niching strategies, following the idea proposed in [21], the region size is decreased along the search, as it is detailed in the following subsection.

3.2. General Scheme

Considering the classification described in Section 2.3, RMAwA uses an adaptive hyper-heuristic strategy. It alternatively applies an EA and a LS method. The EA is applied over the population during I_{EA} evaluations and then the best solution of the population s_{best} is selected for local improvements by the LS until the LS cannot bring about any other significant improvement. This loop is repeated until the given maximum number of evaluations Max_{FEs} is reached. The general scheme of the algorithm can be seen in Algorithm 1.

Algorithm 1 Pseudo-code for general scheme of the RMAwA

Initialise population with uniform distribution over the whole search space
while Max_{FEs} is not reached **do**
    Apply SSGA with i_{EA} evaluations following Algorithm 2
    Select the best individual in the population s_{best}
    Apply LS method following Algorithm 3 on s_{best}
    if conditions for number of divisions update **then**
        Update number of divisions: $ND_i = m_u \cdot ND_{i-1}$
        Update index of the archive
    end if
end while

In the proposal, when the EA generates a solution in a region with a existing solution, the worst is removed. By increasing the number of regions, we also try to reduce the possibility for the EA to encounter more and more difficulties in finding new solutions falling in regions not already represented in the archive.

With the region definition of a niche, the region size is defined by the number of divisions per dimension ND. We consider that the stopping criterion is a predefined maximum number of fitness evaluations Max_{FEs}. ND starts with a initial value ND_0. Then, ND is increased u times throughout the search by $ND_i = m_u \cdot ND_{i-1}$ where m_u is the multiplier of the number of division. An update occurs every $Max_{FEs}/(u+1)$. The values for parameters ND_0, u and m_u are indicated in Section 4. In order to prevent the search from stalling, an update of ND also occurs if every region has been explored by the LS and are represented in the archive. This situation is very likely to happen in low dimensionality. For each update, the corresponding regions of each solution in the population are recalculated and the archive updates the regions according to the solutions presented.

The following two sections describe the EA and the LS method used and how they are incorporated in the RMAwA.

3.3. The EA

The EA in RMAwA evolves a population of solutions over the whole search space seeking promising solutions for the LS method to refine. The evolution process is orientated by the region-based niching strategy and the set of excluded regions from the archive.

Algorithm 2 Pseudo-code for the EA in RMAwA

$i = 0$
while $i < i_{EA}$ **do**
    Select two parents in the population
    repeat
        Create an offspring s_n using crossover and mutation
        Calculate the region r_n to which s_n belongs
    until r_n is not represented in the archive
    Evaluate s_n, $i = i + 1$
    Retrieve from the population the set of solutions S_{r_n} of solutions belonging to the region r_n
    if $S_{r_n} \neq \emptyset$ **then**
        set $S_{r_n} = S_{r_n} \cup s_n$
        Remove worst individual from S_{r_n}
    else
        Replace the worst individual s_{worst} in the population if $f(s_n)$ is better than $f(s_{worst})$
    end if
end while

The EA used here, as in the RMA-LSCh, is a steady-state genetic algorithm (SSGA). On each application, the algorithm runs over i_{EA} evaluations. Two parents are selected by means of *negative assortative mating* strategy (NAM) [1] (with a pool size of 3). Offspring are generated using a BLX-α crossover operator [14] and the BGA mutation operator [36]. The EA in the RMAwA is described in Algorithm 2.

When a new solution s_n is generated via the operators described above, it goes through different processes before validation. First, the region r_n it belongs to is calculated. Then, r_n is looked for in the archive. If this region is already represented by one optimum in the archive, s_n is discarded and thus not evaluated. Otherwise, s_n is evaluated and compared with the set of solutions from the population present in the same region r_n. The worst solution is then removed and replaced by s_n. If r_n is not yet represented in the population, then s_n competes with the worst solution of the whole population to replace it.

3.4. The LS method

The continuous LS algorithm used here is CMA-ES [17]. This algorithm is the *state-of-the-art* in continuous optimisation. Thanks to the adaptability of its parameters, its convergence is very fast and obtains very good results. CMA-ES uses a distribution function to obtain new solutions, and adapts the distribution around the best created solutions.

Contrarily to RMA-LSCh, RMAwA does not implement a LS chaining mechanism because the local search here is applied to the same solution until it cannot be improved anymore. This modification is due to the fact that this algorithm considers as optima solutions those which cannot be improved by LS application.

As stated before, the best solution s_{best} of the population is selected for local refinement. To ensure that this solution will not take part in further exploration, it is removed from the population, placed in the archive and replaced by a random solution. The LS is applied multiple times with i_{LS} evaluations until the last application does not bring about any other sufficient improvement. Between each application, the parameters of the previous LS application are retrieved to carry on from the point where it stopped. In the case of CMA-ES, the learnt covariance matrix is thus reused from one application to another. The final solution is then stored in the archive. The application of the LS is described in Algorithm 3.

Algorithm 3 Pseudo-code for the application of the LS in RMAwA

1: Add s_{best} to the archive
2: $s_{LS}^0 = s_{best}$
3: Replace s_{best} by a random solution in the population
4: **repeat**
5: Apply the LS method to s_{LS}^t with i_{LS} evaluations, giving s_{LS}^{t+1}
6: **until** $|f(s_{LS}^t) - f(s_{LS}^{t+1})| < \delta_{LS}^{min}$
7: Add s_{LS}^t to archive

3.5. The archive

As described previously, this algorithm implements an archive aiming at storing solutions considered as optimised (solutions that have been refined by the LS method) and creating an index of regions of the search space considered undesirable for further exploration.

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We describe in this section the structure of the archive allowing such mechanisms. We then characterise the solutions which are inserted in the archive to define their region as undesirable.

3.5.1. Structure

The archive is composed of two collections and its size is not limited. The first one is a simple list of real-value solutions that store the detected optima. The second one is a sorted index of the regions represented by the solutions in the previous list. The regions listed in the index are considered as forbidden areas for the generation of future solutions by the EA. The index is a self-balancing binary search tree which offers an insertion and search complexity of $O(\log n)$. This low complexity allows a large amount of solutions to be stored in the archive with a limited computational cost. Moreover, it only allows unique elements to be stored.

In Figure 2, we show an example of the archive structures in the continuity of the representation of the search space in Figure 1. We can see how a new solution, composed by the actual real-value solution s_n and the indices of the region it belongs to r_n, are used. The former is stored in the archive while the latter is added to the index. If a region is represented by multiple solutions in the archive, there will be only one entry in the index for that region. The following section describes what regions are considered as restricted to further exploration.

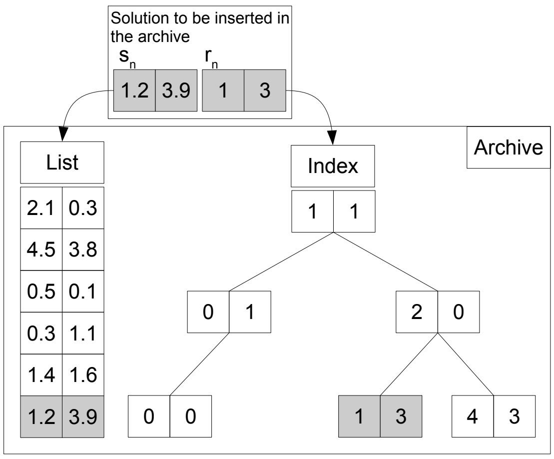


Figure 2: Example of the representation of the archive and its index for two-dimensional problems

3.5.2. Solutions stored the archive

The main purpose of the archive is to store optima identified during the search. Knowing when an optima is found can however be complicated if the fitness value of the optima is unknown. Thanks to the use of an LS method, we consider a solution as an optimum (local or global) when the last LS application does not bring sufficient improvement. Insufficient improvement occurs when the difference between the fitness of the starting point of the LS and the fitness of the obtained solution is below δ_{LS}^{min}.

Apart from storing the optima found by means of LS, the archive also saves the solution that serves as the starting point of each LS application. The idea behind this is to also eliminate from the search space regions that lead to already identified optima.

To summarise, the archive stores the solutions that have undergone LS applications. The rationale behind this is to ensure that the regions in the archive and thus removed from the search space have been intensively explored. However, depending on the characteristics of the fitness landscape, it is not guaranteed that several optima are not in the same region. This risk is reduced by decreasing the niche size during the search as is described above.

3.5.3. Updating the niche size

The update of the number of divisions per dimensions, i.e. the niche size, is performed in order to prevent the presence of multiple optima in the same region. This process is particularly important in this model as some of the regions are completely discarded from the search which may lead to ignoring a number of optima. When an update is performed, as the regions indices are modified and the archive index is wiped:

- A new index is created from the resulting list of regions. Because the solutions are kept in the population, its corresponding regions (using the new size) are calculated again and stored in the archive. The number of stored regions is maintained but the indexes make reference to smaller regions.
- The regions of the solutions stored in the archive are recalculated according to the new partitioning of the search space.

In summary, the archive has to be recalculated with each update of the niche size, thus its structure is designed to carry out the operation easily and efficiently.

4. Experimental framework

The experiments in this paper were carried out using the benchmark proposed for the special session and competition on niching methods for multimodal function optimisation of the IEEE Congress on Evolutionary Computation in 2013 (CEC'2013) [25]. In this section, we describe the framework used to perform these experiments: first we describe the benchmark used and the evaluation method, and then we explain the parameter tuning used for the final version of the algorithm.

4.1. The CEC'2013 benchmark

The CEC'2013 benchmark offers a set of continuous objective functions $f : \mathcal{D} \to \mathbb{R}$ where $\mathcal{D} \subset \mathbb{R}^D$ defines the bounded subset of $\mathbb{R}^D$. The objective consists in identifying every $x \in \mathcal{D}$ such that $x = argmin_{z \in \mathcal{D}}\{f(z)\}$. Functions in this benchmark are to be tackled as black-box problems, i.e. the use of differential based methods is not allowed. Each function contains a finite number of global of optima.

The CEC'2013 benchmark is composed of 12 bounded functions :

- f_1 : Five-Uneven-Peak Trap, $f_1(x)$ where $x \in [0, 30]$, $D = 1$
- f_2 : Equal Maxima, $f_2(x)$ where $x \in [0, 1]$, $D = 1$
- f_3 : Uneven Decreasing Maxima, $f_3(x)$ where $x \in [0, 1]$, $D = 1$
- f_4 : Himmelblau, $f_4(\vec{x})$ where $\vec{x} \in [-6, 6]^D$, $D = 2$
- f_5 : Six-Hump Camel Back, $f_5(x_1, x_2)$ where $x_1 \in [-1.9, 1.9]$ and $x_2 \in [-1.1, 1.1]$, $D = 2$
- f_6 : Shubert, $f_6(\vec{x})$ where $\vec{x} \in [-10, 10]^D$, $D = \{2, 3\}$
- f_7 : Vincent, $f_7(\vec{x})$ where $\vec{x} \in [0.25, 10]^D$, $D = \{2, 3\}$
- f_8 : Modified Rastrigin - All Global Optima, $f_8(\vec{x})$ where $\vec{x} \in [0, 1]^D$, $D = 2$
- f_9 : Composition Function 1, $f_9(\vec{x})$ where $\vec{x} \in [-5, 5]^D$, $D = 2$
- f_{10} : Composition Function 2, $f_{10}(\vec{x})$ where $\vec{x} \in [-5, 5]^D$, $D = 2$
- f_{11} : Composition Function 3, $f_{11}(\vec{x})$ where $\vec{x} \in [-5, 5]^D$, $D = \{2, 3, 5, 10\}$
- f_{12} : Composition Function 4, $f_{12}(\vec{x})$ where $\vec{x} \in [-5, 5]^D$, $D = \{3, 5, 10, 20\}$

Some function are presented with different dimensionality creating a total of 20 problems. Table 1 details the 20 problems and their characteristics. In this paper, we refer by f_i to i-th function and F_j to the j-th problem, a problem consisting of the pair $\{f_i, D\}$ where D is the dimensionality of the problem. We are only interested here in identifying the global optima. The number of global optima is known and finite, but this information cannot be used in the optimisation process. More details on each function can be seen in [25].

