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Asymptotic MIMO Channel Model for Diffusive MC with Fully-absorbing Receivers

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***Abstract*—This letter introduces an analytical model that gives the expected asymptotic cumulative number of molecules absorbed by each spherical receiver in a diffusive multiple-input multiple-output (MIMO) molecular communication (MC) system with pointwise transmitters. The reciprocal effect among the fully absorbing (FA) receivers is taken into account by using the recently introduced concept of fictitious pointwise negative source of molecules. An agreement is shown between the proposed asymptotic model and the numerical solution of the exact analytical one from the literature describing the interaction among the receivers, which is computed for a sufficient long time.**

***Index Terms*—Asymptotic analysis, molecular communication, diffusive MIMO channels, fully absorbing receiver.**

I. Introduction

MOLECULAR communication (MC) is a bio-inspired communication paradigm where signals are exchanged between nanoscale devices by using particles, *i.e.* molecules, as information carriers [1]. Applications of MC revolve around health sector (e.g. targeted drug delivery, nanomedicine, etc.) [2], [3], where nanomachines are the most integral units that are capable of performing primary functions like sensing, actuation, and computation. Since nanomachines are unable to do complicated tasks, they need to establish reliable cooperation in nanonetworks to perform complex activities.

Although nanonetworks are characterized by the presence of multiple transmitting and receiving nanomachines [4], so far research in MC has mainly focused on systems with a single transmitter and a single receiver. This highlights the importance of studying and defining new models for multiple-input multiple-output (MIMO) MC systems. Receivers in MC can be basically divided into two different categories [5]. The first is defined by passive receivers, where there is no interaction with information molecules. The second by active receivers, in which there is reciprocal interaction that can occur through an absorption process or via chemical reactions. Thus, the case of multiple active receivers requires extra consideration due to their interaction and, for this reason, in this letter we focus on a diffusive MIMO MC scenario with fully absorbing (FA) spherical receivers.

The diffusive MIMO MC system was already considered in the literature [6], [7]. Recently, in [8] an analytical model has been introduced to describe the channel impulse response between a pointwise transmitter and a given number of FA receivers. The approach is based on the idea of describing the effect of all the FA receivers, except the one considered for the derivation of the impulse response, as pointwise sources of negative molecules. A key contribution of [8] is to show that the position of the pointwise source of negative molecules is not necessarily the center of the receivers and that its position varies according to the time of observation. The *absorption barycenter*, which depends on the relative position of receivers and transmitter, is proposed to locate the negative source.

By following the analysis in [8], in this letter we model the diffusive MIMO MC scenario with a system of equations and derive an analytical expression for the expected asymptotic value of the cumulative number of molecules absorbed by each FA receiver. To the best of the authors' knowledge, this is the first work providing an analytical expression that allows us to evaluate such an asymptotic number.

The letter is organized as follows. Section II defines the baseline diffusive MC scenario of one pointwise transmitter and multiple FA receivers. Its asymptotic behavior and extension to the MIMO MC case are studied in Sec. III. Numerical results and validation of the proposed asymptotic model are presented in Sec. IV. Concluding remarks are given in Sec. V.

II. System model

The considered scenario consists of a diffusive channel where there are pointwise transmitters and spherical FA receivers. Each transmitter instantaneously releases N_T molecules in an unbounded three-dimensional environment. The released molecules diffuse through the medium with a constant diffusion coefficient D $[\mu\mathrm{m}^2/\mathrm{s}]$. Receivers absorb messenger molecules hitting their surface and trap them. Figure 1 shows an example with one transmitter and two receivers. The FA characteristic of the receivers introduces a coupling effect which leads to a reduction in the number of molecules absorbed by each receiver [8]. In what follows, we first review the single-input single-output (SISO) case, then we move to the single-input two-output (SITO) scenario, and finally generalize it to single-input multiple-output (SIMO).

