# Design of Hybrids for the Minimum Sum-of-Squares Clustering Problem

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#### Abstract

A series of metaheuristic algorithms is proposed and analyzed for the non-hierarchical clustering problem under the criterion of minimum Sum-of-Squares Clustering. These algorithms incorporate genetic operators and Local Search and Tabu Search procedures. The aim is to obtain quality solutions with short computation times. A series of computational experiments has been performed. The proposed algorithms obtain better results than previously reported methods, especially with small numbers of clusters.

*Keywords:* Clusterization, Metaheuristics, Tabu Search, Genetic Algorithms, Memetic Algorithms, Hybrid Algorithms.

### 1. Introduction

Consider a set  $X = \{x_1, x_2, ..., x_N\}$  of N points in  $R^q$  and let m be a predetermined positive integer. The Minimum Sum-of-Squares Clustering (MSSC) problem is to find a partition of X into m disjoint subsets (clusters) so that the sum of squared distances from each point to the centroid of its cluster is minimum. Specifically, let  $P_m$  denote the set of all the partitions of X in m sets, where each partition  $P \in P_m$  is defined as  $P = (C_1, C_2, ..., C_m)$  and where  $C_i$  denotes each of the clusters that forms P. Thus, the problem can be expressed as:

$$\min_{P \in \mathsf{P}_m} \sum_{i=1}^m \sum_{x_i \in C_i} \|x_i - \bar{x}_i\|^2,$$

where the centroid  $x_i$  is defined as

$$\overline{x}_i = \frac{1}{n_i} \sum_{x_l \in C_i} x_l$$
, with  $n_i = |C_i|$ .

Equivalently the problem can be written as

$$\min \sum_{l=1}^{N} \left\| x_{l} - \overline{x}_{c(l)} \right\|^{2}$$

where c(l) is the cluster to which point  $x_l$  belongs.

The design of clusters is a well known exploratory Data Analysis issue called Pattern Recognition. The aim is to find whether a given set of cases X has some structure and, in if so, to display it in the form of a partition. This problem belongs to

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the area of Non-Hierarchical cluster design, which has many applications in Economics, Social and Natural Sciences. It is known to be NP-Hard, (Brucker, 1978).

Various exact methods for MSSC can be found in the literature (see, for example, Koontz et al., 1975 and Diehr, 1985), some of which, such as the method proposed by du Merle et al. (2000), have succeeded in resolving problems with up to 150 points. For larger-sized problems the use of heuristic algorithms is still necessary. The most popular are those based on Local Search methods, such as the well-known K-Means (Jancey, 1966) and H-Means (Howard, 1966) procedures. In a recent work, Hansen and Mladenovic (2001) propose a new Local Search procedure, J-Means, along with variants H-Means+ or HK-Means. In recent years algorithms using Metaheuristic strategies have been designed, such as Simulated Annealing (Klein and Dubes, 1989), Tabu Search (Al-Sultan, 1995), Genetic Algorithms (Babu and Murty, 1993) or most recently Variable Neighborhood Search or VNS (du Merle et al., 2000, and Hansen and Mladenovic, 2001).

A series of algorithms that is able to obtain good solutions in short times is proposed for this problem. Initially, a genetic algorithm is designed using Local Search methods, thus becoming a Memetic Algorithm. A simple procedure based on a Tabu Search method using binary trees is also suggested. This method demonstrates its capacity to improve solutions in very few iterations. The incorporation of this procedure into Memetic Algorithms yields Hybrid Algorithms. Finally, these Memetic and Hybrid Algorithms are analyzed and compared with other techniques. In all cases, the proposed techniques give adequate solutions, compared with other techniques, in reasonable time, especially with small values of m.

This paper is structured as follows: in the next section some of the already existing Local Search algorithms are described. In the third section, the Tabu Search method is presented. Section 4 considers the Genetic Algorithm in detail. In section 5 Memetic and Hybrid Algorithms are described. Section 6 presents the results of different computational experiments and compares the effectiveness and efficiency of the proposed algorithms with other recent techniques. Finally section 7 summarizes the contribution.

