

A Novel Genetic Scan-Matching-Based Registration Algorithm for Supporting Moving Objects Tracking Effectively and Efficiently

KRISTIJAN LENAC^{1,2}, ALFREDO CUZZOCREA³, AND ENZO MUMOLO.⁴

¹Faculty of Engineering, University of Rijeka, Rijeka, Croatia (e-mail: klenac@riteh.hr)

²University of Rijeka, Center for Artificial Intelligence and Cybersecurity, Rijeka, Croatia

³iDEA Lab, University of Calabria, Rende, Italy (e-mail: alfredo.cuzzocrea@unical.it)

⁴Department of Engineering and Architecture, University of Trieste, Trieste, Italy (e-mail: mumolo@units.it)

Corresponding author: Alfredo Cuzzocrea (e-mail: alfredo.cuzzocrea@unical.it).

ABSTRACT In this paper we describe a *scan-matching based registration algorithm* for tracking moving objects which falls in the emerging area that predicates the integration between robotics and *big data applications*. The scan matching approaches track paths of a mobile object by comparing maps of the environment seen by the object during its movement. Algorithms described in this paper are hybrid, i.e. they compare maps by using first a genetic pre-alignment based on a novel metrics, and then performing a finer alignment using a deterministic approach. This kind of hybridization is, indeed, not new. However, the novel metrics used in this paper leads to important new properties, namely to correct arbitrary rotational errors and to cover larger search spaces. The proposed algorithm is experimentally compared to other approaches, and better performance in terms of accuracy and robustness are reported. Finally, our algorithm is also very fast thanks to the genetic pre-alignment task and the novel metrics we propose.

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

I. INTRODUCTION

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., [40]–[42]). 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., [43]–[45]) 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 of the object between these two positions.

In this paper we describe a *scan-matching based registration*

algorithm 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 [2]. 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.

The paper is organized as follows. In Section II we briefly describe the problem and introduce basic terminology. Section III describes principles of the classical rigid registration based on ICP and summarizes numerical derivations. The choice of evolutionary algorithm and ICP for solving the described problem are discussed in Section IV. Section V introduces the proposed hybrid solution. Section VI reports experimental results, by also comparing performance of the proposed algorithm with those of other iterative and genetic algorithms. Section VII provides an overview on the huge research in the field of scan-matching approaches, by dividing it into three main areas: ICP, probabilistic and genetic approaches. Here, as regards genetic approaches, we also provide the principle of the lookup metrics we use in our algorithm. Finally, in Section VIII, concluding remarks and

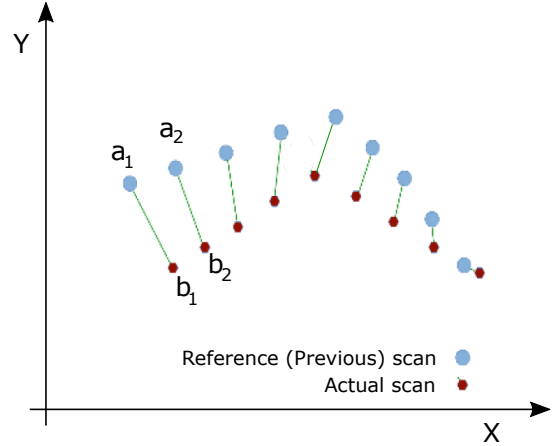


FIGURE 1. An example of point pair correspondences.

future works are reported.

II. PRELIMINARY

We are given two sets of bi-dimensional points $A = a_1, \dots, a_N$ and $B = b_1, \dots, b_M$, where a_i and b_i are 2×1 column vectors. The two sets A and B are scan descriptions of the environment as seen by a range sensor put on a mobile object from two points P_A and P_B . The first scan represented by the set A is the *reference* scan while B is the *new* scan taken after a movement of the mobile object. If we overlap the two scans, that is by determining the optimum rotation and translation of the set B wrt the set A , an estimation of the movement can be obtained. First of all, points correspondences must be estimated between A and B . A generic correspondence search algorithm takes the points from the two scans, $p_{i_k}, i = 1 \dots N$ and $p_{j_k}, j = 1 \dots M$, and establishes a set of k corresponding points pairs (p_{i_k}, p_{j_k}) , $k = 0 \dots K$ where $0 \leq K < M \cdot N$. A straightforward and fast algorithm for establishing point correspondences between two scans simply considers the polar coordinates of the reference and the actual scan points projected in the same coordinate frame of the reference scan. The scan is then traversed with increasing angle and points that belong to the same angle step which are closer than a distance threshold are matched. An example of the correspondence between the points a_i and b_i obtained with such 'polar coordinate' approach is reported in Figure 1 by the lines connecting the points. This 'polar coordinates' approach has been used in [2] in their hybrid two phase genetic + ICP approach for the genetic phase. However the experiments have shown that using this simple approach in iterative correspondence point algorithms leads to convergence failures and poor performance.

