# Localizing the Unknown Receiver in a Diffusive SIMO Molecular Communication System

Fardad Vakilipoor, *Graduate Student Member, IEEE*, Abdulhamid N. M. Ansari, and Maurizio Magarini, *Member, IEEE*

***Abstract*—This letter introduces a method to estimate the position of an unknown fully absorbing (FA) spherical receiver in a diffusive molecular communication (MC) system. This latter consists of a point transmitter and multiple FA spherical receivers in a three-dimensional space. The method relies on a temporal asymptotic single-input multiple-output (SIMO) channel model for diffusive MC systems that takes into account the interaction among receivers. By relying on the asymptotic model, a grid-based likelihood function is a priori created from each known receiver's perspective. The likelihood function's computation requires information about the number of molecules released by the transmitter, its position, and the position of known receivers. From the cumulative number of molecules absorbed by the known FA receivers, different likelihood maps are obtained, where each map corresponds to the likelihood of the position of unknown receiver from a specific known receiver's perspective. By combining the receivers' likelihood maps, which is equivalent to cooperation by sharing their knowledge, the position of the unknown receiver is estimated. The quality of the estimation is evaluated in terms of root mean squared error (RMSE) between the estimated position of the unknown receiver and its true position for different number of released molecules.**

***Index Terms*—Molecular communication, SIMO channel, receiver localization.**

## I. Introduction

MOLECULAR communication (MC) is a paradigm that enables communication among nanomachines in biological environments [1]. In MC, signals are exchanged between nanodevices using particles, *i.e.,* molecules, as information carriers [2]. Usually, in nanonetworks, there are multiple active receivers involved in the communication or sensing process [3]. Hence, a proper model should take into account multiple receivers and their reciprocal interactions with each other. Active receivers' interaction with signaling molecules happens through absorption or chemical reactions [4]. In this work, we take advantage of the interaction and coupling effect among the receivers to estimate the position of an unknown receiver based on the signal observed by the known receivers. The estimation is done by means of the temporal asymptotic cumulative number of molecules absorbed by multiple known fully-absorbing (FA) spherical receivers.

Localization in MC literature is a recent subject of research [5], [6]. In a network of multiple FA receivers it is often needed to localize a receiver. For instance, localizing an inaccessible receiver can be interpreted as localizing the silent receiver for physical security in a communication system [7]. Authors in [8] propose a machine learning approach to localize an unknown receiver (they call it a "silent receiver") based on the observation of a known receiver. The known receiver's surface is segmented into different pieces, each of which is separately able to count the number of absorbed molecules. The absorbed number of molecules by each segment throughout the time is used to train and test a deep neural network.

In this letter, we rely on the single-input multiple-output (SIMO) asymptotic model proposed in [9]. According to the model, the asymptotic behavior can be estimated as a long-time observation[1] that depends on the physical properties of the system such as diffusion coefficient, distance, etc. To begin with, we create a grid in space such that each of its points is a possible position of the unknown receiver. Then, we compute the expected asymptotic cumulative number of absorbed molecules by the known receivers, given that the unknown receiver is located at a specific point on the grid. A probability density function (PDF) is assigned to every point in the grid that describes the likelihood of the unknown receiver located at that point. The likelihood map computation is done a priori in an offline stage on the basis of the information acquired from all the known receivers, their position, that of the transmitter, and its number of released molecules. By substituting the asymptotic observation of a known receiver with its likelihood functions, we can get a map of the likelihood about the position of the unknown receiver from the known receivers' perspective. Finally, the likelihood maps associated with each receiver's perspective are combined to localize the unknown receiver. It is worth noting that, to simplify the visualisation of the results, we create the mesh grid in *xy*-plane, where the receivers and the transmitter are assumed to be located. The proposed estimation method is applicable if the receivers or the transmitter are not in the *xy*-plane. The system model is derived for the case where signalling particles move in a three-dimensional (3D) space.

The rest of this letter is organized as follows. Section II describes the system model. In Section III we discuss how to

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Fardad Vakilipoor and Maurizio Magarini are with the Department of Electronic, Information and Bioengineering, Politecnico di Milano, 20133 Milan, Italy (e-mail: fardad.vakilipoor@polimi.it; maurizio.magarini@polimi.it).