4.2. Evaluation

For the evaluation of an algorithm's performance over multiple run (50 runs to be executed following the competition requirements), we use the now commonly used *peak ratio* (PR). The PR is the average percentage of found optima

Table 1: CEC'2013 benchmark problems

Problem	Function	D	Number of optima	Max_{FEs}
F_1	f_1	1	2	$5 \cdot 10^4$
F_2	f_2	1	5	$5 \cdot 10^4$
F_3	f_3	1	1	$5 \cdot 10^4$
F_4	f_4	2	4	$5 \cdot 10^4$
F_5	f_5	2	2	$5 \cdot 10^4$
F_6	f_6	2	18	$2 \cdot 10^5$
F_7	f_7	2	36	$2 \cdot 10^5$
F_8	f_6	3	81	$4 \cdot 10^5$
F_9	f_7	3	216	$4 \cdot 10^5$
F_{10}	f_8	2	12	$2 \cdot 10^5$
F_{11}	f_9	2	6	$2 \cdot 10^5$
F_{12}	f_{10}	2	8	$2 \cdot 10^5$
F_{13}	f_{11}	2	6	$2 \cdot 10^5$
F_{14}	f_{11}	3	6	$4 \cdot 10^5$
F_{15}	f_{12}	3	8	$4 \cdot 10^5$
F_{16}	f_{11}	5	6	$4 \cdot 10^5$
F_{17}	f_{12}	5	8	$4 \cdot 10^5$
F_{18}	f_{11}	10	6	$4 \cdot 10^5$
F_{19}	f_{12}	10	6	$4 \cdot 10^5$
F_{20}	f_{12}	20	8	$4 \cdot 10^5$

over all global optima within the Max_{FEs} evaluations, and it is calculated by following Eq. 4:

$$PR = \frac{\sum_{i=1}^{NR} NPF_i}{NKP * NR} \tag{4}$$

where NPF_i is the number of global optima found in the ith run, NKP is the number of known global optima and NR is the number of runs (for this benchmark, $NR = 50$). It is considered that an optimum $optim$ is obtained if a solution sol is found where $dist(sol, optim) \leq \epsilon$, where dim is the Euclidean distance, and ϵ is a real value called accuracy level. The PR are calculated according to five different accuracy levels $\epsilon = \{10^{-1}, 10^{-2}, 10^{-3}, 10^{-4}, 10^{-5}\}$.

Comparisons between algorithms have been performed for each accuracy level independently. For the comparison of two algorithms we considered non-parametric statistical tests [9]. More specifically, we used the Wilcoxon matched-pairs signed ranks tests for the direct comparison of two algorithms.

4.3. Automatic configuration

Setting the parameters of a new proposal can be a long and tedious task. Moreover, it does not ensure an optimal setting for these parameters. Considering the novelty of certain components in this algorithm, it is more reliable to use an automatic configuration tool to assist in the design of the algorithm tuning the most critical parameters. To do so, we have used IRACE [29]. The IRACE package has already been extensively tested in several research projects, leading to successful improvement of the state-of-the-art, see for instance [28, 27]. The reader may refer to [41] for more information about IRACE and its parameters (we have used the recommended parameter values).

We selected a set of parameters that we considered the most critical, and tuned them over the 20 problems of the CEC'2013 benchmark. For the non-tuned parameters we have selected commonly used values when not recommended values where given by from its authors. The list of tuned parameters can be seen in Table 2, showing for each parameter the explored range and the final value obtained by IRACE.

Table 2: Tuned parameters and obtained values

Parameters	Descriptions	Ranges	Tuned
i_{EA}	EA intensity, number of evaluations allocated to each EA application	$[100, 1000]$	550
i_{LS}	LS intensity, number of evaluations allocated to each LS application	$[100, 1000]$	150
ND_0	Initial number of divisions, defines the size of the niches/regions	$[2, 10]$	2
u	Number of update to be performed	$[2, 5]$	4
m_u	Update multiplier	$[1, 5]$	1.7
NP	Population size of the EA	$[40, 120]$	70
α	Parameter for the $BLX-\alpha$ crossover	$[0.1, 0.9]$	0.9

We can note that the EA intensity is almost four times the LS intensity. This is due to the fact that the LS is applied multiple times (until the improvements brought not significant enough) in each cycle. Concerning the number of division, we can see that the smallest number of divisions have been preferred ($ND_0 = 2$) along with a slow increase during the search by multiplying four times by 1.7: $ND_{i+1} = ceil(1.7 \cdot ND_i)$. The number of the divisions sequence is then $[2, 4, 7, 12, 21]$. Finally an important thing to note is the value of the α parameter for the BLX-α. Set to a high value ($\alpha = 0.9$), it gives the EA a great exploration range.

The other parameters listed in Table 3 were left to their default values taken from the corresponding papers. δ_{LS}^{min} defines the accuracy required for the search and is set to 10^{-6} as the highest accuracy level required is 10^{-5}. Concerning CMA-ES problems, we have set them to the default values as given in [17]. and the size of NAM selection method is taken from the previous work in [21].

The parameters presented in Table 2 and 3 are the ones used in every experiment performed on every function and dimension of the benchmark.

Table 3: Other parameters

Parameters	Descriptions	Value
λ	Parameter to define the CMA-ES population size $p = 4 + \lambda ln(D)$	3 [17]
μ	Defines the parent size for the CMA-ES p/μ	2 [17]
NAM_{size}	Size of the NAM selection method	3 [21]
δ_{LS}^{min}	Threshold for the LS stopping criterion	10^{-6}

4.4. Possibility of finding all optima

In this section, we discuss the ability of RMAwA to find all optima with an unlimited number evaluation. In other words, we wish to ensure that the search is not restricted to any subset of the whole search domain. For this model, we identify two phenomena that can cause such restriction and we discuss here if their occurrence is possible in the proposal.

First, in population-based algorithm the risk of premature convergence of the population may lead to a genetic drift. The fact that RMAwA regularly generates new random solutions (when a solution is placed in the archive, it is replaced by a random solution) ensures sufficient diversity in the population to prevent premature convergence.

The second risk that can be identified in this model is due to the restriction of the search to regions represented in the archive. Indeed, if a region represented in the archive contains more that one optimum, some optima might be ignored. The probability of having more than one optimum present in the same region (noted M) is directly proportional to the hyper-volume of the regions V_r calculated by Eq. 5:

$$P(M) = a.V_r \tag{5}$$

where a is a variable that is dependent on the objective function f and the search domain. Basically, the smaller the region, the less probable that it will contain multiple optima. Thanks to the region size update, V_r keeps decreasing during the search. In our algorithm, we make a limited number of reductions because the fitness evaluation number is also very limited. For an extremely large fitness evaluation number, the reductions would be applied repeatedly, reducing the hyper-volume of the regions each time. Thus, for an unlimited number of evaluations Max_{FEs}:

$$\lim_{Max_{FEs} \to +\infty} V_r = 0 \tag{6}$$

Hence:

$$\lim_{Max_{FEs} \to +\infty} P(M) = 0 \tag{7}$$

Thus, there is no risk of limiting the search.

5. Experimental results

In this section, we are going to study the behaviour of the different components of our proposal, and we are going to compare our algorithm to previous algorithms in the literature. All the experiments are carried out following the experimental framework explained in previous section.

The analysis of our proposal include the following experiments: First, we prove that using the region definition of a niche compared to the euclidean definition is more efficient in terms of computational time and exploration. Then, we demonstrate that using the solutions in the archive as excluding regions enhance the performance of the model. We also analyse the influence of the region based niching strategy with the archive on the diversity of the population and in the exploration factor. Then, we analyse the memory and computational cost of the archive and the different components of the algorithm. Finally, we compare the proposed algorithm RMAwA with existing algorithms.

5.1. Region niches versus classical niches

Here, we assess the efficiency in terms of computation time and performance of the region definition of niches against the classical definition which implies calculating the euclidean distance between solutions. To do so, we consider the model presented without the use of the archive.

The resulting algorithm here simply referred to as region based memetic algorithm (Region-MA) is opposed to an equivalent algorithm which uses the euclidean distance based definition of a niche as it is used in the classical clearing algorithm. This version is referred to as euclidean-distance based memetic algorithm (Euclidean-MA). On the generation of a new solution by the EA, the offspring created compete with the solutions falling within its niche radius σ, which is set to half the size of a region. In Region-MA, as it is explained in Section 3.1, new solutions created by the EA compete with the solutions already in the same regions.

In order to simplify the display of the results, we will only focus on the highest level of accuracy ($\epsilon = 10^{-5}$). Indeed, the definition of a niche only affects the ability of the algorithm to explore the search space and not the precision of the solutions obtained.

In Table 4, we show the PRs obtained by both versions along with the execution time difference in percentage. We can see that the results of Region-MA are clearly better, and with significant differences (comparing with Wilcoxon's test, the use of regions is statistically better with a p-value< 0.001, see Table 5). Also, the execution time is much smaller, over the whole benchmark, using the region-based niches saves up to 17.4% of time.

Table 4: PRs (for $\epsilon = 10^{-5}$) obtained by Region-MA and Euclidean-MA and execution time difference (in percentage)

Problem	F_1	F_2	F_3	F_4	F_5
Region-MA	**0.81**	0.42	**1**	**0.97**	**0.99**
Euclidean-MA	0.77	**0.56**	**1**	0.36	0.87
Time difference (%)	-35.88	-26.10	-28.36	-45.20	-43.57
Problem	F_6	F_7	F_8	F_9	F_{10}
Region-MA	**0**	**0.7**	**0.06**	**0.22**	**0.94**
Euclidean-MA	**0**	0.05	**0.06**	0.01	0.13
Time difference (%)	-30.26	-39.05	-42.13	-38.96	-24.89
Problem	F_{11}	F_{12}	F_{13}	F_{14}	F_{15}
Region-MA	**0.68**	**0.86**	**0.63**	**0.64**	**0.15**
Euclidean-MA	0.27	0.14	0.2	0.18	0.14
Time difference (%)	-19.42	-20.90	-28.38	-19.20	-21.11
Problem	F_{16}	F_{17}	F_{18}	F_{19}	F_{20}
Region-MA	**0.36**	**0.16**	**0.17**	**0.13**	**0.13**
Euclidean-MA	0.19	0.13	**0.17**	**0.13**	**0.13**
Time difference (%)	-15.93	-1.56	-25.74	-21.19	-7.42

Table 5: Wilcoxon comparison of the PR obtained by Region-MA and Euclidean-MA (for $\epsilon = 10^{-5}$)

R+ Region-MA	R- Euclidean-MA	p-value
189	21	0.0008

5.2. Using the archive to reduce the search space

The archive is used to store solutions considered as optima to allow the algorithm to remove them from the population without losing them. In our algorithm, it is used also to mark some regions as areas excluded for the search. In this section, we are interested in assessing how using the regions represented in the archive as excluded areas for the exploration of the EA improves the exploration of the search space and thus the discovery of more optima.

In order to perform this comparison, we ran two versions of the algorithm. The first one is as presented in Section 3. The second one is the same algorithm without verifying that each solution created by the EA is present or not in the archive (steps 4-7 in Algorithm 2 are ignored). We thus compare here the proposed algorithm which uses an excluding archive (RMAwA) against one with a simple archive called RMA with Simple Archive (RMAwSA).

As in the previous experiment, we will only focus on the highest level of accuracy ($\epsilon = 10^{-5}$). Indeed, the specific use of the archive mainly affects the algorithm's ability to explore the search space and not the precision of the solutions obtained.

Table 6: PRs of the RMA using an excluding archive (RMAwA) and a simple archive (RMAwSA) for $\epsilon = 10^{-5}$ and computational time difference between the two versions.

