Joint Sensing, Communication, and Localization of a Silent Abnormality Using Molecular Diffusion

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Abstract—In this article, 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. This setup consists of three types of devices, each for a different task: mobile sensors for navigation and molecule releasing (for communication), fusion centers (FCs) for sampling, amplifying, and forwarding the signal, and a gateway (GW) for making decision or exchanging the information with an external device. The sensors move randomly in the environment to reach the abnormality. We consider both collaborative and noncollaborative sensors that simultaneously release their molecules to the FCs when the number of activated sensors or the moving time reaches a certain threshold, respectively. The FCs amplify the received signal and forward it to the GW for making a decision using either an ideal or a noisy communication channel. A practical application of the proposed model is drug delivery in a tissue of the human body, to guide the nanomachine-bound drug to the exact location and so to eliminate the adverse effects of the drug on normal cells. Further applications are health-care, treatments of localized disease (e.g., tumors and inflammations), immune system triggering, and nanosurgery. The decision rules and probabilities of error are obtained for two considered sensor types in both ideal and noisy communication channels.

Index Terms—Abnormality localization, cooperative mobile sensors, molecular communication (MC), silent abnormality.

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 for abnormality detection and localization in a variety of applications in biotechnology, medicine, and industry, such as air pollutant monitoring, agriculture, abnormality detection, and drug delivery [1]. For example, abnormality detection in medical applications has received increasing attention in recent years [2], [3], [4], [5], [6]. The goal of these works is to detect the virus, bacteria, infectious microorganisms, or tumors in the body using static [2], [3], [4] or mobile nanomachines [5], [6]. After the abnormalities being detected, the next step would be making treatments for instance using drug delivery, targeted therapy, nanosurgery, regenerative medicine, and tissue engineering [7].

An intermediate step that is necessary between detection and therapy is tracking the target or abnormality localization. This step is crucial to realize the accurate location of the abnormality, eliminate the adverse and side effects of the drug on the other normal cells, and enhance the resolution of abnormality before the surgery and other therapies [7], [8], [9]. Furthermore, in drug delivery applications, it is of crucial importance to find the current locations of the nanomachine carrying the drug as well as their destination (target point) [10]. Moreover, in health-care applications for localized diseases (e.g., tumors and inflammations), finding the location of abnormality is an essential step in treatments, such as immune system triggering, nanosurgery, and tissue engineering in regenerative medicine [7]. Some examples are localizing the unhealthy cells around the capillaries [11], guiding the nanorobots in the human body to the target sites needing treatment [5], [12], [13], and drug delivery, where the drug can be bounded to the mobile nanomachines to be delivered at the target location [9], [10], [14], [15].

In this article, we focus on the abnormality localization in a 2-D microscale medium, without any physical access to each point of it. We use mobile sensors to transmit the location information to the outside environment.

A. Related Works

Using MC setups to localize abnormality has been studied in different scenarios. Some previous works study a scenario, where the target abnormality is a point source that releases molecules into the medium [11], [15], [16]. The goal is to estimate the distance of or localize this target using receivers, that observe the number of received molecules. We call this type of target as molecule releasing targets. In [15], the localization problem is considered in a 3-D environment with three receivers. The target is a point source with impulsive releases. This work proposes an iterative numerical localization method for two cases of known and unknown receivers’ locations. Turan et al. [11] considered a vessel-like medium with a flow and obtained the abnormality location based on the mean peak concentration of received molecules at the receivers. However, the method of obtaining this mean
is not discussed. Gulec and Atakan [16] considered a 3-D environment where the droplets are used as information carriers. They predict the distance using a fluid dynamics algorithm and validate their results with experimental data.

In some scenarios, the target does not release any molecules, but it absorbs the molecules released from a transmitter. Therefore, the concentration of molecules at the receiver is decreased in the presence of the target [17], [18]. We call this type of target as molecule absorbing targets. Kose et al. [17] applied a machine learning method to localize the target using the number of absorbed molecules by the receiver. Bao et al. [18] proposed an algorithm for target localization based on the maximum-likelihood estimation (MLE) method.

In other scenarios, 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 in the vicinity of the target [19], [20]. We call this type of target as silent targets. A solution is to use mobile sensors that reach the target (called navigation) and send their sensory data to receivers by releasing molecules there [6], [21], [22], [23]. This approach is used in both microscale [6], [21], [22] and macroscale applications [23]. The abnormality navigation has two stages. In the first stage, the mobile sensors, injected into the environment, are seeking the variations in the medium to find the target; this stage is called functional navigation [12]. The mobile sensors transfer the sensory data to fusion centers (FCs), which are used to locate the abnormality. Then, to deliver the drug to the abnormality location, the drug is bound to the nanomachines, that know the abnormality location and walk in the determined route to reach the abnormality [8], [13], [24]. This stage is called positional navigation [12].

