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A Spatially Structured Genetic Algorithm for Multi-Robot Localization

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Abstract In this paper the multi-robot localization problem is addressed. A new framework based on a spatially structured genetic algorithm is proposed. Collaboration among robots is considered and is limited to the exchange of sensor data. Additionally, the relative distance and orientation among robots are assumed to be available. The proposed framework (MR-SSGA) takes advantage of the cooperation so that the perceptual capability of each robot is extended. Cooperation can be set-up at any time when robots meet, it is fully decoupled and does not require robots to stop. Several simulations have been performed, either considering cooperation activated or not, in order to emphasize the effectiveness of the collaboration strategy.

Keywords Mobile Robot · Localization · Genetic Algorithms · Complex Networks

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1 Introduction

The possibility of using a team of robots cooperating to achieve a goal has gained great attention in recent years. The reason for this interest comes from the advantage of having a group of robots cooperating to accomplish a required task in various application domains.

The reliability of multi-robot systems is higher than single robot systems, as a team is able to achieve its goal even if a member fails. However, the cooperation inside a multi-robot system comes with several challenges, mainly related to the higher order of complexity in the coordination of the group when compared to single-robot systems.

To achieve cooperation in a robot team, two different approaches can be adopted, *centralized* and *decentralized*. In accordance with the centralized approach all planning execution and monitoring tasks are performed by a single control unit. As the computational overhead grows exponentially with the number of group members, such a scheme can only be applied to small teams. The disadvantages associated with the centralized approach can be overcome removing the central processing unit and spreading the decisional issues over the whole team of robots. This observation leads to decentralized (and distributed) architectures that make the system modular and robust [1].

These two approaches have been adopted in literature to solve the localization problem for multi-robot systems. Localization, i.e., the process of determining the position and orientation (pose) of a robot within the operating environment, is critical for high level navigation tasks.

In a centralized fashion, a supervisor collects all the data coming from the robots and provides an estimate for the poses of the robots in the team. This approach forces all members to continuously communicate with the supervisor. In order to maintain the communication, robots need either to move closely to the supervisor or to implement a mobile ad-hoc network. Therefore some constraints on the robots mobility have to be imposed to guarantee at least one communication-path from any robot to the supervisor at each time instant. The decentralized approach, referred in literature as *collaborative or cooperative* localization, assumes that each robot in the workspace uses its own sensors, exchanges data only with other robots in the neighborhood, and runs a local algorithm to estimate its own pose.

In [2] the concept of *mobile landmark* is introduced. The authors consider a team of robots exploring an unknown environment without any beacon. The exploration is carried out using the robots themselves as landmarks. Each vehicle repeats move-and-stop actions and acts as a landmark for the other robots, while a data fusion algorithm collects data to improve the estimate of the relative positioning of the robots.

A similar solution is proposed in [3,4] where a new sensing strategy, named *robot tracker*, is exploited to improve the accuracy of the pose estimation of each robot. The robots explore the environment in teams of two; each platform is equipped with a robot tracker sensor that reports the relative position of the other robot. Measurements are used in a particle filter to update the poses of the multi-robot system together with the associated uncertainties.

All the solutions mentioned above suffer from the following limitations: only one robot is allowed to move at any given time, and the team has to maintain sensorial contact at all times.

A different collaborative scheme, based on a probabilistic framework, is presented in [5], where two robots are supposed to navigate in a partially known environment. At every meeting they stop and improve their localization by exchanging their *beliefs*, i.e. the posterior probability density over the state space conditioned to measurements. A particle filter is at the base of the algorithm, giving the possibility to handle a non Gaussian shaped belief, and achieve localization.

Another promising solution is proposed in [6,7] and reviewed in [8,9], where a Kalman based algorithm is used to realize collaborative localization. During the navigation cycle, each robot collects data from its proprioceptive sensors to perform the prediction step of a Kalman filter while sharing information from the exteroceptive sensors with the rest of the team during the update. The Authors introduce a distributed algorithm based on singular value decomposition of the covariance matrix. Such an algorithm allows the filter to be decomposed into a number of smaller communicating filters, one for each robot, processing sensory data collected by its hosts. However, in order to properly maintain the cross-correlation terms a reliable inter-robot communication is required. Therefore, its application in a large scale environment is challenging.

This paper represents an extension of the work proposed in [10]. It is devoted to analyze a collaborative procedure for multi-robot localization based on a spatially structured genetic algorithm [11]. The procedure is fully decentralized and considers a group of robots moving in an operating space. During navigation, each robot computes its own localization and cooperates with the other robots to reduce its uncertainty. Cooperation, which does not require robots to stop, is realized in a distributed way by extending the perceptual capability of each robot.