Abdulhamid N. M. Ansari is with the Mechanical Engineering Department, University of Hormozgan, Bandar Abbas 7916193145, Iran (e-mail: a.ansari@hormozgan.ac.ir).

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[1]Determining the minimum time of observation that sufficiently captures the asymptotic behavior is out of the scope of this work.

create the likelihood maps. Section IV presents the numerical results. Concluding remarks are given in Section V.

## II. System Model

The system considered in this work consists of a point transmitter, multiple spherical FA receivers, and a diffusive channel. Without loss of generality, we assume the transmitter is located at the center of the coordinate. The transmitter releases $N_{\mathrm{T}}$ messenger molecules in the environment instantaneously. Molecules diffuse through the medium with a constant diffusion coefficient $D$ in an unbounded 3D environment. Receivers can count the number of molecules absorbed as they hit the receivers' surface. The FA characteristic introduces a coupling effect among the receivers' observations that can be interpreted as a reduction of molecules from the environment [10]. Thus, we need to consider the reciprocal impact to study the number of molecules absorbed by each receiver.

Diffusive propagation of molecules is governed by Fick's second law. Yilmaz et al. [11] specified the boundary and initial conditions for an impulsive release of molecules and an FA receiver $\mathcal{R}_1$. They obtained an analytical expression that describes the hitting rate of the molecules onto the receiver surface, namely $f(d_1,t)$, which depends on the distance $d_1$ between the source $\mathcal{T}$ and the center of the receiver $\mathcal{R}_1$, at time $t$. The channel impulse response of a diffusive MC channel with a single spherical FA receiver of radius $R$, centered at distance $d_1$ from source reads

$$f(d_1,t)=\frac{R(d_1-R)}{d_1\sqrt{4\pi Dt^3}}e^{-\frac{(d_1-R)^2}{4Dt}}. \tag{1}$$

The absorption rate, *i.e.,* the number of molecules absorbed by the receiver per unit time, is given by

$$n_1(t)=N_{\mathrm{T}}f(d_1,t). \tag{2}$$

The overall expected number of absorbed molecules is obtained from integration of (2) up to time $t$

$$N_1(t)=\int_0^t n_1(u)\,du=\frac{N_{\mathrm{T}}R}{d_1}\mathrm{erfc}\left(\frac{d_1-R}{2\sqrt{Dt}}\right), \tag{3}$$

where $\mathrm{erfc}(z)=1-\frac{2}{\sqrt{\pi}}\int_0^z e^{-\tau^2}d\tau$, is the complementary error function.

As shown in [10], the coupling effect among the FA receivers can be modelled by introducing the concept of the negative point source. The negative source position is described by the barycenter that can be associated with each FA receiver. The barycenter is defined as the spatial average of molecules that hit the surface of each receiver according to the geometry of the problem. We can write the absorption rate of each receiver in a SIMO scenario as [10]

$$\begin{cases} n_1(t)=N_{\mathrm{T}}f_1-n_2(t)\star f_{1,2}-n_3(t)\star f_{1,3}\cdots-n_p(t)\star f_{1,p}\\ n_2(t)=N_{\mathrm{T}}f_2-n_1(t)\star f_{2,1}-n_3(t)\star f_{2,3}\cdots-n_p(t)\star f_{2,p}\\ \vdots \qquad\qquad\qquad\qquad \vdots\\ n_p(t)=N_{\mathrm{T}}f_p-n_1(t)\star f_{p,1}-n_2(t)\star f_{p,2}\cdots-n_p(t)\star f_{p,p-1}, \end{cases} \tag{4}$$

where $\star$ is the convolution, $f_i=f(d_i,t), d_i$ is the distance between the transmitter and the center of $\mathcal{R}_i, f_{i,j}=f(d_{i,j},t), d_{i,j}$ is the distance between the center of $\mathcal{R}_i$ and barycenter of $\mathcal{R}_j$. In order to find the number of molecules absorbed by each receiver, it is required to integrate and solve (4). The time domain closed-form solution of (4) for more than two receivers has not been derived yet, while the numerical solution is shown in [10].