The goal of works on the third scenario is tracking a fixed or mobile target [6], [21], [22], or localizing a fixed one [23]. Nakano et al. [6], [21] considered a 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 a second type of nanomachines. The drug is delivered to the target location by the second type to decrease the side effects. In [22], a new type of nanomachines is added to the above model to move randomly and amplify the concentration of molecules in the environment, and hereby improve the accuracy of target tracking. In [23], the detection and localization problems are considered in a macroscale cylindrical and fluidic environment, with laminar flow condition (advection–diffusion channel). The sensors are injected into the medium to move along the channel and detect the silent abnormality. Then, they are activated and release their molecules. Because of flow velocity, all sensors reach the FC, where the abnormality localization is performed using the sensors’ status and the received molecules.

The existing works on target localization, which are reviewed in this section are classified based on different aspects (see Table I).

### B. Our Contribution

In this article, we propose a scheme for silent abnormality localization in a diffusive medium (SALDIM). We consider a general setup to perform joint sensing, communication, and localization of a silent abnormality in a 2-D environment with no flow, where the abnormality has been previously detected. To the best of our knowledge, the silent target localization problem in a diffusive medium has not been previously considered (see Table I). As can be seen in Table I, the goals of SALDIM, [15], [17], and [18] are localization. In SALDIM, the target does not release or receive molecules, but the type of target in [15] is a molecule source and in [17] and [18] is molecule receiver. Furthermore, in SALDIM, we obtain the analytical results but [15], [17], and [18] provide the numerical methods and/or iterative algorithms. We propose a multtier MC network to localize an abnormality in a medium without any physical access to it, and then to transmit the sensory information to the outside environment. We use three types of devices used in four phases and obtain the analytical results.

We consider a target that is identifiable by sensors used in our setup; this is feasible since the target can act as a source of changes in some environmental parameters, such as temperature, PH level, and concentration of a biomarker in the medium. In the first case, the sensors interact with the target surface receptors and identify it, and in the second case, the target releases some molecules in the medium, where the sensors can detect them in the vicinity of the releasing point [6]. In medical applications, for example, in drug delivery, this abnormality can be inflammation, tumor, and other unhealthy cells.

Our localization framework consists of three types of devices used in four phases as shown in Fig. 1: some mobile sensors, a few FCs, and a gateway (GW). The sensors can be some biological cells, bacteria, proteins, amino acids, lipids, viruses, or artificial nanoscale machines [6], [7].

| Phase (1): | The sensors move in the medium randomly and sense the variations in their vicinity. After sensing an abnormal variation, |
| Phase (2): | The sensors send their data to fusion centers (FCs) and then to the gateway (GW). |
| Phase (3): | The FCs process the data and identify the abnormality. |
| Phase (4): | The gateway transmits the information to the outside environment. |

1In some previous works, this type of target is called silent abnormality. But in our classification, the silent abnormality is a different type.

2We assume that the sensing operation is ideal.
they stop and get activated. Phase (2): The activated sensors release their stored molecules into the environment after a short delay. Based on the considered type of sensors (noncollaborative and collaborative), 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 into the medium. These new released molecules will be diffused in the medium to reach the GW. Phase (4): The GW may convert the molecular signal into the electromagnetic (EM) wave to be transmitted to an external device [8], [24] (i.e., computer, laptop, and smartphone), or it may have the sufficient computing capabilities to process the molecular signal itself and make decision about the abnormality location. First, we study the case of the ideal communication channel between the FCs and GW (i.e., noiseless).

1) For the collaborative sensors, we use two FCs. Based on relative abnormality distances to the FCs, we partition the observing area into some clusters to localize the abnormality. We obtain the maximum-likelihood (ML) decision rule and derive the suboptimum thresholds to decide the abnormality location. Then, we derive the probability of error in a closed form.

2) For the noncollaborative sensors, we need three FCs for localization. The observations of FCs are doubly stochastic random variable (RVs). To overcome the difficulty of working with these RVs, we consider the ratio of observations and approximate the new RV with a normal distribution. We apply the optimal ML decision rule based on the ratio of FCs observed molecules, which results in a threshold form. Also, we derive the optimal thresholds and the probability of error.

3) We also study the noisy communication channel between the FCs and GW. To simplify the equations, we assume that all FCs have equal distances to the GW. To overcome the difficulty of working with doubly stochastic RVs, we approximate the random samples of FCs by their mean and obtain the decision rules and probabilities of error.

The remainder of this article is organized as follows. In Section II, the system model is described. Then, the localization problem is investigated for two considered sensor types in Sections III and IV, by obtaining the decision rules and probabilities of error in the case of the ideal channel between the FCs and GW. The case of the noisy channel is analyzed in Section V. The numerical and simulation results are provided in Section VI. Finally, this article is concluded in Section VII.

II. SYSTEM MODEL

We consider a 2-D environment and a \( w \times w \) bounded area \( A = \{[x, y]^T | 0 \leq x \leq w, 0 \leq y \leq w\} \). We assume that an abnormality exists at an unknown location \( \bar{X}^T = [s_x, s_y] \in A \) and the location of abnormality is distributed uniformly in \( A \). We also assume that the abnormality does not release enough molecules itself.\(^3\) Our goal is to localize the abnormality in some resolution. We divide area \( A \) into some clusters, which are described in the next sections.

We use three types of devices: some mobile sensors, a few FCs, and a GW. The functionalities and properties of these devices are described in the following.