Problem	F_1	F_2	F_3	F_4	F_5
RMAwA	**1.000**	**1.000**	**1.000**	**1.000**	**1.000**
RMAwSA	**1.000**	0.312	**1.000**	**1.000**	**1.000**
Time difference (%)	22.6	23.3	7.7	15.5	3.1
Problem	F_6	F_7	F_8	F_9	F_{10}
RMAwA	0.000	**0.917**	0.824	**0.513**	**1.000**
RMAwSA	0.000	0.658	**0.908**	0.343	0.983
Time difference (%)	46.3	34.8	50.8	43.4	4.1
Problem	F_{11}	F_{12}	F_{13}	F_{14}	F_{15}
RMAwA	**1.000**	**1.000**	**0.997**	**0.813**	**0.703**
RMAwSA	0.667	0.930	0.667	0.667	0.648
Time difference (%)	5.8	1.5	2.2	21.8	15.3
Problem	F_{16}	F_{17}	F_{18}	F_{19}	F_{20}
RMAwA	**0.670**	**0.660**	**0.233**	**0.128**	**0.125**
RMAwSA	0.667	0.323	0.183	0.125	0.125
Time difference (%)	5.0	14.1	2.4	0.7	1.2

In Table 6, we show the PRs obtained by both versions of the algorithm and the time difference. Thanks to the excluding property of the archive, the performances of the algorithm are significantly improved (see Table 7 for Wilcoxon comparison). We also display in this table the CPU time increase caused by the use of the archive in the search. As we could have expected, this property implies more computational effort. However, the percentage increase in the computational time is reduced with the complexity and the dimensionality of the problem. This can be easily explained by the fact that in higher dimensions, the computational time of the evaluation increases while the time cost of the archive remains steady regardless the dimensionality. Also, considering the sum of the computational time for the whole benchmark, the runtime of RMAwA is 8.2% higher than RMAwSA's (it cannot be calculated from table 6 because some functions take longer than others).

Table 7: Wilcoxon comparison of the PR of the RMA with and without archive (for $\epsilon = 10^{-5}$)

R+ RMAwA	R- RMAwSA	p-value
186.5	23.5	0.00132

5.3. Diversity and Exploration

In this section we analyse how RMAwA explores the search domain. First, we are going to study how the population diversity evolves along the search. Then, we visually analyse the exploration of the algorithm by plotting for several functions the solutions generated during the exploration phase.

5.3.1. Population diversity: Influence of the Number of Divisions

In this section we analyse the evolution of the population diversity during the search, and the influence of ND over the diversity. To do so, additional runs have been carried out and a diversity measure has been applied to the solutions into the population. The diversity measure applied is the following:

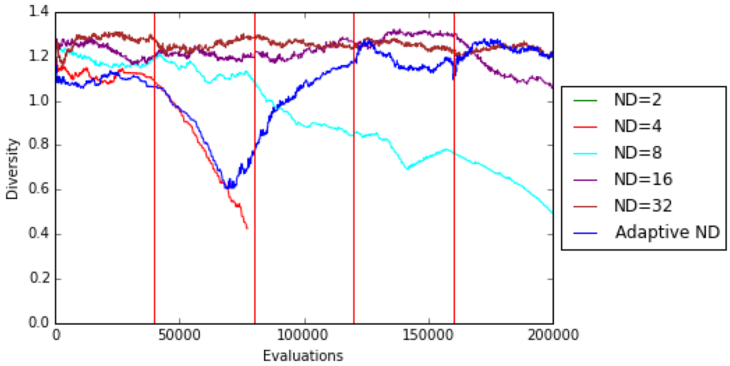
$$Diversity_{Pop} = \frac{\sum_{i=1}^{N-1} \sum_{j=i+1}^{N} dist(x_i, x_j)}{N \cdot (N-1)/2} \tag{8}$$

where Pop is the current population, N is the population size, $dist$ is the Euclidean distance, and x_i, x_j are solutions in the population.

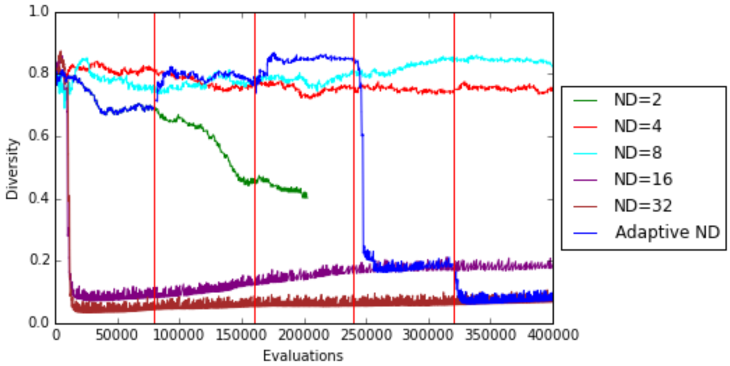
To study the influence of the current ND over the diversity, we are going to visualise and compare the diversity of the proposal (using the adaptive ND mechanism described in 3.2), with using a fixed ND.

Figure 3 shows the evolution of the diversity for functions F_7, F_{16} and F_{18}. These functions have been selected for being representative of the different behaviours detected in this benchmark. In axis x there is the number of evaluations, and in axis y the diversity measure. The vertical lines mark the updates of number of divisions (it only has influence over the adaptive ND version), dividing the axis x in five stages of the algorithm (each stage using a different ND). In the following, we are going to describe the main tendencies:

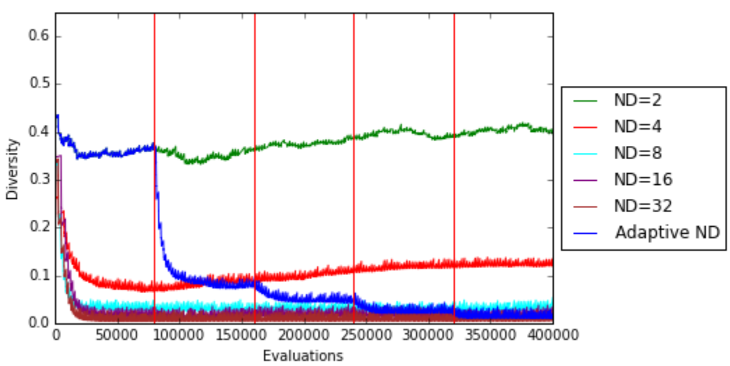
1. In functions with a small dimension, like F_7 (where D=2), we can observe two phases. In the initial stages of the search (ND=2, ND=4), because



(a) F_7



(b) F_{16}



(c) F_{18}

Figure 3: Diversity of the RMAwA population using adaptive number of divisions and using different fixed number of divisions during one run

there are few regions, when a region is avoided the search space is reduced very quickly to a small portion of the whole space, thus the diversity decreases very quickly. Indeed, for these ND values the fixed ND version prematurely stops because all possible regions have a local optima. The subsequent updates in ND increase the number of regions, releasing space for the EA to explore and thus increasing the diversity. As compared with fixed ND, the diversity of adaptive ND is very similar in the first two and final stages, with a greater diversity in the stages inbetween.

2. In functions with medium dimensionality, like F_{16} (D=5), the same phenomena is observed. However, after reaching a certain number of divisions per dimensions (third update) the diversity decreases, because the algorithm allows solutions more closer between them, reducing the diversity to enforce the exploitation of found solutions. Comparing adaptive ND with fixed ND, we can observe that diversity adaptive ND is actually very similar to ND in each stage.
3. In functions with higher dimensionality, like F_{18} (D=10), we can see that the diversity constantly decreases at each increase of the number of divisions. In these functions, it seems that the niching model does not provide a good balance in the population diversity during the search. Comparing adaptive ND with fixed ND, we can observe that adaptive ND obtains very close results to obtained by the fixed ND in each stage.

The previous section has shown the diversity differences comparing several fixed ND and the proposed dynamic ND. However, diversity itself is not our goal, thus we are going to compare the obtained PRs for each case. Table 8 show the results, highlighting the results for those functions whose diversity has been analysed. We can observe that:

- In functions with a small dimension, like F_7, in which a higher ND implies a better diversity, the number of optima increases also with the ND. Better results are obtained with dynamic ND.
- In functions with medium dimensionality, like F_{16}, in which for certain ND values the diversity is reduced very quickly, the PR decreases when ND increases. Dynamic ND, on the contrary, obtains the best PR value.
- Results obtained in functions with higher dimensionality, like F_{18}, proves that there is noy a good balance in the diversity, and that it has bad consecuences for the obtained PR. In this case, dynamic ND obtains worse results than using ND=2 but better than the other values.

In summary, Figure 3 shows that the number of regions and problem dimensionality have strong influence over the diversity in the population and the number of found optima, and that diversity using an adaptive ND is very close to that obtained with a fixed ND in each stage, obtaining the most robust behaviour when finding the optima.

Table 8: PRs of the RMAwA using different fixed numbers of divisions (ND) and with dynamic ND.

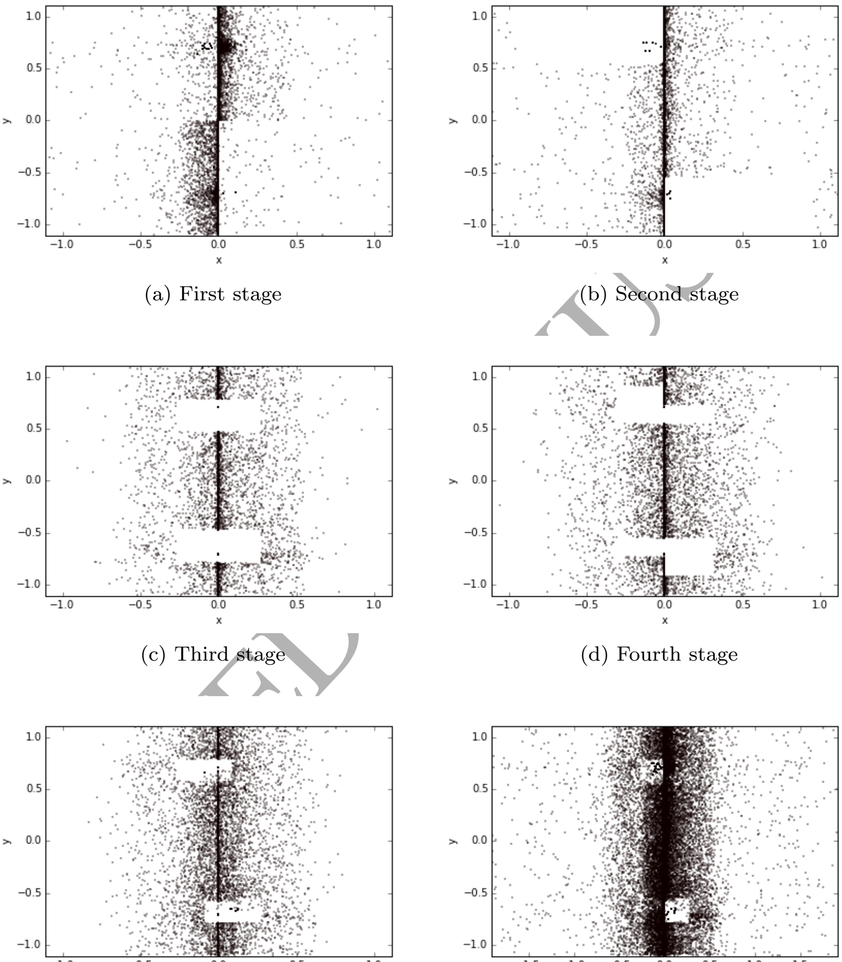
Function	ND=2	ND=4	ND=7	ND=12	ND=21	Dynamic ND
F1	0.900	1.000	1.000	1.000	1.000	1.000
F2	1.000	1.000	1.000	1.000	1.000	1.000
F3	1.000	1.000	1.000	1.000	1.000	1.000
F4	0.750	1.000	1.000	1.000	1.000	1.000
F5	1.000	1.000	1.000	1.000	1.000	1.000
F6	0.000	0.000	0.000	0.000	0.000	0.000
F7	**0.084**	**0.429**	**0.612**	**0.790**	**0.829**	**0.917**
F8	0.023	0.290	0.610	0.458	0.853	0.824
F9	0.035	0.172	0.433	0.660	0.618	0.513
F10	0.923	1.000	1.000	1.000	1.000	1.000
F11	0.733	1.000	1.000	1.000	1.000	1.000
F12	0.470	0.840	0.875	0.955	1.000	1.000
F13	0.680	0.993	1.000	1.000	1.000	0.997
F14	0.760	0.813	0.940	0.727	0.647	0.813
F15	0.665	0.725	0.675	0.640	0.275	0.703
F16	**0.667**	**0.667**	**0.533**	**0.300**	**0.273**	**0.670**
F17	0.660	0.680	0.250	0.185	0.165	0.660
F18	**0.473**	**0.167**	**0.167**	**0.167**	**0.167**	**0.233**
F19	0.160	0.125	0.125	0.125	0.125	0.128
F20	0.125	0.125	0.125	0.125	0.125	0.125
Mean	0.555	0.651	0.667	0.657	0.654	0.729

5.3.2. Exploration of the domain search

In this section, we study the exploration over the search space that RMAwA carries out. First, we observe the solutions generated for each stage of the algorithm to visualise the influence of the number of divisions over the exploration. Then, we analyse if the exploration of the domain search is adapted to the landscape of the function to optimise.

