

A Bacterial Colony Growth Framework for Collaborative Multi-Robot Localization

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Abstract—In this paper the Multi-Robot Localization problem is addressed. A new biology-inspired approach is proposed and implemented: the Bacterial Colony Growth Framework (BCGF). It takes advantage of the models of species reproduction to provide a suitable framework for carrying on the multi-hypothesis, along with proper policies for both autonomous and collaborative contexts. Collaboration among robots is obtained by exchanging sensory data and their relative distance and orientation. This information is integrated into the framework in such a way that the convergence aptitude is enhanced. Several simulations in different environments have been performed, comparing autonomous and collaborative localization, along with proper statistical analysis for performance assessment.

I. INTRODUCTION

The localization problem consists of estimating the pose for a robot moving in an environment using data coming from sensors. Localization has been recognized as one of the most important problems in Robotics. In fact, the availability of reliable pose information turns out to be fundamental to perform almost any task. However, the interaction of the robot with the environment and the noisy nature of sensor data make the problem highly complicated.

The emergence of Multi-Robot Systems (MRS) has introduced new challenges for the localization problem. Working with a MRS leads to several interesting advantages, ranging from an extension of the tasks that can be accomplished to an improvement of the robustness. In addition, the modularity of the system provides a valuable flexibility. In regard to the localization problem, most of the algorithms proposed thus far can be used by means of parallelization: an instance of the algorithm for each robot. However, in general a better localization accuracy can be obtained when collaboration among robots is taken into account. As a consequence, new paradigms have been proposed to exploit all the information available.

From an organizational standpoint, two different architectures can be recognized for multi-robot systems: *centralized* and *decentralized* [2]. Centralized architectures are characterized by a single control robot (leader) that is in charge of organizing the activities of the other robots. The leader takes part in the decision process for the whole team, while the other members act according to the dispositions of the leader. Conversely, decentralized architectures are characterized by “self-organization”, i.e., each robot is autonomous in the decision process with respect to each other. However, all robots share a common goal and their actions are toward

its achievement. Localization algorithms can be developed in respect to these architectures. In a centralized system, a leader collects data provided by the team and performs the localization process for the whole group. In a decentralized system, each robot performs its estimation and exchanges data with the other robots to improve the localization process. Both paradigms present advantages as well as drawbacks. Normally, the assignment of a task is easier in a centralized system compared to a distributed one, as the leader is the only one in charge of it. Furthermore, centralizing the computation requires only one robot with suitable hardware capabilities, or few if redundancy is taken into account. However, this leads to a lack of robustness as once a leader fails, the system becomes unable to accomplish the task. Conversely, the availability of a decentralized system brings robustness as each robot acts autonomously. Obviously, suitable hardware capabilities for all robots are required in this case.

In [7], the authors propose a method called “Cooperative Positioning with Multiple Robots”. The idea is to divide the robots into two groups and let each of them act as a landmark for the other in an alternate fashion in order to improve the localization accuracy. In [8], the previous work is exploited to improve the exploration of an unknown environment. In particular, the authors show how the collaborative exploration can be properly exploited to mitigate the odometry errors which results in a more effective mapping of the environment. In [9], the authors propose an approach in which sensor data, coming from a heterogeneous collection of robots, are combined in a single Kalman Filter. A decentralized version in which each robot runs a smaller filter is presented as well. In [3], a statistical algorithm for collaborative mobile robot localization is proposed. It relies on a sample-based version of the Markov localization approach where probabilistic operators are used when robots detect each other in order to synchronize their beliefs. In [5], a distributed approach based on maximum likelihood estimation is described. In particular, the authors propose a localization approach where each robot acts as a landmark for the others while assuming the availability of relative range, bearing and orientation information. In [10], the authors propose a theoretical analysis for the propagation of position uncertainty for a team of mobile robots. As a result an analytical formula was derived that expresses an upper bound of the uncertainty accumulation as a function of time and the noise characteristics of the robot sensor. In [6], an on-line algorithm for multi-robot simultaneous localization and mapping is described. In this work, the authors propose an

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extension of the single robot Rao-Blackwellized particle-filter for the multi robot scenario. In particular, a technique for the integration of all data coming from all robots into a single map is described.

