New Genetic Algorithm Approach for the Min-Degree Constrained Minimum Spanning Tree

Rui Salgueiro[a], Ana de Almeida[a,b,*], Orlando Oliveira[c]

[a] *CISUC, Pólo II - Pinhal de Marrocos, 3030-290 Coimbra, Portugal*
[b] *ISCTE Instituto Universitário de Lisboa, Av. Forças Armadas, 1649-026 Lisboa, Portugal*
[c] *CFisUC, Department of Physics, University of Coimbra, P-3004 516 Coimbra, Portugal*

Abstract

A novel approach is proposed for the NP-hard *min-degree constrained minimum spanning tree (md-MST)*. The NP-hardness of the md-MST demands that heuristic approximations are used to tackle its intractability and thus an original genetic algorithm strategy is described using an improvement of the Martins-Souza heuristic to obtain a md-MST feasible solution, which is also presented. The genetic approach combines the latter improvement with three new approximations based on different chromosome representations for trees that employ diverse crossover operators. The genetic versions compare very favourably with the best known results in terms of both the run time and obtaining better quality solutions. In particular, new lower bounds are established for instances with higher dimensions.

Keywords: Combinatorial optimization, degree-constrained spanning tree, genetic algorithm, heuristic, lower bound

1. Introduction

Let $G = (V, E)$ be a connected weighted undirected graph, where $V = \{1, \ldots, n\}$ is the set of nodes and $E = \{e = \{i, j\} \, : \, i, j \in V\}$ is the set of m edges. Positive costs, c_{ij}, are associated with each edge connecting nodes i and

*Corresponding author
Email addresses: rps@mat.uc.pt (Rui Salgueiro), ana.almeida@iscte.pt (Ana de Almeida), orlando@teor.fis.uc.pt (Orlando Oliveira)

j. For graph models, a common optimisation task involves finding a connected acyclic subgraph that covers all the nodes of the graph: a spanning tree. In the following, $T = (V, E_T)$ denotes a spanning tree for G, with $E_T \subseteq E$. $deg_T(i)$ is the degree of a node $i \in V$, i.e., the number of edges with node i as an end point. In the following, only connected graphs are considered.

The general *min-degree constrained minimum spanning tree (md-MST)* is defined as follows: given a positive integer $d \in \mathbb{N}$, find a spanning tree T for G with the *minimal total edge cost*[1] such that each tree node either has a degree of at least d, or it is a leaf node (a node with degree one). The solution tree is called *feasible* or *admissible* and the same designation represent each one of its nodes. Examples of feasible and unfeasible md-MST trees are given in Figures 1 for the graph $G1$ defined in Appendix A.

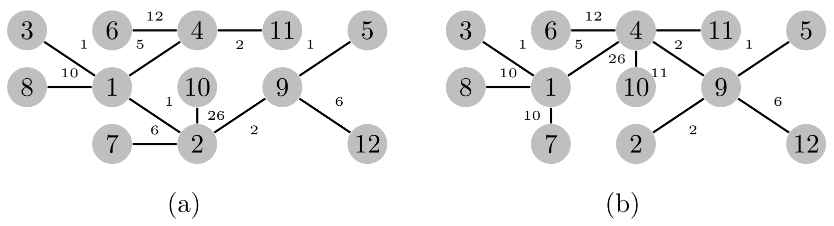


Figure 1: Examples of md–MST problem with $d = 4$, i.e., a m4-MST problem for a given graph G_1 (see Appendix A). (a) Unfeasible tree ; (b) Feasible tree.

The md-MST problem was first described by Almeida *et al.* [1] and it was proved to be an NP-hard problem for $\lfloor n/2 \rfloor > d \geq 3$ [1, 2]. In order to overcome some of the computational difficulties encountered, Martins and Souza [3] designed new algorithmic approaches based on variable neighbourhood search (VNS) metaheuristics transformed for the md-MST and an enhanced version of a second order repetitive technique (ESO) to guide the search during several phases of the VNS method. They also presented an adaptation of a greedy heuristic based on Kruskal's algorithm for determining minimal spanning trees.

[1] As usual, the final cost is given by $\sum_{e \in V} c_e$ and a tree with the minimal cost is known as the minimum spanning tree (MST).

Akgün and Tansel [4] considered a new set of degree-enforcing constraints and used the Miller–Tucker–Zemlin sub-tour elimination constraints as an alternative to single or multi-commodity flow constraints for the tree-defining part of the md–MST formulations. Martinez and Cunha [5] proposed new formulations for the md-MST problem and presented a branch-and-cut algorithm based on the original directed formulation, obtainning several new optimality certificates and new best upper bounds for the md-MST. Murthy and Singh [6, 7] published the only other known evolutionary approach by introducing Artificial Bee Colony and Ant Colony Optimisation heuristics, both tested using Euclidean and random instances for use with Steiner Tree problem instances.

The md-MST requires the computation of a MST with nodes that obey certain degree restrictions. The classical algorithms to construct minimal spanning trees are Prim's algorithm and Kruskal's algorithm (KA). Prim's algorithm [8] starts with a two node tree that contains a minimal edge, and employs a greedy search to build the tree, ensuring that an acyclic tree is obtained. Using a heap as the underlying data structure, this algorithm has a total time bound of $O(m + n \lg n)$, where m is the set of edges and n is the set of nodes. KA [9, 10] also uses a greedy technique but works with forests. Starting with the forest of all the nodes, the algorithm iteratively chooses the cheapest edge to join two disjoint nodes until it obtains the complete tree. This algorithm has an asymptotic time bound of $O(m \log n)$ (assuming that the list of edges is already sorted by cost). The MST algorithm used in our approach is the KA. The rationale behind this choice is due mainly to its good numerical performance with generic dense graphs [11] but also because it can be modified easily for our algorithms.

Due to the NP-hardness of the problem, an exact algorithm is not usable because of the inherent memory limitations. Thus, a genetic algorithm heuristic is presented, exploring new codings for the candidate spanning trees and operators. The remainder of this paper is organised as follows. Next section begins by summarising the method of Martins and Souza[3] for obtaining feasible spanning trees for the md-MST, in order to explain the original computational improvement - MSHOI - of the previous heuristic for generating feasible md-MST trees.

In Section 3, a genetic-based approach to the md-MST problem is introduced, with formulations of three different GA versions. Section 4 reports the results of several computational experiments and the relative efficiency of the different heuristics is discussed. Finally, Section 5 presents concluding remarks as well as suggestions for possible directions for future research.

2. Improvement of the existing heuristic approach to the md-MST

2.1. MSH

Martins and Souza [3] presented a heuristic algorithm (MSH), which uses a modification of Kruskal's algorithm to build a MST, thereby ensuring the feasibility of the spanning tree but without ensuring its optimality. It is based on evaluating the *need* values in each step of the KA, i.e., the number of edges that need to be "added" to unfeasible nodes: the nodes i where $deg_T(i) < d$. The total number of edges in a spanning tree is $n-1$. If a given candidate tree in the forest (F) built by KA has k edges, then $n-1-k$ edges are still needed to obtain the spanning tree. An edge can be included in a tree only if the *need* value is less than $2(n-1-k)$ after edge inclusion; otherwise, it is not necessary to consider this edge ever again [3]. Thus, in every intermediate step, MSH computes the overall need value for a forest: $total\_need(F) = \sum\limits_{\forall T \in F} need(T)$, where $need(T) = \sum_{\forall i : 1 < deg_T(i) < d} 1$. After each KA iteration, the *total_need* value of the forest and the individual tree *need* values are re-evaluated until termination by obtaining a complete feasible tree. For each $T_1, T_2 \in F$ that are required to be joined, the new tree topology depends on the number of nodes in the tree T_1:

1. Size one tree (single node and zero edges): $need(T_1) = 1$. After the connecting edge has been added, the new tree T has this node as a leaf node, so it is admissible for T.
2. Size two tree (two nodes and one edge): $need(T_1) = d - 1$. For the new tree T, at least one of the two connecting nodes in T_1 or T_2 becomes an internal node, and thus there is a $d-2$ need.