Figures 4, 5, and 6 show the generated and evaluated solutions by RMAwA for the 2-D functions: f_5, f_6, and f_7. Solutions generated by the LS have been excluded, because they were too similar to previous solutions to be useful for the analysis. In order to explore the influence of the current ND value over the degree of exploration, in each figure the generated solutions for each stage are shown differently (when the same ND value is applied). From these figures, several conclusions can be extracted:

- In the initial stage the distribution of solutions is around the complete domain search. There are two reasons for this: First, the initial population has been randomly generated. Also, while there are no detected local optima in one region, the new solutions are evaluated to check if they have better fitness than the existing ones.
- In the following stages, several solutions have been detected as local optima, so no more solutions are generated in the same regions. Thus, the exploration shows several empty spaces around the detected optima.
- While the ND value decreases, these empty spaces are reduced, generating solutions closer to current local optimum.
- In subfigures (f) with all the generated solutions, regions can be visualised but not very clearly because they contain solutions generated in the first stage, previous to the detection of local optima.



(a) First stage

(b) Second stage

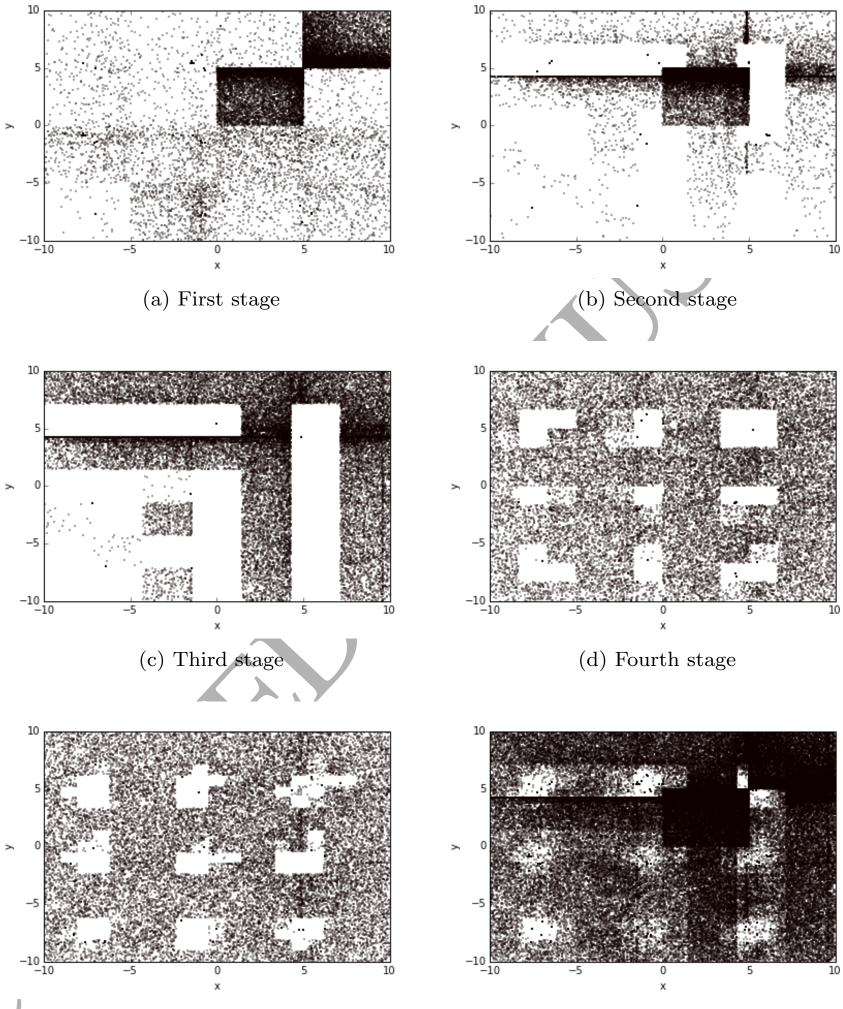
(c) Third stage

(d) Fourth stage

(e) Fifth stage

(f) Total

Figure 4: Generated solutions in function F_5 for each stage

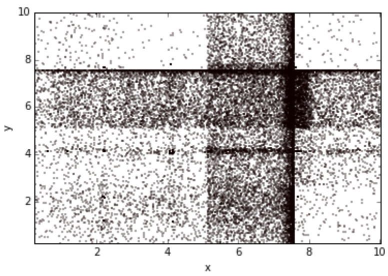


(a) First stage (b) Second stage

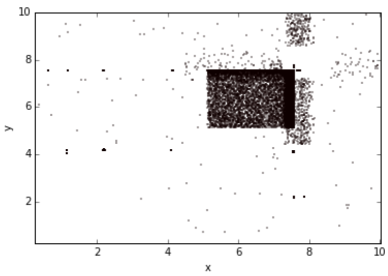
(c) Third stage (d) Fourth stage

(e) Fifth stage (f) Total

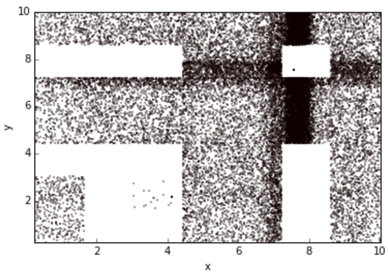
Figure 5: Generated solutions in function F_6 for each stage



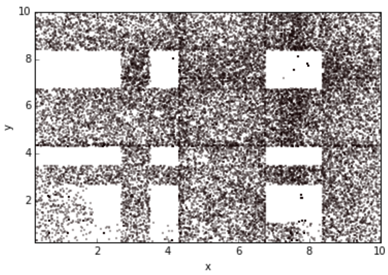
(a) First stage



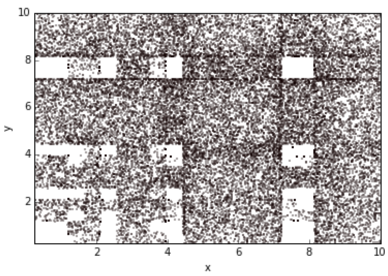
(b) Second stage



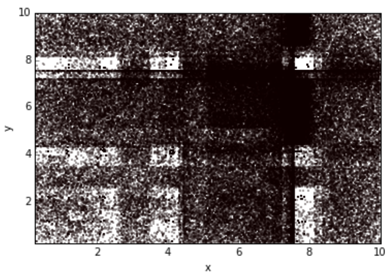
(c) Third stage



(d) Fourth stage



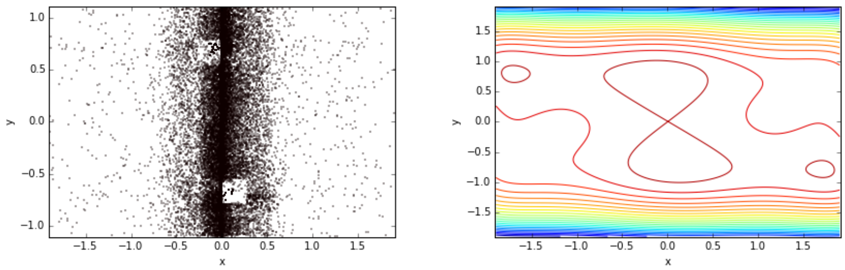
(e) Fifth stage



(f) Total

Figure 6: Generated solutions in function F_7 for each stage

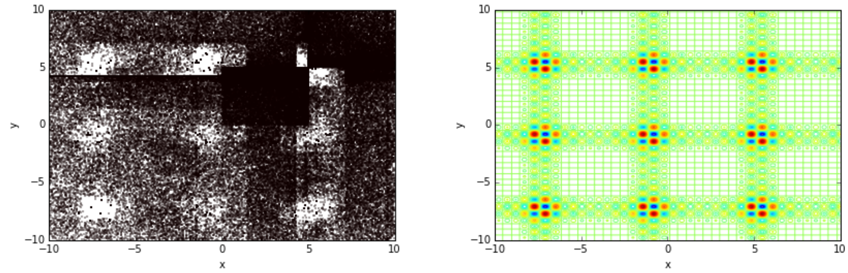
In order to show the exploration done for the algorithm, we plot for functions F_5, F_6 and F_7 in Figures 7, 8, 9 respectively, the total solutions generated and evaluated by the algorithm (no using the LS method). To help the analysis, the contour of the studied functions are also plotted.



(a) Explored Solutions (b) Contour of real function

Figure 7: Function F_5

In Figure 7, we can see that all the domain search is explored, even when the best values are concentrated in one particular area. Also, the area close to each optimum has a reduced number of solutions, because the algorithm has identified them as optima and the region niching avoids solutions in the same region.

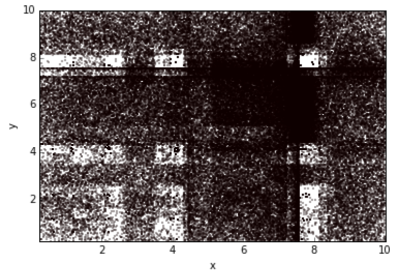


(a) Explored Solutions (b) Contour of real function

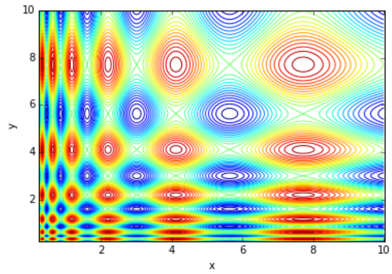
Figure 8: Function F_6

In Figures 8 and 9 we can observe the same behaviour, showing less dense areas surrounding each optimum, thus concentrating the majority of the solutions in regions with no detected optima. It is remarkable that the area of the landscape with the optima have been correctly identified.

In summary, the pattern drawn by the solutions generated during the exploration phase matches the landscape of the objective function. Also, RMAwA behaves as expected: exploring around all the domain search and avoiding at the



(a) Explored Solutions



(b) Contour of real function

Figure 9: Function F_7

same time solutions which are very close to detected optima, defining regions with decreasing size.

5.4. Time and memory cost of RMAwA

In this section, we study the time and memory cost of RMAwA. First, we assess the memory used by the archive. Then we study the computational cost implied by the exclusive property of the archive and the different components of the algorithm.

5.4.1. Memory cost

We present in this section the memory cost implied by the archive. As explained in Section 3.5, the archive list stores two kinds of solutions, the starting and final points of LS applications. In order to evaluate the memory cost of the archive in both cases, we retrieved the number of solutions stored in the archive's list and the number of their corresponding regions represented in the index at the end of each run. From these data, we estimate the total memory size of the archive. The archive's list is a collection of real-value vectors and the index is a collection of integer vectors. In our implementation, real values are represented by "double", coded on eight bytes and integers are represented by "int" coded on four bytes, the space used by the archive is thus calculated by:

$$ArchiveSize = |S| \cdot D \cdot 8 + |R| \cdot D \cdot 4 \tag{9}$$

where $|S|$ is the number of solutions in the archive's list, $|R|$ is the number of regions in the index and D is the dimensionality of the problem. The final size is thus proportionate to the dimensionality. It is also dependant on the maximum number of evaluations allowed by the problem. Indeed, an increase in the number of evaluations increases the number of LS applications and thus the number of solutions stored in the archive. In Table 9, we present the average of 50 runs of these data along with the dimensionality and the maximum number of evaluation for each function of the CEC'2013 benchmark.

As expected, we can observe a strong increase of the physical size used by the archive for the most complex problems. However, the memory used remains reasonable for today's machines. In the most extreme problem, F_{20} where $D = 20$, the archive only uses 64.88 kB of memory. Even if it might appear irrelevant for such problems, the size of the archive can increase exponetially with the dimensionality and the number of evaluation. When tackling large scale problems, one may consider limiting the size of the archive.

