### AN INNOVATIVE FRAMEWORK FOR SUPPORTING BIG-MOVING-OBJECTS TRACKING, ANALYSIS AND MINING EFFECTIVELY AND EFFICIENTLY

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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. In line with these goals, 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, fist, and, second, performing a finer alignment using a deterministic approach.

 $Keywords\colon$  Moving Objects, Scan-Matching Algorithms, Intelligent Systems, Genetic Optimization

### 1. 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., [35, 36, 37]). 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., [38, 39, 40]) 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 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 prealignment 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. On the other hand, even *adaptive metaphors*, perhaps developed in different contexts (e.g., [46]), can be exploited to this end.

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 show that main scan-matching features are improved thanks to the hybrid algorithms proposed in this paper. Furthermore, 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.



Fig. 1. Case Study: A Reference Architecture for Supporting Big Data Analytics in Computer Vision Environments for Security Analysis.

The paper is organized as follows. In Section 2, we report on a relevant case study that confirms the benefits of our proposed framework, by focusing in the issue of *supporting big data analytics tools in computer vision environments for security analysis*. Section 3 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. In Section 4, we briefly describe the problem and introduce basic terminology. Section 5 describes how evolutionary algorithms and ICP can be used to solve the investigated problem. In Section 6, we introduce the proposed hybrid solution. Section 7 contains a collection of open problems and future research directions related to the investigated research area. Finally, in Section 8, concluding remarks and future works are reported.

# 2. CASE STUDY: BIG DATA ANALYTICS TOOLS IN COMPUTER VISION ENVIRONMENTS FOR SECURITY ANALYSIS

In this Section, we describe how our proposed framework GLASM-g can be effectively used in order to support big data analytics in computer vision environments for security analysis, thus depicting a reference case study. Figure 1 shows the reference architecture of the mentioned case study, namely a big data analytics architecture devoted to support security in computer vision environments, particularly oriented to *facial recognition*. As shown in Figure 1, from the facial recognition streams, the whole architecture finally aims at devising *security rules* via big data analytics. These rule finally define the security policy of the target environment.

The GLASM-g framework can be successfully exploited with the core layer of the reference architecture, specifically in a Cloud-based execution mode as to improve efficiency and scalability (see Figure 1).

In more details, looking at Figure 1, in the reference architecture the following layers are identified:

- 1. *Big Moving Object Layer* This layer is the one where the target big moving objects are located.
- 2. Cloud-Based Big-Moving-Object Scan-Matching Layer In this layer, the GLASM-g frame-

work executes in a Cloud-based mode.

- 3. Big Data Lake Layer This layer contains the reference big data lake of the overall architecture, implemented on top of a given well-understood computational platform (e.g., Hadoop).
- 4. Big Data Analytics Layer In this layer, the reference big data analytics tools, for instance those based on machine learning, are used to extract actionable knowledge for security analysis.
- 5. Security Layer This layer embeds the security rules that are derived from the big data analytics procedures implemented in the *Big Data Analytics Layer*.

As discussed in this Section, our proposed framework GLASM-g not only provides significant contributions in the context of scan-matching problems over moving objects, but also it can be effectively and efficiently exploited in the context of a real-life Cloud-based architecture for security analysis in computer vision environments.

# 3. 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.

# 3.1. ICP Scan-Matching Approaches

Since the ICP approach was proposed initially by Besl and McKay in [3], 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 [4] transformed the maps into the spectral domain, while Censi *et al.* used a transformation in the Hough domain, [5, 6]. 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 [7] 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 [5, 1]. Minguez *et al.* describe in [8] 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 [9] 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 [10, 11] or infrared sensors [12].

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.

### 3.2. 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 [13, 14] 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  $\Sigma$  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:

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

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 (1). 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 [15] 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 [16] 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 [17] describe the 3D-NDT algorithm for navigating an autonomous vehicle in a mine. In [18] Magnusson *et al.* compared several recently proposed threedimensional 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 [19] 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 [20] 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 [31] a comparison between NDT and ICP under realistic conditions as two prevailing approaches. They conclude that the two scan matching approaches 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 Newtons 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.

### 3.3. 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.

# 3.3.1. 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 (2). Yamany *et al.* [21] and Robertson and Fisher [22] use the mean squared error objective function. Martinez in [2, 23] introduce the following definition:

$$Fitness = \sum_{k=1}^{N} e_j(k) / N \tag{2}$$

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

### 3.3.2. 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.* [24] 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 2 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 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 5, right panel.

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

Fig. 3. Binary Lookup Fitness Computation

Other interesting approaches that are related to our research are [51, 52]. In particular, [51] proposes a novel GP-based method (GPFD) to extract feature vectors and evolve image



Fig. 2. Lookup-based laser scan scheme.