The paper is organized as follows: in Section 2 a theoretical overview of spatially structured genetic algorithms and complex networks models is provided. In Section 3 the multi-robot localization procedure is given in detail. In Section 4 the robot and sensor modeling are given. In Section 5 the advantages of the collaborative procedure compared with the independent localization are shown. In Section 6 the proposed localization technique is validated by comparison with a simple genetic algorithm and a simple collaborative particle filter. Finally, in Section 7 conclusions are drawn.

2 Theoretical Background

2.1 Spatially Structured Genetic Algorithms

Genetic Algorithms (GAs) are a family of search techniques inspired by Darwin's Theory of Evolution. These techniques provide approximated solutions for problems in which other approaches, e.g., the gradient-based techniques, cannot be applied because of the high non-linearity of the objective functions.

These algorithms use a population of encoded strings (*chromosomes*) as candidate solutions to explore the search space. The candidate's evaluation is performed by means of an objective function (*fitness function*) and improvements at each iteration (*epoch*) result from the application of probabilistic transition operators (*crossover* and *mutation*) acting onto chromosomes. A simple genetic algorithm (SGA) usually provides three steps: initialization, selection and reproduction [12]. Initialization generates a population randomly picking up elements over the whole search space, selection draws an intermediate population relying on a fitness-based approach, and reproduction causes the population to evolve combining elements from the intermediate population. Usually, *crossover* picks up two elements and performs a convex combination of them with probability p_χ, while *mutation* picks up an element and modifies its chromosome, inversely proportional to its fitness, with probability p_μ. This means that some individuals, likely having high fitness, will be exactly copied in the new population (*elitism*). For a comprehensive overview on genetic algorithms the reader is referred to [12].

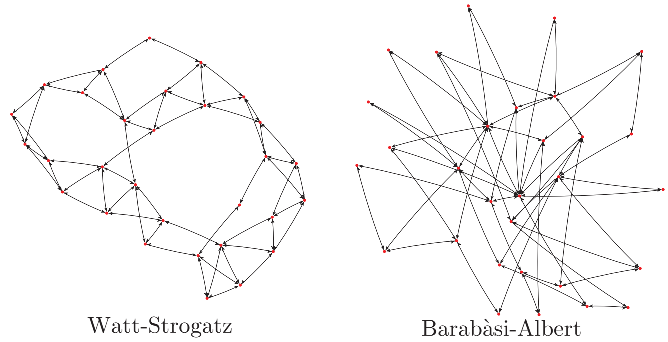
A spatially structured genetic algorithm (SSGA) is a specialization of a SGA, where the population is spatially distributed with respect to some discrete topology. If the topology is a network, these methods are also known as *graph based genetic algorithms* [13]. Following the latter approach, a population P can be defined through a set $V = \{v_1, \ldots, v_n\}$ of vertices and an incidence matrix $M = \{(i,j) = 1 : \exists \textit{ link between i and j}\}$ as P:={ V, M}. According to this structure, selection picks up pairs of vertices which show a relationship into the incidence matrix M, and reproduction generates new elements preserving the network topology. A exhaustive treatment of SSGA can be found in [11].

Therefore, differences between SGA and SSGA are mainly related to the selection approach: the former performs this step by means of a fitness-based approach, such as the roulette wheel, whereas the latter exploits the network topology of the population. In this way topological approaches are able to capture several phenomena that occur in the evolution of a population, like the persistency of niches and selection rules based on elective affinity between individuals.

2.2 Complex Networks

Complex networks are characterized by certain non-trivial topological features that do not occur in simple networks. They can be properly applied to model several natural systems, such as social networks or neural networks, and artificial systems such as the World-Wide-Web.

Several investigations have been performed by the research community in order to provide models able to properly describe these topological features. In particular, three fundamental properties have been recognized: the average path length, the cluster coefficient and finally the degree distribution. The *average path length* L of the network is the mean distance between two nodes, averaged over all pairs of nodes, where the distance between two nodes is



Watt-Strogatz Barabàsi-Albert

Fig. 1 Watt–Strogatz and Barabási–Albert models with 30 nodes

defined as the number of the edge along the shortest path connecting them. The *cluster coefficient* C of the network is the average of C_i over all nodes i, where the coefficient C_i of node i is the average fraction of pairs of neighbors of the node i that are also neighbors of each other. The *degree distribution* of the network is the distribution function $P(k)$ describing the probability that a randomly selected node has exactly degree k, that is the number of links a node owns.

By means of these properties, a classification of complex network models is possible. Among them, the most significant are the scale-free [14] and the small-world models [15]. The scale-free model, proposed by Barabási-Albert, is used to describe networks with a power-law degree distribution. Such networks, built through preferential attachments, are exploited to describe many real world network, e.g., the World-Wide-Web or an airline routing map. The small-world model, introduced by Watts-Strogaz, has its root in social networks. In fact, with its high cluster coefficient and its short average path, it perfectly reflects the dynamics of a circle of acquaintances described by the famous six degree of separation statement.