Here, an approach based on the models of species reproduction is proposed. This work represents an evolution of a study previously performed by the authors for the single-robot context [4], and for which a new strategy able to take into account collaboration is provided. The novelty consists in exploiting information coming from the exchange of data in such a way that the environmental perception of each robot is refined. The rest of the paper is organized as follows. In section II some theoretical insights are given: the robotic and sensor systems are reported in II-A, while models of species evolution are presented in II-B. The proposed (Collaborative) Bacterial Colony Growth framework is described in section III. Finally, simulation results are presented and conclusions are discussed respectively in section IV and V.

II. THEORETICAL BACKGROUND

A. Robot and Sensor Modelling

The robot pose, denoted by the state variable x , can be entirely described on a plane by its position (x, y) and its orientation θ . Here, the unicycle model has been adopted as the kinematic model for the robot. Specifically, $u_{k-1} = (\delta s_k, \delta \phi_k)$ is the system input, where δs_k is the vehicle displacement, and $\delta \theta_k$ the rotation during the sample time interval δt_k , both measured by proprioceptive sensors. As a consequence, the system model equation is:

$$\begin{aligned} x_k &= f(x_{k-1}, u_{k-1}, n_{k-1}) \\ &= x_{k-1} + \begin{bmatrix} \cos \tilde{\phi}_{k-1} & 0 \\ \sin \tilde{\phi}_{k-1} & 0 \\ 0 & 1 \end{bmatrix} u_{k-1} + n_{k-1} \end{aligned} \quad (1)$$

where $\tilde{\phi}_{k-1} = \phi_{k-1} + \delta \phi_k / 2$ is the mean orientation of the robot during the sample time interval δt_k , and n_{k-1} is a white zero mean noise.

The robot, which is moving in an environment completely described by a list of \mathcal{M} segments, has been equipped with L laser range finders arrayed on 360° . The resulting observation model for each laser beam is:

$$z_{j,k} = h(x_k, \mathcal{M}) = \frac{|a_r l_j^x + b_r l_j^y + c_r|}{|a_r \cos \theta_j + b_r \sin \theta_j|} + v_k \quad (2)$$

where (a_r, b_r, c_r) are the coefficients of the r -th segment, (l_j^x, l_j^y, θ_j) is the configuration of the laser beam detecting the segment considered and v_k is a white zero mean noise.

B. Model of Species Evolution

The evolution of species has been modeled mathematically with different approaches. Historically, systems of ordinary deterministic differential equations (ODE) were the first proposed, suitable for large population dynamics [12] [13]. More recently, different models such as stochastic differential equations (SDE) [1] or lattice gas automata using Monte Carlo Algorithms [11] have been introduced. However these models are more suitable to model in-vivo reactions like

metabolic or gene regulations, which exhibit strong stochastic behaviors and multiple equilibria. In this paper the ODE approach will be explored as an effective mean to deal with the localization problem.

A robust basic model for describing species evolution is the *logistic* equation introduced by Verhulst [12]. It describes an *auto-regulation* linked to the numerosness of a species and is defined as:

$$\frac{dN(t)}{dt} = R_0 N(t) \left(1 - \frac{N(t)}{K} \right), \quad (3)$$

where R_0 is the population growth rate and K is the *carrying capacity* (maximum population size). The solution is:

$$N(t) = \frac{K}{1 + \left(\frac{K}{N(0)} - 1 \right) e^{-R_0 t}} \quad (4)$$

A more complex scenario arises when considering different species in the same environment: cohabitant species can start to compete when sharing the same resources or being limited by some related factors. This suggests to modify the logistic model in order to take into account this competition, where the overall numerosness ($N(t) = (N_1(t) + N_2(t))$) is the evolution limit factor. For two species holds:

$$\frac{dN_1(t)}{dt} = \left(1 - \frac{(N_1(t) + N_2(t))}{K_1} \right) R_1 N_1(t) \quad (5)$$

$$\frac{dN_2(t)}{dt} = \left(1 - \frac{(N_1(t) + N_2(t))}{K_2} \right) R_2 N_2(t) \quad (6)$$