Table 9: Average number of elements in the archive's list ($|S|$), the index ($|R|$) and total memory used by the archive (in kB) at the end of each run

Problem	D	Max_{FEs}	$\|S\|$	$\|R\|$	ArchiveSize
F_1	1	$5.00 \cdot 10^4$	135.92	4.58	1.08
F_2	1	$5.00 \cdot 10^4$	130.24	9.96	1.06
F_3	1	$5.00 \cdot 10^4$	129.32	10.52	1.05
F_4	2	$5.00 \cdot 10^4$	106	22.76	1.83
F_5	2	$5.00 \cdot 10^4$	112.76	14.5	1.88
F_6	2	$2.00 \cdot 10^5$	425.52	112.64	7.53
F_7	2	$2.00 \cdot 10^5$	448.28	100.18	7.79
F_8	3	$4.00 \cdot 10^5$	681.84	398.62	20.65
F_9	3	$4.00 \cdot 10^5$	811.64	389.08	23.58
F_{10}	2	$2.00 \cdot 10^5$	431.28	100.68	7.53
F_{11}	2	$2.00 \cdot 10^5$	372.72	106.42	6.66
F_{12}	2	$2.00 \cdot 10^5$	326.04	104.42	5.91
F_{13}	2	$2.00 \cdot 10^5$	349.52	121.84	6.41
F_{14}	3	$4.00 \cdot 10^5$	583	283.48	16.99
F_{15}	3	$4.00 \cdot 10^5$	581.6	278.68	16.90
F_{16}	5	$4.00 \cdot 10^5$	524	259.42	25.54
F_{17}	5	$4.00 \cdot 10^5$	516.64	270.26	25.46
F_{18}	10	$4.00 \cdot 10^5$	446.84	187.36	42.23
F_{19}	10	$4.00 \cdot 10^5$	338.52	168.28	33.02
F_{20}	20	$4.00 \cdot 10^5$	343.8	142.92	64.88

5.4.2. Computational time of the different components of RMAwA

In this section, we analyse the amount of time taken by the different components of RMAwA over a whole run, namely:

- LS operations: the operations performed by CMA-ES during its search process.
- EA operations: the operations performed by the SSGA to evolve the population.
- Niching: the time it takes for a new solution to go through the niching process (retrieval and comparison of the solutions present in the same

region in the population).

- Archive: the time implied by the excluding property of the archive (assessing the presence of the solution's region in the archive's index).

First, to assess the computational time of each component, we use function f_{12}. This function presents the advantage of being implemented in 4 dimensions, $D = \{3, 5, 10, 20\}$, allowing us to evaluate the scalability of the proposal. For those four problems, we calculate the CPU time used by each component to assess their scalability. The search effort is unequally divided between the LS and the EA (the number of evaluation at each EA application is fixed while the number of evaluation for each LS application is not limited). Thus, to perform a fair comparison, we only select the average time per evaluation. We plot the results in Figure 10.

As far as we can see, the complexity of the niching strategy and the use of the archive are barely affected by an increase of the dimensionality. In the same way, the operations of the SSGA algorithms show interesting scalable properties. The main weakness lies in the use of CMA-ES as LS method. Although it offers a low complexity in the lowest dimensions, with more than ten variables, CMA-ES shows poor scalability in terms of complexity.

In order to counterbalance the importance of this drawback, we show in table 10 the CPU time of each of the components along with the evaluation time. Here, we remind the reader of the notation used in this paper, we grouped the problems F_j by function f_i in order to make for easier reading and see the relations between the different dimensions of each function. From this table, when increasing the dimensionality, even if the proportion of the LS (*i.e.* CMA-ES) operations increases, the total CPU time is particularly affected by the computational time of the evaluation which is independent of the algorithm. However, as the complexity of CMA-ES increases exponentially with the dimension, larger scale problems may require the use of another LS method.

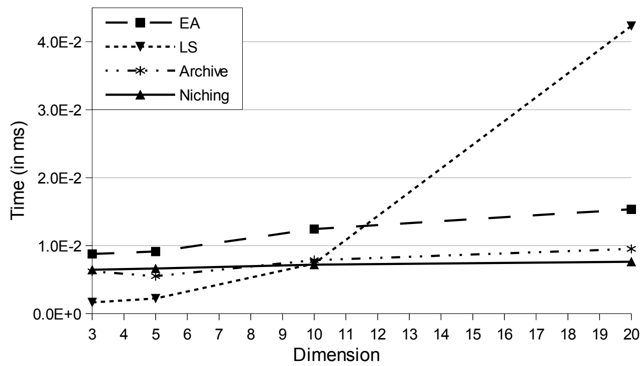


Figure 10: CPU time (in ms) of each component per evaluations for problem f_{12} for different dimensions

Table 10: CPU time (in seconds) details of RMAwA for each problem $F_j = \{f_i, D\}$ with the percentage in the whole optimisatioc process

Problem	$F_1 = \{f_1, 1\}$	$F_2 = \{f_2, 1\}$	$F_3 = \{f_3, 1\}$	$F_4 = \{f_4, 2\}$
Archive	0.150 (18.41%)	0.355 (40.84%)	0.148 (18.99%)	0.099 (14.96%)
Niching	0.236 (28.91%)	0.221 (25.39%)	0.254 (32.43%)	0.180 (27.17%)
EA	0.260 (31.86%)	0.257 (29.59%)	0.282 (36.08%)	0.207 (31.18%)
LS	0.164 (20.08%)	0.027 (3.07%)	0.064 (8.23%)	0.172 (25.93%)
Evaluations	0.006 (0.73%)	0.010 (1.11%)	0.033 (4.27%)	0.005 (0.76%)
Total	0.816	0.869	0.782	0.664
Problem	$F_5 = \{f_5, 2\}$	$F_6 = \{f_6, 2\}$	$F_8 = \{f_6, 3\}$	$F_7 = \{f_7, 2\}$
Archive	0.127 (9.96%)	1.085 (35.82%)	1.512 (29.74%)	1.354 (40.56%)
Niching	0.204 (16.01%)	0.759 (25.05%)	1.188 (23.37%)	0.787 (23.58%)
EA	0.233 (18.27%)	0.884 (29.18%)	1.513 (29.75%)	0.942 (28.23%)
LS	0.696 (54.67%)	0.159 (5.24%)	0.494 (9.72%)	0.173 (5.18%)
Evaluations	0.014 (1.10%)	0.143 (4.70%)	0.377 (7.41%)	0.081 (2.44%)
Total	1.273	3.029	5.085	3.338
Problem	$F_9 = \{f_7, 3\}$	$F_{10} = \{f_8, 2\}$	$F_{11} = \{f_9, 2\}$	$F_{12} = \{f_{10}, 2\}$
Archive	2.210 (35.27%)	0.740 (28.09%)	0.615 (6.15%)	0.521 (5.38%)
Niching	1.403 (22.38%)	0.759 (28.80%)	0.675 (6.74%)	0.586 (6.05%)
EA	1.793 (28.61%)	0.934 (35.41%)	0.903 (9.02%)	0.802 (8.28%)
LS	0.661 (10.55%)	0.153 (5.82%)	0.332 (3.32%)	0.207 (2.13%)
Evaluations	0.200 (3.19%)	0.050 (1.88%)	7.479 (74.77%)	7.571 (78.16%)
Total	6.267	2.636	10.003	9.687
Problem	$F_{13} = \{f_{11}, 2\}$	$F_{14} = \{f_{11}, 3\}$	$F_{16} = \{f_{11}, 5\}$	$F_{18} = \{f_{11}, 10\}$
Archive	0.604 (6.15%)	0.910 (3.88%)	0.853 (2.60%)	1.065 (1.81%)
Niching	0.630 (6.42%)	1.028 (4.39%)	0.951 (2.90%)	0.868 (1.48%)
EA	0.852 (8.69%)	1.441 (6.15%)	1.300 (3.96%)	1.267 (2.16%)
LS	0.210 (2.14%)	0.412 (1.76%)	0.671 (2.04%)	2.099 (3.58%)
Evaluations	7.515 (76.59%)	19.641 (83.82%)	29.054 (88.50%)	53.400 (90.97%)
Total	9.812	23.431	32.829	58.698
Problem	$F_{15} = \{f_{12}, 3\}$	$F_{17} = \{f_{12}, 5\}$	$F_{19} = \{f_{12}, 10\}$	$F_{20} = \{f_{12}, 20\}$
Archive	0.982 (4.15%)	0.773 (2.33%)	0.723 (1.22%)	0.891 (0.71%)
Niching	1.020 (4.31%)	0.932 (2.81%)	0.663 (1.12%)	0.714 (0.57%)
EA	1.387 (5.86%)	1.282 (3.87%)	1.144 (1.93%)	1.435 (1.15%)
LS	0.399 (1.69%)	0.580 (1.75%)	2.267 (3.81%)	12.974 (10.37%)
Evaluations	19.867 (83.98%)	29.560 (89.23%)	54.636 (91.93%)	109.063 (87.20%)
Total	23.655	33.127	59.434	125.077

5.5. Comparison with existing algorithms

In this section we compare the results obtained by our algorithm, RMAwA. We selected a number of algorithms from the literature along with algorithms presented for the CEC'2013 competition:

- PNA-NSGAII [2] proposed for the competition, this algorithm is an improvement of A-NSGAII [8]. These algorithms tackle the multimodal optimisation problem by turning them into bi-objective problems. The first objective is the minimisation of the original function and the second one is the maximisation of the diversity brought by the evaluated individual.
- dADE/nrand/1/bin [12] : a DE using a neighbourhood based mutation strategy and a dynamically updated archive.
- DE/nrand/2 [13] : a DE using the neighbourhood based mutation strategy.
- NVMO [34]: a Variable Mesh optimisation algorithm with niching strategy.
- CMA-ES [18]: A version of CMA-ES that implements a simple archive.
- NEA2 [43]: A version of CMA-ES that uses nearest-better clustering as niching strategy.

These algorithms are the top six algorithms of the CEC'2013 competition. All the results used here were provided by the authors and used during the competition. The detailed results of each algorithm can be seen in the Appendix. We first analyse the overall performance of each algorithm on the benchmark and compare them with RMAwA. Then we study in detail their behaviour according to the problem's characteristics.

5.5.1. Accuracy level analysis

We analyse here the general performance of these algorithms on the CEC'2013 benchmark for each accuracy level. To support this analysis, we show in Table 11 the mean rankings of each algorithm according to the different accuracy levels and in Table 12 the Wilcoxon comparison of RMAwA with the other algorithms.

First, when comparing with other algorithms using CMA-ES, we can see that RMAwA significantly outperforms the classical CMA-ES (with $\alpha = 0.1$). This algorithm is not particularly designed for multimodal optimisation as it does not implement any niching mechanism. When comparing with NEA2, RMAwA offers similar performance.

Then, we can see that RMAwA is third best for the smallest accuracy level ($\epsilon = 1E{-}1$) behind NVMO and dADE although no statistical difference can be observed in Table 12.

Excluding NEA2, RMAwA obtains better results than the other algorithms, and this superiority increases with the accuracy level, being specially remarkable

Table 11: Mean rankings obtained by different algorithms over all functions CEC'2013 benchmark for each accuracy level

Accuracy level	$1E{-}1$	$1E{-}2$	$1E{-}3$	$1E{-}4$	$1E{-}5$
PNA-NSGAII	4.53	5.18	5.28	5.45	5.43
DE/nrand/2	5.53	5.05	4.95	4.83	4.30
CMA-ES	4.58	4.00	4.08	3.93	3.90
NVMO	**2.73**	3.68	4.15	4.43	5.08
dADE	3.43	4.10	4.10	4.08	3.90
NEA2	3.70	**2.75**	**2.55**	2.68	**2.70**
RMAwA	3.53	3.25	2.90	**2.63**	**2.70**

for $\epsilon = \{1E{-}4, 1E{-}5\}$. Between NEA2 and RMAwA there is no statistical difference detected.

This analysis highlights the difficulty of algorithms to properly balance the exploration and the exploitation. Indeed, when algorithms use the original CMA-ES, a very efficient method to obtain accurate solutions but also very costly, they generally perform better for higher accuracy levels. On the other hand, other algorithms (DE-based, NVMO, PNA-NSGAII) have better exploration efficiency but fail to identify accurate solutions.

5.5.2. Problem specific performance analysis

Let us now consider every problem individually. As it is the most challenging for this benchmark, we will consider here only the highest accuracy level ($\epsilon = 1E{-}5$). Table 13 lists the PRs obtained by each algorithm for this accuracy level.