A. Single Input Single Output (SISO)

The diffusive propagation of molecules is governed by Fick's second law, which links the time derivative of the flux to the Laplacian of the molecules concentration $p(r,t)$ at distance r and time t as [5]

$$\frac{\partial p(r,t)}{\partial t} = D\nabla^2 p(r,t)\,. \tag{1}$$

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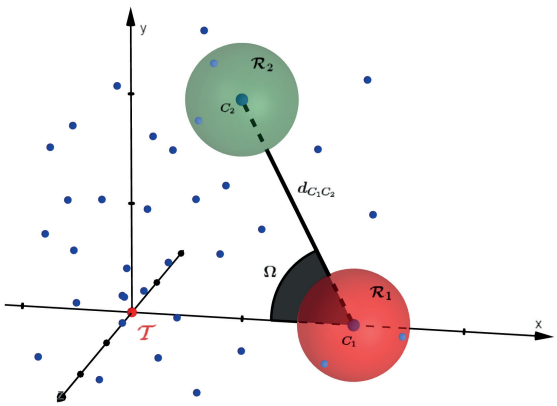

Fig. 1. MCvD system with two FA receivers centered at points C_1 and C_2.

The initial and boundary conditions of (1) vary subject to the MC system characterization. Yilmaz *et al.* [9] 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 receiving cell surface, namely $f(d_1, t)$, which depends on the distance d_1 between the transmitter $\mathcal{T}$ 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 the transmitter reads

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

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

$$n_1(t) = N_T f(d_1, t). \tag{3}$$

The overall expected number of absorbed molecules is obtained from integration of (3) up to time t

$$N_1(t) = \int_0^t n_1(u)\, du = \frac{N_T R}{d_1} \operatorname{erfc}\left(\frac{d_1 - R}{2\sqrt{Dt}}\right), \tag{4}$$

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

B. Single Input Two Output (SITO)

The absorption rate of a single FA receiver is given by (3). The presence of a second FA receiver has the effect of removing molecules from the environment, thus reducing the absorption rate of the first.From the $\mathcal{R}_1$ perspective, $\mathcal{R}_2$ can be interpreted as a fictitious pointwise source of "negative" molecules characterized by a number of released molecules equal to the amount absorbed. As shown in [8], the best position where to place the fictitious pointwise negative source is given by its absorption barycenter[1]. The reciprocal interaction between the two FA receivers can be modelled by applying the superposition principle. Mathematically, we can evaluate the absorption rates of the two receivers by the following system of equations

$$\begin{cases} n_1(t) = N_T f_1 - n_2(t) \star f_{1,2}, \\ n_2(t) = N_T f_2 - n_1(t) \star f_{2,1}, \end{cases} \tag{5}$$

where $\star$ is the convolution, $f_1 = f(d_1, t)$, $f_{1,2} = f(d_{1,2}, t)$, and $d_{1,2}$ is the distance between the center of $\mathcal{R}_1$ and barycenter of $\mathcal{R}_2$. On the other hand, $f_2 = f(d_2, t)$, $f_{2,1} = f(d_{2,1}, t)$, and $d_{2,1}$ is the distance between the center of $\mathcal{R}_2$ and barycenter of $\mathcal{R}_1$. With reference to $\mathcal{R}_1$, (5) takes into account the effect of $\mathcal{R}_2$ by subtracting the number of molecules absorbed, filtered by the impulse response $f_{1,2}$, from the number of molecules that would have been absorbed by $\mathcal{R}_1$ if it had been alone. Note that, for the considered scenario, the release of molecules from the fictitious negative source is not impulsive but varies with time as $n_2(t)$. Due to the reciprocity of the problem, the same reasoning can be applied to evaluate the effect of $\mathcal{R}_1$ on $\mathcal{R}_2$.