## 2. Principal Local Search Algorithms

Some important local search algorithms are described. These are the well-known H-Means and K-Means, their variants H-Means+ and HK-Means, as well as the more recent J-Means and J-Means+. In all cases, we begin by obtaining an arbitrary initial solution (or partition),  $(C_1, C_2, ..., C_M)$ .

Algorithm 1. H-Means

Repeat

(a) Calculate centroids  $x_i$ , for i=1....m;

(b) Reassign every point to its closest centroid (→ new clusters: clusters are composed by the points assigned to the same centroid);

until convergence (that is, no modifications in the composition of clusters)

#### Algorithm 2. H-Means+

Repeat

(a) *Run steps* (a) *and* (b) *of* H-Means (Algorithm 1);

<sup>(</sup>b) If there are no modifications:

(b.1) Verify if empty clusters exist (degeneration);

(b.2) *If there are k empty clusters select the farthest k points from their* 

centroids and insert them into the solution as k new single-point clusters;

until convergence.

Algorithm 3. K-Means

Repeat

(a) ∀ i =1..m. ∀ x<sub>j</sub> ∉ C<sub>i</sub> calculate v<sub>ij</sub> (that is: change in the value of the objective function when x<sub>j</sub> is reassigned to C<sub>i</sub>);
(b) If v<sub>i\*j\*</sub> = min v<sub>ij</sub> < 0 then reassign x<sub>j\*</sub> to C<sub>i\*</sub>; until v<sub>i\*j\*</sub> ≥0

#### Algorithm 4. J-Means

Repeat

- (a)  $\forall j = 1...N$  such that  $x_j$  do not coincide with any actual centroid:
  - (a.1) Add a fictitious cluster  $C_{M+1}$  whose centroid is  $x_j$ ;
    - (a.2)  $\forall i=1...m$ , calculate  $J_{ij}$ ; that is: the change in the value of the objective function when cluster  $C_i$  is 'dissolved' and each one of its entities is reassigned to its closest centroid cluster among the remaining ones (including  $C_{M+1}$  and not including  $C_i$ ) ('Jump-move');
- (b) If  $J_{i^*j^*} = \min J_{ij} < 0$  then undo  $C_{i^*}$  and reassign the elements of  $C_i$  to the closest centroid cluster among the remaining ones (including  $C_{M+1}$  of centroid  $x_{j^*}$ ), redefine  $C_i = C_{M+1}$  and eliminate  $C_{M+1}$ .

until  $J_{i^*i^*} \geq 0$ .

Observe that H-Means+ simply modifies H-Means to prevent the algorithm from ending in a degenerate solution. This modification is very effective according to Hansen and Mladenovic's (2001) experiments.

The following formulas are obtained from Späth (1980) to simplify the calculations in K-Means. Let  $C_l$  be the cluster to which  $x_j$  belongs, then the value of  $v_{ij}$  is calculated as follows:

$$v_{ij} = \frac{n_i}{n_i + 1} \cdot \left\| \overline{x}_i - x_j \right\|^2 - \frac{n_l}{n_l - 1} \cdot \left\| \overline{x}_l - x_j \right\|^2,$$

and the centroids are easily updated as  $x_j$  is changed from  $C_l$  to  $C_i$ . It should be noted that a K-Means local optimum is also a local optimum for H-Means (and H-Means+), but the reverse is not necessarily true. This suggests using H-Means+ followed by K-Means and not the reverse. We shall denote this two phase heuristic by HK-Means.Finally, J-Means+ consists in applying HK-Means once every time 'Jumpmove' is run in J-Means.

# 3. Tabu Algorithm

#### 3.1. Description of a basic algorithm

Tabu Search (TS) is a strategy proposed by Glover (1989) and (1990). "Tabu Search is dramatically changing our possibilities of solving a host of combinatorial problems in different areas" (Glover and Laguna, 2002). This is a procedure that explores the

solution space beyond the local optimum. Once a local optimum is reached, upward moves or those that worsen the solutions are allowed. Simultaneously, the last moves are marked as *tabus* during the following iterations to avoid cycling. Recent and comprehensive tutorials on Tabu Search, that include all types of applications, can be found in Glover and Laguna (1997) and (2002).