Starting from this latter model, the *predator-prey* was derived by Volterra and Lotka [13]. Here authors consider an environment composed by two populations in which predators eat prey:

$$\frac{dH(t)}{dt} = (a - bP(t))H(t) \quad (7)$$

$$\frac{dP(t)}{dt} = (kH(t) - c)P(t) \quad (8)$$

where $P(t)$ and $H(t)$ are respectively the predator and prey populations. Note that, depending on the constant values, the populations can present different behaviors, including periodic ones.

Competition and cooperation can be modeled in a more general way. Let's consider again a biological system composed by two populations P_1, P_2 and a limited resource that both populations need. To use this resource the two populations P_1 and P_2 start to compete. Now, let's assume that if one population extinguishes, the other one grows with logistic law $\frac{dP_i(t)}{dt} = a_i P_i(t) - b_i P_i^2(t)$. In addition, let's consider an encounter term $cP_1(t)P_2(t)$ in the cohabitation that has a control effect. The evolution is then described by:

$$\frac{dP_1(t)}{dt} = (a_1 - b_1 P_1(t) - c_1 P_2(t)) P_1(t) \quad (9)$$

$$\frac{dP_2(t)}{dt} = (a_2 - b_2 P_2(t) - c_2 P_1(t)) P_2(t) \quad (10)$$

where a_i s are the growth rates, b_i s are the *intra-specific* competition coefficients, c_i s are *inter-specific* competition

coefficients. In the same way, the cooperation can be simply defined rearranging terms so that a population would experience extinction if the other one lacked. Note that in these models the genetic evolution of species is not defined. Models can be extended in several ways. For instance, genetic variation among individuals can be achieved with additional equations defining species. Alternatively, the genetic evolution can be accounted for considering the reproduction rates as time-varying functions (i.e. the genetic evolution of a species intrinsically driven by the time-varying reproduction terms).

III. THE BACTERIAL COLONY GROWTH FRAMEWORK

In this section the Bacterial Colony Growth Framework (BCGF) is introduced. First the use of models of species reproduction for robot localization is described. Then, the autonomous localization proposed in [4] is recalled. Next, the novel collaborative localization strategy is described and finally, an effective policy for the choice of the best hypothesis from the generated distributions is discussed.

A. Model of Species Reproduction for Robot Localization

Consider a *bacterium* or a *protozoon* which reproduces asexually in a biological environment. The environment is composed of several areas with different time-varying compounds and concentrations. In this context protozoa can eventually form colonies when in presence of favorable conditions. Conversely, they can die or move far from noxious areas in order to find better zones to reproduce (*bet-hedging*).

In the mobile robot localization context, each bacterium represents a hypothetical robot location, described by its position and orientation $p_i = [x_i \ y_i \ \theta_i]^T$. The nutrient areas define regions where the measures \vec{m}_{r_t} , provided by the real robot, match with some of the population estimated measures $\vec{m}_{p_{i,t}} = [m_{p_{i,t}}^1, \dots, m_{p_{i,t}}^L]$, while bad matches define noxious areas. Bacteria, which move according to the model adopted for robot kinematics, can reproduce and form colonies in the nutrient areas. However, their growth is limited by the total resources of the environment and by the colony size. Therefore, the multi-hypothesis is given by the possibility to form colonies in different areas. In addition, the growth limitation curbs the unbounded growth of the best hypothesis as well as the extinction of other small-medium size colonies. Specifically, when a bacterium is in a nutrient area, the probability to reproduce and form a colony is higher, but if the area is overpopulated the replication chances are lowered. If the environment becomes noxious, for instance in the case of a wrong hypothesis, the colony first tries to expand, then starts to die if nutriment is no longer available.