In order to find the expected number of molecules absorbed by each receiver, it is required to integrate and solve (5). By taking the Laplace transform $\mathscr{L}\{\cdot\}$ of the integral of (5) and rearranging the resulting equation, we can write it in matrix form as

$$\begin{bmatrix} 1 & \hat{f}_{1,2} \\ \hat{f}_{2,1} & 1 \end{bmatrix} \begin{bmatrix} \hat{N}_1(s) \\ \hat{N}_2(s) \end{bmatrix} = \begin{bmatrix} \frac{N_T \hat{f}_1}{s} \\ \frac{N_T \hat{f}_2}{s} \end{bmatrix}, \tag{6}$$

where $\hat{f} = \mathscr{L}\{f\}$ and $\hat{N} = \mathscr{L}\{N\}$. The closed-form solution for the expected cumulative number of absorbed molecules by $\mathcal{R}_1$ can be obtained by matrix inversion and computation of the inverse Laplace transform of as [8, eq. (21)]

$$\begin{aligned} N_1(t) = {} & \frac{N_T R}{d_1} \sum_{n=0}^{\infty} \frac{R^{2n}}{(d_{1,2} d_{2,1})^n} \\ & \operatorname{erfc}\left(\frac{(d_1 - R) + n(d_{1,2} + d_{2,1} - 2R)}{2\sqrt{Dt}}\right) \\ & - \frac{N_T R^2}{d_{1,2} d_2} \sum_{n=0}^{\infty} \frac{R^{2n}}{(d_{1,2} d_{2,1})^n} \\ & \operatorname{erfc}\left(\frac{(d_{1,2} + d_2 - 2R) + n(d_{1,2} + d_{2,1} - 2R)}{2\sqrt{Dt}}\right). \end{aligned} \tag{7}$$

C. Single-Input Multiple-Output (SIMO)

By following the same approach of the SITO case seen in Sec. II-B, for the SIMO case one can write the generalized form of (6) as

$$\begin{bmatrix} 1 & \hat{f}_{1,2} & \hat{f}_{1,3} & \dots & \hat{f}_{1,p} \\ \hat{f}_{2,1} & 1 & \hat{f}_{2,3} & \dots & \hat{f}_{2,p} \\ \hat{f}_{3,1} & \hat{f}_{3,2} & 1 & \dots & \hat{f}_{3,p} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ \hat{f}_{p,1} & \hat{f}_{p,2} & \hat{f}_{p,3} & \dots & 1 \end{bmatrix} \begin{bmatrix} \hat{N}_1(s) \\ \hat{N}_2(s) \\ \vdots \\ \hat{N}_p(s) \end{bmatrix} = \begin{bmatrix} \frac{N_T \hat{f}_1}{s} \\ \frac{N_T \hat{f}_2}{s} \\ \vdots \\ \frac{N_T \hat{f}_p}{s} \end{bmatrix}. \tag{8}$$

Unlike the SITO case, the time domain closed-form solution of (8) has not been derived yet. However, since the original system of equations before applying the Laplace transform corresponds to a time domain integration it can be solved numerically as shown in [8].

[1]For a given geometry of the problem, the barycenter of each receiver is defined as the spatial average of its surface points hit by molecules.

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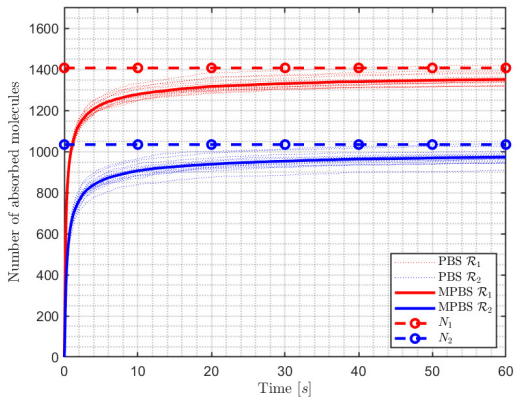

Fig. 2. Cumulative number of molecules absorbed by both receivers according to Fig. 1 where $d_{C_1C_2} = 4\,\mu$m and $\Omega = 90°$.