Next, we design a simple Tabu Search algorithm that uses the neighboring moves employed in K-Means. These moves consist at each step in the movement of an entity from a cluster to a different one. In order to avoid repetitive cycling when a move which consists in moving point  $x_j$  from cluster  $C_l$  to cluster  $C_i$  is performed, point  $x_j$  is prevented from returning to the cluster  $C_l$  for a certain number of iterations. Specifically, let's define

*Matrix\_tabu* (l, j) = the number of the iteration in which point  $x_i$  leaves cluster  $C_l$ .

The Tabu Search method is described by Algorithm 5, where *P* denotes a initial solution with a value *f*. The parameter *Tabu\_Tenure* indicates the number of iterations during which a point is not allowed to return to the leaving cluster. The parameter *max\_iter* indicates the maximum number of unimproved iterations. After different tests, *Tabu\_Tenure* was set as *m*.

Algorithm 5. Tabu Search (a) Do Matrix\_tabu(i,j) = - Tabu\_Tenure, i = 1..m, j = 1,..N(b) Do niter = 0 and  $P^* = P$ ,  $f^* = f$  and iter\_better =0; (c) Repeat (c.1) niter = niter + 1 (c.2) Determine  $v_{i*j*} = min \{v_{ij} / i = 1..m. j = 1,...N; x_j \notin C_i verifying niter > Matrix_tabu (i,j) + Tabu_Tenure or <math>f + v_{ij} < f^*$  ('aspiration criterion')} (c.3) Reassign  $x_{j*}$  to  $C_{i*}$ ; (c.4) Do Matrix\_tabu  $(l^*, j^*) = niter (l^* being the previous cluster of <math>x_{j*}$ ); (c.5) If f (the value of the current solution P) < f\* then do:  $P^* = P$ ,  $f^* = f$  and iter\_better = niter; until (niter - iter\_better > max\_iter) or another termination criterion

#### 3.2. The Use of a Binary Tree structure

Next, a strategy based on the use of binary trees (Williams, 1964) is proposed for storing and arranging the different possible moves, defined for each (i, j) pair, according to the corresponding value  $v_{ij}$ . For each node k of the binary tree, a given move (i, j) is located so that, in the leaving nodes, 2k to 2k+1, two moves (i', j') and (i'', j'') are located that are either equal to or worse than move (i, j), (i.e.,  $v_{ij} \le v_{i'j'}$  and  $v_{ij} \le v_{i''j''}$ ). Clearly, in any iteration, the best move will be located in the root node. The binary tree does not include the tabu moves. A binary tree can be programmed using a vector *HP* and a matrix *QP*:

- HP(k) : indicates move (i, j) located in node k of the tree

- Q(i, j) : indicates the number of the node where move (i, j) is found; if this move is not in the tree (i.e.,  $x_j \in C_i$  or *niter* > *Matrix\_tabu* (i,j)+ *Tabu\_Ternure*) then Q(i, j) = 0.

Figure 1 illustrates a binary tree. In this case *HP* must be equal to ((1,2), (2,4), (3,5), (2,1), (4,6)) and QP(1,2) = 1, QP(2,4) = 2, QP(3,5) = 3, QP(2,1) = 4, and QP(4,6) = 5.



Fig. 1. An example of a binary tree to arrange the moves.

When a move defined for  $i^*$  and  $j^*$  is run, the positions of the moves with values located in the binary tree must be updated. Thus, move  $(i^*, j^*)$  in that iteration must be eliminated, and the move that is no longer tabu must be reincorporated in the tree. As the number of nodes of the binary tree is at most  $N \cdot (m-1)$ , each of these binary tree update operations can be implemented in  $O(\log_2 (N \cdot m))$  time. As can easily be shown, the number of moves (i, j) that must be updated is on the order of  $2 \cdot N + (|C_{i^*}| + |C_{l^*}|) \cdot (m-3)$ . Thus, the number of operations in each iteration is  $O(N \cdot \log_2(N \cdot m))$ . We denote by Tabu\_Search\_with Binary tree the procedure incorporating the above binary tree into the Tabu Search algorithm. Logically, the use of the binary tree does not affect the final result. However, important savings in calculation time are expected.

