

Supporting Big Moving Objects Tracking and Analysis: An Innovative Scan-Matching Algorithm*

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Abstract

In this paper we propose a novel family of *scan matching algorithms* based on registration, which are enhanced by using a genetic pre-alignment phase based on a novel metrics, first, and, second, performing a finer alignment using a deterministic approach. Our experimental assessment and analysis confirms the benefits deriving from the proposed novel family of such algorithms.

Keywords

Moving Objects, Scan-Matching Algorithms, Intelligent Systems, Genetic Optimization

1. Introduction

Big moving objects arise as a novel class of big data objects in emerging environments. Here, the main problems are the following: (i) tracking, which represents the baseline operation for a plethora of higher-level functionalities, such as detection, classification, and so forth; (ii) analysis, which meaningfully marries with *big data analytics scenarios*.

Nowadays, a great deal of interest is growing around the mobile object tracking problem, especially due to the emerging integration between robotics and *big data applications* (e.g., [8, 25, 12]). Following this trend, several mobile object tracking approaches have recently appeared in literature, considering different aspects of the target issue, such as coverage, completeness, effectiveness, efficiency, etc. The category of algorithms that goes under the name of *scan-matching* (e.g., [22, 20, 16]) supports mobile objects positioning in indoor environments based on the acquisition of maps of the environment surrounding the target mobile objects. Maps are acquired from two successive points in the objects' path using a range-scanner sensor positioned on mobile objects themselves. The first acquisition is called reference scan and the second actual scan. The actual scan is sometimes also called new scan. By overlapping the maps acquired at two successive positions on the path it is possible to estimate the relative movement

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of the object between these two positions. It should be noted that the proposed approach strictly follows a recent methodology appeared in literature, where artificial intelligence paradigms marry data analytics methods (e.g., [1, 19, 2]).

In this paper we describe a family of *scan-matching based registration algorithms* called HGLASM-g which perform scan-matching based on a hybrid approach. First, an approximate pre-alignment of two adjacent maps is performed via a new genetic optimization method called GLASM-g; then a variant of the Iterative Closest Point (ICP) algorithm is applied to pre-aligned maps to obtain the final overlap.

In other proposed genetic scan-matching pre-alignment algorithms, the fitness functions are based on metrics between actual and reference scan points that require to know the correspondence of point pairs and the translation and rotation between the two scans. However, when scan acquisitions include noise, correspondence errors may arise. Moreover, also translation and rotation corrections can lead to errors when they are too large.

In order to overcome such issues, in this paper we propose a novel metric which does not require neither points pair correspondences nor translations and rotation corrections. Indeed, our metric is based on lookup tables built around the reference scan points. The fitness function weights the hits of actual scan points in the lookup table. The genetic pre-alignment then finds the scan with the highest fitness within a search space of given size. This guarantees also the maximum robustness towards both the acquisition errors and the Initial Position Errors (IPE). It is well known that ICP performance depends on the quality of points pair correspondence and on the accuracy of the starting point estimation. We overcome this limitation by choosing the initial guess of ICP via genetic pre-alignment, which makes it close to the true solution. This way, point correspondence, translation and rotation estimations are performed correctly and, as a consequence, iteration failures are reduced.

The algorithms described in this paper form a family in the sense that each algorithm is characterized by different values of the target search space size. Each size allows us to solve different registration problems and hence different mobile object tracking scenarios. If the search space size is small, in fact, the algorithm can recover from small errors only, while, if the search space is higher, also higher errors can be recovered. However, computation complexity increases as the search space size gets higher.

A similar hybrid algorithm is described by Martinez *et al.* in [17]. Therefore, we consider the latter algorithm in a comparative approach, and we experimentally show that all the terms of comparison with this algorithm are improved thanks to the hybrid algorithms proposed in this paper. Furthermore, we also show that our approach is able to recover from greater initial positioning and acquisition errors. The key for improvement is the definition of a new metric used for computing the fitness function of the genetic procedure. The proposed target scan-matching algorithm is described for the 2D case, but it can be used in the 3D case as well. Improvements obtained with our proposed algorithm are measured *both* in terms of accuracy and noise robustness. Indeed, the estimation of the initial position of target mobile object often comprises significant errors. For instance, when the mobile object is equipped with a legged or wheeled locomotion, and the initial position is estimated by means of odometric approaches, there may be slippage with respect to the floor, which entails significant errors in the initial position of the object. As a consequence, accuracy of algorithms is seriously affected by IPE.