Examples of these models are depicted in Fig. 1; a comprehensive overview on complex network can be found in the [16] and the references therein.

3 Multi-Robot Spatially Structured Genetic Algorithm

The proposed Multi-Robot Spatially Structured Genetic Algorithm (MR-SSGA)provides a decentralized framework for the multi-robot localization problem. It takes advantage of the complex network theory for the deployment of the population. Giving such a structure to the population leads to several interesting advantages, such as the capability to carry on the multi-hypothesis paradigm. In this context, a chromosome encodes the state of the robot, represented through its position and orientation (x, y, θ).

From an algorithmic standpoint, an SSGA reflects the classical SGA schema with a specialization in regard to the structure of the population. Specifically, initialization creates a population over a complex network, selection picks up all the pairs of linked elements according to the incidence matrix, and reproduction determines which probabilistic transition operator needs to be applied.

In detail, reproduction comes along with two steps:

- Assignment of a state for each individual,
- Evaluation of a mating rule over each pair.

The state of each element, either HIGH or LOW, is computed by comparison of its fitness value against the average value over the whole population. As three different combinations can arise when considering a pair of individuals, a local mating rule is provided for each of them (Table 1).

Table 1 Mating rules

Node 1	**Node 2**	**Action**	**Basic principles**
High	High	The lower is replaced with the Crossover on the two	Elitism and Crossover
High	Low	Node 2 is replaced with a Mutation of Node 1	Elitism and Mutation
Low	Low	Both self-mutate	Mutation

3.1 Independent Evolution

Anytime a robot is moving and no other robot is within its communication range, the only information available are the data coming from its sensors. The algorithm proposed in [10] is used to address the independent evolution of each robot. The idea is to perform a measure of similarity between data coming from a real robot and the expected one computed for a given hypothesis. In order to achieve that, the following fitness function is exploited for robot r:

$$\Phi_i^r(z_k, \hat{z}_{k,i}) = \frac{1}{L} \sum_{j=1}^{L} \frac{1}{\sqrt{2\pi}\sigma} e^{-\left(z_k^j - \hat{z}_{k,i}^j\right)^2 / 2\sigma} \tag{1}$$

where, $z_k = [z_k^1, \ldots, z_k^L]$ represents the sensor data, $\hat{z}_{k,i} = [\hat{z}_{k,i}^1, \ldots, \hat{z}_{k,i}^L]$ is the expected one for the considered hypothesis i and finally σ is a measure of confidence.

3.2 Cooperative Evolution

The same approach holds when considering multi-robot localization. In this case, although for each robot a population is initialized and lets evolve independently, a collaboration can be set-up any time when robots meet. The key idea is to integrate the observations coming from the components in such a way that the sensory system capability of each robot is extended. In order to achieve that, the relative position and orientation of the robots in the team

Algorithm 1: The proposed Cooperative SSGA - step k and robot r

```
Data: Population of size $N_r$: $\{V_r = \{p_{i,k}\}, M_r\}$ $i = 1 \dots N_r$, Fitness $\Phi_i(\cdot)$
Result: $V = \{p_{i,k+1}\}$

/* Average Fitness Evaluation                                    */
$\bar{\Phi} = \sum_{j=1}^{N_r} \Phi_j(\cdot)/N_r$

/* Incidence Matrix Selection                                    */
for $i$=1 to $N_r$ do
    for $j$=$i$ to $N_r$ do
        if $M(i,j) = 1$ then
            switch $Compare(\{\Phi_i(\cdot)), \Phi_j(\cdot)\}, \bar{\Phi})$ do
                case High-High
                    if $\{\Phi_i(\cdot)) > \{\Phi_j(\cdot))$ then
                        $p_{j,k} \ = \ Crossover(p_{i,k}, p_{j,k})$
                    else
                        $p_{i,k} \ = \ Crossover(p_{i,k}, p_{j,k})$
                    end
                case High-Low
                    $p_{j,k} \ = \ Mutation(p_{i,k})$
                case Low-High
                    $p_{i,k} \ = \ Mutation(p_{j,k})$
                case Low-Low
                    $p_{i,k} \ = \ Mutation(p_{i,k})$ $p_{j,k} \ = \ Mutation(p_{j,k})$
            end
        end
    end
end
$\{p_{i,k+1}\} = \{p_{i,k}\}$
```

are assumed available along with the sensor data, while the fitness function is augmented in the following way

$$\Phi_i^r(Z_k, \hat{Z}_{k,i}) = \frac{1}{L}\sum_{j=1}^{L}\frac{1}{\sqrt{2\pi\sigma}}e^{\frac{-(z_k^j-\hat{z}_{k,i}^j)^2}{2\sigma}} + \sum_{s=1}^{R}\frac{1}{L_s}\sum_{l=1}^{L_s}\frac{1}{\sqrt{2\pi\sigma}}e^{\frac{-(z_k^l-\hat{z}_{k,i}^l)^2}{2\sigma}} \tag{2}$$