1) Mobile Sensors: We utilize \( N_m \) mobile sensors, which are injected into the medium at time \( t = 0 \) from the center of the observing area,\(^4\) \( C = [w/2, w/2]^T \). They can move in the area randomly. If a sensor reaches the boundaries, it is reflected back into the area. The sensors measure an environmental parameter (such as temperature, PH level, and concentration of a biomarker) and are activated by the changes in this parameter at the abnormality location compared with the normal points. Each sensor has a molecular storage where it can store \( K \) types of molecules; \( M \) molecules from each type. Note that all sensors have stored the same \( K \) types of molecules. For simplicity, we assume the diffusion coefficients of all these types of molecules in the medium are the same and equal to \( D \).

2) Fusion Centers: We use two or three fixed FCs (FC\(_i\), \( i \in \{1, 2\} \) or \( i \in \{1, 2, 3\} \)) depending on the types of sensors, which will be explained later. The FCs are located at three vertices of the observing area \( A \), as shown in Fig. 2. Each FC\(_i\) has a transparent receiver with the

\(^3\)It may release some molecules but their concentration is very low, detectable only in the vicinity of the abnormality point, not in the early stage.

\(^4\)Or any arbitrary point in the observing area.
ability to receive the sensors molecules with volume $V_F$. Each FC$_i$ stores $K_{FC}$ types of molecules, different from sensors’ molecules. We call the FCs molecules as markers. These markers are used to transfer the gathered sensory data to the GW. Each FC includes a transmitter that controls the number of its released markers. An example of this model is proposed in [25] and [26], where the transmitter has a molecule storage with some surface outlets. The number of released molecules is a Poisson RV whose parameter is determined by the opening size of the outlets [25]. This size is controlled by a gating parameter signal, which is voltage or ligand concentration in [26].

3) Gateway: The GW is located far from the observing area; for example, for the in-body applications, at a close point to the skin. It receives the FCs markers in its observing volume $V_G$, at its sampling times. The GW has a larger volume and more computational capabilities compared to the FCs. Thus, it decides the abnormality location itself or converts its observed samples into an EM wave and transmits it to an external device for decision making. Yang et al. [27] proposed an implemented graphene-based nanodevice, which can convert the molecular signal to an electrical signal. In [24], a smart wristband or other interfaces are used to interconnect the in-body MC and the external environments. For simplicity, we assume that the distances between the GW and all FCs are equal.

Using the above three types of devices, our proposed abnormality localization setup consists of four phases. The outline of these phases is as follows. The sensors move in the observing area. When a sensor reaches the abnormality, it gets activated and releases its stored molecules in the medium, which are received by the FCs. They amplify and forward the received molecular signal to the GW, where either a decision is made or a signal is transmitted to an external device. One of the practical applications of this model is drug delivery in a tissue of the human body, where the goal is to guide the nanomachines-bound drugs to the exact location in order to eliminate the adverse side effects of the drug on the normal cells around the abnormality. Thus, a localization step (functional navigation) is necessary before guiding the nanomachines to the target (positional navigation). In the following, these phases are described in more detail.

1) Phase (1): The sensors move randomly in the observing area and sense the medium, looking for the abnormality by measuring an environmental parameter. When a sensor reaches the abnormality location, it gets activated and stops moving. We denote the number of activated sensors by $N_r$.

2) Phase (2): The activated sensors release all of their stored molecules into the medium from the abnormality location to be received at the FCs (shown in Fig. 1). The types and number of released molecules are the same for all sensors. These sensors will be degraded in the medium after releasing their molecules.

3) Phase (3): The molecules released by the activated sensors diffuse in the medium and some of them reach the FCs. Each FC has $K$ types of receptors to receive all $K$ types of released molecules. It samples the number of molecules in its volume at some sampling times, amplifies the samples, and noninstantaneously releases its markers into the medium, where the number of released markers is proportional to its received samples. We remind that each FC has a different type of markers. As mentioned before, this number is controlled with a gating parameter, such as voltage or ligand concentration. Unlike the amplification process in [30], our FCs do not require the full-duplex mode and perfect time synchronization with the sensors. It means that the release time and duration of the FCs may be different from the sensors. Thus, an FC can send its $K$ samples to the GW in one of these two ways: 1) using only one type of markers (i.e., $K_{FC} = 1$) and $K$ time slots to send FC

We consider two different types of sensors based on their molecule releasing scheme, described as follows.

a) Collaborative Sensors: The sensors used in microscale MC are engineered cells, bacteria, or artificial nanomachines. Some engineered bacteria behave socially based on Quorum sensing [28], [29]. It means that they simultaneously respond to an environmental change by cooperating with each other. For example, when the concentration of some signaling molecules around them reaches a critical threshold, they respond together. We consider a time-slotted system with a slot duration of $T$ and the activated sensors cooperate in signaling time durations of $T_{sig}$, where $T_{sig} < T$. When the number of activated sensors reaches a threshold $N_{th}$, the signaling is finished (we denote this time by $t_r$). The $N_{th}$ sensors release their stored molecules into the medium at the beginning of the next time slot (at $t = nT$, where $n \in \mathbb{N}$ and $(n - 1)T < t_r \leq nT$). Therefore, in this case, $N_r$ is a fixed number and equals $N_{th}$. But, the time of this event (releasing time), $t_r$, is not deterministic. For this type of sensors, two FCs (FC$_i$, $i \in \{1, 2\}$) are used.