2. A Novel Family of Enhanced Hybrid Scan Matching Algorithms

The pre-alignment step is inspired by the algorithm called Genetic Lookup based Algorithm for Scan Matching (GLASM) described by Lenac *et al.* in [14]. The algorithm described in [14] uses a metric based on a binary lookup table.

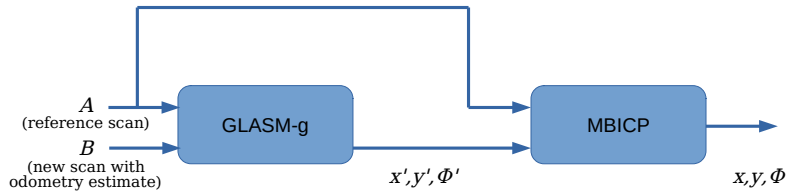


Figure 1: Block diagram of the proposed technique.

In the proposed approach we first improve GLASM by using the 8-bit encoding to store the probability density of measurements being close to points of reference scan in the lookup table. We call this improved variant of the existing binary GLASM technique as *GLASM-g*. Then, this improved variant of the existing GLASM technique is combined with MbICP [18]. In more details, Figure 1 shows a block diagram of the proposed approach. Here, the new scan *B*, evaluated starting from the odometric estimation of robot movements, is fed as input to *GLASM-g*, together with the previous scan, *A*. The output of *GLASM-g* x', y', ϕ' , is then used as starting point of the MbICP algorithm that compares *A* and *B*, thus producing the final output x, y, ϕ .

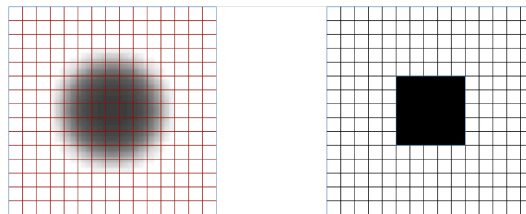


Figure 2: A detail of a lookup table surrounding an isolated point of the reference scan. Left: Radial, Gradual. Right: Squared, Binary.

In Figure 2 the difference between the two algorithms is shown: in the *GLASM-g* version the lookup table is displayed as a gray scale image, while in the *GLASM* version the lookup table is seen as a black and white image.

While in the *GLASM* lookup table each cell was either 1 or 0 the *GLASM-g* table can contain a range of values that model the probability of matching a point using a normal distribution. In the proposed implementation 256 different values are used requiring 1 byte of memory per cell.

The computation of the fitness function works as follows. For each point of the new scan a roto-translation and a discretization are performed to bring the point in the same reference

frame of the lookup table and select the corresponding cell. However, once the cell is selected, instead of simply incrementing the fitness with a binary value, the fitness is incremented with a value corresponding to the probability of matching a point that was saved in the lookup table. A representation of this probability is shown in Figure 2, left panel, with gray levels.

In Algorithm 1 we report the pseudo code of the fitness computation used in GLASM-g.

Algorithm 1 GLASM-g Fitness Computation

Input: B // new scan
Output: $fitness$
 $fitness = 0;$
for (each point p of B) **do**
 // roto-translation to lookup reference frame
 $p' = \text{changereferenceframe}(p)$
 $fitness = fitness \cdot \text{lookup}(p');$
return $fitness;$

The fitness function is essential for the proper functioning of genetic optimization algorithms. For each individual and for each execution it is computed only once. Its correct definition is therefore fundamental also from the point of view of computational complexity, given that a fitness function that requires simple calculations translates into a fast execution of the entire algorithm, leading to an exploration of a greater search space with a greater success ratio.