where R is the number of the robot of the team in the viewing area, L_s the number of sensor of the s–th robot, Z_k is the set of real data retrieved by the robots and $\hat{Z}_{k,i}$ the expected one computed by the robot r for the hypothesis i. The second addendum weights the compliance of the measurement of the team formation with respect to the formation replicated around the i-th individual. In this way the localization algorithm results completely distributed and collaboration is possible even when robots move. Cooperation turns out to be fundamental in reducing the perceptual aliasing, as the more data available the higher the probability to converge to a single location. It is well known that a genetic approach helps to maintain a population of multiple hypotheses. In particular, SSGA, due to their convergence proprieties, usually maintain equally probable hypotheses and, in presence of sufficient and not ambiguous information, converge to a neighborhood of the solution. This fast takeover is related to the structure of the space of interactions and can be exploited monitoring the formation of a single cluster.

4 Robot and Sensor Modeling

The robot pose $\mathbf{x}$ can be entirely described on a plane by means of it position and orientation (x, y, θ). The unicycle model is assumed as the kinematic model for the robot:

$$\begin{aligned} \mathbf{x}_k &= g(\mathbf{x}_{k-1}, u_{k-1}, n_{s,k-1}) \\ &= \mathbf{x}_{k-1} + \begin{bmatrix} \cos\tilde{\phi}_{k-1} & 0 \\ \sin\tilde{\phi}_{k-1} & 0 \\ 0 & 1 \end{bmatrix} u_{k-1} + n_{s,k-1} \end{aligned} \tag{3}$$

where $u_{k-1} = (\delta s_k, \delta\phi_k)$ is the system input (the vehicle displacement and the vehicle rotation respectively), $\tilde{\phi}_{k-1} = \phi_{k-1} + \delta\phi_{k-1}/2$ is the average robot orientation, and n_{k-1} is a white zero mean noise.

The robot is assumed to be equipped with 8 laser rangefinders arrayed on 360°. Given an environment entirely described by a list $\mathcal{M}$ of pairs of points, the related observation model is:

$$z_{j,k} = h(\mathbf{x}_k, \mathcal{M}, n_{s,k-1}) = \frac{|a_r l_j^x + b_r l_j^y + c_r|}{|a_r \cos\theta_j + b_r \sin\theta_j|} + n_{b,k-1} \tag{4}$$

where (a_r, b_r, c_r) are the coefficients of the r-th segment and (l_j^x, l_j^y, θ_j) is the configuration of the laser beam detecting the segment considered. Fig. 2 depicts the proposed robot and sensor modeling.

5 On the advantages of Collaborative vs. Independent Evolution

In section 3 the independent evolution technique proposed in [10] for the autonomous localization has been recalled. Successively, the collaborative procedure proposed for the multi-robot scenario has been described. In this section, a qualitative comparison is provided in order to highlight the advantages introduced by the collaborative procedure against the independent evolution.

5.1 First environment

The first simulation has been carried out in a simple environment with only one wall and two landmarks. Due to the particular structure of the environment, hypotheses cannot be fully distinguished relying only on information coming from laser rangefinders.

Fig. 3 shows the behavior of the algorithm at three different time-steps when the collaboration among robots is deactivated. Robots are represented

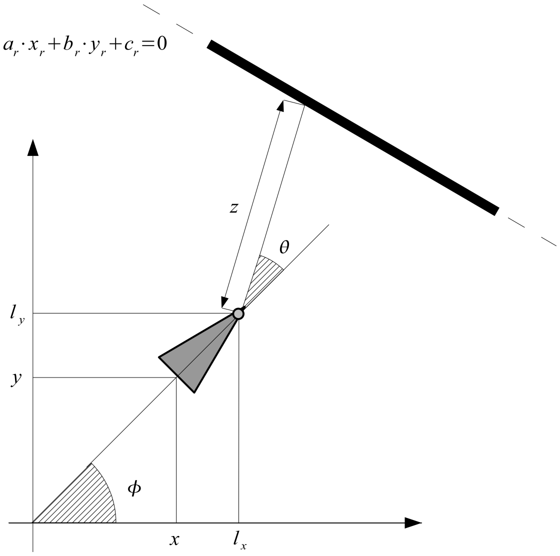


Fig. 2 Robot and Sensor Modeling

by triangles and populations are reported as dots with orientation given by small segments. In (a) each robot recognizes only one landmark, as a consequence each population tends to dispose along a circle whose radius is the measured distance. In (b), in reference to robot 1, hypotheses tend to dispose along a line as soon as the wall is recognized. Specifically, the shape of this line is given by integrating the observation of the wall with the observations of the landmark. In (c) the situation after a few iterations is shown: as predictable, robots cannot fully localize themselves due to the lack of information available.