b) Noncollaborative Sensors: Another type of sensors, for example, artificial nanomachines, have limited energy storage for their mechanical motions (e.g., movements), pumping, etc. This energy may be used for missions with limited durations [12]. Thus, the sensors may have limited energy to move for a limited time duration of $T_{th}$. After this time duration, they stop, and the activated sensors, which arrive at the abnormality, release their stored molecules into the environment. For the noncollaborative sensors, $N_r$ is an RV. They release the molecules at the beginning of the next time slot (i.e., at $t = nT$, where $n \in \mathbb{N}$ and $(n - 1)T < T_{th} \leq nT$). So the releasing time of molecules is deterministic. For this type of sensors, three FCs (FC$_i$, $i \in \{1, 2, 3\}$) are used.
observations to the GW or 2) using \( K_{FC} = K \) types of markers in one time slot. Moreover, the communication channel between the FC and the GW can be considered ideal (noiseless) or nonideal (noisy). In the ideal case, there is no need to signal amplification at the FC and the GW observes the same signals as the FCs.

4) **Phase (4):** The GW receives the markers sent by the FCs. Using the number of sampled markers, the abnormality location is decided. We consider that the GW decides the abnormality location itself instead of an external device.

**Remark 1:** We wish to emphasize the following statements.

1) In our system model, we consider a bounded observing area, which is a suitable model for practical applications. We assume that the sensors do not exit this area to guarantee that enough number of sensors reach the abnormality. Without this assumption, we need more sensors.

2) The signaling time duration of collaborative sensors, \( T_{sig} \), is very short compared with the time intervals between the sensors arriving at the abnormality. Therefore, the probability of that two or more sensors simultaneously arrive at the abnormality (and being activated) is negligible.

3) The reason for using \( K \) different types of molecules for each sensor is to create \( K \) independent observations at the FCs (using \( K \) types of receptors). An alternative solution is to use sensors with one molecule type (the total number of molecules is \( K M \)) and the activated sensors release molecules in \( K \) time slots (\( M \) molecules in each time slot). The FCs receive the molecules in all these \( K \) time slots. Note that the slot duration \( T \) is sufficiently large such that the intersymbol interference (ISI) of the previous time slot is negligible, and the observations at each FC can be assumed to be independent.

4) For simplicity, we study the localization problem for a 2-D area. This model can also be extended into a 3-D environment easily by utilizing one more FC.

In the following section, we study Phases (2) and (3) for collaborative and noncollaborative sensors, where the channels between the FCs and the GW in Phase (3) are ideal (noiseless) or nonideal (noisy). We derive the decision rules and obtain the probabilities of error.

### III. Ideal Channel: Collaborative Sensors

In this section, we investigate the localization problem for collaborative sensors, with the assumption of the ideal channels between FCs and GW. As mentioned, when the number of \( N_{th} \) collaborative sensors reach the abnormality location (at time \( t_i \)), they get activated and each one releases its stored molecules into the environment at \( t = nT \), where \( n \in \mathbb{N} \) and \( (n-1)T < t_i \leq nT \). Since \( t_i \) is not deterministic for the collaborative sensors, \( n \) is an RV. As each activated sensor releases all its stored molecules (\( M \) molecules of each type), the total number of \( N_{th}M \) molecules of each type is released by all activated sensors. Note that there are \( K \) types of molecules. The FCs sample the number of molecules observed in their volume, at sampling time \( t_s = nT + T_{obs} \), where \( T_{obs} \) is the observing time, which is obtained later. We denote the number of \( k \)th type of molecules observed at FC \( i \) by \( Y_i^k \). Since \( n \) is an RV, the FC does not know its realization to decide the sampling time. Thus, it observes the molecules in all time slots \( (n = 1, 2, \ldots) \) as long as \( Y_i^k > 0 \). If we denote the distance between the FC \( i \) and the abnormality point by \( d_i \) (i.e., \( d_i = \|FC_i - \gamma_i\|_2 \)), the probability of a molecule to be observed at \( t_s \) in the receiver volume at FC \( i, i \in \{1, 2, 3\} \) is\(^6\) [31]

\[
\mu(d_i, t_s - nT = T_{obs}) = \frac{V_F}{(4\pi DT_{obs})^{3/2}} \exp\left(-\frac{d_i^2}{4DT_{obs}}\right) \tag{1}
\]

where \( N \) is equal to the dimension of the observing area, which is \( N = 2 \) in our system. Each FC \( i \) obtains \( K \) independent samples as \( \{Y_i^1, Y_i^2, \ldots, Y_i^K\} \), by sampling \( K \) types of molecules, where \( Y_i^k \sim Binomial(N_{th}M, \mu(d_i, T_{obs})) \) for \( k = 1, \ldots, K \). Since the number of released molecules \( M \) is large enough, the Binomial distribution can be approximated by a Gaussian distribution as \([32, p. 105]\)

\[
Y_i^k \sim \mathcal{N}(N_{th}M\mu(d_i, T_{obs}), N_{th}M\mu(d_i, T_{obs})) \tag{2}
\]

where \( \mathcal{N}(\eta, \sigma^2) \) indicates the Gaussian distribution with a mean of \( \eta \) and variance of \( \sigma^2 \). The best observing time is the peak time of the concentration of molecules, which is obtained from (1) as

\[
T_{obs} = \frac{d_i^2}{2ND} \tag{3}
\]