III. LASER SCAN MATCHING OVERVIEW

Scan matching can be described according to several interpretations, for example geometric, correlative or probabilistic. According to a geometric interpretation, the scan

matching approach can briefly be described as follows. Starting from two scans acquired by a range sensor from two consecutive different positions in which the object is located during its movements, the environment maps are obtained. The correspondence between two maps is obtained by finding the translation and rotation of the actual scan which lead to the best overlap of the two maps. The resulting translation and rotation describe the movement of the object between the two positions and its integration leads to the mobile object path estimate. We now give a sketch of the derivations involved in the scan matching approach.

The problem is to determine the translation vector t and the rotation matrix R that minimize the quadratic error reported in Equation (1).

$$E(R, t) = \frac{1}{N} \sum_{i=1}^N (R \cdot b_i + t - a_i)^2 \quad (1)$$

The translation vector t can be found by setting $\frac{\partial E(R, t)}{\partial t} = 0$. Developing the partial derivative we obtain:

$$\begin{aligned} \frac{\partial E}{\partial t} &= \frac{2}{N} \sum_{i=1}^N (R b_i + t - a_i) = \frac{2}{N} \left(R \sum_{i=1}^N b_i + N t - \sum_{i=1}^N a_i \right) \\ &= 2 (R \cdot \mu_B + t - \mu_A) \end{aligned} \quad (2)$$

where

$$\mu_A = \frac{1}{N} \sum_{i=1}^N a_i \quad \text{and} \quad \mu_B = \frac{1}{N} \sum_{i=1}^N b_i \quad (3)$$

are the barycenters of the two sets of points. By setting the partial derivative developed in Equation (2) equal to zero it turns out that the translation vector t is given by Equation (4).

$$t = \mu_A - R \cdot \mu_B \quad (4)$$

Rotation matrix derivation is more complex. Aron *et al.* and Horn proposed two different methods to compute the rotation matrix, described in [3] and [4] respectively. The first method uses SVD and the second is based on quaternions. Later, Horn *et al.* proposed an algorithm based on orthonormal matrices [5] and Walker *et al.* proposed an algorithm based on dual quaternion [6]. Stability and accuracy comparison among [3], [4], [5] and [6], reported in [7] shows that there are no significant differences among the four algorithms, although the method based on SVD has slightly lower computational complexity.

We now briefly summarize the SVD approach for the estimation of the rotation matrix reported in [3]. Substitute Equation (4) into the error function defined above by Equa-

tion (1).

$$\begin{aligned} E(R, t) &= \frac{\sum_{i=1}^N (R \cdot b_i + \mu_A - R \cdot \mu_B - a_i)^2}{N} = \\ &= \frac{\sum_{i=1}^N (R \cdot b'_i - a'_i)^2}{N} = \\ &= \frac{1}{N} \sum_{i=1}^N \left((R \cdot b')^T \cdot R \cdot b'_i + a_i'^T a'_i - 2(R \cdot b'_i)^T \cdot a'_i \right) = \\ &= \frac{1}{N} \sum_{i=1}^N \left(b_i'^T b'_i + a_i'^T a'_i - 2b_i'^T R^T a'_i \right) \end{aligned} \quad (5)$$

The points a'_i, b'_i in Equation (5) are obtained by subtracting from each original point the barycenters of the two sets of points, namely $a'_i = a_i - \mu_A$ and $b'_i = b_i - \mu_B$.

From Equation (5) the minimum of $E(R, t)$ is obtained by maximizing Equation (6).

$$\sum_{i=1}^N b_i'^T R^T a'_i = \text{trace}(RW) \quad (6)$$

where $W = \sum_{i=1}^N a'_i b_i'^T$. In other terms, the minimization of the squared error described by Equation (1) is obtained with the translation vector t described in Equation (4) and with the rotation matrix R given by:

$$\bar{R} = \underset{R}{\text{argmax}} (\text{trace}(R \cdot W)) \quad (7)$$

Let us consider the Singular Value Decomposition of the W matrix.

$$W = U \Sigma V^T \quad (8)$$

where U, V are orthonormal and Σ is a diagonal matrix whose diagonal values are the singular values of W . As shown in [3], the matrix

$$\bar{R} = UV^T \quad (9)$$

maximizes $\text{trace}(RW)$ and therefore minimizes Equation (5). In conclusion the translation vector t and the rotation matrix \bar{R} which minimizes the quadratic error reported in Equation (1) are given by Equations (4) and (9) respectively.

However, the correspondences between actual and reference scans points is not known in advance. Therefore the solution may be obtained using an iterative approach, called Iterative Closest Point algorithm (ICP), which is the most popular registration approach. The scheme of the ICP algorithm is reported in Algorithm 1.

Typically, this method converges if the starting position is close enough to the true position. We remark that the initial position of scan matching algorithms is given by other position estimation methods, for example odometry. Since odometry measurements can often fail, due for instance to wheel slippage, IPE can be high. In this paper the performances of scan matching algorithms are measured versus initial translation and rotation errors.