Fig. 4 shows the behavior of the algorithm at three different time-steps when the collaboration among robots is activated. Robots are assumed to be able to communicate to each other within a range of 5 m. In this case, even after few steps the situation is less ambiguous (a). In fact, in (b) robots are already localized but a perceptible uncertainty (underlined by the hypotheses arrangement) is experienced. In (c), having the cooperation activated long enough, robots are fully localized proving that cooperation can better exploit data.

5.2 Second environment

The second simulation has been carried out in a fully symmetrical environment. As in the previous environment, information coming only from rangefinders are not adequate to fully distinguish hypotheses.

Fig. 5 shows the behavior of the algorithm at three different time-steps when the collaboration among robots is deactivated. At the beginning, as

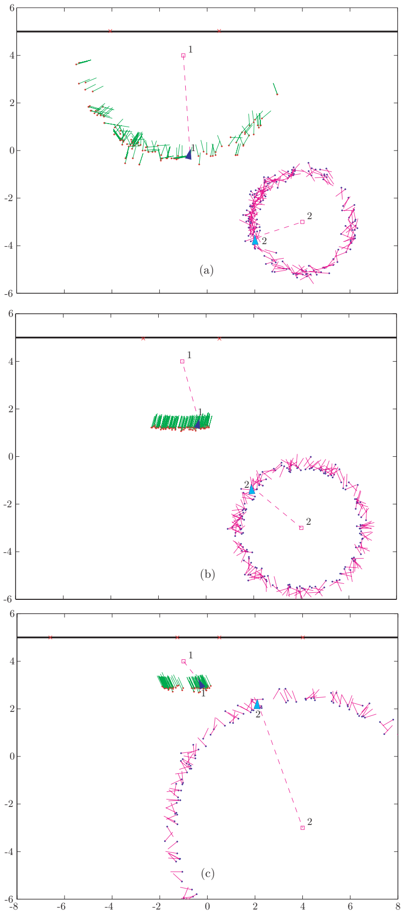


Fig. 3 First simulation in independent mode: iterations 4 (a), 24 (b) and 48 (c)

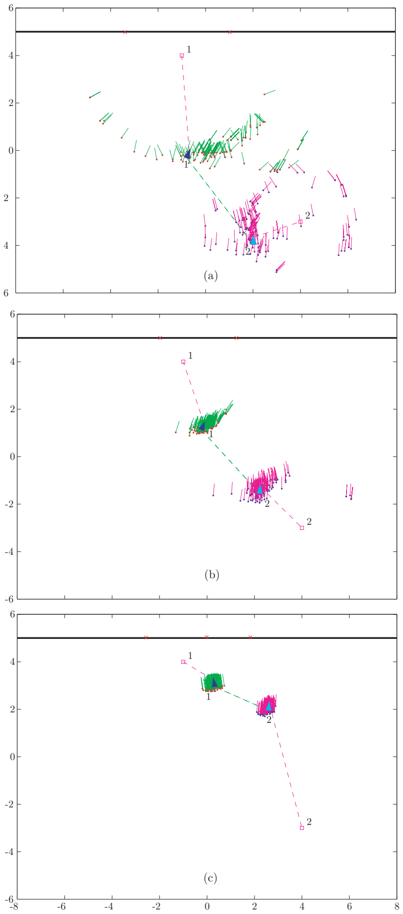


Fig. 4 First simulation in collaborative mode: iterations 4 (a), 24 (b) and 48 (c)

no prior information are available, hypotheses are uniformly spread over the whole environment. After, according to data coming from sensors, some regions turn out to be more likely than others. As a result, individuals tend to cover these areas. However, as expected, robots cannot fully localize themselves relying only on the rangefinder data because of the nature of the environment.

Fig. 6 shows the behavior of the algorithm at some time-steps when the collaboration among robots is activated. Robots are assumed to be able to communicate with each other within a range of 5 m. Also in this case, as no prior information are available at the beginning, hypotheses are spread uniformly over the whole environment. However, due to the cooperation between the two robots, a different behavior is experienced. In fact, extending