To begin with the derivation of the asymptotic model, we take the Laplace transform of the integral of (4) and write it as matrix multiplication

$$\begin{bmatrix}\hat{N}_1(s)\\ \hat{N}_2(s)\\ \vdots\\ \hat{N}_p(s)\end{bmatrix}=\begin{bmatrix}1 & \hat{f}_{1,2} & \hat{f}_{1,3} & \cdots & \hat{f}_{1,p}\\ \hat{f}_{2,1} & 1 & \hat{f}_{2,3} & \cdots & \hat{f}_{2,p}\\ \hat{f}_{3,1} & \hat{f}_{3,2} & 1 & \cdots & \hat{f}_{3,p}\\ \vdots & \vdots & \vdots & \ddots & \vdots\\ \hat{f}_{p,1} & \hat{f}_{p,2} & \hat{f}_{p,3} & \cdots & 1\end{bmatrix}^{-1}\begin{bmatrix}\frac{N_{\mathrm{T}}\hat{f}_1}{s}\\ \frac{N_{\mathrm{T}}\hat{f}_2}{s}\\ \vdots\\ \frac{N_{\mathrm{T}}\hat{f}_p}{s}\end{bmatrix}, \tag{5}$$

where $\mathscr{L}\{f\}=\hat{f}$ and $\mathscr{L}\{N\}=\hat{N}$. Next, we use the final value theorem to achieve the temporal asymptotic behavior, as $t\to\infty$, of FA receivers' observation [9]

$$\begin{bmatrix}N_1\\ N_2\\ \vdots\\ N_p\end{bmatrix}=\begin{bmatrix}\frac{1}{R} & \frac{1}{d_{1,2}} & \frac{1}{d_{1,3}} & \cdots & \frac{1}{d_{1,p}}\\ \frac{1}{d_{2,1}} & \frac{1}{R} & \frac{1}{d_{2,3}} & \cdots & \frac{1}{d_{2,p}}\\ \frac{1}{d_{3,1}} & \frac{1}{d_{3,2}} & \frac{1}{R} & \cdots & \frac{1}{d_{3,p}}\\ \vdots & \vdots & \vdots & \ddots & \vdots\\ \frac{1}{d_{p,1}} & \frac{1}{d_{p,2}} & \frac{1}{d_{p,3}} & \cdots & \frac{1}{R}\end{bmatrix}^{-1}\begin{bmatrix}\frac{N_{\mathrm{T}}}{d_1}\\ \frac{N_{\mathrm{T}}}{d_2}\\ \vdots\\ \frac{N_{\mathrm{T}}}{d_p}\end{bmatrix}, \tag{6}$$

where $N_i$ is the expected asymptotic cumulative number of the molecules absorbed by receiver $\mathcal{R}_i, i=1,\ldots,p$. Note that when the transmitter and receivers are not extremely at close distance, the barycenter location converges to the center of the receivers as the observation time increases. This assumption goes back to the definition of the barycenter. As time increases, the molecules spread in the space and hit the receivers uniformly unless the distance between the transmitter and receivers is very close. Thus, barycenters of receivers are assumed to be at the centers of the spherical FA receivers, as $t\to\infty$. Hence, $d_{i,j}$ is approximated as the distance between the center of $\mathcal{R}_i$ and $\mathcal{R}_j$ [9].