3. Other cases:

$$need(T_1) = \begin{cases} \displaystyle\sum_{\forall i : 1 < deg_T(i) < d} d - deg_T(i) & \text{if sum not null} \\ 1 & \text{otherwise} \end{cases}$$

If the sum is null and this is not the final tree, it is necessary to add one edge to connect with another.

2.2. MSHOI - Computatinal improvement of the MSH

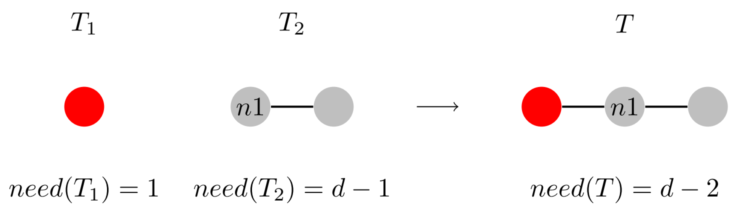
As described previously, the MSH's requirement to compute all of the *need* tree values at each iteration fundamentally determines the complexity of the algorithm. However, the overall efficiency can be improved by modifying the algorithm so it evaluates only each new *need* value iteratively based on the previous values. We refer to this improvement as the MSHOI heuristic.

It should be noted that at each step k of the MSH, a pair of trees in the forest F_k, T_1 and T_2, are joined to form a larger tree T. Therefore, the new *total need* of the forest can be evaluated only by using the knowledge of T_1 and T_2 (which are removed from the forest) and the new tree T. Since now we also use the another tree T_2 besides the T_1, there's a total of six possible cases (excluding symmetry) to be considered.

Case 1 + 1: Trees T_1 and T_2 both have size one. Tree T will have two nodes of degree 1 and one edge, and thus $need(T) = d - 1$. The new forest F_{k+1} has a total need of:

$$total\_need(F_{k+1}) = total\_need(F_k) - 2 + (d-1) = total\_need(F_k) + d - 3\,.$$

Case 1 + 2 and Case 2 + 1: Assume that T_1 has size one and that T_2 has size two, and $need = d - 1$. Then, $need(T) = d - 2$ since T will have one degree 2 node, and thus it is unfeasible.



The total need changes to

$$total\_need(F_{k+1}) = total\_need(F_k) - 1 - (d-1) + (d-2) = total\_need(F_k) - 2\,.$$

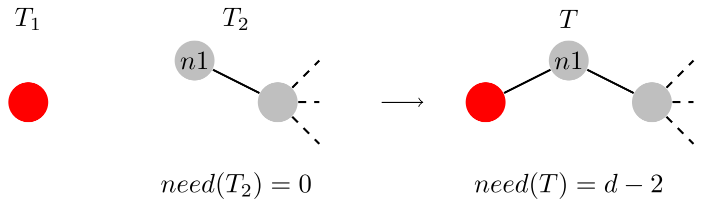
<u>*Case 2 + 2*</u>: Trees T_1 and T_2 both have size two. Then, two of the nodes of T will have degree 2, and $need(T) = 2(d-2)$. Thus,

$$total\_need(F_{k+1}) = total\_need(F_k) - 2(d-1) + 2(d-2) = total\_need(F_k) - 2\,.$$

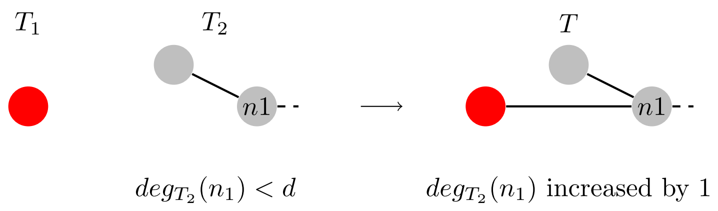
The last two cases imply exactly the same change in the *total_need* so they can be aggregated. All of the previous cases yield a new tree T with unfeasible nodes.

The resulting tree may become feasible when we combine a tree with size three or more with another. This is a special case, so a new variable is introduced, $inadm_{T_i}$, to represent the sum of *needs* for the nodes of a tree T_i. After joining T_1 with T_2, if the number of *needs* for T is zero but it is not a complete tree (has less than $|V|$ nodes), then the *need* of T will be 1; otherwise, it will be equal to *new_inadm*, where *new_inadm* is calculated in the following way.
<u>*Case 1 + 3 and 3 + 1*</u>: Consider T_1 of size one joining T_2 of size 3 or greater. Then, $need(T) = need(T_2)$. However, three different situations may occur depending on the node n_1 of T_2 used for joining:

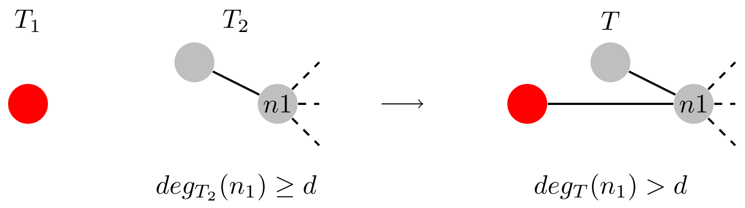
1. If $deg_{T_2}(n_1) = 1$, then it becomes an unfeasible node by increasing its degree and the new unfeasibility is $new\_inadm = inadm_{T_2} + d - 2$;



2. In the case where the degree of n_1 is less than d, the general unfeasibility is reduced by 1 to become $new\_inadm = inadm_{T_2} - 1$;



3. If the degree of n_1 is greater than or equal to d, the unfeasibility value does not change: $new\_inadm = inadm_{T_2}$.



Case 2 + 3 and 3 + 2: Consider tree T_1 of size 2 and $need = d - 1$, which is joined with a (bigger) tree T_2. The degree of the node in T used for the connection increases by 2, so it will contribute with $d-2$ to the new unfeasibility. Again, the node n_1 to which T_1 will be connected influences the feasibility of the new joint tree.

1. If n_1 had degree 1, the new unfeasibility is $new\_inadm = inadm_{T_2} + 2 \times (d-2)$.
2. If the degree is less than d, the unfeasibility is reduced by 1 and increased by $d-2$ or $new\_inadm = inadm_{T_2} + d - 3$.
3. If the degree was greater than or equal to d, the node is already feasible and so the change in unfeasibility is increased by $d-2$ compared with joining with T_1, i.e., $new\_inadm = inadm_{T_2} + d - 2$.

Case 3 + 3: Two trees of size greater than 2 are joined. In this case, the sum of *needs* will be calculated separately for each. For T_1 and depending on the node n_1 to which T_2 is connected, we have the same possibilities described in (4) when changing $inadm_{T_2}$ for $inadm_{T_1}$. The new unfeasibility for T_2, $new\_inadm_{T_2}$, is calculated in a similar manner and for the new tree T, we have, $new\_inadm = new\_inadm_{T_1} + new\_inadm_{T_2}$.

Determining the new total need (after joining trees T_1 and T_2) employs the same iterative procedure,

$$total\_need = total\_need - need(T_1) - need(T_2) + need(T) \ , \qquad (1)$$

thereby proving the following new result.

Theorem 1. *For each iteration of the MSH algorithm where 2 sub-trees, T_1 and T_2, are joined into a new tree T, the new total need is equal to subtracting the previous total need value of the associated needs for T_1 and T_2 plus the need of the new tree T.*

This implementation results in a few code decision instructions, which are independent of the size of the graph being processed. Consequently, this improvement does not require additional usage of resources and the general algorithmic complexity remains the same as that of the original MSH algorithm.

The genetic algorithm approach needs to insure that feasible trees are generated for a successful evolution phase. Therefore, in the following, the improved MSHOI method is used for spanning tree construction.

3. GAs for the m*d*–MST

The proposed approach relies on genetic algorithm (GA) metaheuristics, which are used to investigate a large number of different types of optimisation problems. This class of algorithms is inspired by the Darwinian process of evolution by natural selection [12, 13]. A GA aims to mimic the evolutionary process of species by starting with an *initial population* of randomly generated candidate solutions, where each individual is represented by a *chromosome* (its genotype) and each step (or iteration) involves the *evolution* of the population of candidates guided by a *fitness function.* This type of heuristic approach is used in the combinatorial optimisation of NP-hard problems [14], where the fitness function is usually referred to as the *cost function.* The evaluation of the cost function is performed based on the phenotypes, i.e., the individual chromosomes in the population, which is also known as the *search space.*

The same basic evolutionary strategy is used for all of the genetic variants described in the following, i.e., the classical GA using a predefined number of generations as the stopping criterion.