# 4. Genetic Algorithm

According to Goldberg (1989) "Genetic Algorithms are search techniques based on the mechanics of natural selection and genetics". These techniques are probably the best-known and widespread evolutionary algorithms. They were originally conceived by John Holland and described in the classic monograph "Adaptation in Natural and Artificial Systems" (Holland, 1975). This text has had a great influence on the later development of these techniques since the mechanisms described in it have long since been adopted as dogma.

They are based on a close analogy with the natural processes of the evolution of species. The base is an ensemble (population) of solutions on which are performed operations such as Selection, Crossover, Reproduction, Renovation or Mutation. An outline of how a Genetic algorithm operates is described by Algorithm 6:

<u>Algorithm 6</u>. Genetic Algorithm

Generate an initial population of solutions;

Repeat

- (a) Randomly select a subset of elements (even) of the population with a probability proportional to its goodness;
- (b) Cross reproduction: pair or cross these solutions (Parents) to give rise to new solutions (Children). From each pair of parents a new pair of 'child' solutions has to be generated;

(c) *Mutation: the solutions of the population can change some of its elements (genes) with a small probability;* 

(d) Substitute the worst solutions of the population with the new child solutions; until reaching some stop criterion

The solutions are represented by a set of *m* seed points  $S = \{s_1, s_2, ..., s_m\} \subset \mathbb{R}^q$ . The corresponding partition  $P = (C_1, C_2, ..., C_m)$  is the one resulting from assigning each point of X to its closest seed point.

The 'non-goodness' of each solution of the population will be given by the value of the objective function f of the corresponding partition. The selection probability of a given solution  $S_i$  will be proportional to  $fmax - f_i$ ; where  $f_i$  is its non-goodness value and fmax is the maximum value of  $f_i$  of this population. Once selected, the parent solution pairs are crossed as illustrated in the following example. Let m = 3 and let two parent solutions be  $S^1 = \{A_1, B_1, C_1\}$  and  $S^2 = \{A_2, B_2, C_2\}$ , then the matrix of distances between the *seeds* of  $S^1$  and  $S^2$  is calculated assuming the results shown in Table 1.

Table 1								
Example of distances between seeds								
$S^1 \downarrow S^2 \rightarrow$	$A_2$	$\mathbf{B}_2$	C <sub>2</sub>					
A <sub>1</sub>	7	9	6					
$B_1$	3	5	4					
$C_1$	5	4	9					

Then the seeds of  $S^2$  are rearranged according to their proximity to  $S^1$  as follows: starting from A<sub>1</sub> the closest seed of  $S^2$ , C<sub>2</sub>, is chosen and positioned in the first place. The column of C<sub>2</sub> is eliminated for consecutive choices. Next, out of the remaining seeds of  $S^2$  the one closest to B<sub>1</sub> is selected, A<sub>2</sub> in this case, and its column is eliminated. Finally, the only remaining seed B<sub>2</sub> is selected. In this way, the elements of S<sub>1</sub> and S<sub>2</sub> are arranged as follows:

$$S' \rightarrow (A_1, B_1, C_1)$$
 and  $S' \rightarrow (C_2, A_2, B_2)$ .

Subsequently, an integer value between 1 and *m*-1 is randomly selected as an intersection point (*cross\_pt*), (in the example *cross\_pt* = 1), and two child solutions  $S^3$  and  $S^4$  are generated as shown in Tables 2 and 3.

Table 2							
Parent Solutions							
$S^1 \rightarrow$	$A_1$	$B_1$	$C_1$				
$S^2 \rightarrow$	$C_2$	$A_2$	$B_2$				
Table 3							
Child Solutions							
$S^3 \rightarrow$	A <sub>1</sub>	$A_2$	$B_2$				
$S^4 \rightarrow$	$C_2$	$B_1$	$C_1$				

The aim of pairing the elements  $S^1$  and  $S^2$  according to their closeness is to prevent entities or seeds that are close to each other from forming the same child solution. Experience shows, in general, that if there are very close pairs of seeds-points of a solution *S*, the corresponding partition is poor (Cano, 1999). A series of tests has been performed to verify the efficiency of this arrangement process. First, N = 1000 is set and random values of X between 0 and 100 are uniformly generated. The results clearly show the positive effect of this arrangement process for every value of *m* considered, (m = 10, 20, ..., 150).