Algorithm 1 ICP Scheme

Input: $A, B, threshold$

Output: R, t

$k = 0;$

$B^k = B;$

$\mu_A = compute\mu_A(A);$

$\mu_B = compute\mu_B(B);$

repeat

for (each point of A) **do**

 find its closest point in B^k ;

$W = \sum_{i=1}^{N_p} a_i' b_i'^T$;

$SVD = SVD(W);$

$R = (SVD.U) \cdot (SVD.V)^T$;

$t = \mu_A - R\mu_B$;

$B^k = transform(B^k, R, t);$

$k = k + 1$;

until $E(R, t) < threshold$;

return (R, t) ;

IV. PRE-ALIGNMENT BY MEANS OF EVOLUTIONARY ALGORITHMS

Evolutionary Algorithms, such as for example Genetic Algorithms (GA) or Particle Swarm Optimization (PSO) algorithms are heuristic processes inspired by the natural evolution in biological systems. Evolutionary optimization algorithms are popular in solving complex or nonlinear problems such as for example optimization or classification. These algorithms are characterized by some key concepts, such as the generation of an initial number of solutions, called the population or swarm of individuals, the calculation of the function to optimize, called fitness, and the generation of a new population until the best individual survives. These steps are represented in Algorithm 2.

Algorithm 2 Generic Evolutionary Algorithm

Input: gen

Output: $best\ individual$

$k = 0;$

$P = generateInitialPopulation(\odot);$

repeat

$f = computeFitness(P);$

$P = generateNewPopulation(P);$

$k = k + 1$;

until $k > gen$;

return $best\ individual$;

The procedures for initial creation and generation of the new population are different in the various versions of the evolutionary algorithms. Since in GA each solution is encoded in binary notation, GA performs basically discrete optimization. PSO instead represents the solutions as particles with position and speed encoded as real variables. All the particles form a swarm, while positions are the real variable to be optimized.

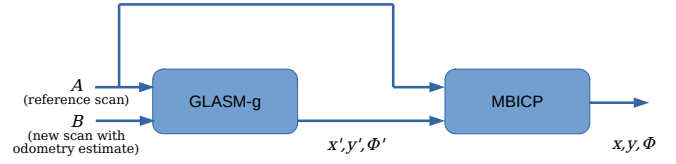


FIGURE 2. Block diagram of the proposed technique.

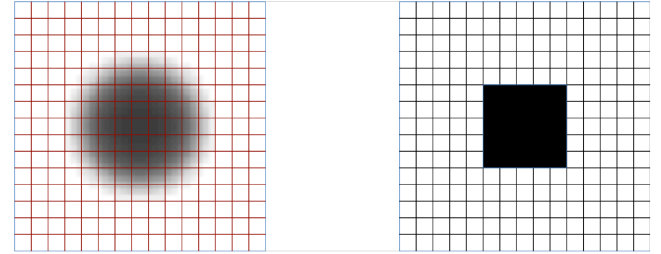


FIGURE 3. A detail of a lookup table surrounding an isolated point of the reference scan. Left: Radial, Gradual. Right: Squared, Binary.

The proposed hybrid algorithm consists in the discrete estimation of translation and rotation by means of an evolutionary algorithm followed by a fine optimization by means of a deterministic algorithm. It has to be remarked that the discrete variables (x, y, ϕ) are related to the discretization of the search space. Sub-optimal values of the variables can be obtained by discrete optimization algorithms and a finer optimization by continuous optimization algorithms. In this paper we perform discrete optimization with Genetic Algorithms and finer optimization with Iterative Closest Point algorithms which are very efficient if the starting point is close to the true value.

V. NOVEL 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 [29]. The algorithm described in [29] uses a metric based on a binary lookup table.

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 [13]. In more details, Figure 2 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 .

In Figure 3 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 3, left panel, with gray levels.

In Algorithm 3 we report the pseudo code of the fitness computation used in GLASM-g.

Algorithm 3 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.

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 4 and listed in Table 1. The Table 1

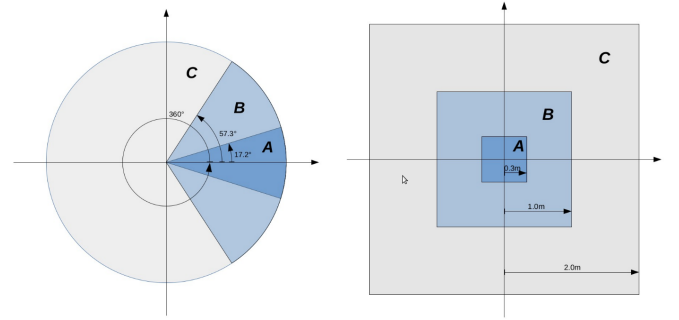


FIGURE 4. Search space size of the algorithms *small* (A), *medium* (B), and *large* (C).

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 [13] 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 [32], [33].

Visual examples of the algorithm in operation are shown in Figure 5. 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.

VI. EXPERIMENTAL ASSESSMENT AND ANALYSIS

The performance of the 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, [34], [35]. 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

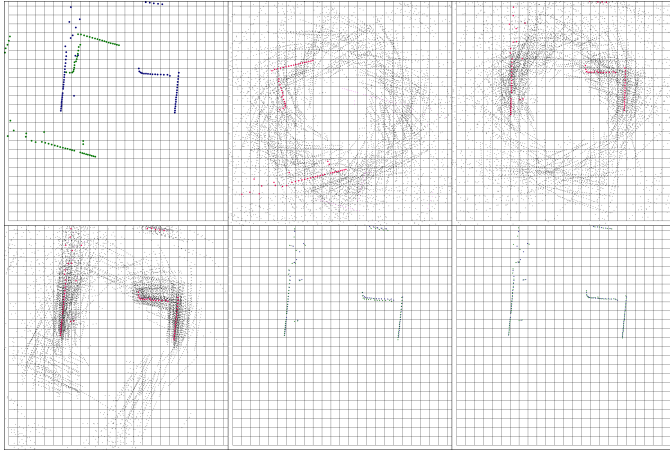


FIGURE 5. Visualization of HGLASM-g operation. In the top-left frame the initial position estimate of the new scan is depicted in green and the reference scan in blue. The next three frames show the pre-alignment process depicting the population after 0, 5, and 12 generations of the genetic algorithm 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).