Algorithm 1 Genetic Algorithm

```
Initial population random generated using the MSHOI;
Sort individuals based on their fitness value;
Choose $K$ with the best fitness as the first evolutionary population;
repeat
    Select the parental mating pool for reproduction ($MP$);
    Crossover: use the $MP$ to choose two parents for reproduction to obtain a child;
    Mutation: decide on the gene mutation for each child;
    Selection: select individuals to form the next evolutionary population.
until termination criterion is satisfied.
```

In this genetic approach, selection is mostly elitist. Thus, the selection mechanism retains 50% of the elements with the greatest fitness from the previous evolutionary population and replaces the least fit 50% with the best children of the new offspring. The general reproductive plan of the evolutionary algorithm, i.e, the evolution strategy after crossover is the $(\mu + \mu)$-ES [15].

Chromosome mutations are controlled by a random function where there is only a low probability of a mutation occurring.

3.1. Fitness function

To evaluate the fitness of a *tree*, the most obvious choice would be a linear combination of the cost of the tree T and a measurement of its unfeasibility as a penalty function. The latter can be defined by adding the difference between any unfeasible node's degree and the desired value d, $c_{na}(T)$. For each candidate tree T, both costs would then be combined to obtain a fitness function by using the parameter α in a convex combination: $\alpha \sum_{e \in E_T} c_e + (1-\alpha)\, c_{na}(T)$. Initially,

α can be set at 0.9 and decreased gradually, thereby forcing infeasible solutions to be rejected increasingly. However, intensive computational tests have shown that the GA versions using this fitness function seldom find admissible trees for values of d above 8 or 9. In order to obtain an effective GA approach, we decided to use the MSHOI heuristic (Section 2.2) so that admissible tree candidate solutions (chromosomes) are always build. Therefore, the fitness function needs no penalty evaluation and is simply taken as the total edge cost of the tree,

$$F(T) = \sum_{e \in E_T} c_e$$

3.2. Chromosome representations and operators

Based on a thorough investigation of previous studies, we only found two suitable chromosome representations for trees. The first proposes the use of Prüfer numbers, where according to the constructive demonstration of Cayley's formula discovered by Prüfer [16], every such number represents a different spanning tree. Nevertheless, despite its general use, it was argued [17] that this is a poor choice for the implementation of GAs because small changes in the chromosome might cause large differences in the corresponding spanning tree. The second was suggested by Raidl and Julstrom[18] who used a completely different representation based on the vector of node weights introduced by Palmer and Kershenbaum [19]. In the following, we describe three different encodings of candidate spanning tree structures with two original representations.

3.2.1. Version gen0 - Using node weights

The authors of [18] suggest the use of a vector based on the weights of the nodes since it can influence the performance of Kruskal's algorithm. The vector is initialised randomly with weights w_i, $\forall i \in V$. When MSHOI is used to generate a feasible tree, the w_i and w_j values of each of the edge's $\{i, j\}$ extreme nodes will be temporarily added to the current costs of the edge weights:

$$c'_{ij} = c_{ij} + w_i + w_j \,.$$

To improve efficiency, the edges must be kept in an ordered list. The edges then need to be re-sorted for each candidate solution. A *bucket sort*[2] linear sorting algorithm is used due to the unusual number of orderings required and because the range of the weights of the edges (known a priori) is limited.

For each generation, the reproduction operator alternates between uniform crossover, where each weight is copied randomly either from the father or the mother, and blending with extrapolation. In the latter process, the weight w_{child} of the new chromosome (child) is obtained by the linear combination of the parents' weights as: $w_{child} = \beta * w_{dad} + (1 - \beta) * w_{mom}$, $-0.5 \leq \beta < 1.5$. Next, each element of the chromosome can be mutated according to a given mutation probability parameter by the addition or subtraction of a random amount relative to the respective weight.

3.2.2. Version gen1 - Using the leaf set

A different chromosome representation involves using a set of randomly selected leaves. In this case, an array of bits is used to represent the edges in the set. For this version, we need to modify KA in order to avoid choosing edges whose leaves are already joined in the tree. However, not using these might prevent the construction of a spanning tree for non-complete graphs. To overcome this problem, the algorithm goes through the edges again, but without excluding any this time. This phase is never used in a complete graph because all of the leaf nodes are connected to central nodes.

In general, it should be noted that this representation will not guarantee the depiction of all the possible existing trees. For instance, if we consider a graph with eight nodes where the first six are leaves (Figure 2), we need to find a tree with the minimum internal vertex degree $d = 3$. KA is a greedy strategy, so it always chooses the edges with lower costs to connect leaves to internal nodes, but this will generate a non-admissible solution for the m3-MST problem. For the graph G_2, KA will build a tree where five of the leaves are connected to one

[2]The bucket sort is a similar algorithm to the radix sort[20].

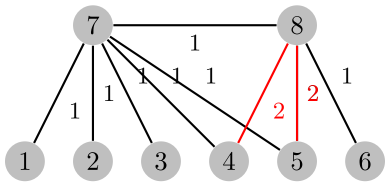


Figure 2: Example: Graph G_2

internal node of the tree and the remaining internal nodes will be connected with only one leaf, and thus it has an unfeasible degree of 2. However, all of the solutions generated are admissible trees because we use the MSHOI to build the trees.

The *gen1* version uses uniform crossover, where each bit is copied at random either from the father or the mother. Before adding the child to the population, mutations are applied with a low probability by flipping bits in the chromosome.

3.2.3. Version gen2 - Using the Edge set

This version represents the chromosome by storing the set of edges in the tree as an array of bits.

When we generate a random set, the probability of hitting a spanning tree is low. In fact, for a complete graph with n nodes and m edges, there are $2^m = 2^{n^2-n/2}$ possible sets of edges. However, only $n^{(n-2)}$ are spanning trees. For instance, in a complete graph with 25 nodes, only 25^{23} out of 2^{300} possible sets represent a spanning tree (only one out of $1.43E + 58$). Again, KA is employed to overcome this drawback. When a randomly generated set that does not represent a spanning tree, a second phase occurs where KA is repeated but considering all of the edges this time. Unlike the previous version, even for complete graphs this version generally needs to use the second phase to complete the tree.

For *gen2* version, reproduction and mutation are alternated between generations. Uniform crossover is used for each even generation, whereas for the odd generations, every individual in the population except the best is subjected to mutations with a low probability. The mutations are implemented by flipping bits in the chromosome.

4. Computational tests

For comparison with the works of Martinez and Cunha [5] and Martins and Souza [3], the experiments were performed using exactly the same instances as the test-bed. In particular, the three classes of instances, CRD, SYM, and ALM classes, are classic benchmark instances for testing the performance of algorithms for the degree-constrained problem [e.g. 21, 22]. For the weights of the edges, the CRD class uses the Euclidean distance between n randomly generated points within a square. The instances used have 30, 50, 70, and 100 nodes. The SYM class can be defined in a similar manner, except the points are generated in a Euclidean space with higher dimension. In this study, we used 30, 50, and 70 nodes. The ALM class represents larger dimension problems with 100, 200, 300, 400, and 500 nodes. These nodes are evenly distributed points in a grid measuring 480×640 and the weights of the edges are the truncated Euclidean distances between the points.

Murthy and Singh [7] use different test sets, namely Euclidean instances for Euclidean Steiner tree problem available from `http://people.brunel.ac.uk/~mastjjb/jeb/info.html`. These consist of randomly distributed points in a unit square considered as nodes of a complete graph, whose edge weights are the Euclidean distances among them.

The minimum bound on the node degree restriction d used as a control parameter depends on the size and of the instances, with values ranging from 3 to 20. All the graphs were complete, and thus $m = n^2 - n$.