Every seed of every generated child solution can change or mutate with a small probability,  $mut_p$ . To decide whether a given seed changes, a random value in the interval (0,1) is uniformly generated. If this value is less than  $mut_p$  the change takes place: the seed is randomly placed in a point in the range of defined values for X (Mutation). This mutation process supplies diversity to the process and prevents the search from getting boxed into a zone around the local minimum.

Once an even number of child solutions is generated (equal to the number of selected parents), the worst solutions of the population are deleted and replaced by the child solutions such that the number of elements remains constant (Renovation).

Each iteration (Parent Selection  $\rightarrow$  Crossover or Reproduction  $\rightarrow$  Mutation  $\rightarrow$  Renovation) is also denoted as 'generation'. The algorithm ends when a given number of generations without improvement (*max\_iter*) occurs, or when a certain preset time elapses. Besides the parameters mentioned before, *p\_mut* and *max\_iter*, two other parameters are used: *n\_pop*, the number of solutions that constitute the population, and *n\_sel*, the number of solutions selected as parents.

# 5. Memetic and Hybrid Algorithms

Memetic Algorithms are also population-based methods and have been demonstrated to be faster than Genetic Algorithms for certain classes of problems, (Moscato and Laguna, 1996). In brief, they combine local search procedures with crossing or mutating operators; due to their structure some researchers have called them Hybrid Genetic Algorithms, Parallel Genetic Algorithms (PGAs) or Genetic Local Search methods. The method is gaining wide acceptance particularly for the well-known problems of combinatorial optimization. A recent tutorial can be found in Moscato, (2002).

In our case, the proposed Memetic Algorithm acts like the Genetic Algorithm described in section 4, except Local Search procedures are added each time a new solution is generated. The Local Search procedures can be any of those described above: HK-Means, J-Means or J-Means+. When a new solution is generated, these processes act on the corresponding partition leading to a new improved partition P. The set S of seed points of this new partition P is defined as the set of centroids of the clusters in P. It must be noted that, after running HK-Means or J-Means+, the new partition P will not vary if we reassign the points of X to the closer seeds (centroids in this case), because P is the local optimum with respect to H-Means. In other words, the partition corresponding to S continues to be P.

In many cases the incorporation of Local Search methods improves the performance of the original genetic algorithms, although sometimes this has the effect of accelerating the process towards a local minimum. The use of higher values in the mutation probability  $(p\_mut)$  is recommended to ensure a certain degree of diversification to avoid this problem.

The Tabu Search procedure with only a few iterations demonstrates its capacity to improve solutions, even 'good' local optima (see section 6.2). Therefore, we propose modifying the Memetic proposed algorithm by appending Tabu Search (with *max\_iter* = 50 to avoid excessive computation time) to the local search procedure. The aim is to obtain a Hybrid method that gives better results than the original Memetic one.

## 6. Computational Results

Next the results of a set of computational experiments using the proposed algorithms are shown. For each case, the TSPLIB library file (Reinelt, 1991) with N = 1060 points is used with different numbers of clusters, m = 10, 20, 30, ..., 150. These test data were previously used in Hansen and Mladenovic (2001), where the best solution known for every value of m (except m = 40) is reported. These were obtained on a SUN Ultra I System workstation with 10 minutes computation time. All the tests in the current work are performed on a personal computer with a Pentium III 600 MHz processor.

# 6.1. Empirical Analysis of using the Binary Tree in Tabu Search

We present the results of a series of tests carried out in order to verify the reduction in computation time achieved by using the binary tree in Tabu Search. For each value of m, both Tabu Search (*TS*) and Tabu Search with Binary Tree (*TSB*) are run. Each uses the same initial solution and performs a fixed number (500) of iterations. The initial solution (SA) is obtained as follows: m centroids (with uniform distribution in the X value range) are randomly generated and each point is directly assigned to the closest centroid. The obtained computation times (in seconds) are shown in figure 2. It is clear that a reduction in computation time is achieved using the binary tree, especially as mgrows (except for m = 10). Thus, from now on, the TSB variant will be used when Tabu Search is employed.

#### **Calculation Time Evolution**



Fig. 2. Calculation Times of TS and TSB.