In this analysis we will focus on the problems offering the major differences between the results obtained by the compared algorithms. Concerning problems with highly multimodal fitness landscapes, F_7 to F_9 where the number of optima ranges from 36 to 216, RMAwA ranks amongst the best algorithm. It obtains the best results for problem F_7 and obtains the second best results of problem F_8 and F_9 after respectively dADE and NEA2.

RMAwA also shows the best results in the problems with composition functions (F_{10} to F_{17}). However the quality of the results decreases with the dimensionality (F_{18} to F_{20}), being clearly worse than that obtained by NEA2.

The improvable behaviour of RMAwA when the dimensionality increases is clear because for f_{11} and f_{12} results are very good with dimension 2, but not good with a higher dimension, like 10 (F_{18}-F_{20}). In Section 5.3.1, it can be observed that for these functions the results obtained are low for each possible ND, thus the results are not due to the ND adaptation mechanism. Another possible reason of the improvable results could be that the parameter values have been automatically tuned considering all functions, in which the majority has a very low dimension. Because of this, these parameter values could not be the more adequate for lower dimension problems. In order to reject or confirm

Table 12: Wilcoxon comparison of the PRs of the RMAwA ($R+$) with other algorithms ($R-$) (for $\epsilon = \{1E-1, 1E-2, 1E-3, 1E-4, 1E-5\}$)

$\epsilon = 1E-1$			
RMAwA vs	$R+$	$R-$	p-value
PNA-NSGAII	128.5	65	2.27E-1
DE/nrand/2	180.5	29.5	**3.40E-3**
CMA-ES	168.5	41.5	**1.62E-2**
NVMO	62	132.5	1.96E-1
dADE	71.5	122	3.44E-1
NEA2	117.5	92.5	6.41E-1
$\epsilon = 1E-2$			
RMAwA vs	$R+$	$R-$	p-value
PNA-NSGAII	199.5	10.5	**9.35E-5**
DE/nrand/2	171.5	38.5	**1.14E-2**
CMA-ES	150.5	59.5	**9.35E-2**
NVMO	124.5	85.5	4.67E-1
dADE	134.5	75.5	2.71E-1
NEA2	82.5	127.5	4.01E-1
$\epsilon = 1E-3$			
RMAwA vs	$R+$	$R-$	p-value
PNA-NSGAII	185	7.5	**8.39E-5**
DE/nrand/2	171.5	38.5	**1.14E-2**
CMA-ES	139	53.5	**9.98E-2**
NVMO	166.5	43.5	**2.04E-2**
dADE	147.5	62.5	1.19E-1
NEA2	91.5	118.5	6.14E-1
$\epsilon = 1E-4$			
RMAwA vs	$R+$	$R-$	p-value
PNA-NSGAII	185	7.5	**8.39E-5**
DE/nrand/2	171.5	38.5	**1.14E-2**
CMA-ES	139	53.5	**9.98E-2**
NVMO	185.5	24.5	**1.56E-3**
dADE	165.5	44.5	**2.27E-2**
NEA2	95	97.5	1.00E+0
$\epsilon = 1E-5$			
RMAwA vs	$R+$	$R-$	p-value
PNA-NSGAII	199.5	10.5	**9.35E-5**
DE/nrand/2	151.5	42	**3.23E-2**
CMA-ES	138	54.5	1.09E-1
NVMO	189.5	20.5	**7.79E-4**
dADE	151.5	42	**3.23E-2**
NEA2	96.5	96	9.68E-1

Table 13: PRs obtained by each algorithm for $\epsilon = 1E{-}5$ on the CEC'2013 benchmark. Values in the parenthesis represent the standard competition ranking of each algorithm for each problem

Problem	PNA-NSGAII	DE/nrand/2	CMA-ES	NVMO	dADE	NEA2	RMAwA
F_1	1.000 (1)	1.000 (1)	1.000 (1)	1.000 (1)	1.000 (1)	1.000 (1)	1.000 (1)
F_2	1.000 (1)	1.000 (1)	1.000 (1)	1.000 (1)	1.000 (1)	1.000 (1)	1.000 (1)
F_3	1.000 (1)	1.000 (1)	1.000 (1)	1.000 (1)	1.000 (1)	1.000 (1)	1.000 (1)
F_4	0.805 (7)	1.000 (1)	0.990 (5)	1.000 (1)	1.000 (1)	0.990 (5)	1.000 (1)
F_5	1.000 (1)	1.000 (1)	1.000 (1)	1.000 (1)	1.000 (1)	1.000 (1)	1.000 (1)
F_6	0.000 (1)	0.000 (1)	0.000 (1)	0.000 (1)	0.000 (1)	0.000 (1)	0.000 (1)
F_7	0.683 (5)	0.275 (7)	0.516 (6)	0.804 (3)	0.714 (4)	0.911 (2)	0.917 (1)
F_8	0.252 (4)	0.363 (3)	0.115 (6)	0.027 (7)	0.947 (1)	0.239 (5)	0.824 (2)
F_9	0.276 (4)	0.065 (7)	0.272 (5)	0.194 (6)	0.349 (3)	0.579 (1)	0.513 (2)
F_{10}	1.000 (1)	1.000 (1)	0.978 (6)	0.967 (7)	1.000 (1)	0.980 (5)	1.000 (1)
F_{11}	0.663 (7)	0.667 (5)	0.953 (3)	0.667 (4)	0.667 (5)	0.960 (2)	1.000 (1)
F_{12}	0.573 (7)	0.618 (5)	0.760 (3)	0.593 (6)	0.735 (4)	0.833 (2)	1.000 (1)
F_{13}	0.623 (7)	0.667 (4)	0.947 (2)	0.663 (6)	0.667 (4)	0.947 (2)	0.997 (1)
F_{14}	0.610 (7)	0.667 (4)	0.743 (3)	0.627 (6)	0.667 (4)	0.800 (2)	0.813 (1)
F_{15}	0.443 (5)	0.400 (6)	0.653 (3)	0.378 (7)	0.620 (4)	0.713 (1)	0.703 (2)
F_{16}	0.323 (7)	0.667 (3)	0.663 (5)	0.653 (6)	0.667 (3)	0.673 (1)	0.670 (2)
F_{17}	0.245 (7)	0.280 (6)	0.583 (3)	0.325 (5)	0.358 (4)	0.695 (1)	0.660 (2)
F_{18}	0.093 (7)	0.507 (3)	0.340 (4)	0.327 (5)	0.603 (2)	0.663 (1)	0.233 (6)
F_{19}	0.010 (6)	0.180 (3)	0.597 (2)	0.093 (5)	0.000 (7)	0.667 (1)	0.128 (4)
F_{20}	0.000 (5)	0.230 (3)	0.425 (1)	0.000 (5)	0.000 (5)	0.350 (2)	0.125 (4)

that hypothesis, we have carried out another automatic tuning considering only functions $F_{18} - F_{20}$, but the results obtained were very similar. Thus, the improvable behaviour or RMAwA in higher dimensionality problems is kept as a open issue to be solved in the future.

However, this previous behaviour is not unsurprising, because it has happened to many others, as can be observed in Table 13. As was formulated by the No Free Lunch Theorem, designing an algorithm for an heterogeneous test bed of problems is very challenging. It is common for algorithms to perform well in problems with certain characteristics and poorly on others.

In summary, the algorithm proposed of this paper, RMAwA, offers an overall performance significantly superior to the other algorithms by obtaining competitive if not better results in most problems (except in higher dimension problems) proposed in the CEC'2013 benchmark. Only NEA2, the winner of the CEC'2013 competition obtains equivalent results.

6. Conclusions

In this paper, we present a novel model based on region-based MA to tackle multimodal optimisation problems. It uses a clearing strategy where niches are defined as regions. It implements an archive of solutions and indexed regions considered as explored and thus excluded from further exploration.

In order to asses the efficiency of the model against existing ones, we have tested it on a MA which alternatively applies an EA (SSGA) to explore the search space and an LS (CMA-ES) to the best one until it does not improve for a certain number of evaluations.

Various studies have been performed to study the performances of this model. First, we have demonstrated that the use of region-based niches was more efficient than that of the classical euclidean niches. We have shown that excluding regions explored by the LS allows the algorithm to reduce the search space leading to a more efficient exploration. Also, we have analysed the population diversity during the run and the degree of exploration in several functions. Finally, complexity testing show the good scalability of the proposal.

We compared the resulting algorithm using the benchmark issued for the special session and competition on niching methods for multimodal function optimisation of the IEEE Congress on Evolutionary Computation in 2013. We noted that our algorithm was fairly independent to the different accuracy levels tested in this benchmark compared to the other algorithms obtaining significantly better results than most algorithms and similar performance to NEA2.

This work opens the way of various potential future studies:

- First, the behaviour of RMAwA with higher dimension problems should be studied more in detailed and improved it. Also, the memory cost of the archive may become consequent when tackling higher dimension problems and it could be interesting to study techniques which reduce or limit the size of the archive or remove similar solutions representing the same region.

- As is often the case when the parameter defining the size of a niche, the number of divisions per dimensions is highly sensitive. Although the idea of a constant increasing during the search might offer interesting results, it may not be optimal in some cases. A more adapted strategy could be identified and researched. An other option would be to implement multi-population where, as it is done in Hierarchical Genetic Strategy [53], each population uses different numbers of divisions.
- This model has proved to obtain interesting results when applied with both SSGA and CMAES as its EA and LS. Further experiments using different components or in a different memetic framework could lead to new efficient algorithms. If tested in higher dimensions, the necessity of changing CMAES to a more scalable LS method would be compulsory.

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References

[1] C. F. Agostinho, C. Fernandes, A. Rosa, A Study on Non-random Mating and Varying Population Size in Genetic Algorithms Using a Royal Road Function, in: Proceedings of the 2001 IEEE Congress on Evolutionary Computation, IEEE Press, 2001, pp. 60–66.

[2] S. Bandaru, K. Deb, A parameterless-niching-assisted bi-objective approach to multimodal optimization, in: Evolutionary Computation (CEC), 2013 IEEE Congress on, 2013, pp. 95–102.

[3] S. Bird, X. Li, Adaptively choosing niching parameters in a PSO, in: Proceedings of the 8th annual conference on Genetic and evolutionary computation, GECCO '06, ACM, New York, NY, USA, 2006, pp. 3–10.

[4] S. Biswas, S. Kundu, S. Das, An improved parent-centric mutation with normalized neighborhoods for inducing niching behavior in differential evolution, Cybernetics, IEEE Transactions on 44 (10) (2014) 1726–1737.

[5] X. Chen, Y.-S. Ong, M.-H. Lim, K. C. Tan, A multi-facet survey on memetic computation, Evolutionary Computation, IEEE Transactions on 15 (5) (2011) 591–607.

[6] S. Das, S. Maity, B.-Y. Qu, P. Suganthan, Real-parameter evolutionary multimodal optimization a survey of the state-of-the-art, Swarm and Evolutionary Computation 1 (2) (2011) 71 – 88.

[7] K. A. De Jong, An analysis of the behavior of a class of genetic adaptive systems., Ph.D. thesis, Ann Arbor, MI, USA (1975).

[8] K. Deb, A. Saha, Multimodal optimization using a bi-objective evolutionary algorithm, Evolutionary Computation 20 (1) (2012) 27–62.

[9] J. Derrac, S. García, D. Molina, F. Herrera, A practical tutorial on the use of nonparametric statistical tests as a methodology for comparing evolutionary and swarm intelligence algorithms, Swarm and Evolutionary Computation 1 (1) (2011) 3–18.

[10] G. Dick, P. Whigham, Weighted local sharing and local clearing for multimodal optimisation, Soft Computing 15 (9) (2011) 1707–1721.

[11] M. Ellabaan, Y.-S. Ong, Valley-adaptive clearing scheme for multimodal optimization evolutionary search, in: Intelligent Systems Design and Applications, 2009. ISDA '09. Ninth International Conference on, 2009, pp. 1–6.

[12] M. Epitropakis, X. Li, E. Burke, A dynamic archive niching differential evolution algorithm for multimodal optimization, in: Evolutionary Computation (CEC), 2013 IEEE Congress on, 2013, pp. 79–86.

[13] M. Epitropakis, V. Plagianakos, M. Vrahatis, Finding multiple global optima exploiting differential evolution's niching capability, in: Differential Evolution (SDE), 2011 IEEE Symposium on, 2011, pp. 1–8.

[14] L. J. Eshelman, J. D. Schaffer, Real-coded Genetic Algorithms in Genetic Algorithms by Preventing Incest, Foundation of Genetic Algorithms 2 (1993) 187–202.