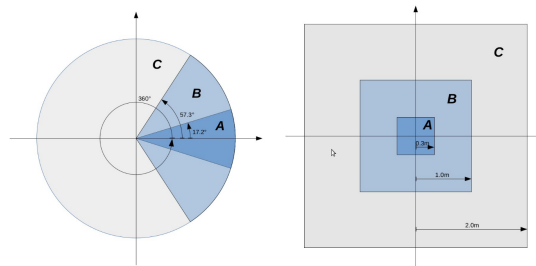


Figure 3: Search space size of the algorithms *small* (A), *medium* (B), and *large* (C).

The goal of two-dimensional scan matching algorithms is to obtain the path of a mobile object by estimating its relative movements during the path. In other words, we can speak of a space ($translation_x \times translation_y, rotation$) within which the scan matching algorithm searches for its estimate.

The individual algorithms within the family differ in the search space size and the parameters selected for the genetic algorithm. Typically, in order to cover a larger search space, a larger population is used, as well as the number of generations and runs of the genetic algorithm.

In this paper we selected and studied three different algorithms from within the family that we simply call *small*, *medium*, and *large*. The search space size and the combination of genetic parameters of the selected algorithms are depicted in Figure 3 and listed in Table 1.

Table 1

Search space size of the selected algorithms and the corresponding parameters used for the genetic algorithm

Algorithm	Search Space Size	Genetic Configuration
	$(dX, dY, dRot)$	$(pop \times gen \times runs)$
<i>small</i> (A)	$\pm 0.3m, \pm 0.3m, \pm 17.2^\circ$	$20 \times 6 \times 1$
<i>medium</i> (B)	$\pm 1.0m, \pm 1.0m, \pm 57.3^\circ$	$100 \times 10 \times 1$
<i>large</i> (C)	$\pm 2.0m, \pm 2.0m, \pm 180.0^\circ$	$200 \times 12 \times 2$

The search space of the *small* algorithm is sufficient to recover from small initial errors, while *medium* and *large* are able to correct progressively larger errors, at the cost of computational time. The *large* algorithm is able to recover from arbitrary orientation errors and large translation errors. The search space is obviously centered on the reference scan.

For the refinement step we selected the MbICP algorithm [18] which determines the correspondences between the points of the current scan and the reference scan considering both the rotation and the distance between the points. The algorithm has characteristics of accuracy and low calculation times. MbICP has better characteristics than other iterative scan matching algorithms based on point correspondences, for example [21, 23].

Visual examples of the algorithm in operation are shown in Figure 4. In addition a video file is available attached to this manuscript that illustrates the problem and shows in more detail the proposed algorithms in operation.

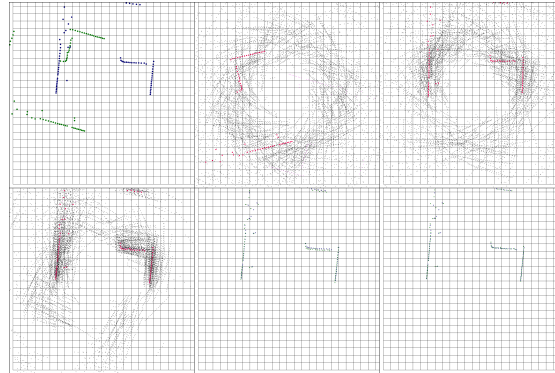


Figure 4: Visualization of HGLASM-g operation. In the top-left frame the initial position estimate of the new scan is depicted in green and the reference scan in blue. The next three frames show the pre-alignment process depicting the population after 0,5, and 12 generations of the genetic algorithm with the best estimate shown in red. The last two frames show the refinement of the solution using the MbICP algorithm (the first and the last iteration are shown).

3. Experimental Study

The performance of the family of algorithms described in this paper has been verified through several experiments carried out with a publicly available scan dataset. The dataset used in our experiments was produced by the RAWSEED project, [4, 6]. The aim of the RAWSEED project was to produce tools to compare the performance of robotic systems. The laser data considered in this dataset was obtained from a Sick sensor. To simplify the experiments, a significant subset of the whole data was randomly extracted across the entire dataset.

The dataset concerns internal and external environments. The movable objects traced in the dataset entered and exited from various environments, and also covered urban environments. The dataset thus provides the opportunity to study the performance of complex navigation algorithms in various types of environments.

It is worth to note moreover that the results reported in this Section have been obtained with a PC equipped with Intel Core 2 Quad Q9550 CPU running at 2,83 GHz.