#### 6.2. Tabu Search to improve Local Minima: Empirical Analysis

To demonstrate the efficiency of this *Tabu Search* method, a series of tests is run. In these tests the two-part solutions obtained by the greedy-random method - as proposed by Beltrán and Pacheco, (2001) - are improved by the J-Means+ algorithm. The solutions obtained by this Local Search method are in turn improved by the Tabu Search algorithm. In this case, Tabu Search uses the stop criterion *max\_iter* = 50. The process is repeated ten times for each number of clusters *m*. The corresponding average percent deviation with respect to the best solution known is presented in figure 3.



Fig. 3. Tabu Search Behavior

The following conclusions can be drawn from results of figure 3:

- As presented in Beltrán and Pacheco, (2001), the local optima obtained using greedy-random initial solutions are better than the local optima obtained with initial random centroids (SA).
- However, these local optima can still be slightly improved by exploring their neighboring regions with a simple Tabu Search method as suggested in section 3. This is interesting, since the local optima obtained by J-Means+ are local optima with respect to J-Means, H-Means, and K-Means. Thus, apparently, it would be very difficult to improve on them with solutions nearby. Moreover, the computation time employed by Tabu Search using the binary tree is very short. This allows their addition to other metaheuristics that use Local Search procedures, such as GRASP, VNS, Memetics, Scatter Search, to improve on the results and produce Hybrids of higher quality.

# 6.3. Genetics and Memetics: Empirical Analysis

To compare the efficiency of the proposed Genetic and Memetic algorithms, a series of tests has been performed:

- the Genetic Algorithm proposed in section 4,
- Memetic-HK: the Memetic Algorithm proposed in section 5 with HK-Means as the Local Search method,
- Memetic-J: the same Memetic Algorithm with J-Means as the Local Search method.

For each number of clusters *m* the algorithms are run once, all employing the same population of initial solutions. To obtain the elements of these initial populations, partitions are randomly generated with the SA algorithm previously described. The centroids of the corresponding clusters are used as a set of seeds. A calculation time of 30 seconds is used for all algorithms as a stop criterion. The values of the parameters are the following:  $n_pop = 10$ ,  $n_sel = 6$ , and  $p_mut = 0.3$ . A graph with the minimal percent deviations with respect to the best-known solution is shown in figure 4.



Fig. 4. Evolution of the minimal deviations

In the light of these results the following conclusions can be drawn:

- Among the evolutionary algorithms analyzed, the Memetic methods clearly perform better than the genetic ones, at least with this computational time. To obtain quality results, it is necessary to incorporate a local search procedure. Within the memetic methods, it is clear that HK-Means gives better results than J-Means. This is due to the poor functioning of the J-Means method using a start from partitions obtained by random seed points (generated by SA) as shown by Beltrán and Pacheco (2001). Therefore, in the following sections the Memetic-HK variant is used.

# 6.4. The proposed algorithms versus other recent strategies

To compare the efficiencies of the algorithms proposed in the previous sections and those of other recent strategies, a series of tests is performed. The following algorithms are tested:

proposed in section 5
Memetic Algorithm to which Tabu Search is incorporated
the GRASP Algorithm described in Beltrán and Pacheco (2000),
with HK-Means as the Local Search method
the GRASP Algorithm with J-Means as the Local Search method
the VNS Algorithm, proposed in Hansen and Mladenovic (2001),
with HK-Means as the Local Search method
the VNS Algorithm, with J-Means as the Local Search method.

The GRASP strategy (*Greedy Randomize Adaptive Search Procedures*), although initially presented in the work of Feo and Resende (1989), has undergone development more recently than other metaheuristics. A thorough description can be found in a paper published in 1995 by the same authors, (Feo and Resende, 1995). Variable Neighborhood Search (VNS) is a recent metaheuristic method for solving combinatorial problems and is described in the works of Mladenovic (1995), Mladenovic and Hansen

(1997), and Hansen and Mladenovic, (1998). Both these recent strategies use Local Search procedures repeatedly.