III. Asymptotic Analysis

The goal of this letter is to explore the asymptotic behavior, as $t \to \infty$, of FA receivers observation through the study of their interaction. Since as time goes to infinity molecules tend to be distributed more and more evenly in space, we assume here that the barycenters are asymptotically located in the center of the spherical FA receivers. As will be shown, this assumption is well assessed by numerical validation. Hence, $d_{i,j}$ represents the distance between the centers of $\mathcal{R}_i$ and $\mathcal{R}_j$. In the following, we analyze the asymptotic behavior of the three scenarios discussed in the previous section and, finally, we extend the SIMO model to MIMO.

A. SISO

The expected asymptotic number of molecules absorbed by $\mathcal{R}_1$ in the SISO case is calculated by taking the limit of (4) as

$$\lim_{t\to\infty} N_1(t) = \lim_{t\to\infty} \frac{N_T R}{d_1} \operatorname{erfc}\left(\frac{d_1 - R}{2\sqrt{Dt}}\right) = \frac{N_T R}{d_1}. \tag{9}$$

In the remaining of this letter for compactness we denote the expected asymptotic values by only removing the argument t in front of the N. For example $\lim_{t\to\infty} N_1(t) = N_1$.

B. SITO

The expected asymptotic value in this case is obtained from (7) as

$$\begin{aligned} N_1 = \sum_{n=0}^{\infty} \left(\frac{R^2}{d_{C_R S_I 1,2} d_{2,1}}\right)^n \lim_{t\to\infty} \Bigg[& \frac{N_T R}{d_1} \\ & \operatorname{erfc}\left(\frac{(d_1 - R) + n(d_{1,2} + d_{2,1} - 2R)}{2\sqrt{Dt}}\right) - \frac{N_T R^2}{d_{1,2} d_2} \\ & \operatorname{erfc}\left(\frac{(d_{1,2} + d_2 - 2R) + n(d_{1,2} + d_{2,1} - 2R)}{2\sqrt{Dt}}\right)\Bigg]. \end{aligned} \tag{10}$$

Since the value of erfc converges to one as the argument goes to zero, (10) simplifies to

$$N_1 = \sum_{n=0}^{\infty} \left(\frac{R^2}{d_{1,2} d_{2,1}}\right)^n \left(\frac{N_T R}{d_1} - \frac{N_T R^2}{d_{1,2} d_2}\right). \tag{11}$$

Assuming $\frac{R^2}{d_{1,2} d_{2,1}} < 1$, *i.e.*, receivers do not touch nor interfere with each other, by using the geometrical series limit we get

$$N_1 = N_T R \left(\frac{d_{1,2} d_2 - R d_1}{d_1 d_2 d_{1,2}}\right)\left(\frac{d_{1,2} d_{2,1}}{d_{1,2} d_{2,1} - R^2}\right). \tag{12}$$

It is expected that in a SITO scenario if $\mathcal{R}_2$ is located far from $\mathcal{R}_1$, then N_1 must behave as there was no other FA receivers around. This characteristic is perfectly observable in our derivations. In fact, if we fix the position of $\mathcal{R}_1$ and move $\mathcal{R}_2$ far away, *i.e.*, $d_2, d_{1,2}, d_{2,1} \to \infty$, (12) converges to (9).