The assessment of the accuracy obtained by the algorithms requires not only the laser scanning data but also the ground truth data. The Rawseed dataset contains ground truth data, but not for all scans. Furthermore, the reported positioning error is 1 cm, which is not sufficient for our evaluations. To address this inadequacy, the ground truth values were constructed by using a translated and rotated copy of the reference scan as the new scan. The ground truth value is thus known exactly as it corresponds to the position of the reference scan. To prevent the scan from being compared to a copy of itself the scan was split between the two scans with the reference scan consisting of the odd readings in the scan, and the new scan consisting of the even ones.

In all experiments it is important to study how algorithms converge under different conditions. To quantitatively express the robustness of the algorithms with respect to initialization errors, scanning noise and falling in local minima, we defined the Success Ratio. Success Ratio is the percentage of successful comparisons, computed as the number of successful comparisons divided by the total number of comparisons. A success is the case in which the resulting translation and rotation fall within a fixed size ellipsoid around the true values. In all the experiments the pre-established size is 10 cm for distance and 0.57° ($0.01[rad]$) for rotation, respectively. In cases where genetic optimization was used to achieve a coarse pre-alignment of the hybrid algorithm, the predetermined size was 30 cm and 5.73° ($0.1[rad]$) respectively. This relaxation of the thresholds was introduced because the purpose of the pre-alignment is not to provide an accurate estimate, but an estimate that is close enough to the true position to be significant for the next step of the algorithm. When the scan matching reached convergence, the mean and standard deviation of the error (estimated position - true position) were computed for the considered algorithms.

In the first set of experiments, the MbICP algorithm was studied. In addition to the obtainable accuracy, it is important to study how robust is the MbICP to the initial position estimate errors, i.e. to establish its convergence area. Since the MbICP algorithm is used in the refinement step of the proposed hybrid approach the pre-alignment step should always produce a good enough alignment that falls inside this area thus enabling MbICP to further refine the solution.

In the second set of experiments we compared the genetic algorithm using three different definitions of the fitness function. The results are described in the 3.1 Section. The results

presented are fundamental to the algorithm described in this paper.

Finally, the third set of experiments concerns the comparison of the algorithms proposed in this paper with the algorithm proposed by Almeida *et al.* (MbICP) [18] that we have taken as a reference. These comparisons are listed in the 3.2 Section.

3.1. Genetic Pre-Alignment: Performance Analysis

The performance of the genetic algorithm has been studied by varying the configuration of genetic parameters such as the size of the population and the number of generations. Figure 5 shows the translation (left) and rotation (right) errors versus the number of evaluations of the fitness function for the Polar Genetic Algorithm (PGA), GLASM and GLASM-g.

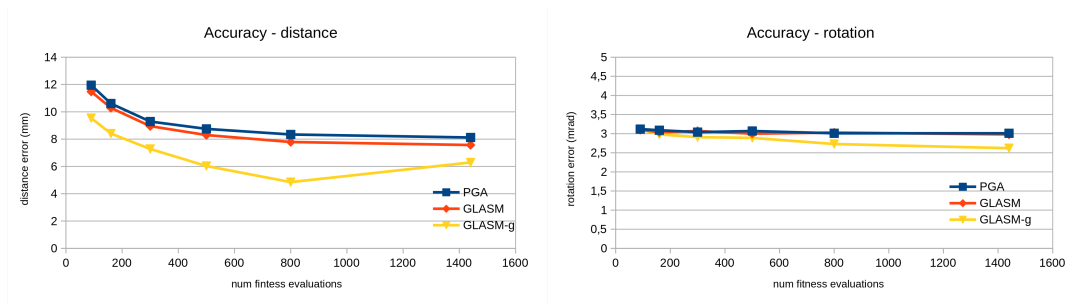


Figure 5: Translation Error (Left) and Rotation Error (Right) Versus the Number of Fitness Evaluations (Right).

The calculation time of the algorithms based on the GLASM and GLASM-g lookup tables respectively represents the time taken only by the matching of the new scan with respect to the reference scan and not by the initialization phase of the lookup table. The figures show the times in milliseconds relating to various Success Ratios for *small* and *large* search spaces.

