Silent Target Localization Using Molecular Diffusion

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***Abstract*—In this paper, we propose a molecular communication system to localize an abnormality in a diffusion based medium. We consider a general setup to perform joint sensing, communication and localization. An application of this setup is targeted drug delivery. This setup consists of three types of devices: *mobile sensors* for navigation and molecule releasing, *fusion centers* for sampling, amplifying and forwarding the signal, and a *gateway* for making decision or exchanging the signal with an external device. The sensors move randomly in the medium to reach the abnormality and transfer their sensory data to the FCs. The decision rules and probabilities of error are obtained for two considered sensors types (collaborative and non-collaborative).**

I. Introduction

Molecular communication (MC) is a new communication paradigm, where the molecules or ions are used as information carriers. MC has been proposed as a promising approach in variety of applications. For example, the abnormality detection in medical applications has been received increasing attention in recent years [1], [2]. The goal of these works is detecting the virus, tumors, or unhealthy cells in human body by means of nanomachines. If an abnormality is detected, the next step would be treatments such as drug delivery, targeted therapy, and nanosurgery [3]. An intermediate step which is necessary between detection and therapy is tracking the target or abnormality localization, in order to improve the efficiency of surgery and other therapies [3].

In some scenarios of abnormality localization, physical access to the abnormality point is not feasible and the target either does not release molecules or the concentration of its released molecules becomes very low at the receivers, such that it is detectable only at the vicinity of the target [4]. A solution is to use mobile sensors that reach the target and send their sensory data to receivers by releasing molecules there [2], [5], [6]. The goal of these works is tracking a fixed or mobile target [2], [5], or localizing a fixed one [6]. [2] considers a two dimensional (2-D) bounded area where two types of nanomachines can move with Brownian motion. When the first type reaches the target, it releases molecules to guide the second type, who delivers the drug to the target location. In [5], a new type of nanomachines is added to the above model to amplify the number of molecules, improving the accuracy of target tracking. In [6], a macro-scale cylindrical and fluidic medium is considered, where the sensors are used to detect the abnormality, being activated and releasing molecules. The fusion center (FC) localizes the abnormality using the sensors status and received molecules.

In the following, we outline our proposed system that the full version and proofs are provided in [8]. We consider a general setup to perform joint sensing, communication, and localization of a silent abnormality in a 2-D $w \times w$ area with no flow, where the abnormality has been previously detected. We assume that the sensing operation is ideal, and an abnormality exists at an unknown location $\overrightarrow{sJ} = [s_x, s_y]^T$. Our localization framework consists of three types of devices used in four phases as shown in Fig. 1: some mobile sensors, a few FCs (i.e., FC_i, $i \in \{1, 2, 3\}$), and a gateway. The sensors can be some biological cells, bacteria, or artificial nano-scale machines [2], [3], and each one stores M molecules. Phase (1): The sensors move in the medium randomly and sense the variations in their vicinity. After sensing an abnormal variation, they stop and get activated. Phase (2): The activated sensors release their molecules into the environment after a short delay. Based on the considered type of sensors, this delay can be deterministic or random. These molecules are diffused and arrive the FCs located at the vertices of the observing area. Phase (3): Each FC samples the number of received molecules in its volume at some sampling times, amplifies the samples and releases other type of molecules (called *markers*) into the medium, which will be diffused in the medium to reach the gateway. Phase (4): The gateway may convert the molecular signal into the electromagnetic wave to be transmitted to an external device, or it may have the sufficient computing capabilities to process the molecular signal itself and make decision about the abnormality location. We assume that the channels of Phases (3) and (4) are ideal.

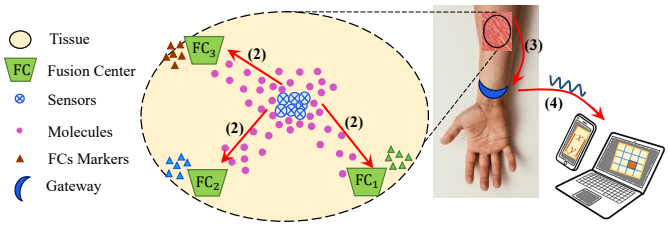

Fig. 1. The Phases (2), (3) and (4) are shown [8].

II. System Model

We consider two types of sensors: 1) collaborative sensors, which release the molecules when their activated number reach a threshold, N_{th}, (e.g., some bacterias that behaves socially based on Quorum sensing), and 2) non-collaborative sensors, which release the molecules after a deterministic time duration (e.g., some artificial nanomachines that have limited energy for their motions). Therefore, the number of sensors that release molecules, N_r, is deterministic and random for the collaborative and non-collaborative sensors, respectively. If D is the