## III. Localization of the Unknown Receiver

The main objective of this work is to introduce a method to estimate the position of an unknown receiver, $\mathcal{R}^u$, from the cumulative asymptotic number of molecules absorbed by the $p-1$ number of known receivers, $\mathcal{R}_i$, $i\in\{1,\ldots,p-1\}$. To this aim, we create a grid of points over the *xy*-plane such that each point can be presumed to be the coordinate of the center of the unknown receiver, $c_{\mathcal{R}^u}=c_l$, $l\in\{1,\ldots,|\mathcal{S}|\}$, where $c_{\mathcal{R}^u}$ is the coordinate of the center of the unknown receiver, $c_l$ is the coordinate of the $l$th point on the grid, and $|\mathcal{S}|$ is the total number of points on the grid. For every point on the grid, we locate the unknown receiver and compute the asymptotic expected number of absorbed molecules by the receivers in the environment (*i.e.,* known and unknown receivers) by using (6). In practice, the number of absorbed molecules by the receivers follows a Binomial distribution due to the independent molecule behavior assumption and since any given molecule released by the transmitter is either absorbed by the receiver or not

$$\tilde{N}_i\sim\mathcal{B}\left(N_{\mathrm{T}},\frac{N_i}{N_{\mathrm{T}}}\right). \tag{7}$$

TABLE I
DEFAULT VALUES FOR SYSTEM PARAMETERS

| Variable | Definition | Value |
|---|---|---|
| $N_{\mathrm{T}}$ | Number of released molecules | $\{10^4, 10^5\}$ |
| $c_{\mathcal{R}_1}$ | Coordinate of the center of $\mathcal{R}_1$ | $(10, 0, 0)$ [$\mu$m] |
| $c_{\mathcal{R}_2}$ | Coordinate of the center of $\mathcal{R}_2$ | $(4, 6, 0)$ [$\mu$m] |
| $c_{\mathcal{R}_3}$ | Coordinate of the center of $\mathcal{R}_3$ | $(-7, -2, 0)$ [$\mu$m] |
| $c_{\mathcal{R}^u}$ | Coordinate of the center of $\mathcal{R}^u$ | $(-6, 7, 0)$ [$\mu$m] |
| $R$ | Radius of receivers | 1 [$\mu$m] |

It is worth noting that, the binomial distribution of the number of absorbed molecules can be approximated as Gaussian distribution if $N_i > 15$ [12] or $N_i > 5$ and $N_{\mathrm{T}} - N_i > 5$ [13]. Since both of the above conditions hold in our simulations, we can assume that the number of absorbed molecules is a Gaussian random variable described as

$$\tilde{N}_i \sim \mathcal{N}\left(N_i, N_i\left(1 - \frac{N_i}{N_{\mathrm{T}}}\right)\right). \tag{8}$$

For every point $c_l$ on the grid, which defines the possible position of the unknown receiver, we compute $N_{i|c_{\mathcal{R}^u}=c_l}$ $i \in \{1, \ldots, p-1\}$ by using (6). The variable $N_{i|c_{\mathcal{R}^u}=c_l}$, can be read as the expected asymptotic cumulative number of absorbed molecules by $\mathcal{R}_i$ given that the unknown receiver is located at coordinate $c_{\mathcal{R}^u} = c_l$. For every coordinate on the grid, we can compute $p-1$ different Gaussian PDF as

$$g_i(\tau|c_{\mathcal{R}^u} = c_l) = \frac{1}{\sqrt{2\pi N_i\left(1 - \frac{N_i}{N_{\mathrm{T}}}\right)}} \exp\left(-\frac{(\tau - N_i)^2}{N_i\left(1 - \frac{N_i}{N_{\mathrm{T}}}\right)}\right). \tag{9}$$

Every $g_i(\tau|c_{\mathcal{R}^u} = c_l)$ describes the likelihood of $c_{\mathcal{R}^u}$ being equal to $c_l$ from the view point of the receiver $\mathcal{R}_i$. By assuming no prior knowledge about the position of the unknown receiver, $c_{\mathcal{R}^u}$, we can employ $g_i$s to estimate $c_{\mathcal{R}^u}$. We create the function that computes the likelihood about the location of $\mathcal{R}^u$ in space from different known receiver's perspectives by considering their asymptotic cumulative number of absorbed molecules, $\tilde{N}_i$, as the input of the likelihood function.