C. SIMO

For the SIMO scenario we use (8) and take advantage of finite value theorem [10], which reads

$$\begin{bmatrix} N_1 \\ \vdots \\ N_p \end{bmatrix} = \lim_{s\to 0} s \begin{bmatrix} \hat{N}_1(s) \\ \vdots \\ \hat{N}_p(s) \end{bmatrix}. \tag{13}$$

Substituting the vector of expected absorbed number of molecules from (8) in (13) we get

$$\begin{bmatrix} N_1 \\ N_2 \\ \vdots \\ N_p \end{bmatrix} = \lim_{s\to 0} \begin{bmatrix} 1 & \hat{f}_{1,2} & \hat{f}_{1,3} & \cdots & \hat{f}_{1,p} \\ \hat{f}_{2,1} & 1 & \hat{f}_{2,3} & \cdots & \hat{f}_{2,p} \\ \hat{f}_{3,1} & \hat{f}_{3,2} & 1 & \cdots & \hat{f}_{3,p} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ \hat{f}_{p,1} & \hat{f}_{p,2} & \hat{f}_{p,3} & \cdots & 1 \end{bmatrix}^{-1} \begin{bmatrix} N_T \hat{f}_1 \\ N_T \hat{f}_2 \\ \vdots \\ N_T \hat{f}_p \end{bmatrix}. \tag{14}$$

The limit of $\hat{f}$ as $s \to 0$ is found by taking the Laplace transform of f, and computing the limit

$$\lim_{s\to 0} \hat{f}(d, s) = \lim_{s\to 0} \frac{R}{d} e^{-\frac{d-R}{\sqrt{D}}\sqrt{s}} = \frac{R}{d}. \tag{15}$$

We can substitute the result from (15) in (14) to get

$$\begin{bmatrix} N_1 \\ N_2 \\ \vdots \\ N_p \end{bmatrix} = \underbrace{\begin{bmatrix} 1 & \frac{R}{d_{1,2}} & \frac{R}{d_{1,3}} & \cdots & \frac{R}{d_{1,p}} \\ \frac{R}{d_{2,1}} & 1 & \frac{R}{d_{2,3}} & \cdots & \frac{R}{d_{2,p}} \\ \frac{R}{d_{3,1}} & \frac{R}{d_{3,2}} & 1 & \cdots & \frac{R}{d_{3,p}} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ \frac{R}{d_{p,1}} & \frac{R}{d_{p,2}} & \frac{R}{d_{p,3}} & \cdots & 1 \end{bmatrix}^{-1}}_{\mathscr{R}} \underbrace{\begin{bmatrix} N_T \frac{R}{d_1} \\ N_T \frac{R}{d_2} \\ \vdots \\ N_T \frac{R}{d_p} \end{bmatrix}}_{\mathscr{T}}. \tag{16}$$

D. MIMO

The MIMO case occurs with multiple transmitters in the system. All of them are assumed to be pointwise. Considering their independency, we can generalize matrix $\mathscr{T}$ to multiple transmitters by introducing a new notation for the distance between each receiver and transmitter. We define the distance between $\mathcal{T}_i$ and $\mathcal{R}_j$ by ${}_i d_j$. Imposing the superposition effect on $\mathscr{T}$, we can extend it to the case of q transmitters as

$$\mathscr{T} = N_T \left[\sum_{i=1}^{i=q} \frac{R}{{}_i d_1}, \sum_{i=1}^{i=q} \frac{R}{{}_i d_2}, \ldots, \sum_{i=1}^{i=q} \frac{R}{{}_i d_p}\right]^{\mathsf{T}}. \tag{17}$$

All the derivations up to (17) can be extended to a scenario with different receivers' radius. The key for such an extension is in (8), where each row corresponds to a specific receiver.