From the above equation, the observing time depends on the distance between the releasing and receiving points of molecules (i.e., \( d_i \)). As mentioned, the releasing point is the abnormality location, which is unknown for the FCs. We choose a sampling time assuming that the abnormality locates at the center of the observing area \( A \). Thus, we assume \( d_i = (w\sqrt{2}/2) \) and thus the observing time is \( T_{obs} = (w^2/4ND) \). By defining \( m(d_i) \triangleq N_{th}M\mu(d_i, [w^2/4ND]) \), (2) results in

\[
Y_i^k \sim \mathcal{N}(m(d_i), m(d_i)) \tag{4}
\]

Each FC \( i \) observes \( K \) samples by receiving \( K \) molecule types (released from the abnormality point), at the sampling time \( t_s \) (i.e., \( Y_i^k \), for \( k = 1, \ldots, K \) and \( i = 1, 2 \)). The mean of distribution in (4), \( m(d_i) \), is a function of \( d_i \). Therefore, the distance between FC \( i \) and the abnormality point \( (d_i) \) can be obtained by using the number of FCs’ sampled molecules. Note that each point in the bounded observing area \( A \) can be uniquely presented by its distances to FC1 and FC2. To localize the abnormality, we cluster the observing area as follows.

**Clustering:** The abnormality can be located by obtaining the distances \( d_1 \) and \( d_2 \). Let \( L \) be a clustering parameter and \( L \in \mathbb{N}, L \geq 2 \). We consider intervals of length \( (w/L) \) for distance \( d_i, i \in \{1, 2\} \) as \( \{j(w/L) \leq d_i < (j + 1)(w/L) | j = 0, 1, \ldots\} \). By defining \( \beta_j = j(w/L) \). Therefore, the observing area is partitioned into some clusters as shown in Fig. 3 and the localization is performed by deciding the correct cluster, where the abnormality exists. Note that the shapes of clusters

\(^6\)We assume that the volume \( V_F \) is small enough, such that the concentration of molecules in this volume is uniform.
are different and we do not know the abnormality distribution in each cluster. Thus, we approximately assume that the abnormality is placed at the center of each cluster, as shown in Fig. 3. We call these points as indicator points (IPs), which are placed at distance \( d_i \in \{ r_j = (j + (1/2))(W/L) | j = 0, 1, 2, \ldots \} \) from FC \( i \) \((i \in \{1, 2\})\). To localize the abnormality with higher resolution, we should choose a higher value of \( L \) (clusters with a smaller area), as our numerical results indicate.

### A. Decision Rule

Each FC amplifies the samples and transmits them to the GW. The obtained number of markers by the GW from FC \( i \) is denoted as \( W_i = \{W_i^1, W_i^2, \ldots, W_i^K\} \), corresponding to \( K \) samples of FC \( i \). Note that in this section, we assume that the communication channels between the FCS and GW are ideal (noiseless). Thus, the GW observes the same samples as the FCSs, i.e., \( W_k = Y_{k}^i(\text{for} k = 1, \ldots, K) \).

As shown in Fig. 3, the IPs are probable points for the abnormality location. If we show the distances between an IP and FC \( i \) by \( d_i \in \{ d_i \in \{ r_j = (j + (1/2))(W/L) | j = 0, 1, 2, \ldots \} \) from FC \( i \) \((i \in \{1, 2\})\), the location can be found at the GW by the ML decision rule as

\[
\hat{d}_i = \arg \max_{r_j=1,2,\ldots} P(W_i^1, W_i^2, \ldots, W_i^K|d_i = r_j) = \arg \max_{r_j=1,2,\ldots} P(Y_i^1, Y_i^2, \ldots, Y_i^K|d_i = r_j). \tag{5}
\]

As mentioned before, \( K \) observations are obtained by sampling different types of molecules. Thus, \( Y_1^1, \ldots, Y_i^K \) are independent, and thus

\[
P(Y_i^1, \ldots, Y_i^K|d_i = r_j) = \prod_{k=1}^{K} P(Y_i^k|d_i = r_j) \\
= \frac{1}{\sqrt{2\pi m(r_j)}} \exp\left(-\frac{\sum_{k=1}^{K} (Y_i^k - m(r_j))^2}{2m(r_j)}\right) \tag{a}
\]

where (a) results from (4). By substituting the above equation in (5) and using some simplifications, (5) is reduced to

\[
\hat{d}_i = \arg \min_{r_j=1,2,\ldots} K \ln(m(r_j)) + \frac{\sum_{k=1}^{K} (Y_i^k - m(r_j))^2}{m(r_j)}. \tag{6}
\]