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 $0.57^\circ (0.01[rad])$ 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 $5.73^\circ (0.1 [rad])$

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, and the results using the described dataset are reported in Section VI-A. 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 VI-B 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) [13] that we have taken as a reference. These comparisons are listed in the VI-C Section..

A. MBICP

To verify the robustness of the algorithm, before the scan matching process, an initial error was added to the position of the new scan. The error has been added both in the Cartesian directions and in the rotational component. Scan matching was then performed for all error combinations ($\pm Ex$, $\pm Ey$, $\pm Erot$) for a total of 8000 scan matchings. Table 2 shows the accuracy of different combinations of initial positioning errors. The table shows the Success Ratio, the average calculation time and the average translation and rotation accuracy respectively.

We can see in the table that the initial error has a strong impact on the performance of the MbICP algorithm. In particular conditions, the iteration does not end and remains stacked in local minimums. The algorithm converges only for small initial error values but in any case the Success Ratio remains lower than 100%. If the initial error exceeds 15° , the Success Ratio collapses because the algorithm is not able to associate a sufficient number of points of the new scan with the reference one. These results are perfectly understandable and they are indeed what is expected from an iterative algorithm based on point correspondences. In cases where the MbICP algorithm converges correctly, the accuracy and standard deviation results remain fairly constant with respect to different initial error values.

TABLE 2. Performances of MbICP for three Initial Orientation Errors – The numbers in each cell are Success Ratio, computation time, displacement and rotation accuracies respectively.

IPE	MbICP $\pm 5^\circ$	MbICP $\pm 30^\circ$	MbICP $\pm 60^\circ$
$\pm 0.2\text{m}, \pm 0.2\text{m}$	82.3% 0.68ms 1.78mm 2.91mrad	6.0% 1.24ms 1.13mm 2.70mrad	0.1% 1.08ms 0.95mm 1.26mrad
$\pm 0.3\text{m}, \pm 0.3\text{m}$	77.9% 0.74ms 1.77mm 2.95mrad	5.8% 1.23ms 1.18mm 2.76mrad	0.1% 1.10ms 1.37mm 2.36mrad
$\pm 0.4\text{m}, \pm 0.4\text{m}$	69.6% 0.79ms 1.79mm 3.00mrad	5.6% 1.20ms 1.27mm 2.78mrad	0.1% 1.01ms 0.99mm 1.89mrad
$\pm 1.0\text{m}, \pm 1.0\text{m}$	14.9% 1.02ms 2.87mm 3.13mrad	2.5% 1.04ms 2.38mm 2.97mrad	0.2% 0.86ms 2.17mm 2.69mrad
$\pm 1.5\text{m}, \pm 1.5\text{m}$	1.5% 1.02ms 3.67mm 2.61mrad	0.6% 0.86ms 2.51mm 3.90mrad	0.1% 0.82ms 1.35mm 2.10mrad

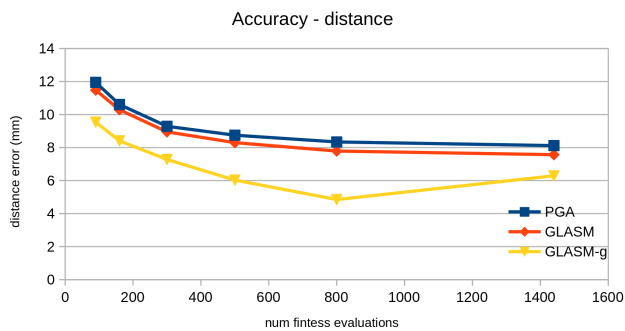


FIGURE 6. Translation Error Versus the Number of Fitness Evaluations.

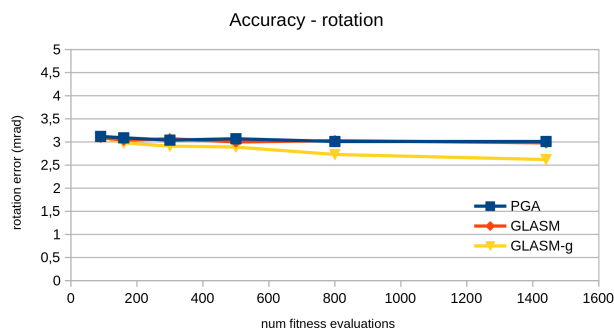


FIGURE 7. Rotation error versus the number of fitness evaluations.

B. GENETIC PRE-ALIGNMENT

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 6 and Figure 7 show the translation and rotation errors versus the number of evaluations of the fitness function for the Polar Genetic Algorithm (PGA), GLASM and GLASM-g.