Memetic-HK and HybMem use the same parameters as in section 5. For each value of *m*, the algorithms are run ten times. The Memetic-HK and HybMem algorithms use an initial population whose elements are generated as follows: partitions are generated in two phases with a greedy-random method described in Beltrán and Pacheco (2001). The centroids of the corresponding clusters are taken as sets of seeds. The VNS-HK and VNS-J algorithms use the best of these partitions as the initial solution. The two GRASP variants generate their own initial solutions. The running time is limited to 300 seconds for all the algorithms. In table 4 a series of statistics is presented corresponding to the best-known solution (minimum and average). Also, the minimal deviations are presented in figure 5.

amn.	<i>imn</i> . Minimal percent Deviation, <i>ame</i> . mean percent Deviation,							
т	Est.	Memetic	HybMem	GRASP-HK	GRASP-J	VNS-HK	VNS-J	
10	dmn	0	0	0.026	0.082	0	0	
	dme	0	0	0.032	0.213	0.028	0.029	
20	dmn	0	0	0.066	0.142	0	0.077	
	dme	0.026	0	1.412	1.645	1.301	1.393	
30	dmn	0.0	0.048	1.512	0.270	0.56	0.582	
	dme	0.862	1.312	2.841	2.081	1.954	2.473	
50	dmn	0.602	0.545	1.698	0.972	0.403	0.871	
	dme	1.321	1.014	2.444	1.976	1.358	1.619	
60	dmn	1.236	0.984	2.158	2.120	0.971	1.777	
	dme	1.964	1.891	2.955	3.402	1.943	2.636	
70	dmn	0.835	0.778	1.725	2.064	0.379	0.817	
	dme	1.985	1.304	2.988	2.458	1.231	1.976	
80	dmn	1.715	1.541	2.386	2.185	0.345	1.617	
	dme	2.267	2.059	3.430	3.825	1.804	2.162	
90	dmn	1.759	1.286	2.428	2.761	0.492	1.66	
	dme	2.642	2.453	3.712	4.159	1.623	3.128	
100	dmn	2.005	1.491	3.805	3.021	0.523	1.563	
	dme	2.418	2.391	4.246	3.941	1.583	2.646	
110	dmn	2.241	1.905	3.620	3.036	0.335	2.347	
	dme	3.406	2.931	4.614	4.276	2.229	3.645	
120	dmn	1.891	1.724	3.823	4.281	1.798	2.146	
	dme	3.461	3.107	4.810	5.274	3.001	3.509	
130	dmn	2.590	2.256	4.190	3.497	2.103	2.928	
	dme	4.336	4.431	6.012	4.918	3.691	4.615	
140	dmn	2.699	2.801	4.061	4.051	1.423	3.011	
	dme	3.371	3.427	5.925	5.791	3.321	3.913	
150	dmn	2.401	2.256	3.938	4.130	1.011	2.398	
	dme	3.321	3.198	4.830	5.203	2.989	3.345	

*dmn*: Minimal percent Deviation; *dme*: mean percent Deviation;

Table 4.



Fig. 5. Evolution of the minimal deviations (300" run)

The following conclusions can be drawn from the previous results:

- Among the techniques analyzed, the two GRASP variants yield slightly worse results.
- Among the other four, Memetic-HK and HybMem obtain excellent results for a low number of clusters (until m = 50).
- For 60 or 70 clusters VNS-HK obtains the best results, both for the least and average values. Moreover, in almost all cases, Memetic-HK and HybMem yield better results than VNS-J, (particularly regarding average results).
- Finally, HybMem tends to give better results than Memetic-HK as the number of clusters increases.

# 7. Conclusions

Methods that give adequate solutions to the cluster design problem in short time have been proposed. The methods proposed have obtained solutions equal to the best-known solutions for small values of m, and only slightly worse for higher values of m.

In the former case, (m  $\leq$  50), the new methods proposed obtain the best overall solutions from among those included in the comparison. In the latter case, they are only surpassed by the VNS algorithm proposed by Hansen and Mladenovic (2001), with HK-Means as the Local Search Procedure. However, the following is worth noting: in their work, VNS is used with J-Means and J-Means+ as a local search procedure, whereas in our work the use of J-Means in VNS leads to worse solutions than VNS with HK-Means and also to worse solutions than the methods we propose.

In future work the behavior of these new proposed methods and/or variants using long calculation times will be studied.

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