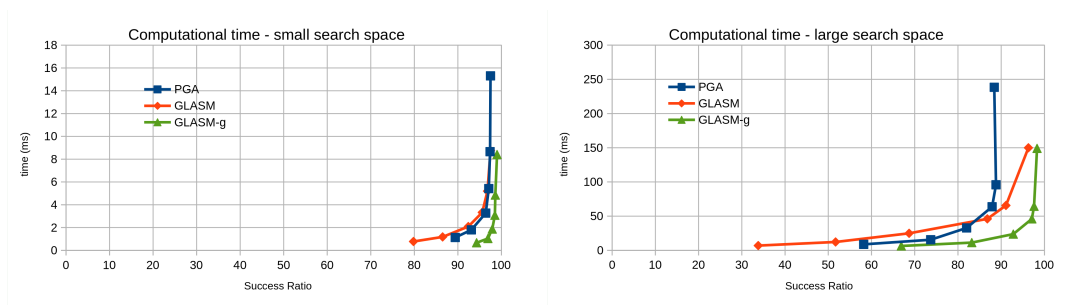


Figure 6: Time Needed to Get Various Levels of Success Ratio for Different Sets of Genetic Algorithms with *Small* (Left) and *Large* (Right) Search Size.

As we can see in Figure 6, the best Success Ratio results, calculation time and accuracy are always obtained with the fitness function used by the GLASM-g algorithm. In particular we see

that the GLASM-g algorithm always offers better Success Ratio and calculation speed results than the PGA algorithm of Martinez *et al.*. The GLASM algorithm provides the same results as GLASM-g if the size of the population and the number of generations are both high.

This slower convergence toward high Success Ratios is explained by the nature of the GLASM fitness function. Actually, in addition to the smaller marking pattern, the GLASM fitness function also produces variations of the fitness score that are less refined than GLASM-g.

3.2. Proposed Hybrid Algorithms: Performance Analysis

The objectives of the hybrid algorithm proposed in this paper is to improve the robustness of the approaches based on Iterative Correspondence Point with respect to the initial positioning errors, to convergence issues and to the presence of noise in the scans. The increase in robustness must maintain accuracy and must not be introduced at the expense of computing time. Here we report the results of the third set of experiments, i.e. those obtained with the hybrid approach presented in this paper. The parameters of the genetic algorithm are described in the previous section and shown in Table 1 for the search spaces *small*, *medium* and *large*.

We describe now some results concerning the Success Ratios obtained with different values of initial position errors, both rotation and translation errors. On the other hand, the computation time slightly increases going from *small* to *large* sizes. But it is very important to observe that also the range of errors that can be corrected increases going from *small* to *large* sizes.

Figure 7 shows the Success Ratio curves versus different values of rotation and translation initial positioning errors, for *large* (left) and *medium* (right) search spaces. In addition to this, Figure 8 (left) shows the same experimental patterns for *small* search space.

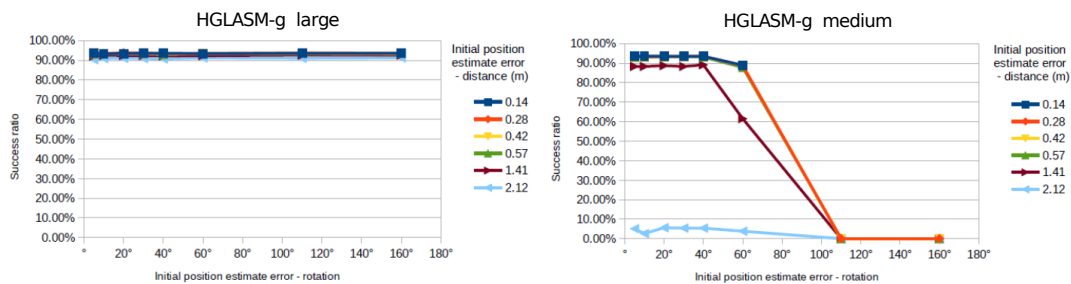


Figure 7: Success Ratio Behavior Versus Rotation and Translation Errors for *large* (Left) and *medium* (Right) Search Space Size.