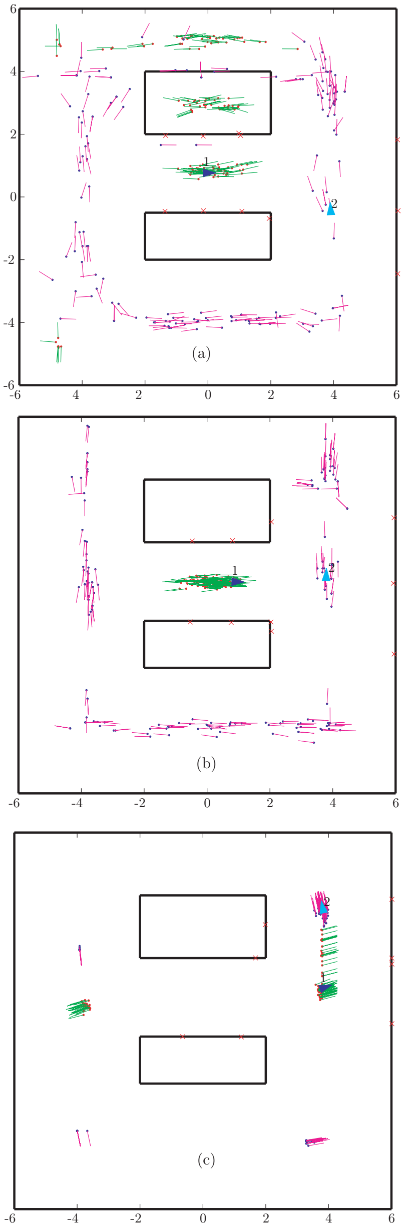


Fig. 5 Second simulation in independent mode: iterations 12 (a), 24 (b) and 48 (c)

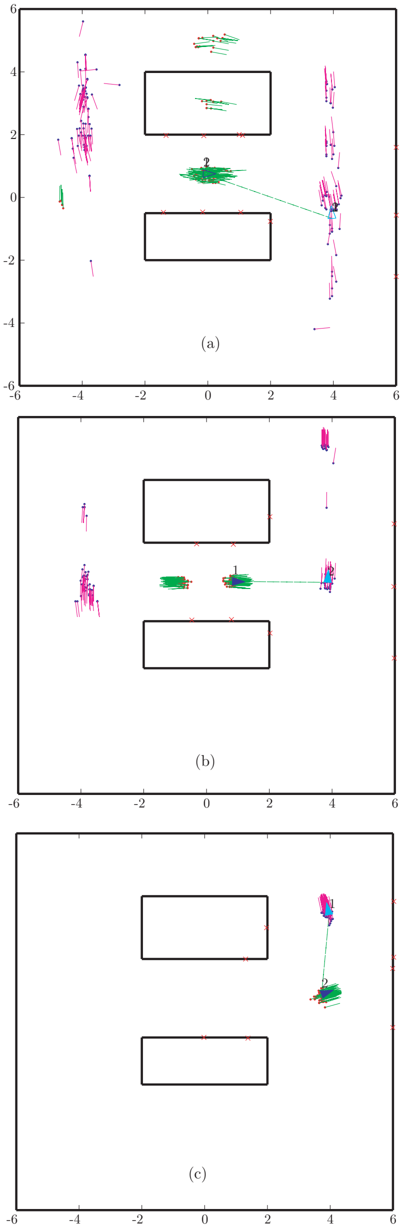


Fig. 6 Second simulation in collaborative mode: iterations 12 (a), 24 (b) and 48 (c)

the perceptual capability of a robot, a better “sight” of the environment can be obtained. Therefore, some structural ambiguities can be easily overcome.

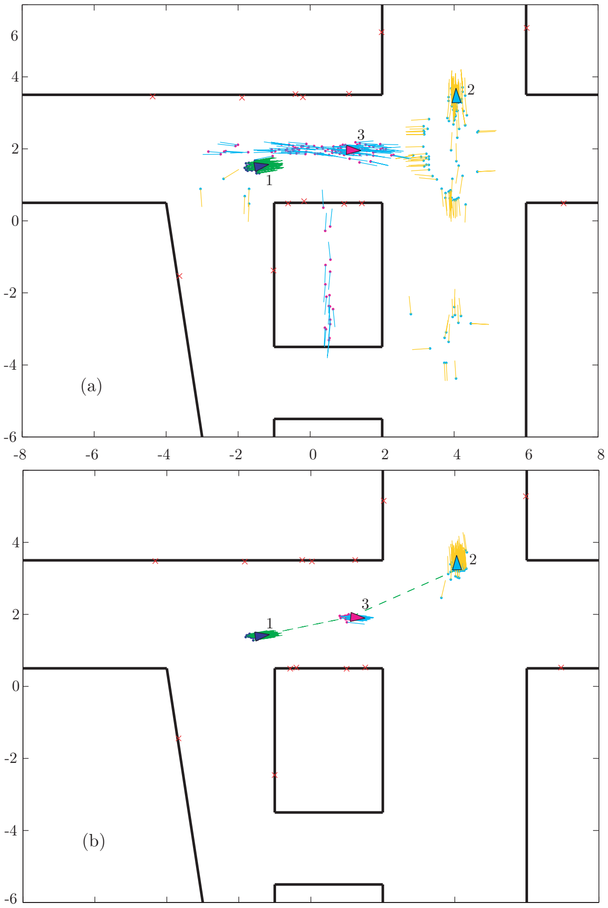


Fig. 7 Third simulation in independent (a) and collaborative (b) mode: iteration 55