B. Autonomous Localization

The Bacterial Colony Growth Algorithm for Autonomous localization (BCGA) is given in detail in Algorithm 1: each bacterium-robot reproduces according to both the match with the real robot measures and the colony density in the local

area. This algorithm, originally proposed in [4] for the single-robot context, can be naively applied to the multi-robot context simply by means of parallelization: an instance of the algorithm for each robot.

Algorithm 1: Bacterial Colony Growth Algorithm for Autonomous localization (BCGA)

Data: $P_t = \{p_{1,t} \dots p_{N,t}\}$
Result: $P_{t+1} = \{p_{1,t+1} \dots p_{N,t+1}\}$

$i = 1;$
while ($i \leq N$) **do**
 latency flag $l = TRUE;$
 $j = 1;$
 while ($j \leq N \wedge i \leq N$) **do**
 generate $r \in \mathcal{U}[0, 1];$
 calculate $f_1(\vec{m}_{p_{j,t}}, \vec{m}_{r_{obot_t}}) = n \in [0, 1];$
 calculate $f_2(p_{j,t}, P_{t+1}) = d \in [0, 1];$
 if ($r < n \cdot (1 - d)$) **then**
 $p_{i,t+1} = reproduction(p_{j,t}, n);$
 $i = i + 1;$
 $l = FALSE;$
 end
 $j = j + 1;$
 end
 if ($l = TRUE$) **then**
 /* Uniform random deployment */
 $p_{i,t+1} = betHedging(P_t);$
 $i = i + 1;$
 end
end

The nutrient or noxious environmental condition is given by the function:

$$f_1(\vec{m}_{p_{j,t}}, \vec{m}_{r_t}) = \frac{1}{L} \sum_{i=1}^L e^{-\frac{(m_{p_{j,t}}^i - m_{r_t}^i)^2}{2\sigma_i^2}} \quad (11)$$

where σ_i is tuned coherently with the robot measure confidence intervals.

The colony density is defined as:

$$f_2(p_j, P) = \min \left\{ 1, \frac{1}{\nu N} \sum_{i=1}^N \left(e^{-\frac{\|p_j - p_i\|^2}{2\sigma_p^2}} \right) \right\} \quad (12)$$

where N is the bacterial population size and $\|\cdot\|$ is the Euclidean distance between two points, with $\nu \in [0, 1]$ and σ_p controlling the maximum colony size and the spatial radius respectively.

If a bacterium belonging to a colony C_i in a determined spatial radius is considered as an individual in a single species S_i , the corresponding deterministic differential equation, which holds for large populations, is:

$$\frac{dS_i}{dt} = f_1(S_i) \left(1 - \left(f_2(S_i, N) + \sum_{k \neq i} f_2(S_k, N) \right) \right) S_i \quad (13)$$

Note that if $f_2(S_i)$ is approximated with $\frac{S_i}{N}$ the logistic law is obtained; the growth is limited by the density and the size of the other colonies, being $\sum_k S_k \leq N$ the boundary condition. Here it is assumed that a colony is determined

by a small radius in which nutriment conditions and density can be considered constant. If a bacterium reproduces out of this radius, then it is considered migrating to another colony or forming a new colony (species). The spatial reproduction of a bacterium p depends on the environmental condition: if the ambient is favorable, the bacterium reproduces in a small neighborhood, otherwise it migrates according to a normal distribution, whose variance is inversely proportional to the nutriment conditions:

$$\text{reproduction}(p) = \begin{cases} x_p = \mathcal{N}(x_p, \frac{\sigma_1}{f_1(p)}) \\ y_p = \mathcal{N}(y_p, \frac{\sigma_1}{f_1(p)}) \\ \vartheta_p = \mathcal{N}(\vartheta_p, \frac{\sigma_2}{f_1(p)}) \end{cases} \quad (14)$$

It is clear that as $f_1(p)$ approaches zero the normal distribution tends to the uniform one. Therefore, the bacterium is randomly dragged wandering for attractive areas and the bet-hedging strategy is achieved.