To further simplify (6), we propose a suboptimal and efficient method by comparing two probable IPs with distances \( r_{j_1} \) and \( r_{j_2} \) from FC \( i \) in the following. Using (6), we have

\[
K \ln(m(r_{j_1})) + \frac{\sum_{k=1}^{K} (Y_i^k - m(r_{j_1}))^2}{m(r_{j_1})} \\
K \ln(m(r_{j_2})) + \frac{\sum_{k=1}^{K} (Y_i^k - m(r_{j_2}))^2}{m(r_{j_2})}.
\]

Noting that \( r_{j_1} < r_{j_2} \), the above decision rule is simplified as

\[
\sum_{k=1}^{K} \left(Y_i^k \right)^2 \frac{\hat{d}_i = r_{j_1}}{m(r_{j_1})} + \frac{\ln \left(\frac{m(r_{j_1})}{m(r_{j_2})}\right)}{m(r_{j_1}) - m(r_{j_2})}. \tag{7}
\]

The right-hand side of (7) is a threshold that depends on distances \( r_{j_1} \) and \( r_{j_2} \), defined as

\[
\tau(r_{j_1}, r_{j_2}) = \ln \left(\frac{m(r_{j_1})}{m(r_{j_2})}\right) \frac{1}{m(r_{j_1}) - m(r_{j_2})}. \tag{8}
\]

Therefore, the proposed suboptimal method compares the sum squares of samples with a threshold \( \tau(r_{j_1}, r_{j_2}) \). In the following section, we derive the probability of error.

### B. Probability of Error

Assume that the distances of abnormality point from FC \( i = 1, 2 \), the probability of error is

\[
P_e = 1 - \sum_{(x_1, x_2) \in \Psi} P(d_1, d_2 = (x_1, x_2) | (d_1, d_2) = (x_1, x_2)) \times P(d_1, d_2 = (x_1, x_2)). \tag{9}
\]

As observations at FC \( 1 \) and FC \( 2 \) given in (4) are independent, we have

\[
P(d_1, d_2|d_1, d_2) = P(d_1|d_1, d_2)P(d_2|d_2, d_1)
\]

where \( P(.) \) represents the probability mass function (PMF). As the decision on \( d_1 \) only is made based on \( d_1 \), conditioned on \( d_1 \), \( d_1 \) is independent of \( d_2 \). Thus, \( p(d_1|d_1, d_2) = p(d_1|d_1) \). Similarly, \( p(d_2|d_2, d_1) = p(d_2|d_2) \). Therefore, (9) results in

\[
P_e = 1 - \frac{1}{N_p} \sum_{(x_1, x_2) \in \Psi} \prod_{i=1,2} P(d_i = x_i | d_i = x_i) \tag{10}
\]

where from (8) we have

\[
P(d_i = x_i | d_i = x_i) = P\left(\tau(x_i + \frac{w}{2}, x_i) < \sum_{k=1}^{K} \left(Y_i^k | d_i = x_i\right)^2 < \tau(x_i, x_i - \frac{w}{2})\right).
\]

To simplify (11), we obtain the distribution of \( \sum_{k=1}^{K} \left(Y_i^k | d_i = x_i\right)^2 \). \( Y_i^k | d_i = x_i \) has a Gaussian distribution as
\( N(m(x_i), m(x_i)) \), where its mean is not zero. Now, we write (11) as
\[
P[\hat{d}_i = x_i|d_i = x_i] = \frac{1}{m(x_i)} \sum_{k=1}^{K} \left( \frac{Y_i^k}{\sqrt{m(x_i)}} \right)^2 \mathcal{N} \left( \frac{\tau(x_i, x_i - w)}{m(x_i)} \right).
\]
(12)

All \( (Y_i^k|d_i = x_i) \)s have the same variance of \( m(x_i) \). Therefore, \( \sum_{k=1}^{K} (Y_i^k|d_i = x_i/\sqrt{m(x_i)})^2 \) has a noncentral Chi-squared distribution, using Lemma 1 in the Appendix. Thus, we write (12) as
\[
P[\hat{d}_i = x_i|d_i = x_i] = Q_{\frac{\tau(x_i, x_i - w)}{m(x_i)}}(\sqrt{m(x_i)}, \sqrt{\frac{\tau(x_i, x_i + w)}{m(x_i)}}).
\]
(13)

The probability of localization error is obtained by substituting (13) in (10).

IV. IDEAL CHANNEL: NONCOLLABORATIVE SENSORS

In this section, we investigate the localization problem for noncollaborative sensors, with the assumption of the ideal channels between FCs and GW. Thus, the GW observes the same samples as the FCs (i.e., \( W_i^k = Y_i^k \) for \( k = 1, \ldots, K \) and \( i \in \{1, 2, 3\} \)). We denote the number of noncollaborative sensors that reach the abnormality location at the stop time by \( N_r \), which is an RV. These sensors release their stored molecules into the environment at \( t = nT \), where \( n \in \mathbb{N} \) and \( (n-1)T < T_{obs} \leq nT \). So \( N_rM \) molecules of each type are released, and the FCs’ sampling times are deterministic as \( t_s = nT + T_{obs} \). The number of received molecules is a Gaussian RV as (4), where \( m(d_i) = MN_r\mu(d_i, T_{obs}) \) and \( i \in \{1, 2, 3\} \). In this section, our goal is to find the abnormality location \( \hat{y}_j = [s_x, s_y]^T \). As illustrated in Fig. 2, we have
\[
\begin{align*}
d_1^2 &= \left( \frac{FC_1 - \hat{y}_j}{s_x} \right)^2 = (w - s_x)^2 + s_y^2, \\
d_2^2 &= \left( \frac{FC_2 - \hat{y}_j}{s_y} \right)^2 = s_x^2 + s_y^2, \\
d_3^2 &= \left( \frac{FC_3 - \hat{y}_j}{s_y} \right)^2 = s_x^2 + (w - s_y)^2.
\end{align*}
\]