5.3 Third environment

The third simulation has been carried out considering three robots. Fig. 7 describes the 55th iteration. In (a) the algorithm behavior when the cooperation is deactivated is reported, while in (b) the same situation with the support of the cooperation is shown. Also in this context, it can be easily noticed as extending the perceptual capability of a robot improves its localization. In particular, due to the nature of the environment, robots 2 and 3 take advantage of the collaboration to disambiguate their position, while robot 1 can localize itself simply exploiting the rangefinder data. Moreover, the framework allows different perceptual extensions to exist. In fact, while robot 3 extends its perception using data coming from both robots 1 and 2, these robots exploit only data coming from one robot. Note that, the full video is available at the web address previously given.

6 Performance Analysis

A statistical analysis has been carried out in order to assess the effectiveness of the proposed MR-SSGA. Fig. 8 shows the environment exploited for the analysis. This environment presents several ambiguities due to the perceptual aliasing of the laser rangefinders and the symmetry of the rooms. In particular, three robots have been considered and their relative paths are given (dots represent starting points). Three indexes of quality have been taken into account to investigate the accuracy of the estimation: minimum, maximum and average error. The analysis, involving 100 trials for each configuration (size of the population), has been performed comparing the proposed MR-SSGA with a simple GA and a collaborative particle filter (PF) algorithm. Table 2 shows the common parameters setting for the algorithms.

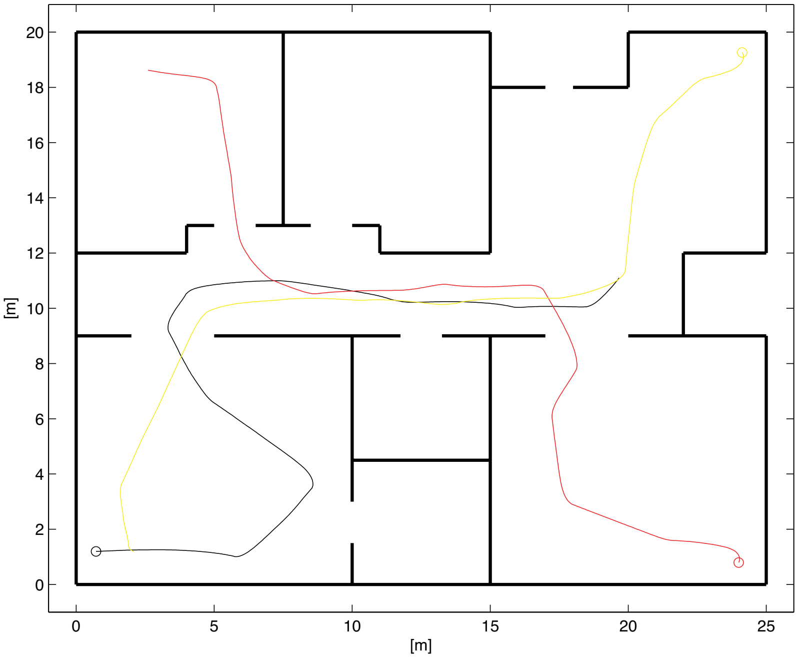


Fig. 8 Environment exploited for the analysis. Lines represent the robots' paths while dots represent the starting points.

Table 3 summarizes the simulation results: the MR-SSGA shows an accuracy of roughly one order of magnitude lower than the other two approaches.

Table 2 Common Parameters Setting

Parameter	Description	Value
L	No. of Pattern Beams	8
l	Beam Range [m]	6
σ_s	Std. Dev. System Model Noise [cm rad/sec]	[3 0.2]
σ_b	Std. Dev. Laser Beam Noise [cm]	10
σ_d	Std. Dev. Relative Distance Sensor Noise [cm]	5
σ_o	Std. Dev. Relative Orientation Sensor Noise [rad]	3
V	Range of Robot's Visibility [m]	8

Moreover, Fig. 9 points out the advantages related to the spatially structured deployment. Indeed, the use of a complex network reduces the jittering of the error estimation due to the particular topology.

In detail, at the beginning the robots start in three different rooms and perform a non-collaborative localization that, due to the high symmetry, has a large error in all the cases. First disambiguation (at about iteration 100, as shown in Fig.9) occurs when red and yellow robots meet in the corridor and, exchanging data, better their estimations. It is possible to note that the genetic approaches are more sensitive to the collaborative exchange of data, rapidly improving the estimate while the particles filter is less prone to exploit this situation. The third robot joins the group around iteration 250 and, with the genetic approaches has a very fast convergence to the right estimate. Not so with the PF, that tends to maintain the previous belief.