Creating the $g_i$ functions is equivalent to the concept of interference cancellation because thanks to the full knowledge of the position of the known receivers and the analytical model, the PDF maps corresponding to each known receiver become independent of the PDF associated with the other known receivers. The reason behind the independence of the PDFs is that all the information concerning the effect of other known receivers has already been taken into account in the PDF map due to the channel model (6). Hence, we can multiply the PDF maps by one another due to their independence. The estimated position of the unknown receiver can be formulated as

$$\tilde{c}_{\mathcal{R}^u} = \arg\max_{c_l}\left\{\Pi_{i=1}^{p-1} g_i\left(\tilde{N}_i|c_{\mathcal{R}^u} = c_l\right)\right\}. \tag{10}$$

## IV. NUMERICAL EVALUATION AND RESULTS

In this section, we show the estimator's performance in localizing the unknown receiver. Simulation system parameters are taken from [10] and are reported in Tab. I. Fig. 1 demonstrates the topology of the simulation scenario projected on *xy*-plane for most of the simulations in this letter. The circles with checkerboard patterns are the 2D reflection of the known receivers. Receivers $\mathcal{R}_1$, $\mathcal{R}_2$, and $\mathcal{R}_3$ are depicted with green, blue, and orange color, respectively. The red circle corresponds to the reflection of the unknown receiver, $\mathcal{R}^u$, on *xy*-plane. The estimation accuracy depends on the grid resolution, and we consider the spacing of 0.2 $\mu$m on both $x$ and $y$ axes.

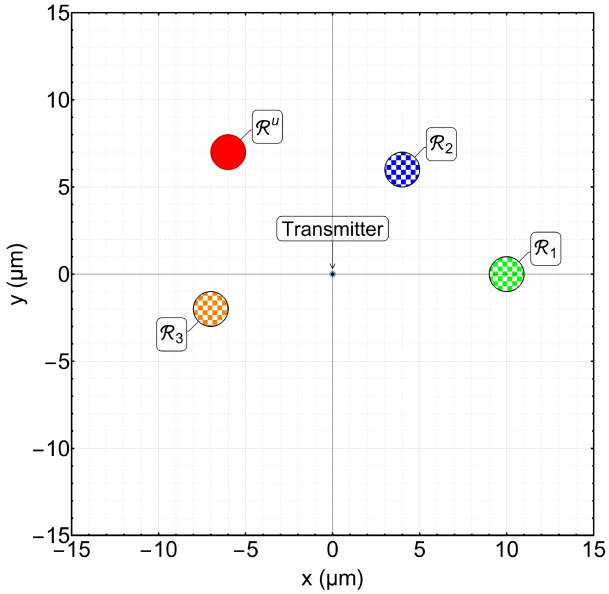


Fig. 1. Topology of simulation scenario. The red circle is the unknown receiver. Receivers $\mathcal{R}_1$, $\mathcal{R}_2$, and $\mathcal{R}_3$ are depicted with checkerboard patterns and green, blue, and orange color respectively. The transmitter is located at the center of the coordinate.

Fig. 2a shows the PDF map from the $\mathcal{R}_1$ perspective when there are two known receivers in the environment. The transmitter releases $10^4$ molecules. From the contour lines and their dispersion, we can interpret there is huge uncertainty about the position of the unknown receiver from the $\mathcal{R}_1$ perspective. Fig. 2b shows the PDF map from the $\mathcal{R}_2$ perspective in the same scenario as Fig. 2a. Fig. 2c shows the product of the PDFs shown in Fig. 2a and Fig. 2b. We can observe that by merging both receivers' perspective, the contour levels gets narrower and more concentrated. This shrinkage of the contour area indicates the improvement in the confidence of the decision about $c_{\mathcal{R}^u}$. In Fig. 2d, we demonstrate the PDF map as if there are three known receivers in the environment. We can observe that the PDF of the points around the unknown receiver have higher values, which can be interpreted as an improvement in the confidence level of the estimation.

Fig. 3 depicts the 3D version of Fig. 2d. We can observe two bulges on the PDF map; however, the one where the unknown receiver is located has a higher value. Fig. 4 computes the likelihood map for the same scenario as Fig. 3 with $N_{\mathrm{T}} = 10^5$. Despite Fig. 3, here we can see that there is only a single peak and the contour area shrinkage is also noticeable, which implies a dramatic improvement in the estimation of the unknown receiver's position.