C. Collaborative Localization

The BCGA algorithm provides an effective localization strategy when the single-robot context is considered. However, it does not take into account collaboration among robots. An algorithmic extension (CBCG) can be devised in order to exploit information derived by collaboration among robots. In detail, once two real robots (say r_1 and r_2) meet, i.e, they are within their range of visibility V , sensor data along with relative distance and orientation are exchanged. This information will be used to improve the localization process as follows (supposing two robots are moving in the environment):

- Consider two robot populations P_1 and P_2 , composed by single hypotheses $p_{1,i} \in P_1$ and $p_{2,j} \in P_2$, and let the real robot r_1 be seen by r_2 .
- The robot r_2 communicates to the robot r_1 its relative distance and orientation along with a subset of its population for which $f_1(p_{2,j}) \geq \phi$ (where ϕ can be set arbitrarily) holds.
- Each $p_{1,i}$ exploits this information to refine areas potentially nutrient with regard to its own estimate. Specifically, $p_{1,i}$ updates its fitness through a modified version of the (11) able to take into account data sent by r_2 .

The modified version of the nutrient or noxious environmental condition, for each $p_{1,i} \in P_1$, is given by:

$$\hat{f}_1(p_{1,i}) = f_1(p_{1,i}) + f_3(p_{1,i}) - f_1(p_{1,i}) \cdot f_3(p_{1,i}) \quad (15)$$

where $f_1(p_{1,i}) = f_1(\vec{m}_{p_{1,i}}, \vec{m}_{r_1})$ (time index is not shown) and $f_3(p_{1,i})$ represents the weighted projection of the estimate of r_2 on r_1 , which can be defined as:

$$f_3(p_{1,i}) = \max \left\{ f_1(p_{2,j}) \cdot e^{-\frac{\|p_{2,j} - p_{1 \rightarrow 2,i}\|^2}{2\sigma^2}} \right\}, \quad (16)$$

$$\forall p_{1,i} \in P_1, \forall p_{2,j} \in P_2$$

where $p_{1 \rightarrow 2,i}$ is the estimate of robot r_2 with respect to the hypothesis $p_{1,i}$ of the robot r_1 . Furthermore, (15) can be viewed, from a probabilistic perspective, as a “union” that

redefines a probability distribution with regard to additional information coming from another source.

D. Best Hypothesis Choice Policies

In the global localization problem, when the environment map is given but a plausible hypothesis of the start pose is not available, one major issue is to maintain a set of hypotheses about the robot pose until a reasonable confidence level of estimation is reached. This consideration has been taken into account when devising the algorithm. As a result the Bacterial Colony Growth Framework provides two-level modeling:

- *Background*: To provide a suitable framework for modeling the multi-hypotheses (i.e. algorithms implementing the ODE theory), either in the autonomous or in the collaborative scenario,
- *Foreground*: To exploit several exchangeable strategies to track the robot pose.

The second point refers to the definition of a set of functions that report an actual estimated robot pose, regardless of the multiple optimal hypothesis set. Different approaches can be devised: clustering, mobile mean, naive best fitness choice, etc. For the various simulation environments tested, the formula:

$$\max_{p_i \in P} \{f_1(p_i) \cdot f_2(p_i) \cdot \text{age}(p_i)\} \quad (17)$$

turned out to be an effective and robust strategy. According to the (17), the best hypothesis is obtained at each iteration by exploiting the nutriment condition f_1 , the population density f_2 and the age (a variable that records how long a bacterium was able to reproduce at each generation).