4.1. Parameters: study and evaluation

The behavior of any GA is affected by various parameters associated with the genetic operators. Those with major effects on the performance comprise the population size (both the original and evolved population sizes), number of generations, and mutation rate. The first two parameters are crucial because their product is an important measure of the computational efficiency of a GA, and factors such as genetic diversity can be obtained using specifically devised strategies for the crossover and mutation operators. The optimal values are unknown for the md-MST, so we must rely entirely on empirical tests[3]. After trial-and-error experiments, it was clear that the best mutation rate value was 3% (although the difference was not significant for 1% or 2%), which agreed with previous studies.

We studied the number of generations and population sizes and their relationship. However, the major difficulty involved is that the algorithm is not deterministic, so the results obtained from each run depend on the pseudo-random generator employed. To determine whether changing a parameter is beneficial for the GA, a statistical criterion must be used to infer the actual significance of differences in performance. We considered two random variables, X_1 and X_2, to represent the costs of the spanning trees obtained after executing the two versions of the algorithm compared. Given two samples of each, n_1 and n_2, with dimensions greater than[4] 30, where $\bar{X}_1$, $\bar{X}_2$ and the corrected standard deviations are $\hat{S}_1$ and $\hat{S}_2$, respectively:

$$|\bar{X}_1 - \bar{X}_2| - 1,65\sqrt{\frac{\hat{S}_1^2}{n_1} + \frac{\hat{S}_2^2}{n_2}}. \tag{2}$$

If (2) returns a negative value, the difference between the two means is not statistically significant at a level of significance equal to 5% [24].

After several experiments based on evaluations using the significance criterion (2), we decided to generate an initial random population twice the size of the evolutionary population. It should be noted that the number of generations required to obtain the best average value did not vary significantly as the population size increased. Although this increase continually improved the

[3]Another possibility, which we did not explore, is to use online or offline automatic parameter tuning methods such as the F-Race method (see [23]).

[4] Note that 30 represents the theoretical value above which the validity of the test is proved [24].

quality of the results, only slight changes occur when the population exceeds a thousand (Figure 3). The improvement was no longer significant so the number

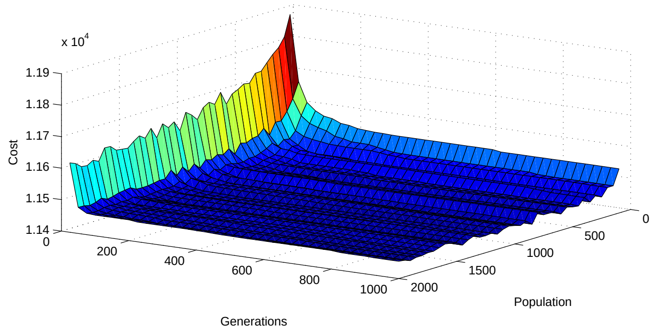


Figure 3: CRD70-2, a 70-node graph instance using $d = 10$.

of generations required to obtain the best result did not vary greatly with the size of the evolutionary population.

Unlike the size of the evolutionary population, the initial population dimension did not have any significant effects on the final values obtained.

4.2. Comparisons of algorithms' performance

To evaluate the true effectiveness of the various versions of the GAs, their results were compared with the best published previously. Complete comparison tables can be found in Appendices B and C. The genetic algorithm results are compared with results presented by the authors using the same benchmark graph instances (CRD, SYM and ALM), namely Martinez and Cunha (BC) [5] and Martins and Souza (VNS) [3]. Albeit not sharing the same benchmark instance set, GA results are also compared with the ones reported by Murthy and Singh [7], being at the moment the only other known evolutionary approach.

Akgün and Tansel ([4]) also presented comparative results for their methods over some the benchmark instances. However, having only used some of the smaller instances that only improved the run times previously reported by Almeida *et al.*[1], the results are not effective for use this comparison. Moreover, this potential partial advantage is lost when compared with the fastest results included in [5]. Thus, we will not include Akgün and Tansel results in our analysis.

Table 1: Summary of the performance comparisons: GA approach versus Martins-Souza's final results (VNS) and Martinez-Cunha (BC).

		Genetic x VNS			Genetic x BC		
Problems	#Instances	Better	Equal	Worse	Better	Equal	Worse
CRD 30-100	30	14	14	2	4	23	3
SYM 30-70	24	9	15	-	-	19	5
ALM 100-500	36	36	-	-	23	2	11
Total	90	59	29	2	27	44	19

4.2.1. Genetic versions versus other heuristics

On most occasions, some version of the GA obtained better (or at least equal) results than the best produced by the VNS heuristics of Martins and Souza [3]. The summary in Table 1 shows that the GA approach obtained better values in 66% of the tests and in only two cases with worse results. The BC heuristics of Martinez and Cunha [5] achieved generally lower values than the previous VNS in terms of the final lower bounds obtained, but the new GA versions are still competitive. In fact, comparing only with BC results, although the percentage of better solutions declined to 30%, the GA approach obtained exactly the same values for 70% of the remaining instances, and presented higher values on only 19 occasions.

In the tables in Appendix B, it is shown that the best value found by the genetic versions has better than all of the best VNS values, with only two exceptions: CRD-2 and CRD-3 using $d = 5$ (Appendix B, Table 7). The GA strategy is always better than VNS with the hardest instances, the ALM class (Appendix B, Table 7). In terms of the gap values, $\frac{\text{VNS}-\text{min GA}}{\text{VNS}}$, the genetic algorithms achieved an average value of $8,17\%$ over all ALM results. In fact, the differences between the final GA values and VNS approaches were significant in terms of the new lower values obtained by GA (Appendix B). Over all test set

Table 2: BC and VNS best values versus minimum GA versions value performance evaluation - ALM 500 nodes instances.

Instance	d	VNS	BC	min GA	gap VNS	gap BC
ALM500-1	5	14626	13328	**12334**	18.58%	8.06%
ALM500-2	5	14039	12990	**12405**	13.17%	4.72%
ALM500-3	5	13521	12997	**11730**	15.27%	10.80%
ALM500-1	10	19342	17652	**17415**	11.07%	1.36%
ALM500-2	10	18138	17891	**17653**	2.75%	1.35%
ALM500-3	10	18269	18644	**16539**	10.46%	12.73%
ALM500-1	20	24999	24508	**22346**	11.87%	9.68%
ALM500-2	20	24823	24900	**22285**	11.39%	11.73%
ALM500-3	20	25468	25064	**22643**	12.48%	10.69%

instances, the average gap for VNS versus best GA value is $5,59\%$.

Comparing only BC and GA results, for the hardest ALM class the average gap value for the better GA results is $4,52\%$ as detailed in Appendix B. Table 1 shows that 27 new lower bounds were established. It should be noticed that the new GA's lower values are particularly relevant for the hardest of the instances, the 500 nodes ALM instances (Table 2).

Overall, for the benchmark test set, the GA strategy presents itself as an effective heuristic approach for the md-MST problem, and the more so over the hardest of the instances of the set.

In relation with the works of Murthy and Singh [7], Table 3 is self-explanatory: for the hardest of the fixed Euclidean instances used by these authors, both gen_1 and gen_2 always perform better. The genetic version gen_0 was not tested since is was designed to work specifically with integer weights and these instances use reals. The GA versions achieved an average gap of $11,5\%$ and $10,5\%$ better performance than ABC and ACO heuristics, respectively (AppendixB, Table 5).

Table 3: GA *versus* ACO and ABC ([7]) for the hardest Euclidean Instances (best and average results for each instance).