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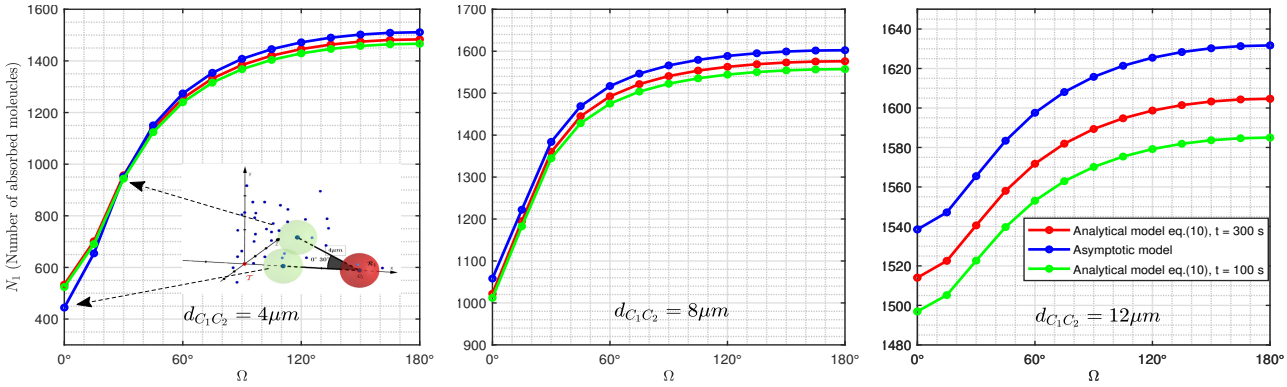

(a) (b) (c)

Fig. 3. Cumulative expected number of molecules $N_1(t)$ absorbed by $\mathcal{R}_1$ after $t \in \{100, 300\}$ seconds, in the scenario of Fig. 1 with $d_1 = 6\,\mu$m, for various positions of $\mathcal{R}_2$ identified by Ω and $d_{C_1C_2} = \{4, 8, 12\}\,\mu$m in (a), (b), and (c), respectively.

TABLE I
VALUES FOR SYSTEM PARAMETERS

Variable	Definition	Value
N_T	Number of released molecules	10^4
R	Receivers radius	1 [μm]
d_1	Distance between receiver $\mathcal{R}_1$ and transmitter	6 [μm]
D	Diffusion coefficient for the signaling molecule	79.4 [μm^2/s]

Thus, we can write each line for a receiver with an arbitrary radius. We skip the proof and just write the asymptotic results

$$\begin{bmatrix} N_1 \\ N_2 \\ \vdots \\ N_p \end{bmatrix} = \begin{bmatrix} 1 & \frac{R_1}{d_{1,2}} & \frac{R_1}{d_{1,3}} & \cdots & \frac{R_1}{d_{1,p}} \\ \frac{R_2}{d_{2,1}} & 1 & \frac{R_2}{d_{2,3}} & \cdots & \frac{R_2}{d_{2,p}} \\ \frac{R_3}{d_{3,1}} & \frac{R_3}{d_{3,2}} & 1 & \cdots & \frac{R_3}{d_{3,p}} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ \frac{R_p}{d_{p,1}} & \frac{R_p}{d_{p,2}} & \frac{R_p}{d_{p,3}} & \cdots & 1 \end{bmatrix}^{-1} \begin{bmatrix} N_T \sum_{i=1}^{i=q} \frac{R_1}{{}_id_1} \\ N_T \sum_{i=1}^{i=q} \frac{R_2}{{}_id_2} \\ \vdots \\ N_T \sum_{i=1}^{i=q} \frac{R_p}{{}_id_p} \end{bmatrix}, \quad (18)$$

where R_i is the radius of the receiver $\mathcal{R}_i$, $i = 1, \cdots, p$.

IV. NUMERICAL EVALUATION AND RESULTS

This section validates the results obtained from the asymptotic model by comparing them with the particle based simulation (PBS) results for a fixed topology according to Fig. 1 and then the exact analytical expressions defined in [8], which was computed for a large value of the time ,t. Both SITO and 2×2 MIMO cases in different relative positions of the receivers are investigated. With reference to the system of coordinates defined in Fig. 1, in the two considered scenarios the position of $\mathcal{R}_1$ is fixed in $(d_1, 0, 0)$ while that of $\mathcal{R}_2$ varies based on $\Omega \in [0, \pi]$ and $d_{C_1C_2} \in \{4, 8, 12\}\,\mu$m. The angle Ω is on xy-plane. Table I reports the values of the parameters we used to obtain the results shown in the following.