**Clustering:** We localize the abnormality by deciding \( s_x \) and \( s_y \). These variables are dependent. We consider intervals of length \( (w/L) \) for \( s_x \) and \( s_y \), as \( [j(w/L)] \leq s_x, s_y < (j + 1)(w/L)] \) for \( j = 0, 1, \ldots, L - 1 \). Therefore, the observing area is partitioned into some clusters as shown in Fig. 2, and the localization is performed by deciding the correct cluster, where the abnormality exists. Note that in this case, the shapes of clusters are the same. Thus, the abnormality location is distributed uniformly in each cluster. We approximately assume that the abnormality would be located at the IPs placed at \([i - (1/2)](w/L), (j - (1/2))(w/L)]^2 \), where \( i, j \in \{1, \ldots, L\} \) as shown in Fig. 2. To localize the abnormality with higher resolution, we should choose a higher value of \( L \) (clusters with a smaller area), as our numerical results indicate.

Our approach is to find \( s_x \) using the observations of FC1 and FC2, and \( s_y \) using the observations of FC2 and FC3. First, we focus on finding \( s_x \). The procedure for \( s_y \) is similar. We convert \( K \) samples into one sample by averaging and define a new RV as
\[
V_i = \frac{1}{K} \sum_{k=1}^{K} W_i^k = \frac{1}{K} \sum_{k=1}^{K} Y_i^k \\
\sim \mathcal{N}\left( \frac{m(d_i)}{1/K}, \frac{1}{K} \right).
\]

If \( \sqrt{Km(d_i)} \geq 10 \), we use Lemma 2 and define a positive RV as \( Z_{12} = (V_1/V_2) \), which has approximately a normal distribution as \( Z_{12} \sim \mathcal{N}(\mu_{Z_{12}}, \sigma_{Z_{12}}^2) \), where
\[
\mu_{Z_{12}} = \frac{m(d_1)}{m(d_2)} = \exp\left(\frac{2ws_x - w^2}{4D_{obs}}\right),
\]
(14)
\[
\sigma_{Z_{12}}^2 = \frac{m(d_1)}{Km(d_2)} \left( \frac{1 + m(d_1)}{m(d_2)} \right) = \frac{\mu_{Z_{12}}}{Km(d_2)} (1 + \mu_{Z_{12}}).
\]
(15)

Note that the mean and variance of \( Y_i^k, i \in \{1, 2, 3\} \) depend on \( N_r \), which is an RV. But the mean of \( \mu_{Z_{12}} \) is deterministic and does not depend on \( N_r \). The variance \( \sigma_{Z_{12}}^2 \) in (15) depends on \( m(d_2) \), which is the mean number of received molecules by FC2. It is an RV and its realization is unknown at FC2. In the following, we approximate \( m(d_2) \) to find \( \sigma_{Z_{12}}^2 \).

We estimate \( m(d_2) \) using the observations \( Y_i^k, k \in \{1, \ldots, K\}; \) \( m(d_2) \) is chosen as the minimizer of the mean-square error (MSE)
\[
m(d_2) \simeq \arg\min_{m} \frac{K}{k=1} (m - Y_i^k)^2 = \frac{1}{K} \sum_{k=1}^{K} Y_i^k.
\]
(16)

We use the above approximation for designing the system and deriving the decision rules, and it does not affect the performance analysis of the system (i.e., the probability of error derivations). The accuracy of this approximation is validated in Section VI.

**A. Decision Rule**

To decide the abnormality location \( (s_x, s_y) \), we define \( i_s = s_x(L/w) + 1/2 \) and \( i_y = s_y(L/w) + 1/2 \), where \( i_s \) and \( i_y \) are independently and uniformly distributed over \( \{1, \ldots, L\} \) (i.e., \( p(i_s) = p(i_y) = (1/L) \)). Thus, the optimal ML decision rule is
\[
\hat{i}_s = \arg\max_{j=1,2,\ldots} P[Z_{12} = z_{12}|i_s]
\]
where \( z_{12} \) denotes the realization of \( Z_{12} \). To find a threshold-based decision rule, we consider the log-likelihood ratio (LLR) as
\[
\Lambda(z_{12}) = \ln \left( \frac{P[Z_{12} = z_{12}|i_s]}{P[Z_{12} = z_{12}|i_s + 1]} \right).
\]
(17)