		ABC		ACO		gen1		gen2	
Name	d	Best	Avg.	Best	Avg.	Best	Avg.	Best	Avg.
E250.1	3	15.92	16.08	15.59	15.70	13.077	13.243	**12.456**	**12.762**
E250.2	3	15.65	15.85	15.35	15.57	12.852	13.015	**12.603**	**12.865**
E250.3	3	15.56	15.72	15.39	15.48	12.854	12.973	**12.428**	**12.760**
E250.4	3	15.95	16.09	15.72	15.91	**12.788**	13.046	12.860	**13.021**
E250.5	3	15.82	15.95	15.49	15.64	12.895	13.065	**12.746**	**12.888**
E250.1	5	19.22	19.59	18.54	19.05	**16.454**	**16.672**	16.658	17.254
E250.2	5	19.05	19.29	18.69	19.03	**15.552**	**15.836**	16.047	16.355
E250.3	5	18.29	19.10	18.54	18.74	17.087	17.375	**15.364**	**15.735**
E250.4	5	19.20	19.73	19.10	19.37	**15.940**	**16.342**	16.227	16.642
E250.5	5	18.77	19.23	18.81	19.03	**15.882**	**16.081**	16.220	16.449
E250.1	10	24.05	25.23	24.11	24.66	**23.359**	**23.827**	23.812	24.222
E250.2	10	24.81	25.49	24.91	25.16	**22.303**	**22.674**	22.656	24.094
E250.3	10	24.13	24.88	23.87	24.20	**21.755**	**22.210**	22.413	22.933
E250.4	10	25.08	25.69	24.36	25.11	**22.745**	24.309	23.172	**24.016**
E250.5	10	24.14	25.06	24.57	25.02	**22.494**	**23.485**	23.272	23.682

4.2.2. Run times for the GA versions

This section presents an analysis of the time performance of the GA. The reported times are average run times over 64 runs for each of the GA versions, evolving over 3000 generations with a population size of 3000.

The computer used has an Intel Q9550 processor (Core2 2.83 GHz quadruple core) and 4 GB RAM, so slightly slower than the systems used in the works used for comparison [3, 5, 7]. The RAM capacity was of no consequence because the instance's dimensions were rather small and we never needed to use more than a small amount of the overall capacity. Therefore, the results of the performance test are directly comparable with those presented in previous studies.

The running times of the GA versions performance is quite stable for any instance and any number of nodes (Appendix C) when compared to the run times presented by Martins and Souza and Martinez and Cunha [3, 5]. Table 4

Table 4: Run times (seconds) for the genetic versions on CRD and SYM instances (graphs with $n = 50$ nodes).

Instance	d	gen0	gen1	gen2	Instance	d	gen0	gen1	gen2
CRD50-1	3	43.0	24.4	16.5	SYM50-1	3	42.8	14.9	16.3
CRD50-1	5	44.8	15.2	16.5	SYM50-1	5	40.7	13.7	17.1
CRD50-1	10	45.4	12.7	16.4	SYM50-2	3	43.7	12.5	16.3
CRD50-2	5	42.7	17.5	16.3	SYM50-2	5	40.8	8.1	17.3
CRD50-2	3	47.0	16.6	16.4	SYM50-3	3	42.9	13.6	16.3
CRD50-2	10	45.4	18.0	16.6	SYM50-3	5	43.8	12.9	16.1

helps the visualisation of the stability of the time performance for the genetic approach, and the same behaviour was observed in all of the CRD, SYM, and ALM classes. Note that *gen*0 was the slowest of the three versions. In general, for $n \leq 100$, *gen*2 requires less than half the time needed by *gen*0 and *gen*1 is slightly faster than *gen*2, with only a few exceptions. Excluding *gen*0, the genetic versions are not affected by the different classes of instances and there is no direct relationship between the run time and increasing d.

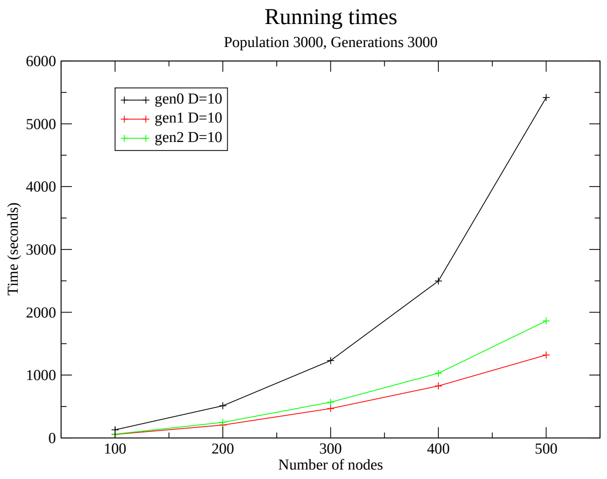


Figure 4: Comparison of the average run times for the GAs over the ALM class instances using $d = 10$ for increasing number of nodes.

In contrast, increasing the number of nodes has a direct effect on the run time for any of the genetic versions (Figure 4), which proves that the number of nodes has impact on the run times while maintaining the relative time performance of the three GA versions. Complete graphs were always used so $m = \mathcal{O}(n^2)$ and the results presented are the worst case example. This explains the higher times required by *gen*0 because it re-sorts the list of edge weights for each candidate solution (the *Bucket Sort* algorithm is linear according to the number of edges sorted).

4.2.3. Run times: comparisons with other results

The run times of the GAs depend on the size of the population, the number of generations, and the number of tests for each instance. When these were kept constant, we have shown that the run times were also a function of the number of nodes n.

Martins and Souza [3] present run times that vary greatly, which is particularly obvious for the smaller instances. For example, for CRD with $n \in \{30, 50\}$, VNS requires times that range from only a few seconds to almost 12 minutes. For the same class but with $n \in \{70, 100\}$, the time ranges from less than 5 minutes to almost 2 hours. For the ALM class, the reported times range from a few thousand to several thousand seconds. These run times do not follow clear patterns of variation relative to the instance dimension or parameters, so it is not possible to directly compare the time required by both approaches. For instance, in the case of ALM300-1 using $d = 10$, Martins and Souza obtained the best solution with a value of 13899 using almost 4 hours. By contrast, the best result found by the GAs with a smaller cost value of 13701 takes about 23 minutes.

Martinez and Cunha report shorter run times for BC [5] with the simplest of the instances in the test data set, but GA performed better for the all remaining instances, i.e., medium to large size and denser graphs (Appendix C). Especially for the larger and harder of the ALM instances class, GA always outperforms BC both in quality as in time, where BC achieves the maximum tolerate iteration time set by the authors. In short, the new GAs generally obtain quality competitive results in much shorter run times compared with both the VNS and the BC heuristics.

In relation with the evolutionary approach of Murthy and Singh, namely the ABC and ACO heuristics, the GA versions average times for the parameters used are always worse than the former: the best averaged times of the GA is around $6,5\%$ worst then the ABC, and around 3% worst than the ACO averaged times (Appendix C, Table 10). Nevertheless, the quality of the GA results is much better (Table 3).

5. Conclusions

In this study, we proposed a new algorithmic approach for the approximation of the NP-hard *md-MST* problem presenting three novel genetic algorithm approaches. An improvement for an existing heuristic procedure for the obtention of feasible md-MST trees (MSHOI) was also described. The results obtained with the new algorithms are quite promising, with computationally consistent run times as the instance dimension increases, unlike previously published direct benchmarking approaches. For these benchmarks, the GA versions achieved lower cost values for over 30% of the instances with competitive and consistent run times. In particular, for the higher instances dimensions, 27 new lower bounds were found, thereby demonstrating that the GA versions provide effective and time efficient solutions to the m*d*-MST problem. Furthermore, when compared with the other known evolutionary approach, using an Artificial Bee Colony and a Ant Colony Optimization heuristics, although more time consuming, the quality of the present GA approach is far superior.

However, some questions remain for future research. First, as usual, the GAs could be made more efficient by enforcing greater genetic diversity in the population throughout the evolutionary phase. This could be achieved by measuring the difference between each solution and the best obtained to date and using this difference to favour more diverse solutions. Naturally, it is difficult to design a difference function that is both useful and fast. Second, on several occasions, we found that an optimal parameter or strategy could not be selected because the performance depended on the instance of the problem tested. It might be interesting to implement an approach that runs diverse genetic strategies with the option of dynamically adjusting the genetic operators and parameters. Finally, we would like to perform exhaustive testing of this novel GA approach using a more comprehensive data set, ranging from smaller to harder larger dimensional instances and including non Euclidean ones, to facilitate a better evaluation of its empirical computational efficiency.

References

[1] A. M. de Almeida, P. Martins, M. C. de Souza, Min-degree constrained minimum spanning tree problem: complexity, properties, and formulations, International Transactions in Operational Research 19 (3) (2012) 323–352.

[2] A. de Almeida, P. Martins, M. C. de Souza, The md-mst problem is np-hard for $d \geq 3$, Electronic Notes for Discrete Mathematics 36 (2010) 9–15.