To verify the derivations, Fig. 2 compares the asymptotic model with the PBS results. However, due to the computational cost of the PBS we only run the simulation to compute the cumulative number of absorbed molecules by both receivers up to 60 s with the temporal step size of 10^{-6} s. Additionally, PBS is stochastic due to the Brownian motion of the molecules thus we run the simulation 15 times. We consider the case where $d_{C_1C_2} = 4\,\mu$m and $\Omega = 90°$. Fig. 2 shows the cumulative absorbed number of molecules by the receivers over 15 trials, thin dashed lines, where the red color corresponds to $\mathcal{R}_1$ and blue color corresponds to $\mathcal{R}_2$. The thick solid lines correspond to the mean of the cumulative number of molecules absorbed by each receiver through the PBS and called mean-PBS (MPBS). In the end the horizontal lines with circular markers represent the expected asymptotic value of the cumulative number of molecules absorbed by both receivers. A very good agreement can be observed since MPBS curves converge towards the asymptotic values.

Fig. 3 shows the expected cumulative number of molecules absorbed by receiver $\mathcal{R}_1$ for the scenario depicted in Fig. 1. The green and red curves are plotted based on analytical model with accurate barycenter position from [8] when $t \in \{100, 300\}$ s. The blue curve resulted from (12) by assuming that the barycenters are located in the center of the spheres. It can be seen that the asymptotic model with the assumption that the barycenters are located in the center of the FA receivers follows the result obtained by the analytical model for a long observation time, which relies on the exact position of the barycenter point. Fig. 3a shows the expected cumulative number of absorbed molecules when the distance between the two FA receivers is $4\,\mu$m. We observe that when $\Omega = 0$, receiver $\mathcal{R}_2$ is between $\mathcal{R}_1$ and $\mathcal{T}$, thus blocking the "line-of-sight" (LOS) between them. In this case N_1 has the lowest value and then it increases as the position of $\mathcal{R}_2$ changes for higher values of Ω. This happens because $\mathcal{R}_2$ absorbs less molecules from the environment, and consequently it has less effect on $\mathcal{R}_1$. In Fig. 3b we increased the distance between the receivers. When $\Omega = 0°$, $\mathcal{R}_2$ is very close to the transmitter and located at $(-2, 0, 0)$. Receiver $\mathcal{R}_2$ absorbs molecules but in comparison with $\Omega = 0°$ at Fig. 3a, N_1 has higher value because $\mathcal{R}_2$ does not block the LOS. Moreover, for $\Omega = 90°$ and higher the variation of N_1 is not so large because $\mathcal{R}_2$ is sufficiently far from both $\mathcal{R}_1$ and transmitter thus, has less effect on N_1. Finally, in Fig. 3c the distance is increased to $12\,\mu$m. In this case, we observe that the variation of N_1 is not large due to the increase of the distance between $\mathcal{R}_2$ and $\mathcal{R}_1$. When $\Omega = 0°$, $\mathcal{R}_2$ is closer to the transmitter compared with $\Omega = 180°$ and, therefore, the value of N_1 is a little bit lower