[15] W. Gao, G. G. Yen, S. Liu, A cluster-based differential evolution with self-adaptive strategy for multimodal optimization, Cybernetics, IEEE Transactions on 44 (8) (2014) 1314–1327.

[16] D. E. Goldberg, J. Richardson, Genetic algorithms with sharing for multimodal function optimization, in: Proceedings of the Second International Conference on Genetic Algorithms on Genetic algorithms and their application, L. Erlbaum Associates Inc., Hillsdale, NJ, USA, 1987, pp. 41–49.

[17] N. Hansen, S. D. Müller, P. Koumoutsakos, Reducing the Time Complexity of the Derandomized Evolution Strategy with Covariance Matrix Adaptation (CMA-ES), Evolutionary Computation 1 (11) (2003) 1–18.

[18] N. Hansen, A. Ostermeier, Completely derandomized self-adaptation in evolution strategies, Evolutionary Computation 9 (2) (2001) 159–195.

[19] A. Kononova, D. Ingham, M. Pourkashanian, Simple scheduled memetic algorithm for inverse problems in higher dimensions: Application to chemical kinetics, in: Evolutionary Computation, 2008. CEC 2008. (IEEE World

Congress on Computational Intelligence). IEEE Congress on, 2008, pp. 3905–3912.

[20] N. Krasnogor, J. Smith, A tutorial for competent memetic algorithms: model, taxonomy, and design issues, IEEE Transactions on Evolutionary Computation 9 (5) (2005) 474 – 488.

[21] B. Lacroix, D. Molina, F. Herrera, Region based memetic algorithm for real-parameter optimisation, Information Sciences 262 (2014) 15 – 31.

[22] J.-P. Li, M. E. Balazs, G. T. Parks, P. J. Clarkson, A species conserving genetic algorithm for multimodal function optimization, Evol. Comput. 10 (3) (2002) 207–234.

[23] X. Li, Adaptively choosing neighbourhood bests using species in a particle swarm optimizer for multimodal function optimization, in: K. Deb (ed.), Genetic and Evolutionary Computation GECCO 2004, vol. 3102 of Lecture Notes in Computer Science, Springer Berlin Heidelberg, 2004, pp. 105–116.

[24] X. Li, Niching without niching parameters: Particle swarm optimization using a ring topology, Evolutionary Computation, IEEE Transactions on 14 (1) (2010) 150–169.

[25] X. Li, A. Engelbrecht, M. Epitropakis, Benchmark functions for cec 2013 special session and competition on niching methods for multimodal function optimization, Tech. rep., Royal Melbourne Institute of Technology (2013).

[26] Li Xiaodong, A multimodal particle swarm optimizer based on fitness euclidean-distance ratio, in: Proceedings of the 9th annual conference on Genetic and evolutionary computation, GECCO '07, ACM, New York, NY, USA, 2007, pp. 78–85.

[27] M. López-Ibáñez, J. Dubois-Lacoste, T. Stützle, Automatic configuration of state-of-the-art multi-objective optimizers using the TP+PLS framework, in: N. Krasnogor, P. L. Lanzi (eds.), Proceedings of the Genetic and Evolutionary Computation Conference, GECCO 2011, ACM Press, New York, NY, 2011, pp. 2019–2026.

[28] M. López-Ibáñez, J. Dubois-Lacoste, T. Stützle, A hybrid TP+PLS algorithm for bi-objective flow-shop scheduling problems, Computers & Operations Research 38 (8) (2011) 1219–1236.

[29] M. López-Ibáñez, J. Dubois-Lacoste, T. Stützle, M. Birattari, The irace package, iterated race for automatic algorithm configuration, Tech. Rep. TR/IRIDIA/2011-004, IRIDIA, Université Libre de Bruxelles, Belgium (2011).

[30] S. W. Mahfoud, Niching methods for genetic algorithms, Ph.D. thesis, Champaign, IL, USA (1995).

[31] O. J. Mengshoel, D. E. Goldberg, Probabilistic crowding: Deterministic crowding with probabilistic replacement, in: Proceedings of the Genetic and Evolutionary Computation Conference (GECCO-99), 1999, pp. 409–416.

[32] D. Molina, M. Lozano, C. García-Martínez, F. Herrera, Memetic Algorithms for Continuous Optimisation Based on Local Search Chains, Evolutionary Computation 18 (1) (2010) 27–63.

[33] D. Molina, M. Lozano, A. M. Sánchez, F. Herrera, Memetic algorithms based on local search chains for large scale continuous optimisation problems: MA-SSW-Chains, Soft Computing 15 (11) (2010) 2201–2220.

[34] D. Molina, A. Puris, R. Bello, F. Herrera, Variable mesh optimization for the 2013 CEC Special Session Niching Methods for Multimodal Optimization, in: Evolutionary Computation (CEC), 2013 IEEE Congress on, 2013, pp. 87–94.

[35] P. Moscato, On Evolution, Search, Optimization, Genetic Algorithms and Martial Arts: Toward Memetic Algorithms, Tech. rep. (1989).

[36] H. Mülenbein, D. Schlierkamp-Voosen, Predictive models for the breeding genetic algorithm in continuous parameter optimization, Evolutionary Computation 1 (1993) 25–49.

[37] F. Neri, C. Cotta, Memetic algorithms and memetic computing optimization: A literature review, Swarm and Evolutionary Computation 2 (2012) 1 – 14.

[38] F. Neri, V. Tirronen, T. Karkkainen, T. Rossi, Fitness diversity based adaptation in multimeme algorithms:a comparative study, in: Evolutionary Computation, 2007. CEC 2007. IEEE Congress on, 2007, pp. 2374–2381.

[39] Y.-S. Ong, A. Keane, Meta-lamarckian learning in memetic algorithms, Evolutionary Computation, IEEE Transactions on 8 (2) (2004) 99–110.

[40] Y.-S. Ong, M.-H. Lim, N. Zhu, K.-W. Wong, Classification of adaptive memetic algorithms: a comparative study, Systems, Man, and Cybernetics, Part B: Cybernetics, IEEE Transactions on 36 (1) (2006) 141–152.

[41] L. Pérez Cáceres, M. López-Ibáez, T. St utzle, An analysis of parameters of IRACE, in: C. Blum, G. Ochoa (eds.), Evolutionary Computation in Combinatorial Optimisation, vol. 8600 of Lecture Notes in Computer Science, Springer Berlin Heidelberg, 2014, pp. 37–48.

[42] A. Petrowski, A clearing procedure as a niching method for genetic algorithms, in: Evolutionary Computation, 1996., Proceedings of IEEE International Conference on, 1996, pp. 798–803.

[43] M. Preuss, Niching the CMA-ES via nearest-better clustering, in: Proceedings of the 12th Annual Conference Companion on Genetic and Evolutionary Computation, GECCO '10, ACM, New York, NY, USA, 2010, pp. 1711–1718.

[44] L. Qing, W. Gang, Y. Zaiyue, W. Qiuping, Crowding clustering genetic algorithm for multimodal function optimization, Applied Soft Computing 8 (1) (2008) 88 – 95.

[45] B. Qu, P. Gouthanan, P. Suganthan, Dynamic grouping crowding differential evolution with ensemble of parameters for multi-modal optimization, in: B. Panigrahi, S. Das, P. Suganthan, S. Dash (eds.), Swarm, Evolutionary, and Memetic Computing, vol. 6466 of Lecture Notes in Computer Science, Springer Berlin Heidelberg, 2010, pp. 19–28.

[46] B. Qu, J. Liang, P. Suganthan, Niching particle swarm optimization with local search for multi-modal optimization, Information Sciences 197 (2012) 131 – 143.

[47] B. Qu, J. Liang, P. Suganthan, T. Chen, Ensemble of clearing differential evolution for multi-modal optimization, in: Y. Tan, Y. Shi, Z. Ji (eds.), Advances in Swarm Intelligence, vol. 7331 of Lecture Notes in Computer Science, Springer Berlin Heidelberg, 2012, pp. 350–357.

[48] B. Y. Qu, P. Suganthan, J. Liang, Differential evolution with neighborhood mutation for multimodal optimization, Evolutionary Computation, IEEE Transactions on 16 (5) (2012) 601–614.

[49] S. Bird and Li Xiaodong, Enhancing the robustness of a speciation-based PSO, in: Evolutionary Computation, 2006. CEC 2006. IEEE Congress on, 2006, pp. 843–850.

[50] W. F. Sacco, M. D. Machado, C. M. Pereira, R. Schirru, The fuzzy clearing approach for a niching genetic algorithm applied to a nuclear reactor core design optimization problem, Annals of Nuclear Energy 31 (1) (2004) 55 – 69.

[51] B. Sareni, L. Krahenbuhl, Fitness sharing and niching methods revisited, Evolutionary Computation, IEEE Transactions on 2 (3) (1998) 97–106.

[52] R. Schaefer, K. Adamska, H. Telega, Clustered genetic search in continuous landscape exploration, Engineering Applications of Artificial Intelligence 17 (4) (2004) 407–416.

[53] R. Schaefer, J. Kolodziej, Genetic search reinforced by the population hierarchy, in: K. A. D. Jong, R. Poli, J. E. Rowe (eds.), FOGA, Morgan Kaufmann, 2002, pp. 383–400.

[54] J. Smith, Coevolving memetic algorithms: A review and progress report, Systems, Man, and Cybernetics, Part B: Cybernetics, IEEE Transactions on 37 (1) (2007) 6–17.

[55] C. Stoean, M. Preuss, R. Stoean, D. Dumitrescu, Ea-powered basin number estimation by means of preservation and exploration, in: G. Rudolph, T. Jansen, S. Lucas, C. Poloni, N. Beume (eds.), Parallel Problem Solving from Nature PPSN X, vol. 5199 of Lecture Notes in Computer Science, Springer Berlin Heidelberg, 2008, pp. 569–578.

[56] H. Telega, R. Schaefer, E. Cabib, A parallel genetic clustering for inverse problems, in: B. Kgstrm, J. Dongarra, E. Elmroth, J. Waniewski (eds.), Applied Parallel Computing Large Scale Scientific and Industrial Problems, vol. 1541 of Lecture Notes in Computer Science, Springer Berlin Heidelberg, 1998, pp. 551–556.

[57] R. Thomsen, Multimodal optimization using crowding-based differential evolution, in: Evolutionary Computation, 2004. CEC2004. Congress on, vol. 2, 2004, pp. 1382–1389 Vol.2.

[58] M. Tomassini, Spatially Structured Evolutionary Algorithms, Springer, 2005.

[59] M. Črepinšek, S.-H. Liu, M. Mernik, Exploration and exploitation in evolutionary algorithms: A survey, ACM Comput. Surv. 45 (3) (2013) 35:1–35:33.

[60] J. E. Vitela, O. Castanos, A real-coded niching memetic algorithm for continuous multimodal function optimization, in: Evolutionary Computation, 2008. CEC 2008. (IEEE World Congress on Computational Intelligence). IEEE Congress on, 2008, pp. 2170–2177.

[61] J. E. Vitela, O. Castaos, A sequential niching memetic algorithm for continuous multimodal function optimization, Applied Mathematics and Computation 218 (17) (2012) 8242 – 8259.

[62] H. Wang, I. Moon, S. Yang, D. Wang, A memetic particle swarm optimization algorithm for multimodal optimization problems, Information Sciences 197 (2012) 38 – 52.

[63] D. Zaharie, Extensions of differential evolution algorithms for multimodal optimization, in: Proceedings of SYNASC, 2004, pp. 523–534.

[64] Z. Zhai, X. Li, A dynamic archive based niching particle swarm optimizer using a small population size, in: Proceedings of the Thirty-Fourth Australasian Computer Science Conference - Volume 113, ACSC'11, Australian Computer Society, Inc., Darlinghurst, Australia, Australia, 2011, pp. 83–90.