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. As we can see in Figure 8 and Figure 9 the best Success Ratio results, calculation time and accuracy are always obtained with the fitness function used by the

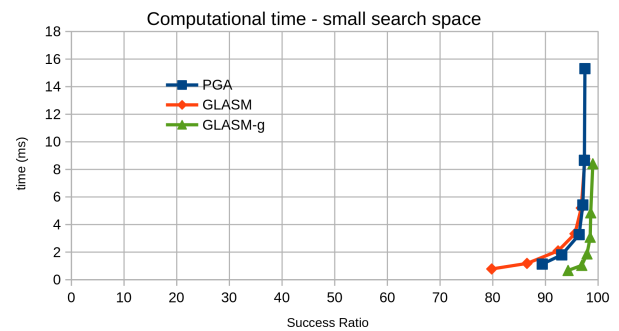


FIGURE 8. Time needed to get various levels of Success Ratio for different sets of genetic algorithms (the search size is *small*).

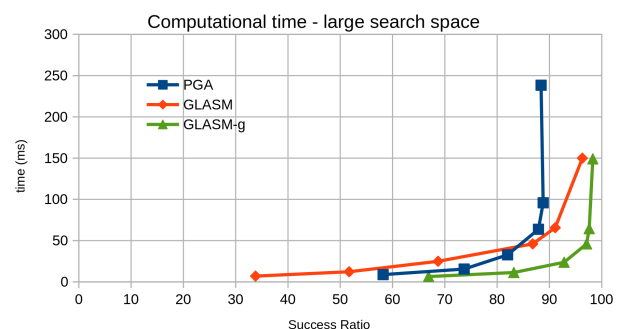


FIGURE 9. Time needed to get various levels of Success Ratio for different sets of genetic algorithms (the search size is *large*).

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.

C. PROPOSED HYBRID ALGORITHM

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

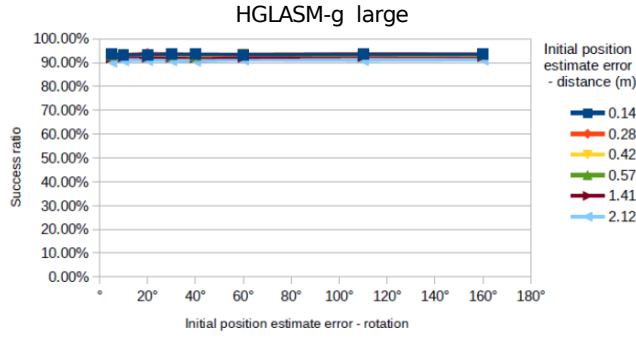


FIGURE 10. Success Ratio behavior versus rotation and translation errors for *large* search space size.

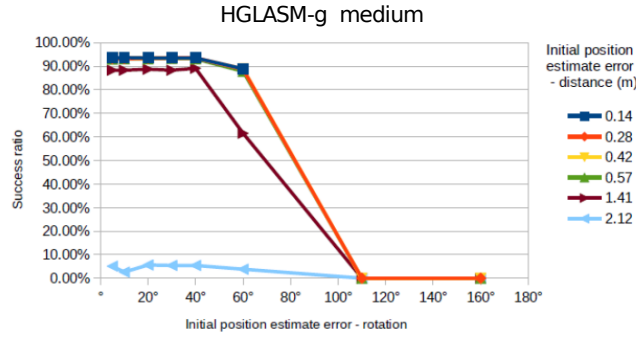


FIGURE 11. Success Ratio behavior versus rotation and translation errors for *medium* search space size.

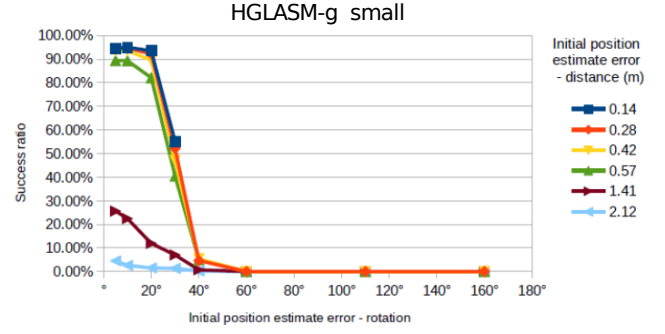


FIGURE 12. Success Ratio behavior versus rotation and translation errors for *small* search space size.

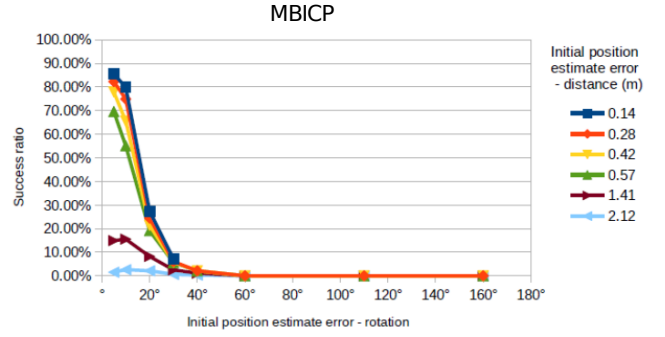


FIGURE 13. Success Ratio behavior versus rotation and translation errors for the MbICP algorithm.