Note that, although some similarities with the standard particle filter localization approach can be noticed, the proposed framework provides several interesting advantages. For example, the availability of a specific framework for carrying on the multi-hypothesis or the de-coupling between the maintenance of the hypotheses (provided by the background level) and their interpretation (provided by the foreground level). More details can be found in [4].

IV. SIMULATION RESULTS

The proposed framework has been widely tested against different simulation environments using a software suite developed by the authors. This suite is composed by several modules, each one providing a specific functionality such as the robot kinematics model or the sensor model, which can be aggregated to model a complex system in depth.

For clarity of exposition, only simulations involving two robots are provided. Indeed, due to the nature of the collaboration, the framework scales well with respect to the number of robots. Moreover, results for two environments, specifically designed to make convergence difficult to achieve, are shown here. In detail, Fig. 1 and 2 show such environments along with the related paths for two robots. Note that, the first environment presents rooms with structural similarity among them, while the second allows for symmetric paths. Thus ambiguous situations can arise in both cases.

TABLE I
ALGORITHM PARAMETERS SETTING

Parameter	Description	Value
N	Population Size	$50 \div 100$
L	No. of Pattern Beams	7
l	Beam Range [m]	12
σ_l	St. Dev. Laser Beam Noise [cm]	10
σ_p	St. Dev. Spatial Radius Bound [m]	2
ν	Density Bound [%]	50
σ_1	St. Dev. x-y Reproduction Area [cm]	10
σ_2	St. Dev. Angle Reproduction Area [rad]	0.05
V	Range of Robot's Visibility [m]	15

In order to assess model performances, a set of 100 independent BCGA and CBCG runs was executed. For each environment, two paths were fixed so that mutual localization was possible. Table I describes the algorithm parameter settings adopted for simulations. Specifically, at each iteration of a given trial, a pose error was computed with respect to the best hypothesis choice policy described above. Median and mean errors over the 100 trials were evaluated as performance indicators, obtaining a non-parametric distribution of the errors over time to be statistically investigated. Note that the initial population was always drawn from a random uniform distribution of bacteria over the whole environment.

Figs. 3 to 6 show the performances of the algorithm for both robots in the two environments. Dashed lines (red) describe localization errors for the autonomous policy, while solid lines (blue) refer to the collaborative policy. In both scenarios communication among robots is available only in the second half path: thus no improvement can be provided from the collaborative approach until this event occurs. The median, which cuts off outliers, underlines the accuracy of the localization technique (showing a negligible error) while the mean reveals the robustness more broadly (taking into account any outcome). According to the experimental results, the CBCG turns out to be more effective than the BCGA in terms of successful trials. This emphasizes the advantage deriving from the collaboration. In particular, significant improvements of the performance are experienced any time the convergence is lacking for a single robot (with the information coming only from its sensorial system). Furthermore, a Wilcoxon rank test [14], detailed in Tab. II, corroborates this result proving a significant statistical difference ($p \leq 1.2 \cdot 10^{-4}$) in performances when considering collaborative strategy against autonomous strategy.

TABLE II
WILCOXON RANK TEST

Robots	p-value	rank sum	z-value
Environment 1			
R1	$4.5368 \cdot 10^{-7}$	$2.6366 \cdot 10^4$	5.0449
R2	$8.2272 \cdot 10^{-9}$	$2.6906 \cdot 10^4$	5.7637
Environment 2			
R1	$5.1633 \cdot 10^{-7}$	$2.3072 \cdot 10^4$	5.0201
R2	$1.2119 \cdot 10^{-4}$	$2.2274 \cdot 10^4$	3.8437

V. CONCLUSIONS

In this paper a new biology-inspired framework (BCGF) is proposed to deal with the Multi-Robot Localization problem. It takes advantage of the models of species reproduction to provide a suitable framework for carrying on the multi-hypothesis, along with proper policies for both autonomous and collaborative contexts.