[3] P. Martins, M. C. de Souza, Vns and second order heuristics for the min-degree constrained minimum spanning tree problem, Computers & Operations Research 36 (11) (2009) 2969–2982.

[4] B. Akgün, I.and Tansel, Min-degree constrained minimum spanning tree problem: New formulation via miller-tucker-zemlin constraints, Computers & Operations Research 37 (1) (2010) 72–82.

[5] L. C. Martinez, A. Cunha, The min-degree constrained minimum spanning tree problem: Formulations and branch-and-cut algorithm, Discrete Applied Mathematics (164) (2014) 210–224.

[6] V. V. R. Murthy, A. Singh, Solving the min-degree constrained minimum spanning tree problem using heuristic and metaheuristic approaches, in: Proc. of the Second IEEE International Conference on Parallel, Distributed and Grid Computing (PDGC 2012), IEEE Press, 2012, pp. 716–720.

[7] V. V. R. Murthy, A. Singh, An ant colony optimization algorithm for the min-degree constrained minimum spanning tree problem, in: B. Panigrahi, P. Suganthan, S. Das, S. Dash (Eds.), Swarm, Evolutionary, and Memetic Computing, Vol. 8298 of Lecture Notes in Computer Science, Springer International Publishing, 2013, pp. 85–94.

[8] R. C. Prim, Shortest connection networks and some generalizations, Bell System Technical Journal (36) (1957) 1389–1401.

[9] J. B. Kruskal, On the shortest spanning subtree of a graph and the travelling salesman problem., in: Proc. of the American Mathematical Society, 1956, pp. 48–50.

[10] M. Gondran, M. Minoux, Graphs and algorithms, John Wiley & Sons, Chichester, UK, 1984.

[11] A. de Almeida, R. Salgueiro, Recovering a labeling algorithm for the disjoint-set problem to improve kruskal's effciency on dense graphs, tR2015/02, CISUC (February 2015).

[12] R. L. Haupt, S. E. Haupt, Practical genetic algorithms, John Wiley & Sons, Inc., New York, NY, USA, 1998.

[13] Z. Michalewicz, Genetic algorithms + data structures = evolution programs, 2nd Edition, Springer-Verlag New York, Inc., New York, NY, USA, 1994.

[14] C. M. Papadimitriou, Computational complexity, Addison-Wesley, Massachusetts, 1994.

[15] H.-G. Beyer, H.-P. Schwefel, Evolution strategies – a comprehensive introduction, Natural Computing 1 (1) (2002) 3–52.

[16] H. Prüffer, Neuer beweis eines satzes über permutationen, Archiv für Mathematik und Physik (1918) 742–744.

[17] J. Gottlieb, B. Julstrom, G. Raidl, F. Rothlauf, Prüfer numbers: A poor representation of spanning trees for evolutionary search, in: L. Spector, E. D. Goodman, A. Wu, W. B. Langdon, H.-M. Voigt, M. Gen, S. Sen, M. Dorigo, S. Pezeshk, M. H. Garzon, E. Burke (Eds.), Proc. of the Genetic and Evolutionary Computation Conference (GECCO-2001), Morgan Kaufmann, San Francisco, California, USA, 2001, pp. 343–350.

[18] G. Raidl, B. Julstrom, A weighted coding in a genetic algorithm for the degree-constrained minimum spanning tree problem, in: Proc. in the ACM Symposium in Applied Computing, 2000, pp. 440–445.

[19] C. Palmer, A. Kershenbaum, Representing trees in genetic algorithms, in: Proc. of the First IEEE Conference on Evolutionary Computation, Vol. 1, 1994, pp. 379–384.

[20] T. H. Cormen, C. E. Leiserson, R. L. Rivest, C. Stein, Introduction to Algorithms, 2nd Edition, The MIT Press, 2001.

[21] M. Krishnamoorthy, A. Ernst, Y. Sharaiha, Comparison of algorithms for the degree constrained spanning tree, Journal of Heuristics 7 (2001) 587–611.

[22] C. Ribeiro, M. de Souza, Variable neighborhood search for the degree constrained minimum spanning tree problem, Discrete Applied Mathematics 118 (2002) 43–54.

[23] M. Birattari, Tuning Metaheuristics: A Machine Learning Perspective, 1st Edition, Springer, 2009.

[24] S. M. Ross, Introduction to Probability and Statistics for Engineers and Scientists, 3rd Edition, Elsevier Academic Press, 2004.

Appendix A

Let $G_1 = (V, E)$, where $V = \{1, 2, 3, \ldots, 12\}$ is the graph.

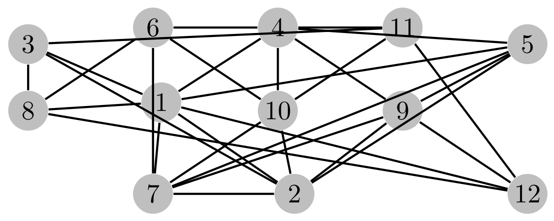


Figure 5: Graph G_1.

The associated edge costs are given by the adjacency matrix C, as follows.

$$C = \begin{bmatrix}
- & 1 & 1 & 5 & 26 & - & 10 & 10 & - & - & - & 48 \\
1 & - & 28 & - & 67 & - & 6 & - & 2 & 26 & - & - \\
1 & 28 & - & - & - & 40 & - & 38 & - & - & 57 & - \\
5 & - & - & - & 34 & 12 & - & - & 11 & 26 & 2 & - \\
26 & 67 & - & 34 & - & - & 102 & - & 1 & - & - & - \\
- & - & 40 & 12 & - & - & 65 & 30 & - & 53 & - & - \\
10 & 6 & - & - & 102 & 65 & - & - & 110 & - & - & - \\
10 & - & 38 & - & - & 30 & - & - & 54 & - & - & 67 \\
- & 2 & - & 11 & 1 & - & 110 & - & - & - & - & 6 \\
- & 26 & - & 26 & - & 53 & 54 & - & - & - & 45 & - \\
- & - & 57 & 2 & - & - & - & - & - & 45 & - & 90 \\
48 & - & - & - & - & - & - & 67 & 6 & - & 90 & -
\end{bmatrix} \qquad (3)$$

Appendix B: Genetic Algorithms Strategy Quality Performance Evaluation

Comparison of the minimum of objective function values obtained by the GA approaches (*gen*0, *gen*1, and *gen*2), min GA, with the lower bounds of VNS [3] and BC [5] heuristics, and the best values of ACO and ABC heuristics [7]. Also shown are the gap differences $\frac{X - \text{min GA}}{\text{min GA}}$, where min GA stands for the minimum value obtained between the genetic algorithm versions and X is the heuristics value in comparison (VNS, BC, ABC, or ACO).

Table 5: Comparison of gen1 and gen2 with ACO and ABC heuristics [7] for the 250 nodes Euclidean instances.

		ABC		ACO		gen1		gen2		gap ABC	gap ACO
Name	d	Best	Avg.	Best	Avg	Best	Avg.	Best	Avg.		
E250.1	3	15.92	16.08	15.59	15.70	13.08	13.24	**12.46**	**12.76**	27,77%	25,12%
E250.2	3	15.65	15.85	15.35	15.57	12.85	13.02	**12.61**	**12.87**	24,11%	21,73%
E250.3	3	15.56	15.72	15.39	15.48	12.85	12.97	**12.43**	**12.76**	25,18%	23,81%
E250.4	3	15.95	16.09	15.72	15.91	**12.79**	13.05	12.86	**13.02**	24,71%	22,91%
E250.5	3	15.82	15.95	15.49	15.64	12.9	13.07	**12.75**	**12.89**	24,08%	21,49%
E250.1	5	19.22	19.59	18.54	19.05	**16.45**	**16.67**	16.66	17.25	16,84%	12,71%
E250.2	5	19.05	19.29	18.69	19.03	**15.55**	**15.84**	16.05	16.36	22,51%	20,19%
E250.3	5	18.29	19.10	18.54	18.74	17.09	17.38	**15.36**	**15.74**	19,08%	20,70%
E250.4	5	19.20	19.73	19.10	19.37	**15.94**	**16.34**	16.23	16.64	20,45%	19,82%
E250.5	5	18.77	19.23	18.81	19.03	**15.88**	**16.08**	16.22	16.45	18,20%	18,45%
E250.1	10	24.05	25.23	24.11	24.66	**23.36**	**23.83**	23.81	24.22	2,95%	3,21%
E250.2	10	24.81	25.49	24.91	25.16	**22.30**	**22.67**	22.66	24.09	11,26%	11,70%
E250.3	10	24.13	24.88	23.87	24.20	**21.76**	**22.21**	22.413	22.93	10,89%	9,70%
E250.4	10	25.08	25.69	24.36	25.11	**22.75**	24.31	23.17	**24.02**	10,24%	7,08%
E250.5	10	24.14	25.06	24.57	25.02	**22.49**	**23.49**	23.27	23.68	7,34%	9,25%

Table 6: BC and VNS versus GA: performance evaluation - ALM class.