As we can see in these figures, the Success Ratio for *large* search space size is about 90% for arbitrarily large rotation errors and all considered translation errors up to 2.12 meters. This large range of errors that can be corrected means that global positioning and tracking applications are possible. As the search space size decreases the range of errors that can be corrected is reduced, because the solution is searched in a reduced space. This allows to reduce the computation time in applications where a smaller search space size is sufficient.

For comparison we report in the following the Success Ratios obtained with the MbICP algorithm. Figure 8 (right) shows that the rotation and translation errors that can be corrected

by the MbICP algorithm are much worse than that corrected by the hybrid algorithm described in this paper. Just to highlight a couple of results reported in Figure 8 (right), consider the following initial positioning errors: 20 degree of rotation error and 0.57 meter of translation error. With these errors we have a Success Ratio of about 93% for large and medium search space sizes and about 85% for small search space size.

In the same condition the Success Ratio of the MbICP algorithm drops at about 20%. It is also important to consider the rotation error after which it is not possible to get significant Success Ratio. While HGLASM-g medium cannot get significant Success Ratio after 110 degrees and HGLASM-g small after 60 degree, the MbICP algorithm stops at 40 degrees.

If the IPE is inside the realignment margins of the local scan matcher, the addition of the pre-alignment step in theory would not be necessary since the ICP based algorithms is capable by itself of successful matching. On the first thought the addition of the pre-alignment step would then just add to execution time incurring speed penalty. However, in practice this often is not true because the addition of the pre-alignment step typically reduces the number of iterations for the ICP step. The reason for this speed-up lies in the iterative nature of ICP based algorithms. If the iteration starts from an initial point that is very far from the true position, it normally requires many iterations to improve the position. If we look at the last row of the table we see that if the search space is large, the proposed algorithm obtains a high Success Ratio in a very short time even if the initial position error is high.

An important aspect of the proposed algorithms is their robustness against uncertainty. Scan matching algorithms in general cannot adequately overcome singularity cases like navigation in long hallways. The uncertainty alongside the direction of the corridor cannot be addressed using the information contained in the scan alone. The proposed approach however manages to correct the error along the direction orthogonal to the direction of the hallways even for large errors of the initial position.

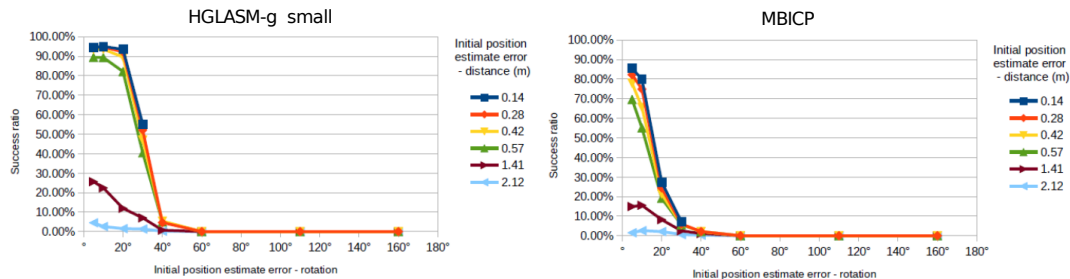


Figure 8: Success Ratio Behavior Versus Rotation and Translation Errors for *small* Search Space Size (Left) and with respect to the MbICP algorithm (Right).

4. Conclusions and Future Work

In this paper we have presented a hybrid algorithm for the problem of scan matching. The algorithm was tested with a dataset consisting of laser scans obtained in various environments.

The main contribution is that better results of the scan matching operation are obtained in terms of accuracy and robustness. The main reason is due to the new metric adopted that allows to compare not just single points but an entire scan. This permits to avoid the preliminary steps of point correspondence and the translation and rotation computation, that introduce errors in classical scan matching algorithms.

Future works will be directed towards the extension of the described hybrid algorithms to the 3-D case, and higher dimensions. Also, we plan to make our comprehensive framework suitable to the emerging *big data trend* (e.g., [10, 7, 9, 5, 3]), as to make it able of dealing with specific features of such innovative settings, like also dictated by some recent studies (e.g., [13, 15, 11]).

Acknowledgments

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