Collaboration can be set-up at any time when two robots are within their range of visibility. It involves the exchange of sensory data along with relative distance and orientation. This information is integrated into the proposed framework so that the convergence aptitude is enhanced. In detail, the sender's information is exploited by the receiver to redefine areas that can be nutrient with regard to its estimate. In this way, the sensorial capabilities of the receiver are extended and its localization capability is enhanced.

Several simulations in different environments have been performed comparing autonomous and collaborative localization. According to the simulation results, the localization effectiveness is significantly increased (in terms of robustness) when collaboration is properly exploited. In addition, a rank sum test was performed to further validate this result by comparing median error vectors of both autonomous and collaborative localization.

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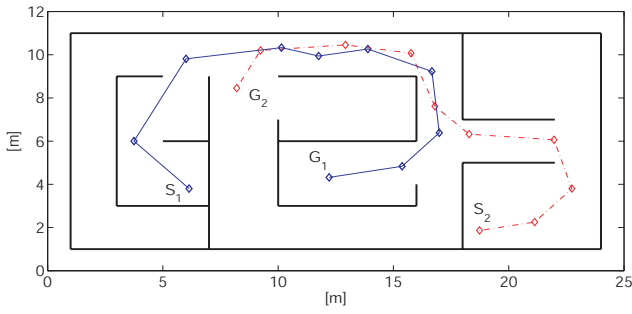


Fig. 1. Environment 1: $S_{\{1,2\}}$ are start points, $G_{\{1,2\}}$ are goal points.

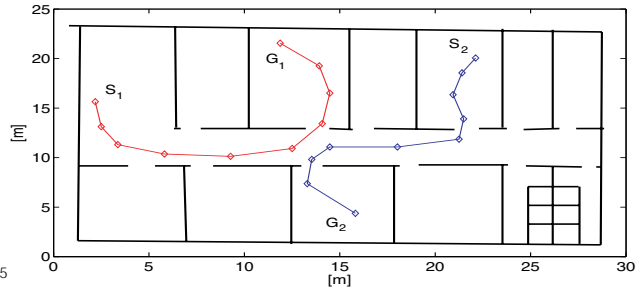


Fig. 2. Environment 2: $S_{\{1,2\}}$ are start points, $G_{\{1,2\}}$ are goal points.

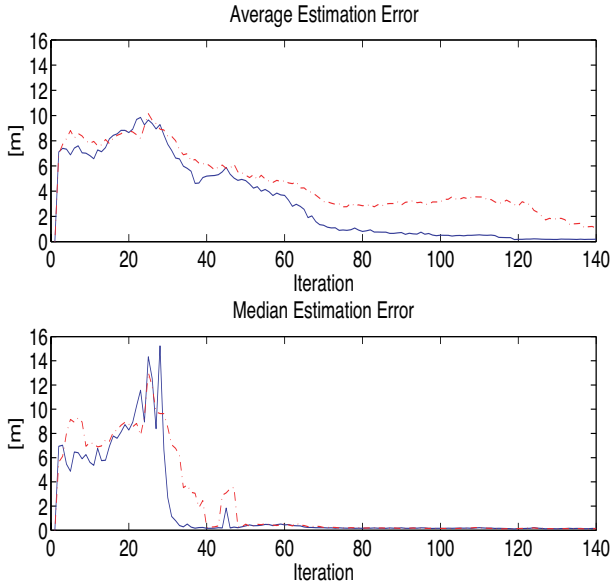


Fig. 3. Robot 1. First Environment. Independent policy (dashed line) vs Collaborative policy (solid line).