Instance	n	d	VNS	BC	min GA	gap VNS	gap BC	Instance	n	d	VNS	BC	min GA	gap VNS	gap BC
ALM100-1	100	5	5439	5363	**5353**	1.61%	0.19%	ALM400-1	400	5	12487	10859	**10811**	15.50%	0.44%
ALM100-2	100	5	5207	5072	**5022**	3.68%	1.00%	ALM400-2	400	5	13877	**11001**	11090	25.13%	-0.80%
ALM100-3	100	5	5456	5457	**5441**	0.28%	0.29%	ALM400-3	400	5	12379	**10834**	11098	11.54%	-2.38%
ALM100-1	100	10	7180	**7164**	**7164**	0.22%	- -	ALM400-1	400	10	17309	**15068**	15788	9.63%	-4.56%
ALM100-2	100	10	6915	**6886**	**6886**	0.42%	- -	ALM400-2	400	10	16595	**15016**	15318	8.34%	-1.97%
ALM100-3	100	10	7509	**7394**	7443	0.89%	-0.66%	ALM400-3	400	10	16439	15239	**15214**	8.05%	0.16%
ALM200-1	200	5	7467	**7072**	7246	3.05%	-2.40%	ALM400-1	400	20	21339	22905	**20000**	6.70%	14.53%
ALM200-2	200	5	7680	**7225**	7367	4.25%	-1.93%	ALM400-2	400	20	21299	22772	**20013**	6.43%	13.79%
ALM200-3	200	5	8217	**7522**	7797	5.39%	-3.53%	ALM400-3	400	20	22049	21478	**20289**	8.67%	5.86%
ALM200-1	200	10	10391	9615	**9595**	8.30%	0.21%	ALM500-1	500	5	14626	13328	**12334**	18.58%	8.06%
ALM200-2	200	10	10238	9847	**9792**	4.55%	0.56%	ALM500-2	500	5	14039	12990	**12405**	13.17%	4.72%
ALM200-3	200	10	10533	10018	**9955**	5.81%	0.63%	ALM500-3	500	5	13521	12997	**11730**	15.27%	10.80%
ALM300-1	300	5	9871	**8933**	9520	3.69%	-6.17%	ALM500-1	500	10	19342	17652	**17415**	11.07%	1.36%
ALM300-2	300	5	10532	9326	**9276**	13.54%	0.54%	ALM500-2	500	10	18138	17891	**17653**	2.75%	1.35%
ALM300-3	300	5	10887	**9501**	10016	8.70%	-5.14%	ALM500-3	500	10	18269	18644	**16539**	10.46%	12.73%
ALM300-1	300	10	13899	12838	**12771**	8.83%	0.52%	ALM500-1	500	20	24999	24508	**22346**	11.87%	9.68%
ALM300-2	300	10	13210	**12375**	12535	5.38%	-1.28%	ALM500-2	500	20	24823	24900	**22285**	11.39%	11.73%
ALM300-3	300	10	13792	13116	**12715**	8.47%	3.15%	ALM500-3	500	20	25468	25064	**22643**	12.48%	10.69%

Table 7: BC and VNS versus GA: performance evaluation - CRD and SYM classes.

Instance	n	d	VNS	BC	min GA	improv VNS	improv BC	Instance	n	d	VNS	BC	min GA	improv VNS	improv BC
CRD30-1	30	3	**4026**	**4026**	**4026**	- -	- -	CRD70-1	70	3	6609	**6516**	**6516**	1.43%	- -
CRD30-2	30	3	**3793**	**3793**	**3793**	- -	- -	CRD70-2	70	3	6621	**6586**	6619	0.03%	-0.50%
CRD30-3	30	3	**4293**	**4293**	**4293**	- -	- -	CRD70-3	70	3	7058	**7053**	**7053**	0.07%	- -
CRD30-1	30	5	**5026**	**5026**	**5026**	- -	- -	CRD70-1	70	5	8177	8144	**8139**	0.47%	0.06%
CRD30-2	30	5	**4648**	**4648**	**4648**	- -	- -	CRD70-2	70	5	7971	**7943**	**7943**	0.35%	- -
CRD30-3	30	5	**5425**	**5425**	**5425**	- -	- -	CRD70-3	70	5	8628	**8419**	**8419**	2.48%	- -
CRD50-1	50	3	**5512**	**5512**	**5512**	- -	- -	CRD70-1	70	10	11355	**11235**	**11235**	1.07%	- -
CRD50-2	50	3	**5813**	**5813**	**5813**	- -	- -	CRD70-2	70	10	11395	**11373**	**11373**	0.19%	- -
CRD50-3	50	3	**5590**	**5590**	**5590**	- -	- -	CRD70-3	70	10	11986	**11979**	**11979**	0.06%	- -
CRD50-1	50	5	**6908**	**6908**	**6908**	- -	- -	CRD100-1	100	5	9387	9352	**9283**	1.12%	0.74%
CRD50-2	50	5	**7238**	**7204**	7244	-0.08%	-0.55%	CRD100-2	100	5	9728	9623	**9587**	1.47%	0.38%
CRD50-3	50	5	**7277**	**7277**	7295	-0.25%	-0.25%	CRD100-3	100	5	9739	9656	**9653**	0.89%	0.03%
CRD50-1	50	10	**9633**	**9633**	**9633**	- -	- -	CRD100-1	100	10	13006	**12916**	**12916**	0.70%	- -
CRD50-2	50	10	**9743**	**9743**	**9743**	- -	- -	CRD100-2	100	10	13255	**13026**	**13026**	1.76%	- -
CRD50-3	50	10	**9855**	**9855**	**9855**	- -	- -	CRD100-3	100	10	**13365**	**13365**	**13365**	- -	- -
SYM30-1	30	3	**1197**	**1197**	**1197**	- -	- -								
SYM30-2	30	3	**1435**	**1435**	**1435**	- -	- -								
SYM30-3	30	3	**1408**	**1408**	**1408**	- -	- -								
SYM30-1	30	5	**1765**	**1765**	**1765**	- -	- -								
SYM30-2	30	5	**2090**	**2090**	**2090**	- -	- -								
SYM30-3	30	5	**2008**	**2008**	**2008**	- -	- -								
SYM50-1	50	3	**1278**	**1278**	**1278**	- -	- -	SYM70-1	70	3	1362	**1360**	**1360**	0.15%	- -
SYM50-2	50	3	**1178**	**1178**	**1178**	- -	- -	SYM70-2	70	3	1471	**1448**	1465	0.41%	-1.16%
SYM50-3	50	3	**1615**	**1615**	**1615**	- -	- -	SYM70-3	70	3	1551	**1521**	1534	1.11%	-0.85%
SYM50-1	50	5	**2054**	**2054**	**2054**	- -	- -	SYM70-1	70	5	2240	**2028**	2087	7.33%	-2.83%
SYM50-2	50	5	**1760**	**1760**	**1760**	- -	- -	SYM70-2	70	5	2496	**2165**	2293	8.85%	-5.58%
SYM50-3	50	5	**2525**	**2525**	**2525**	- -	- -	SYM70-3	70	5	2242	**2210**	**2210**	1.45%	- -
SYM50-1	50	10	**4121**	**4121**	**4121**	- -	- -	SYM70-1	70	10	5055	**4979**	**4979**	1.53%	- -
SYM50-2	50	10	**4166**	**4166**	**4166**	- -	- -	SYM70-2	70	10	4912	**4787**	4887	0.51%	-2.05%
SYM50-3	50	10	**4979**	**4979**	**4979**	- -	- -	SYM70-3	70	10	5098	**4997**	**4997**	2.02%	- -

Appendix C: Run times for the GA versions

Average performance times based on 64 runs of each test instance for each genetic version: *gen*0, *gen*1, and *gen*2 and the respective BC [5] run times, with the exception of the last table, were the vast majority of run times reported for BC are maximum tolerated iteration times.