In Fig. 5, we demonstrate the PDF maps when there are two known receivers in the environment. We can observe that

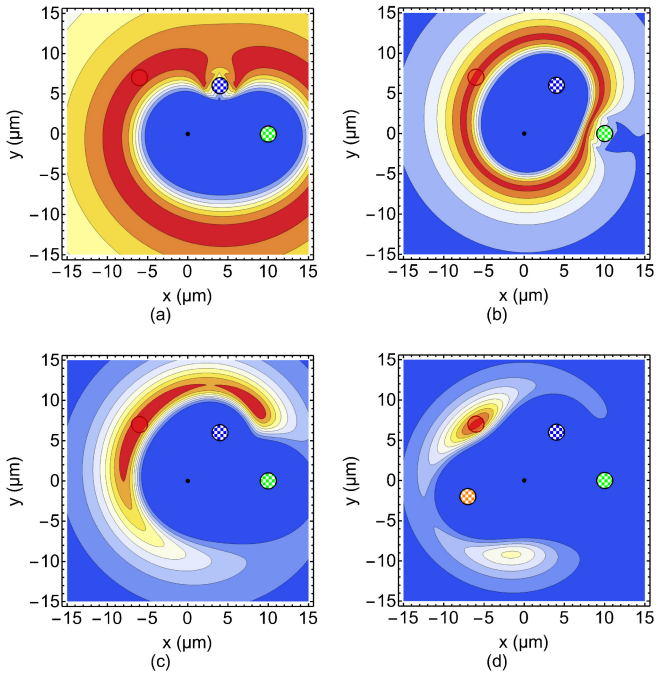


Fig. 2. PDF maps with $N_{\mathrm{T}} = 10^4$. a) The value of $g_1(N_1)$ corresponding to the $\mathcal{R}_1$ (the green circle) perspective when there are two known receivers in the environment. b) The value of $g_2(N_2)$ corresponding to the $\mathcal{R}_2$ (the blue circle) perspective when there are two known receivers in the environment. c) Cooperative PDF when there are two known receivers in the environment. d) Cooperative PDF when there are three known receivers in the environment.

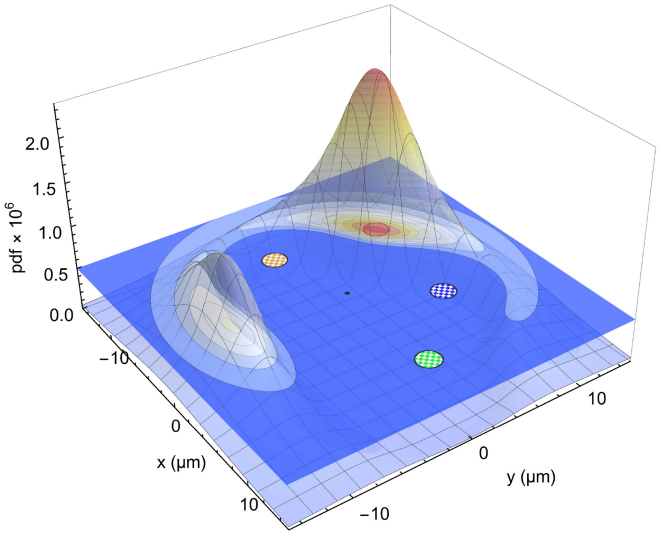


Fig. 3. PDF map of the position of the unknown receiver from the perspective of all three receivers with $N_{\mathrm{T}} = 10^4$.