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 10, Figure 11, Figure 12 show the Success Ratio curves versus different values of rotation and translation initial positioning errors.

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 13 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 13, 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.

VII. RELATED WORK

A large literature is available concerning the scan matching problem. In this Section we briefly describe some relevant approaches, namely the ICP, the Probabilistic and the Genetic-based scan matching approaches. The Section concludes with a highlight of Hybrid approaches.

A. ICP SCAN-MATCHING APPROACHES

Since the ICP approach was proposed initially by Besl and McKay in [8], numerous variants of the original technique have been proposed. The variants mainly concerned the following issues: Selection of points; Correspondence weighing; Association of data; Rejection of anomalous pairs of points. The variants modify different characteristics of the original algorithm, for example its speed, the stability of the solution and the management of local minima, its robustness to noise or anomalous values and the maximum initial error.

Data acquired by range sensors describe the environment considering two or three dimensions. The environment seen by the sensor in adjacent positions along the path of the mobile object is described by a sequence of points. Data can be elaborated point by point or using a suitable transformation of the sequences. The sensors measures the distance of the object closest to the sensor itself along its current orientation. The orientation of the sensor is periodically changed. The environment map seen by the sensor is represented by a series of points described by two (distance of the closest point, polar angle) or three parameters (distance of the closest point to the sensor, polar angle, azimuth angle) depending on the dimension considered. For example Park and Kee in [9] transformed the maps into the spectral domain, while Censi *et al.* used a transformation in the Hough domain, [10], [11]. The advantage of a comparison between the maps through a transformation of the maps into suitable domains is that the amount of data compared to a point-to-point comparison is much less and therefore the computational complexity of the comparison is less than that required by a point to point comparison. On the other hand, the robustness and accuracy

of the comparison worsen as the level of structure of the environment increases.

Some of the proposed variants use various reference systems. For example, Lu and Milios propose in [12] an ICP based on Cartesian coordinate frame called Iterative Dual Correspondence (IDC). The IDC variant evaluates translation with ICP and the rotation with an iterative matching-range-point. Their variant brings to an accurate estimation of the translation and rotation but its efficiency is lower than that of [1], [10]. Minguez *et al.* describe in [13] the MbICP variant. The family of ICP algorithms uses the minimum Euclidean distance criteria to establish the points correspondences and to apply the least squares for estimating the pose. MbICP adopts a new metric distance, which takes into account both the translation and rotation error to improve the rotation estimating.

Diosi *et al.* propose in [14] an ICP variant called Polar Scan Matching based on polar coordinate frame. Unlike ICP or MbICP, the Polar Scan Matching separately estimates the robot pose including the rotation estimation and translation estimation at each iteration. The problem of Polar Scan Matching is that it fails if two consecutive scans in polar coordinate frame have similar distribution.

Other variants concern the devices used to acquire the maps. Normally these are laser devices, more rarely acoustic sensors [15], [16] or infrared sensors [17].

In the case of laser sensors, the distance of the robot with the obstacles in the environment is estimated by sending a laser pulse and measuring the arrival time of the impulse reflected by the obstacle. The distance to the nearest obstacle is given by the minimum arrival time. In this way we obtain the map of the room where the mobile object is located, also including any fixed objects. In the context of locating a mobile object, the range-finder sensors are positioned on the robot.

B. PROBABILISTIC SCAN-MATCHING APPROACHES

The approaches described so far are essentially variants of the Iterative Closest Point technique. These techniques have difficulty estimating translation and rotation correctly at the same time. Another limitation is related to noise management and uncertainty introduced by the range sensors used. These limitations were one of the reasons that led to the development of probability-based scan matching approaches. For example, Biber and Strasser in [18], [19] propose using the Normal Distribution Transform (NDT) to describe data collected with laser scans. As in ICP approaches there is a reference scan and a new scan and the purpose of the algorithm is to find the displacement and rotation that allows the two scans to overlap. In this case, the two-dimensional space is divided into cells of equal size. For each cell, all the occupied points contained in it are considered, their average q and their covariance matrix Σ are computed. With these statistical parameters, the probability of each two-dimensional point x of the actual scan is evaluated, according

to a Gaussian bivariate distribution:

$$p(x) = \frac{e^{-\frac{(x-q)^T \Sigma^{-1} (x-q)}{2}}}{\sqrt{(2\pi)^2 |\Sigma|}} \sim e^{-\frac{(x-q)^T \Sigma^{-1} (x-q)}{2}} \quad (10)$$

In this way, a continuous and differentiable description of the points coming from the range sensor is obtained, which can be used to minimize cost factors using classic or numerical methods. The displacement and rotation between two scans correspond to the minimization of a continuous function defined on the rotation and translation between previous and actual scans. Biber and Strasser propose the use of Newton's iterative algorithm to minimize the function (10). Newton's algorithm is particularly suitable for NDT-based approaches because it requires the calculation of first and second order derivatives that are simply obtainable with these approaches. In [20] Montesano *et al.* propose another probabilistic formulation of the problem of scan matching. The approach is divided into two phases: the probabilistic calculation of the correspondences and the estimate of the relative displacements between the two scans. The correspondences between the points of the two scans are evaluated using the Mahalanobis distance between the points. The estimate of the relative displacement between the two scans is obtained through an iterative approach based on the least squares criterion. In [21] Olson presents another probabilistic approach for solving the scan matching problem. The algorithm proposed by Olson is based on the cross-correlations between two laser scans. The algorithm maximizes the probability that two scans overlap. To avoid local maxima, the cross correlation algorithm searches for the maxima in the space of parameters obtained from additional sensors such as odometric sensors.