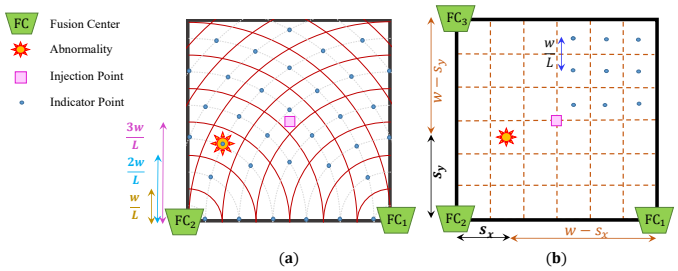

Fig. 2. Clustering for (a) collaborative, (b) non-collaborative sensors

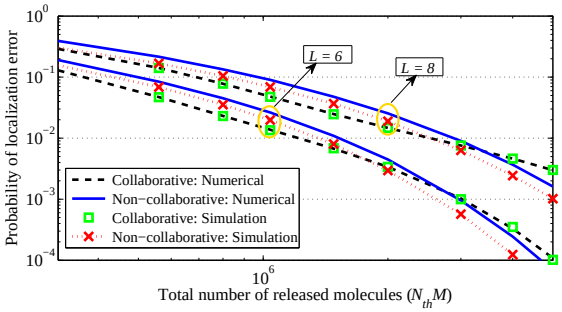

Fig. 3. The probability of error vs. total number of released molecules [8].

diffusion coefficient of molecules in the medium, and d_i be the distance between FC_i and the releasing point, the number of molecules observed in FC_i volume, V_F, after a time duration of τ is a normal distribution as $Y_i \sim \mathcal{N}(m(d_i), m(d_i))$, where $m(d_i)$ depends on d_i^2 as [1],

$$m(d_i) = \frac{V_F N_r}{4\pi D\tau} \exp\left(-\frac{d_i^2}{4D\tau}\right), \tag{1}$$

For collaborative sensors, Y_is are used for localization. But for non-collaborative sensors, Y_is are doubly stochastic random variables, which make our analyzes difficult. To overcome this problem, we use the ratio of observations, $Z_{12} \doteq Y_1/Y_2$, and approximate it as a normal distribution, where its mean depends on s_x and is independent of N_r. Therefore, we use Z_{12} and $Z_{32} \doteq Y_3/Y_2$ to decide the s_x and s_y, respectively.

- **Clustering**: Let L be a clustering parameter, which specifies the resolution of localization. For the collaborative sensors, the abnormality is localized based on its relative distances to $\text{FC}_i, i = 1, 2$. We consider intervals of length w/L for distance d_i. Therefore, the observing area is partitioned into some clusters as Fig. 2 (a). Note that the shape of clusters are different and we do not know the abnormality distribution in each one. Thus, we approximately assume that the abnormality is placed at the center of each cluster, called indicator point (IP), at $d_i \in \{\Delta_j | j \in \mathbb{N}\}$, where $\Delta_j = (j + 1/2)w/L$ (see Fig. 2 (a)). For the non-collaborative sensors, we localize the abnormality by deciding s_x and s_y, which are independent variables. We consider intervals of length w/L for s_x and s_y. Therefore, the observing area is partitioned into some clusters as Fig. 2 (b). The localization is performed by deciding the correct cluster from L^2 ones, i.e., $s_x, s_y \in \{\Delta_j | j = 1, \cdots, L\}$.

III. Results

For the collaborative sensors, the distribution of clusters (IPs) is unknown. Thus, we apply the maximum likelihood (ML) decision rule as $\hat{d}_i = \text{argmax}_{j\in\mathbb{N}} \Pr[Y_i | d_i = \Delta_j]$, and derive the sub-optimum thresholds to decide the abnormality location. For the non-collaborative sensors, we apply the optimal ML decision rule based on the ratio of FCs observed molecules, as $\hat{s}_x = \text{argmax}_{j\in\mathbb{N}} \Pr[Z_{12} | s_x = \Delta_j]$ (similarly for $\hat{s}_y$). It results in a threshold form. Also for both types of sensors, we derive the probability of error in a closed form.

We compare the performance of collaborative and non-collaborative sensors, for two samples at each FC and $w = 0.01\text{m}, D = 10^{-9}\text{m}^2/\text{s}, V_F = 1.11 \times 10^{-7}\text{m}^2, N_{th}M = 10^6$. To have a fair comparison we assume $N_r = N_{th}$. The probability of localization error versus the total number of released molecules, $N_{th}M$, is shown in Fig. 3. As can be seen, the non-collaborative sensors perform better than the collaborative ones when $N_{th}M$ is increased. Since the normal distribution used for the ratio of observations is more accurate for higher number of molecules. Note that for non-collaborative sensors, one more FC is used for deciding the location (see Fig. 2). For higher values of L, the number of clusters and the resolution of localization increased and thus, the error probability increases. Also, We simulate the diffusion of molecules in the medium (Phase (2)). The provided simulation results validate the numerical results.

IV. Conclusion

In this paper, we consider a general setup to localize a silent abnormality with molecular communication. We investigate the localization problem in a 2-D medium, using three types of devices: the mobile sensors, FCs, and a gateway. We consider two types of collaborative and non-collaborative sensors. For both types of sensors, we apply the ML decision rule and derive the thresholds and probabilities of error in closed forms. The proposed model can also be extended into a 3-D environment easily by utilizing one more FC.

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