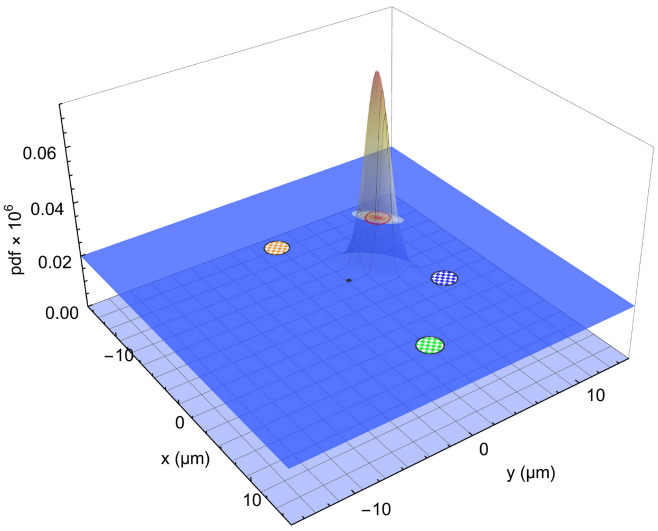


Fig. 4. PDF map of the position of the unknown receiver from the perspective of all three receivers with $N_{\mathrm{T}} = 10^5$.

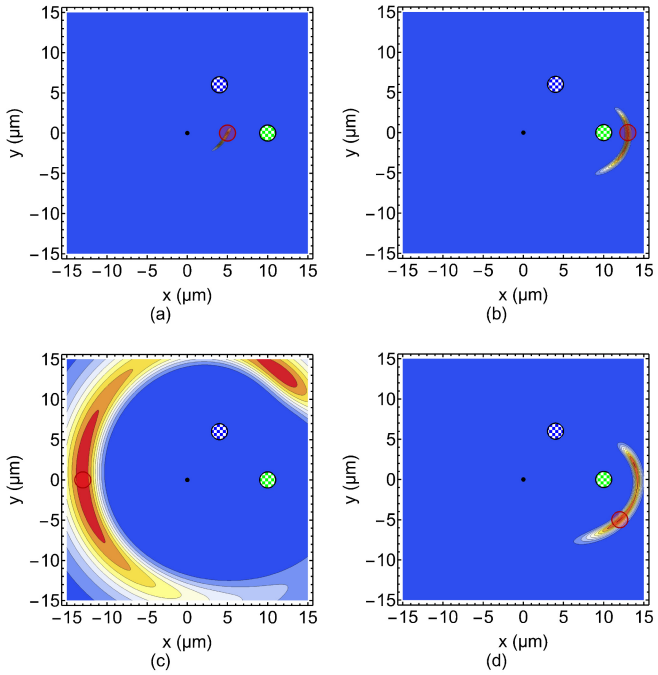


Fig. 5. PDF maps with $N_{\mathrm{T}} = 10^4$ and two known receivers. a) The PDF when $c_{\mathcal{R}^u} = (5, 0, 0)$ [$\mu$m]. b) The PDF when $c_{\mathcal{R}^u} = (13, 0, 0)$ [$\mu$m] c) The PDF when $c_{\mathcal{R}^u} = (-13, 0, 0)$ [$\mu$m]. d) The PDF when $c_{\mathcal{R}^u} = (12, -5, 0)$ [$\mu$m].

in Fig. 5a when the unknown receiver is located between the receiver and transmitter, it can be localized with very high confidence. In another scenario, Fig. 5b we moved the unknown receiver behind the known receiver $\mathcal{R}_1$ at coordinate (13, 0, 0) [$\mu$m]. We can see that although the unknown receiver is closer to $\mathcal{R}_1$, it is characterized by higher uncertainty compared to the scenario of Fig. 5a. In Fig. 5c we move $\mathcal{R}^u$ to $(-13, 0, 0)$ [$\mu$m]. Compared to Fig. 5b. in Fig. 5c, the unknown receiver absorbs more molecules, but since it is far from the known receivers, its detection is not quite confident. In Fig. 5d we put $\mathcal{R}^u$ at (12, −5, 0) [$\mu$m]. In this case, it absorbs more molecules compared to Fig. 5b, but since it is far from $\mathcal{R}_2$, the quality of localization is weaker than what is observed in Fig. 5b. Overall from the observations in Fig. 5 we understand that if the unknown receiver is located in the line of sight between the transmitter and the known receiver, it can be localized with good confidence. On the other hand, if the unknown receiver is located in the shadowing of the receiver, like in Fig. 5b, the estimator becomes less confident. To establish secure communication, it is preferred to surround the source with the receivers so that any appearance of the unknown receiver becomes localizable with high certainty.