Appendix: Detailed Peak Ratio on the CEC'2013 benchmark

This section shows the Peak Ratio obtained on the CEC'2013 benchmark in the 5 accuracy levels by:

- RMAwA (Table 14)
- CMA-ES (Table 15)
- DE/nrand/2 (Table 16)
- dADE/nrand/1/bin (Table 17).
- PNA-NSGAII (Table 18)
- NVMO (Table 19)
- NEA2 (Table 20)

Table 14: Results with RMAwA

Pb	Fun	Dim	Accuracy level				
			$1E{-}1$	$1E{-}2$	$1E{-}3$	$1E{-}4$	$1E{-}5$
F_1	f_1	1	1.000	1.000	1.000	1.000	1.000
F_2	f_2	1	1.000	1.000	1.000	1.000	1.000
F_3	f_3	1	1.000	1.000	1.000	1.000	1.000
F_4	f_4	2	1.000	1.000	1.000	1.000	1.000
F_5	f_5	2	1.000	1.000	1.000	1.000	1.000
F_6	f_6	2	0.992	0.992	0.992	0.992	0.000
F_7	f_7	2	1.000	0.920	0.917	0.917	0.917
F_8	f_6	3	0.824	0.824	0.824	0.824	0.824
F_9	f_7	3	1.000	0.519	0.515	0.514	0.513
F_{10}	f_8	2	1.000	1.000	1.000	1.000	1.000
F_{11}	f_9	2	1.000	1.000	1.000	1.000	1.000
F_{12}	f_{10}	2	1.000	1.000	1.000	1.000	1.000
F_{13}	f_{11}	2	0.997	0.997	0.997	0.997	0.997
F_{14}	f_{11}	3	0.823	0.813	0.813	0.813	0.813
F_{15}	f_{12}	3	0.705	0.703	0.703	0.703	0.703
F_{16}	f_{11}	5	0.683	0.670	0.670	0.670	0.670
F_{17}	f_{12}	5	0.668	0.660	0.660	0.660	0.660
F_{18}	f_{11}	10	0.377	0.237	0.237	0.233	0.233
F_{19}	f_{12}	10	0.128	0.128	0.128	0.128	0.128
F_{20}	f_{12}	20	0.253	0.125	0.125	0.125	0.125

Table 15: Results with CMA-ES

Pb	Fun	Dim	Accuracy level				
			$1E-1$	$1E-2$	$1E-3$	$1E-4$	$1E-5$
F_1	f_1	1	1.000	1.000	1.000	1.000	1.000
F_2	f_2	1	1.000	1.000	1.000	1.000	1.000
F_3	f_3	1	1.000	1.000	1.000	1.000	1.000
F_4	f_4	2	1.000	1.000	1.000	1.000	0.990
F_5	f_5	2	1.000	1.000	1.000	1.000	1.000
F_6	f_6	2	0.783	0.783	0.782	0.776	0.000
F_7	f_7	2	0.531	0.529	0.521	0.518	0.516
F_8	f_6	3	0.115	0.115	0.115	0.115	0.115
F_9	f_7	3	0.282	0.278	0.274	0.273	0.272
F_{10}	f_8	2	1.000	1.000	0.998	0.992	0.978
F_{11}	f_9	2	0.990	0.977	0.970	0.963	0.953
F_{12}	f_{10}	2	0.788	0.788	0.778	0.760	0.760
F_{13}	f_{11}	2	0.980	0.967	0.957	0.950	0.947
F_{14}	f_{11}	3	0.760	0.750	0.743	0.743	0.743
F_{15}	f_{12}	3	0.680	0.658	0.655	0.655	0.653
F_{16}	f_{11}	5	0.667	0.667	0.667	0.667	0.663
F_{17}	f_{12}	5	0.585	0.585	0.585	0.585	0.583
F_{18}	f_{11}	10	0.340	0.340	0.340	0.340	0.340
F_{19}	f_{12}	10	0.597	0.597	0.597	0.597	0.597
F_{20}	f_{12}	20	0.448	0.448	0.448	0.448	0.425

Table 16: Results with DE/nrand/2

Pb	Fun	Dim	Accuracy level				
			$1E{-}1$	$1E{-}2$	$1E{-}3$	$1E{-}4$	$1E{-}5$
F_1	f_1	1	1.000	1.000	1.000	1.000	1.000
F_2	f_2	1	1.000	1.000	1.000	1.000	1.000
F_3	f_3	1	1.000	1.000	1.000	1.000	1.000
F_4	f_4	2	1.000	1.000	1.000	1.000	1.000
F_5	f_5	2	1.000	1.000	1.000	1.000	1.000
F_6	f_6	2	0.669	0.669	0.669	0.669	0.000
F_7	f_7	2	0.276	0.276	0.276	0.276	0.275
F_8	f_6	3	0.365	0.365	0.365	0.365	0.363
F_9	f_7	3	0.066	0.066	0.066	0.066	0.065
F_{10}	f_8	2	1.000	1.000	1.000	1.000	1.000
F_{11}	f_9	2	0.667	0.667	0.667	0.667	0.667
F_{12}	f_{10}	2	0.635	0.628	0.628	0.618	0.618
F_{13}	f_{11}	2	0.667	0.667	0.667	0.667	0.667
F_{14}	f_{11}	3	0.667	0.667	0.667	0.667	0.667
F_{15}	f_{12}	3	0.413	0.408	0.405	0.400	0.400
F_{16}	f_{11}	5	0.667	0.667	0.667	0.667	0.667
F_{17}	f_{12}	5	0.288	0.283	0.283	0.280	0.280
F_{18}	f_{11}	10	0.517	0.513	0.507	0.507	0.507
F_{19}	f_{12}	10	0.230	0.218	0.203	0.190	0.180
F_{20}	f_{12}	20	0.230	0.230	0.230	0.230	0.230

Table 17: Results with dADE/nrand/1/bin

Pb	Fun	Dim	Accuracy level				
			$1E{-}1$	$1E{-}2$	$1E{-}3$	$1E{-}4$	$1E{-}5$
F_1	f_1	1	1.000	1.000	1.000	1.000	1.000
F_2	f_2	1	1.000	1.000	1.000	1.000	1.000
F_3	f_3	1	1.000	1.000	1.000	1.000	1.000
F_4	f_4	2	1.000	1.000	1.000	1.000	1.000
F_5	f_5	2	1.000	1.000	1.000	1.000	1.000
F_6	f_6	2	1.000	1.000	1.000	0.988	0.000
F_7	f_7	2	1.000	0.960	0.878	0.808	0.714
F_8	f_6	3	0.990	0.991	0.985	0.958	0.947
F_9	f_7	3	0.829	0.592	0.552	0.436	0.349
F_{10}	f_8	2	1.000	1.000	1.000	1.000	1.000
F_{11}	f_9	2	0.867	0.667	0.667	0.667	0.667
F_{12}	f_{10}	2	0.750	0.748	0.738	0.740	0.735
F_{13}	f_{11}	2	0.737	0.667	0.667	0.667	0.667
F_{14}	f_{11}	3	0.943	0.667	0.667	0.667	0.667
F_{15}	f_{12}	3	1.000	0.643	0.623	0.600	0.620
F_{16}	f_{11}	5	0.890	0.667	0.667	0.667	0.667
F_{17}	f_{12}	5	0.963	0.480	0.420	0.400	0.358
F_{18}	f_{11}	10	0.663	0.630	0.630	0.613	0.603
F_{19}	f_{12}	10	0.495	0.118	0.080	0.020	0.000
F_{20}	f_{12}	20	0.080	0.005	0.000	0.000	0.000

Table 18: Results with PNA-NSGA

Pb	Fun	Dim	Accuracy level				
			$1E{-}1$	$1E{-}2$	$1E{-}3$	$1E{-}4$	$1E{-}5$
F_1	f_1	1	1.000	1.000	1.000	1.000	1.000
F_2	f_2	1	1.000	1.000	1.000	1.000	1.000
F_3	f_3	1	1.000	1.000	1.000	1.000	1.000
F_4	f_4	2	1.000	1.000	0.995	0.985	0.805
F_5	f_5	2	1.000	1.000	1.000	1.000	1.000
F_6	f_6	2	0.562	0.536	0.523	0.473	0.000
F_7	f_7	2	1.000	0.741	0.726	0.709	0.683
F_8	f_6	3	0.352	0.330	0.310	0.275	0.252
F_9	f_7	3	0.480	0.326	0.318	0.298	0.276
F_{10}	f_8	2	1.000	1.000	1.000	1.000	1.000
F_{11}	f_9	2	0.877	0.677	0.670	0.680	0.663
F_{12}	f_{10}	2	0.752	0.715	0.672	0.642	0.573
F_{13}	f_{11}	2	0.697	0.667	0.667	0.663	0.623
F_{14}	f_{11}	3	0.933	0.667	0.667	0.663	0.610
F_{15}	f_{12}	3	0.665	0.495	0.485	0.470	0.443
F_{16}	f_{11}	5	1.000	0.523	0.523	0.417	0.323
F_{17}	f_{12}	5	0.917	0.347	0.338	0.300	0.245
F_{18}	f_{11}	10	0.640	0.117	0.113	0.110	0.093
F_{19}	f_{12}	10	0.020	0.020	0.043	0.017	0.010

Table 19: Results with NVMO

Pb	Fun	Dim	Accuracy level				
			$1E{-}1$	$1E{-}2$	$1E{-}3$	$1E{-}4$	$1E{-}5$
F_1	f_1	1	1.000	1.000	1.000	1.000	1.000
F_2	f_2	1	1.000	1.000	1.000	1.000	1.000
F_3	f_3	1	1.000	1.000	1.000	1.000	1.000
F_4	f_4	2	1.000	1.000	1.000	1.000	1.000
F_5	f_5	2	1.000	1.000	1.000	1.000	1.000
F_6	f_6	2	1.000	0.996	0.944	0.681	0.000
F_7	f_7	2	1.000	1.000	0.953	0.901	0.804
F_8	f_6	3	0.411	0.300	0.276	0.198	0.027
F_9	f_7	3	1.000	0.686	0.409	0.279	0.194
F_{10}	f_8	2	1.000	1.000	1.000	1.000	0.967
F_{11}	f_9	2	1.000	0.667	0.667	0.667	0.667
F_{12}	f_{10}	2	0.838	0.743	0.730	0.705	0.593
F_{13}	f_{11}	2	0.997	0.667	0.667	0.667	0.663
F_{14}	f_{11}	3	1.000	0.667	0.667	0.667	0.627
F_{15}	f_{12}	3	1.000	0.723	0.675	0.640	0.378
F_{16}	f_{11}	5	1.000	0.673	0.663	0.663	0.653
F_{17}	f_{12}	5	1.000	0.483	0.453	0.438	0.325
F_{18}	f_{11}	10	0.997	0.470	0.460	0.460	0.327
F_{19}	f_{12}	10	0.273	0.133	0.133	0.127	0.093
F_{20}	f_{12}	20	0.000	0.000	0.000	0.000	0.000

Table 20: Results with NEA2

Pb	Fun	Dim	Accuracy level				
			$1E{-}1$	$1E{-}2$	$1E{-}3$	$1E{-}4$	$1E{-}5$
F_1	f_1	1	1.000	1.000	1.000	1.000	1.000
F_2	f_2	1	1.000	1.000	1.000	1.000	1.000
F_3	f_3	1	1.000	1.000	1.000	1.000	1.000
F_4	f_4	2	1.000	1.000	1.000	1.000	0.990
F_5	f_5	2	1.000	1.000	1.000	1.000	1.000
F_6	f_6	2	0.963	0.963	0.958	0.950	0.000
F_7	f_7	2	0.946	0.925	0.918	0.914	0.911
F_8	f_6	3	0.241	0.240	0.240	0.240	0.239
F_9	f_7	3	0.622	0.595	0.584	0.581	0.579
F_{10}	f_8	2	1.000	1.000	1.000	0.988	0.980
F_{11}	f_9	2	0.980	0.967	0.967	0.960	0.960
F_{12}	f_{10}	2	0.853	0.850	0.843	0.840	0.833
F_{13}	f_{11}	2	0.977	0.970	0.960	0.957	0.947
F_{14}	f_{11}	3	0.830	0.817	0.810	0.807	0.800
F_{15}	f_{12}	3	0.743	0.723	0.720	0.718	0.713
F_{16}	f_{11}	5	0.673	0.673	0.673	0.673	0.673
F_{17}	f_{12}	5	0.695	0.695	0.695	0.695	0.695
F_{18}	f_{11}	10	0.667	0.667	0.667	0.667	0.663
F_{19}	f_{12}	10	0.667	0.667	0.667	0.667	0.667
F_{20}	f_{12}	20	0.363	0.360	0.360	0.360	0.350