Recently the NDT approach has been extended to three dimensions by many authors. For example Magnusson in [22] describe the 3D-NDT algorithm for navigating an autonomous vehicle in a mine. In [23] Magnusson *et al.* compared several recently proposed three-dimensional scan matching algorithms. The results confirm that the three-dimensional Normal Distribution Transform algorithm improves the convergence characteristics even with the increase in initial position errors. Takeuchi and Tsubouchi proposed in [24] an extension of Biber's algorithm into a three-dimensional space, dividing the space into voxels and assigning each voxel a normal probability distribution. The authors experiment with the algorithm in a vast indoor space. In [25] Ulas and Temeltas introduce an algorithm that extends the 3D-NDT approach by inserting different layers that depend on how the environment is structured. In each layer the cells are of different sizes. The size of each individual cell is automatically determined by the input data. Unlike the Biber and Strassen algorithm, the function to be minimized is based on the Mahalanobis distance. The probabilistic approaches described above are based on good initial assumptions.

Su Pang *et al.* report in [36] a comparison between NDT and ICP under realistic conditions as two prevailing approaches. They conclude that the two scan matching ap-

proaches are similar in terms of accuracy. However, NDT is more robust versus environmental modifications.

The core concept behind NDT and our idea is very similar: to construct a 2D plane representation with cells of constant size where the cells contain a probability density of measurement being close to points of the reference scan. The main difference is that NDT uses Newton's algorithm to iteratively search for the optimal solution, requiring additional steps in the preparation of the 2D plane representation, while we use a genetic algorithm directly with a lookup table.

C. GENETIC-BASED SCAN-MATCHING APPROACHES

The matching of successive laser scans has been accomplished by several authors using genetic optimization (GA). The main advantage of GA is that it can explore all the solution space avoiding local minima and is more robust to initial alignment errors. Its disadvantage is that its computational complexity is usually high.

1) Fitness Definition based on Squared Error Metric

The alignment between the two scans by genetic optimization is obtained by randomly changing, from one generation to the next, one scan with respect to the other according to the minimization of an objective function, i.e. the fitness. The most important issue of this type of matching is the definition of the fitness to be minimized. The most intuitive fitness definition is that reported in Equation (1). Yamany *et al.* [26] and Robertson and Fisher [27] use the mean squared error objective function. Martinez in [2], [28] introduce the following definition:

$$Fitness = \sum_{k=1}^N e_j(k)/N \quad (11)$$

where N is the number of points and e_j is the distance between the point k in the reference and the new scans.

2) Fitness Definition based on Lookup Metric

However to calculate Squared Error Metric based fitness, it is required to know the correspondences between the points of the two scans. For this reason Lenac *et al.* [29] propose a genetic scan matching algorithm based on a binary lookup table based fitness function called GLASM, which avoids the points pair correspondences. In Figure 14 the idea of the proposed fitness function is depicted. In short, each reference point is surrounded by squares or circles (in this case we consider circles of radius *radius*). The points of the new scan that hit the circles are counted. Using this concept of scan similarity we do not have to compute point correspondences.

The lookup table is built using the reference (i.e. previous) scan. The computation of the fitness function based on the binary lookup table is described in Algorithm 4. As it is shown, for each point of the new scan first a roto-translation is performed to bring the point in the same reference frame as the lookup table, followed by a selection of the corresponding lookup cell. The fitness is then incremented only if the lookup

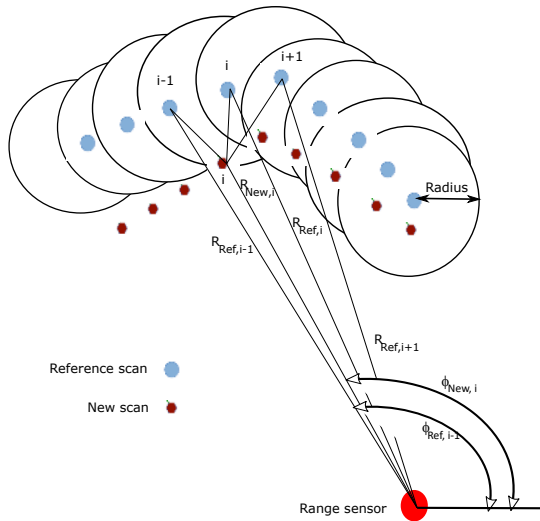


FIGURE 14. Lookup-based laser scan scheme.

cell is marked with value 1, i.e. there was at least one point of the reference scan in the vicinity. A detail of the lookup table is shown in Figure 3, right panel.