Table 8: Average run times (seconds) of the GA versions: CRD and SYM instance graphs ($n \leq 100$).

Instance	d	gen0	gen1	gen2	BC	Instance	d	gen0	gen1	gen2	BC
CRD30-1	3	19.6	13.9	7.3	0.3	SYM30-1	3	19.2	4.7	7.6	0.2
CRD30-1	5	20.5	6.7	7.2	0.9	SYM30-1	5	19.9	5.5	7.4	0.5
CRD30-2	3	19.4	5.6	7.3	0.2	SYM30-2	3	19.1	4.9	7.6	0.1
CRD30-2	5	20.0	8.7	7.2	0.3	SYM30-2	5	20.0	7.2	7.4	0.3
CRD30-3	3	19.3	7.2	7.5	0.2	SYM30-3	3	18.8	4.6	7.8	0.0
CRD30-3	5	20.5	7.2	7.2	3.2	SYM30-3	5	19.5	11.6	7.5	0.1
CRD50-1	3	43.0	24.4	16.5	5.0	SYM50-1	3	42.8	14.9	16.3	0.7
CRD50-1	5	44.8	15.2	16.5	69.0	SYM50-1	5	40.7	13.7	17.1	5.7
CRD50-1	10	45.4	12.7	16.4	13.8	SYM50-2	3	43.7	12.5	16.3	0.7
CRD50-2	5	42.7	17.5	16.3	81.2	SYM50-2	5	40.8	8.1	17.3	1.3
CRD50-2	3	47.0	16.6	16.4	61.6	SYM50-3	3	42.9	13.6	16.3	0.2
CRD50-2	10	45.4	18.0	16.6	7.7	SYM50-3	5	43.8	12.9	16.1	10.9
CRD70-1	3	77.3	33.6	32.5	148.6	SYM70-1	3	70.1	36.6	30.7	1.9
CRD70-1	5	78.1	26.9	30.1	800.0	SYM70-1	5	73.4	18.0	30.1	7.3
CRD70-1	10	78.5	20.7	30.2	138.6	SYM70-1	10	76.6	21.2	30.1	115.9
CRD70-2	3	75.0	23.1	30.4	4785.0	SYM70-2	3	70.9	18.9	30.5	6.0
CRD70-2	5	74.9	23.8	29.8	2416.9	SYM70-2	5	73.4	17.2	30.1	5.0
CRD70-2	10	78.2	28.3	29.9	571.9	SYM70-2	10	75.7	22.6	29.8	53.0
CRD70-3	3	75.7	25.6	30.2	3859.9	SYM70-3	3	72.1	19.5	31.9	4.8
CRD70-3	5	77.1	21.2	29.8	1402.8	SYM70-3	5	73.1	21.8	30.1	31.6
CRD70-3	10	76.6	24.7	30.6	17.9	SYM70-3	10	75.6	21.5	29.7	112.9
CRD100-1	3	137.1	57.5	62.1	-	ALM100-1	3	125.5	52.5	60.0	-
CRD100-1	5	140.6	47.2	60.5	10800.0	ALM100-1	5	129.5	51.2	59.3	21600.0
CRD100-1	10	131.5	51.9	59.8	5741.6	ALM100-1	10	127.6	56.3	59.4	385.4
CRD100-2	3	129.4	91.3	61.3	-	ALM100-2	3	125.7	55.5	62.7	-
CRD100-2	5	146.9	68.0	61.2	10800.0	ALM100-2	5	130.8	59.1	63.4	21600.0
CRD100-2	10	133.9	49.7	59.9	669.4	ALM100-2	10	128.4	51.9	59.6	7706.1
CRD100-3	3	137.9	60.9	63.5	-	ALM100-3	3	126.9	47.3	60.7	-
CRD100-3	5	144.4	63.1	60.5	10800.0	ALM100-3	5	131.8	55.8	60.5	21600.0
CRD100-3	10	134.9	42.1	60.3	1359.4	ALM100-3	10	128.8	58.4	60.5	21600.0

Table 9: Average run times (seconds) of the GA versions: ALM instance graphs ($n > 100$).

Instance	n	d	gen0	gen1	gen2	Instance	n	d	gen0	gen1	gen2
ALM200-1	200	3	497.0	273.2	261.6	ALM300-1	300	3	1169.3	411.3	566.6
ALM200-1	200	5	527.9	219.3	251.7	ALM300-1	300	5	1193.4	438.5	564.5
ALM200-1	200	10	509.7	201.9	245.9	ALM300-1	300	10	1237.0	474.7	553.5
ALM200-2	200	3	504.9	231.3	268.8	ALM300-2	300	3	1181.5	554.0	619.2
ALM200-2	200	5	523.2	256.2	247.9	ALM300-2	300	5	1185.3	443.2	569.7
ALM200-2	200	10	509.7	182.2	247.0	ALM300-2	300	10	1224.6	445.5	573.0
ALM200-3	200	3	501.6	224.9	257.5	ALM300-3	300	3	1173.6	459.4	605.4
ALM200-3	200	5	518.7	210.2	252.4	ALM300-3	300	5	1195.9	506.0	580.6
ALM200-3	200	10	515.1	231.4	250.5	ALM300-3	300	10	1230.6	480.8	577.1
ALM400-1	400	3	2296.7	864.4	1153.0						
ALM400-1	400	5	2503.2	912.3	1044.5	ALM500-1	500	5	5338.9	1652.3	1662.9
ALM400-1	400	10	2498.2	811.4	1028.9	ALM500-1	500	10	5433.9	1260.3	1997.7
ALM400-1	400	20	2526.2	701.6	1285.7	ALM500-1	500	20	5384.2	1302.1	2144.2
ALM400-2	400	3	2321.0	832.0	1035.7						
ALM400-2	400	5	2374.0	906.1	1019.1	ALM500-2	500	5	5292.5	1541.0	1692.1
ALM400-2	400	10	2499.0	850.3	1022.1	ALM500-2	500	10	5444.3	1382.3	1854.3
ALM400-2	400	20	2385.2	719.9	1156.5	ALM500-2	500	20	5285.6	1184.3	1928.3
ALM400-3	400	3	2317.9	878.1	1078.5						
ALM400-3	400	5	2370.4	1022.7	1030.8	ALM500-3	500	5	5257.6	594.7	1666.5
ALM400-3	400	10	2496.4	819.8	1036.8	ALM500-3	500	10	5376.9	1318.7	1735.7
ALM400-3	400	20	2354.3	787.1	1242.9	ALM500-3	500	20	5320.0	1126.2	1809.3

Table 10: Average run times (seconds) of gen1 and gen2 for the 250 nodes Euclidean instances compared with ABC and ACO heuristics [7]

Name	d	ABC	ACO	gen_1	gen_2	Name	d	ABC	ACO	gen_1	gen_2
E250.1	3	96.81	273.51	874.13	918.83	E250.1	10	96.16	108.78	683.07	1037.82
E250.2	3	89.05	296.32	516.04	871.47	E250.2	10	105.29	107.14	613.44	982.23
E250.3	3	89.52	284.62	681.29	852.30	E250.3	10	108.72	106.63	406.26	984.35
E250.4	3	96.59	286.20	605.41	850.86	E250.4	10	104.29	102.73	710.56	1005.81
E250.5	3	103.74	272.22	817.51	789.27	E250.5	10	104.99	101.73	737.53	985.97
E250.1	5	98.34	195.69	650.40	1013.87						
E250.2	5	106.52	203.36	574.67	1013.70						
E250.3	5	95.35	191.98	633.26	992.89						
E250.4	5	99.53	172.76	691.03	1031.76						
E250.5	5	89.88	170.54	506.76	982.03						