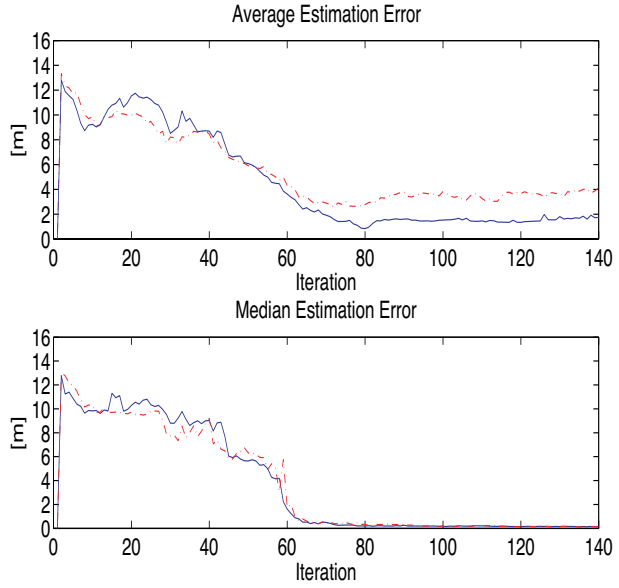


Fig. 4. Robot 1. Second Environment. Independent policy (dashed line) vs Collaborative policy (solid line).

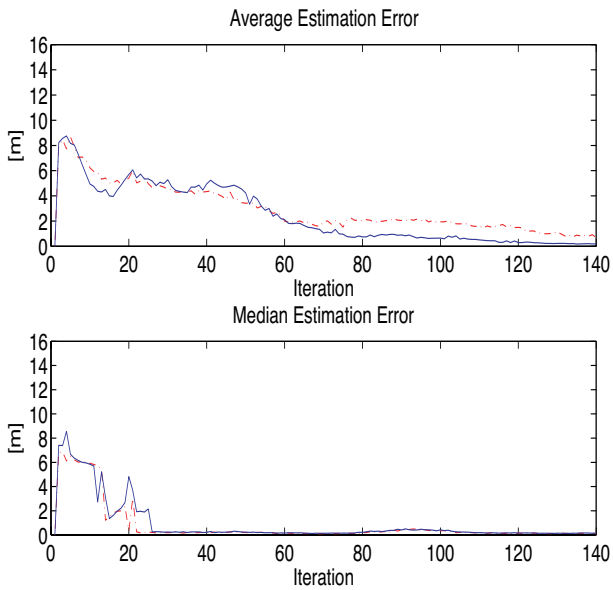


Fig. 5. Robot 2. First Environment. Independent policy (dashed line) vs Collaborative policy (solid line).

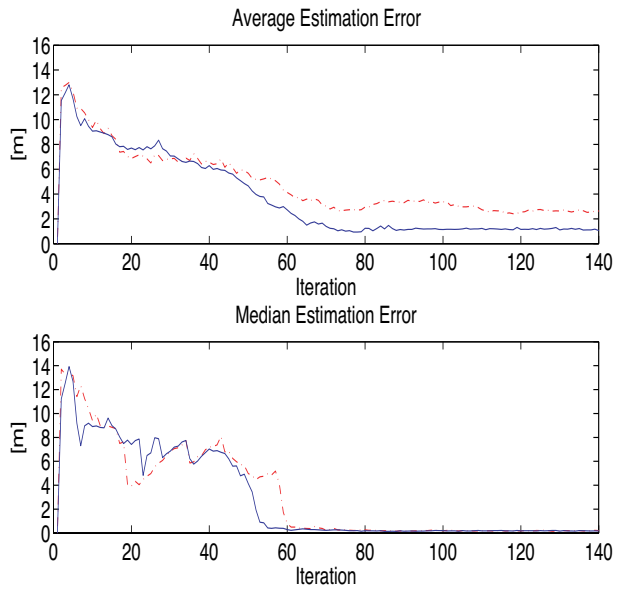


Fig. 6. Robot 2. Second Environment. Independent policy (dashed line) vs Collaborative policy (solid line).