Algorithm 4 Binary Lookup Fitness Computation

Input: B // new scan
Output: $fitness$
 $fitness = 0$;
for (each point p of B) **do**
 // roto-translation to lookup reference frame
 $p' = \text{changereferenceframe}(p)$
 if $\text{lookup}(p') = 1$ **then**
 $fitness++$;
return $fitness$;

Other interesting approaches that are related to our research are [51], [52]. In particular, [51] proposes a novel GP-based method (GPDF) to extract feature vectors and evolve image descriptors for image registration without supervision. The method designs a set of simple arithmetic operators and first-order statistics to construct feature descriptors in order to reduce noise interference. [52] instead introduces a Particle Swarm Optimization (PSO) sample consensus algorithm for remote sensing image registration. Different from Random Sample Consensus (RANSAC) algorithm, the proposed solution directly samples the modal transformation parameter rather than randomly selecting tentative matches. Thus, the method is less sensitive to the correct rate than RANSAC, and it has the ability to handle lower correct rate and more matches. Meanwhile, PSO is utilized to optimize parameter as its efficiency.

D. HYBRID APPROACHES

Several recent works have shown that the combination of different optimization approaches for estimating the rotation and translation of one scan with respect to the other can increase the robustness and accuracy in the registration of laser scans. Moreover, Martinez in [2] shown that the use of the cascade genetic optimization - ICP for estimating the translation and rotation of the second scan with respect to the first one improves the accuracy of ICP alone. They call their fitness function as Polar Fitness Function. Luck *et al.* have shown in [30] that the cascade Simulated Annealing - ICP leads to a better overlap of the two recordings with better iteration convergence. The hybrid pre-registration approach described by Lomonosov *et al.* in [31] is applicable to arbitrarily oriented surfaces and is composed by genetic search followed by iterative alignment. In [29] Lenac *et al.* described a hybrid genetic scan matching based on binary lookup table. Depending on the search space size dimension, the algorithm can be used both in local and global navigation applications. The algorithm described in this paper aims at increasing accuracy and robustness with respect to [29].

VIII. FINAL REMARKS AND FUTURE WORK

In this paper we have presented a hybrid algorithm for the problem of scan matching. The algorithm better solves some scan-matching problems as compared to state-of-the-art algorithms, such as the problem of initial positioning errors and blocking the iterations in local minima. The proposed algorithm introduces a fitness function based on the look up tables whose content is used as a weight in the fitness calculation. Values in look up tables are gradually modified starting from the reference position. 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., [37]–[39]), as to make it able of dealing with specific features of such innovative settings, like also dictated by some recent studies (e.g., [48]–[50]).

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ENZO MUMOLO received the Dr.Eng. Degree in electronic engineering from the University of Trieste, Italy, where he conducted research on signal processing algorithms. In 1984, he joined the Alcatel Italy Laboratory, formerly FACE Research Center, Rome, Italy. In 1985, he was with ITT DCD-West, San Diego, CA, working on the development of realtime speech recognizers. In 1987, he was responsible of research activities within the Speech Processing Dept. of Alcatel Italy Lab.

From 1990 he was with Sincrotrone Trieste, Trieste, Italy, as Head of the Electronics Group, working on photon beam position monitors. Since 1993 he has been working at the Engineering and Architecture Department (DIA) of the University of Trieste. At DIA, he served as scientific responsible of many national projects and he founded two Academic SpinOffs. He also was the founder of the SMART Lab. in 1980, where he developed non visual robotic technologies. He acted as Editor of Computing and Information Technology Journals and as Program Committee member of several International Conferences. He holds several national and international patents and he is a senior member of IEEE.

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KRISTIJAN LENAC is an Associate Professor at the University of Rijeka, Faculty of Engineering. He received his PhD at the University of Trieste, Italy with dissertation in the field of Mobile robotics. He then worked for five years as a project manager and lead developer in AIBSLab Engineering company from Trieste leading several R&D projects commissioned by the industry. On his return to Croatia he joins the University of Rijeka, Faculty of Engineering as professor in the

Computer Engineering department. He is a founder and currently head of Artificial Perception and Autonomous Systems laboratory and one of the founders of Riteh Drone Team. At the Centre for Artificial Intelligence and Cybersecurity (AIRI) he is a founder and currently head of the Laboratory for Applications of Blockchain Technology. His research interests are in the fields of mobile robotics, satellite navigation, embedded systems and blockchain. He is a member of IEEE and Royal Institute of Navigation.



ALFREDO CUZZOCREA is Professor in Computer Engineering at the University of Calabria, Rende, Italy. He is the Head of the Big Data Engineering and Analytics Lab of the University of Calabria. His research focuses on big data, database systems, data mining, data warehousing, and knowledge discovery. He is author or co-author of more than 550 papers. He is recognized in prestigious international research rankings, such as: (i) **Top Scientists in Computer Science and**

Electronics by Guide2Research, Clifton, NJ, USA; (ii) **Top 2% World-Wide Scientists 1996-2019** by METRICS, Stanford, CA, USA; (iii) **Top Researchers in Computer Science 2013-2018** by SciVal – Elsevier, Amsterdam, Netherlands; (iv) **Top Italian Scientists in Computer Sciences** by Virtual Italian Academy, Manchester, UK.