Table 3 Autonomous Localization.

Population Size	**50**			**100**		
Algorithm	SSGA	GA	PF	SSGA	GA	PF
Max Err.	0.054	0.133	0.205	0.021	0.056	0.157
Min Err.	0.012	0.027	0.148	0.010	0.009	0.107
Mean Err.	0.023	0.053	0.178	0.014	0.021	0.133

7 Conclusions

In this paper the multi-robot localization problem is addressed. A new framework based on a spatially structured genetic algorithm is proposed (MR-SSGA). It takes advantage of the complex network theory for the deployment of the population. In fact, modeling the search space by means of complex networks results in a more effective exploration. In addition, giving such a structure to the population leads to several interesting advantages such as the capability to create evolutionary niches. As niches are regions where particular solutions are preserved, a natural way to carry on multi-hypothesis paradigm is obtained.

This paper enhances the approach proposed in [10] through an extension for the multi-robot context. Specifically, any time two robots are within their range of visibility a collaboration can be set-up. It consists of exchanging sensor data, along with a measure of their relative distance and orientation, in order to extend the perceptual capability of each robot. As a result, cooperation is fully decoupled and robots are not required to stop while updating their estimates.

Several simulations have been performed, both considering both cooperation activated and not activated, in order to emphasize the effectiveness of the collaboration strategy. According to the simulation results, the cooperation helps the localization process, especially when the interaction with the environment does not provide enough information. Moreover, a comparative analysis against a simple GA and a simple collaborative PF has been performed. It highlighted the MR-SSGA capability to provide an accuracy of roughly one order of magnitude better than the other approaches. Future works are oriented toward a real implementation of the proposed collaborative strategy in order to validate its effectiveness in a real world environment.

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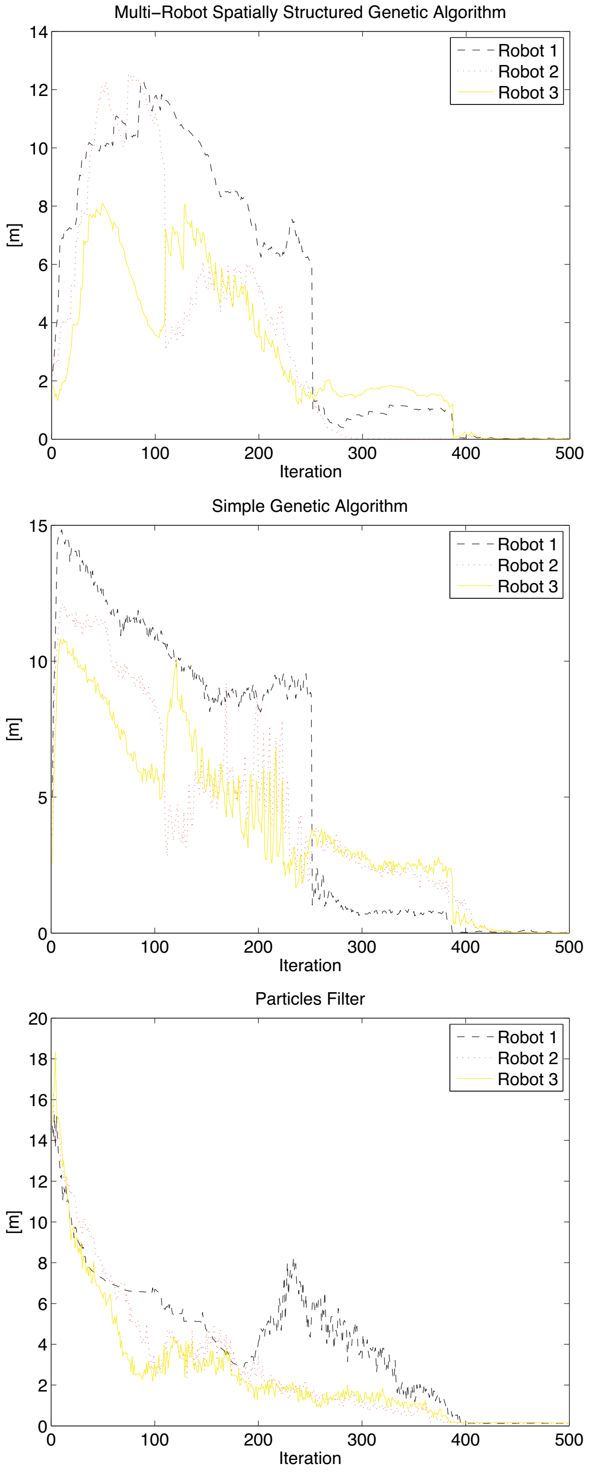

Fig. 9 Comparison of MR-SSGA against a simple GA and a collaborative PF