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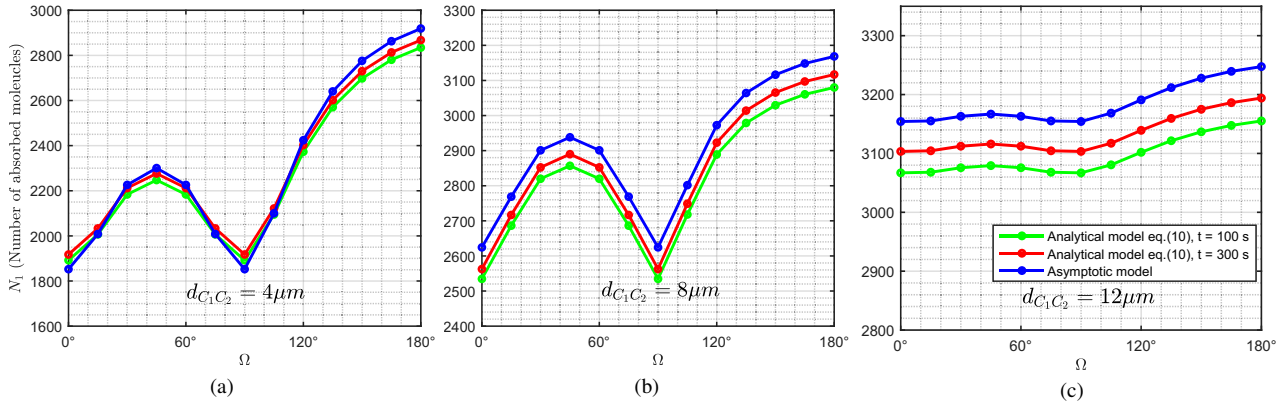

Fig. 4. Cumulative expected number of molecules $N_1(t)$ absorbed by $\mathcal{R}_1$ after $t \in \{100, 300\}$ seconds, in the scenario of Fig. 5 with $d_1 = 6\,\mu$m and $\mathcal{T}_2 = (6, 6, 0)\mu$m, where (a), (b), and (c) corresponds to the same positions of $\mathcal{R}_2$ considered in Fig. 3 .

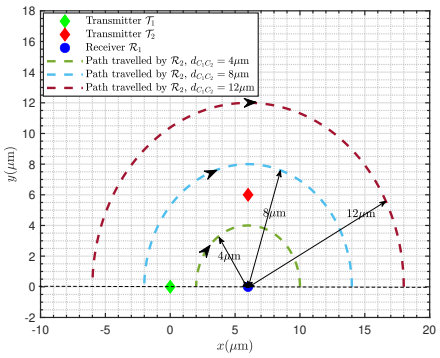

Fig. 5. A 2D perspective of the simulation scenario with two transmitters and two receivers. The dashed lines represents the travelled path by $\mathcal{R}_2$ for different $d_{C_1C_2}$.

than that at $\Omega = 0°$.

Fig. 4 shows the expected cumulative number of molecules absorbed by $\mathcal{R}_1$ for the topology depicted in Fig. 5, where a second pointwise transmitter is present. The results show that our model is able to capture the reciprocal effect of FA receivers in a MIMO scenario. Here, it is assumed that the second transmitter, $\mathcal{T}_2$ is located at $(6, 6, 0)\mu$m. The position of the second transmitter was chosen because it can easily highlight the blocking effect associated with the movement of $\mathcal{R}_2$ from $\Omega = 0°$ to $\Omega = 180°$. As for the previous scenario, in Fig. 4a we can observe a good agreement between our asymptotic model and the exact analytical expected cumulative number of absorbed molecules. Figs. 4b and 4c demonstrate the correctness of the dynamic behavior of the asymptotic model. For these two latter cases we do not have any blocking effect, thus the cumulative number of absorbed molecules is higher and this demonstrates the validity of our model.

V. Conclusion

We derived an analytical model that captures the expected asymptotic value of the cumulative number of molecules absorbed by each receiver in a diffusive MIMO molecular communication (MC) system. The model is validated by comparing it with the results obtained by solving the system of equations that describes the exact analytical model that takes into account the reciprocal effect among the fully absorbing (FA) receivers. In the exact analytical model each FA receiver is described as a pointwise negative source of molecules. The best position of the pointwise negative sources is the barycenter defined by the given geometry. We show that in the temporal asymptotic case the effect of the interfering receivers can be described by approximating their barycenters with the centers of the spheres.

The proposed asymptotic model opens the ways to the investigation of many problems in diffusive MC systems based on the use of multiple FA receivers such as, target localization and sensing based on the number of absorbed molecules that are measured for a temporal interval that is long enough.

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