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.

# 3.4. 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 [25] 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 [26] is applicable to arbitrarily oriented surfaces and is composed by genetic search followed by iterative alignment. In [24] 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 [24].

# 4. BACKGROUND CONCEPTS

We are given two sets of bi-dimensional points  $A = a_1, \ldots, a_N$  and  $B = b_1, \ldots, b_M$ , where  $a_i$  and  $b_i$  are  $2 \times 1$  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 4 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.



Fig. 4. An example of point pair correspondences.

# 5. GENETIC PRE-ALIGNMENT PHASE

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.

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.

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. In has to be remarked that the discrete variables  $(x, y, \phi)$  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.

# 6. A NOVEL FAMILY OF ENHANCED HYBRID SCAN MATCHING ALGO-RITHMS

The pre-alignment step is inspired by the algorithm called Genetic Lookup based Algorithm for Scan Matching (GLASM) described by Lenac *et al.* in [24]. The algorithm described in [24] 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 [8]. 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  $x', y', \phi'$ , is then used as starting point of the MbICP algorithm that compares *A* and *B*, thus producing the final output  $x, y, \phi$ .



Fig. 5. A detail of a lookup table surrounding an isolated point of the reference scan. Left: Radial, Gradual. Right: Squared, Binary.

In Figure 5 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 5, 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' = changereferenceframe(p)
 fitness = fitness · 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.



Fig. 6. 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 withing 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 6 and listed in Table 1.

Algorithm	Search Space Size	Genetic Configuration
	(dX, dY, dRot)	$(pop \times gen \times runs)$
small (A)	$\pm 0.3m, \pm 0.3m, \pm 17.2^{\circ}$	$20 \times 6 \times 1$
medium (B)	$\pm 1.0m, \pm 1.0m, \pm 57.3^{\circ}$	$100 \times 10 \times 1$
large (C)	$\pm 2.0m, \pm 2.0m, \pm 180.0^{\circ}$	$200\times12\times2$

Table 1. Search space size of the selected algorithms and the corresponding parameters used for the genetic algorithm

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 [8] 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 [27, 28].

# 7. OPEN PROBLEMS AND FUTURE RESEARCH DIRECTIONS

In this Section, we focus the attention on some open problems and future research directions related to the more general topics concerning the issue of tracking, analyzing and mining big moving objects.

Among the most relevant ones, we identify the following main research challenges in the area:

- 1. Scalability Issues Systems and frameworks that manage big moving objects usually face-off scalability issues, i.e. the aptitude of core algorithms to keep spatio-temporal computational overheads low (or barely low) when the size of input increases. This is a special feature of approaches that deal with big moving object tracking, analysis and mining, as highlighted by recent studies (e.g., [51, 52]), and it will play more and more a majority role in next-generation research.
- 2. Multidimensional Scan-Matching Scenarios While in our research we investigated twodimensional scenarios, multidimensional scenarios for scan-matching problems are, of course, of great interested at now. This has also been pinpointed by some recent proposals (e.g., [53, 54]). Indeed, actual models and methodologies must be meaningfully

extended towards the most interesting multidimensional case that, indeed, arise in several modern settings like, for instance, *drones* (e.g., [55]). In future, multidimensional scan-matching scenarios will become more and more relevant for research experiences in both the academic and industrial scene.

- 3. Privacy-Preservation Issues Big moving objects very often are built on top of sensitive data. To become convinced about this, it suffices to think of the typical computer vision application scenario represented by facial recognition systems. In this case, innovative models, methodologies and algorithms proposed in this scientific area must comply with the annoying issue of supporting privacy-preserving computations, i.e. computations that preserve the privacy of sensitive data while accomplishing the main big moving objects tracking, analysis and mining goals (e.g., [56, 57]). The latter one is, again, a critical future research direction to be considered by forthcoming efforts.
- 4. Flexible Artificial Intelligence Methodologies As a matter of fact, flexible artificial intelligence methodologies are conquering the scene, for instance those related to the emerging explainable AI trend (e.g., [58]). In this respect, even the problem of tracking, analysis and mining big moving objects can significantly take advantages from these methodologies, also in agreement with latest studies in the active literature (e.g., [59, 60]). Therefore, one of the most probing research challenge of the future consists in grafting flexible artificial intelligence methodologies into big moving object tracking, analysis and mining problems.

### 8. CONCLUSIONS 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 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., [32, 33, 34, 47, 48, 49]), as to make it able of dealing with specific features of such innovative settings, like also dictated by some recent studies (e.g., [41, 42, 43, 50]).

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