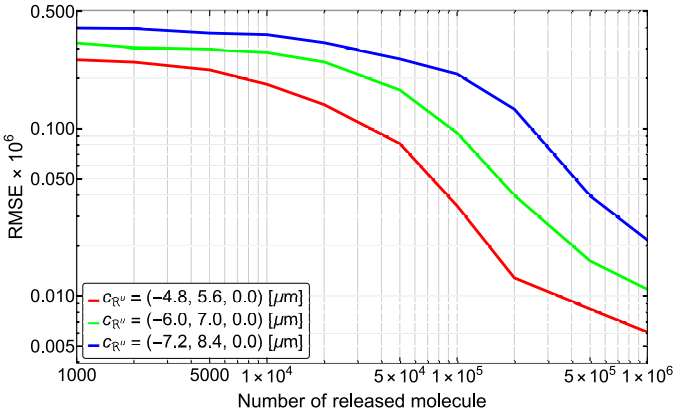


Fig. 6. The RMSE of estimating the position of the unknown receiver in three different coordinates with the same topology as Fig. 2d with three known receivers.

Finally, we evaluate the performance of the estimator (10) by computing the root mean squared error (RMSE) between the estimated position of the unknown receiver obtained based on $\tilde{N}_i$s following (8) and its true position. The estimation process is repeated $Q = 10^3$ times. The RMSE in every condition can be computed as

$$RMSE = \sqrt{\frac{1}{Q}\Sigma_{q=1}^{Q}|\tilde{c}_{\mathcal{R}^u}^{(q)} - c_{\mathcal{R}^u}|^2}, \tag{11}$$

where $\tilde{c}_{\mathcal{R}^u}^{(q)}$ is the estimated position of the unknown receiver at the $q$th run. Fig. 6 reports the RMSE results versus the number of released molecules. We can see that for the closer position of the unknown receiver to the origin (transmitter), its corresponding RMSE line is lower than those farther from the origin. This trend indicates that as the distance between the unknown receiver and the source increases, its localization becomes more challenging. Additionally, Fig. 6 shows the RMSE for different values of $N_{\mathrm{T}}$. We can observe that the RMSE varies with $N_{\mathrm{T}}$, and by increasing $N_{\mathrm{T}}$, RMSE drops, which indicates an improvement in estimation quality.

## V. Conclusion

This letter introduces a method to estimate the position of an unknown fully absorbing (FA) receiver in a diffusive molecular communication system that relies on the knowledge of the number of molecules absorbed by known receivers. The scenario is that of a single-input multiple-output system where molecules are instantaneously released by a point transmitter and captured by FA spherical receivers. Based on the asymptotic number of molecules absorbed by the known receivers, a likelihood map of a grid of points is created offline. Simulation results show that for the considered 3D scenario with one transmitter and three known receivers lying on the surface of a square plane with side of 30 $\mu$m, the RMSE is almost constant around $3 \times 10^{-1}$ $\mu$m when the number of released molecules is between $10^3$ and $10^4$ and then it starts decreasing with a value between $7 \times 10^{-3}$ and $2 \times 10^{-2}$ when the number of released molecules is equal to $10^6$, depending on the positions of the known receivers.

The main idea behind the proposed approach consists of assessing the likelihood of the possible position of the unknown receiver in the space from the perspective of each known receiver. By combining likelihood maps, we can estimate the position of the unknown receiver cooperatively. To ensure the possibility of localizing the unknown receiver with good confidence and not letting it receive enough signalling molecules, it is better to surround the transmitter by receivers uniformly in all directions and keep the distance between the transmitter and known receivers not very small. When the receiver and the transmitter are very close, then a large number of molecules have a chance to go into the shadowing area of the intended receiver due to their stochastic movement nature. Hence, the unknown receiver can gain information due to its position behind the known receiver. As a result of this letter, we introduce a new trade-off in the diffusive communication system design. To ensure secure communication (in terms of unknown receiver detection), an optimum location must be investigated such that it guarantees both reliability of the communication and the detectability of the unknown receiver.

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