\footnote{If \( K \) is large enough and \( E[.] \) be the expectation operator, the MSE approximation tends to \( E[\Lambda] = m(d_2) \) [law of large numbers (LLN)].}
Using the normal distribution of $Z_{i12}$, (17) will be reduced into

$$
\Lambda(z_{i12}) = \ln \left( \frac{\sigma_{Z_{i12}} + 1}{\sigma_{Z_{i12}}} \right) + \frac{(z_{i12} - \mu_{Z_{i12}})^2}{2\sigma_{Z_{i12}}^2} - \frac{(z_{i12} - \mu_{Z_{i12}})^2}{2\sigma_{Z_{i12}}^2}
$$

which can be simplified as

$$
\Lambda(z_{i12}) = a\sigma_{Z_{i12}}^2 + b\gamma_{i12} + c
$$

where

$$
a = \frac{1}{2} \left( \frac{1}{\sigma_{Z_{i12}}^2} - \frac{1}{\sigma_{Z_{i12}}^2} \right)
$$

$$
b = \frac{\mu_{Z_{i12}}}{\sigma_{Z_{i12}}^2} - \frac{\mu_{Z_{i12}}}{\sigma_{Z_{i12}}^2}
$$

$$
c = \frac{1}{2} \left( \ln \left( \frac{\sigma_{Z_{i12}}^2}{\sigma_{Z_{i12}}^2} \right) + \frac{\mu_{Z_{i12}}^2}{\sigma_{Z_{i12}}^2} - \frac{\mu_{Z_{i12}}^2}{\sigma_{Z_{i12}}^2} \right)
$$

We denote the optimal threshold between $i_x$ and $i_x + 1$ by $\gamma(i_x)$, which is obtained by solving $\Lambda(\gamma(i_x)) = 0$, and the optimum decision rule is $\Lambda(z_{i12}) > 0$. Noting that $a < 0$, the decision rule is obtained as

$$
z_{i12} \overset{\sim}{\gtrless} i_x \Rightarrow \gamma(i_x) = \frac{b}{2a} + \sqrt{\left( \frac{b}{2a} \right)^2 - \frac{c}{a}}. \quad (18)
$$

So far, we have discussed the decision rule to find $\hat{s}_x = \hat{s}_x(w/L)$. Note that $\hat{s}_x = \hat{s}_x(w/L)$ can also be decided similarly by considering $Z_{i12} = (X_3/X_2)$. Then, the location of the abnormality in the observing area is obtained as $\hat{Z}_{ij} = [\hat{s}_x, \hat{s}_y]^T$.

B. Probability of Error

An error occurs when $[\hat{s}_x \neq s_x]$ or $[\hat{s}_y \neq s_y]$. Thus, we have

$$
P_e = P[\hat{s}_x \neq s_x \cup \hat{s}_y \neq s_y] = \sum_{i_x=1}^{L} \sum_{i_y=1}^{L} P[\hat{s}_x \neq s_x \cup \hat{s}_y \neq s_y | (i_x, i_y)] \cdot \mathbf{P}[i_x, i_y]. \quad (19)
$$

where $\mathbf{P}[i_x, i_y] = (1/L^2)$. Using (18), we have

$$
P[\hat{s}_x \neq s_x \cup \hat{s}_y \neq s_y | (i_x, i_y)] = P[\hat{s}_x \neq s_x \cup \hat{s}_y \neq s_y | (i_x, i_y)] = 1 - P[\gamma(i_x - 1) < z_{i12} < \gamma(i_x)] P[\gamma(i_y - 1) < z_{j12} < \gamma(i_y)]
$$

Since $Z_{i12} \sim N(\mu_{Z_{i12}}, \sigma_{Z_{i12}}^2)$, we have

$$
P[\gamma(i_x - 1) < z_{i12} < \gamma(i_x)] = Q\left( \frac{\gamma(i_x - 1) - \mu_{Z_{i12}}}{\sigma_{Z_{i12}}} \right) - Q\left( \frac{\gamma(i_x) - \mu_{Z_{i12}}}{\sigma_{Z_{i12}}} \right).
$$

$P[\gamma(i_y - 1) < z_{j12} < \gamma(i_y)]$ can be also obtained similarly.

V. NONIDEAL COMMUNICATION CHANNEL

In this section, we consider the noise of the communication channel between the FCs and GW, which is located at $s_G$. It means that the GW does not receive the same signal as the FC transmitted. In fact, the molecular signal transmitted by the FC is affected by the diffusion noise in the channel, which results the received signal (the number of received molecules) to be an RV with Gaussian distribution. This noise may cause some decision/localization errors at the GW. Each FC samples the number of received molecules in its volume at the sampling times, amplifies the samples, and noninstantaneously releases another type of molecules (called markers) into the medium, where the number of released markers is proportional to the received samples. The FC has a transmitter that controls the number of released markers. An example of this model is proposed in [25] and [26] and used in [33], where the transmitter has a molecule storage with some surface outlets. The number of released molecules is a Poisson RV. The parameter of this variable is determined by the opening size of the outlets [25]. In [26], this size is controlled by a gating parameter signal (i.e., voltage and ligand concentration).

We assume that each FC uses different types of markers to amplify and forward its received signal. The GW is a transparent receiver and has receptors of all types of markers. Thus, it receives all types of markers, independently. For simplicity, we assume that the distances between FCs and GW are the same and equal to $d_{FG}$ and the diffusion coefficients for all types of markers are the same and equal to $D_2$.

In the following sections, we investigate the performance of collaborative and noncollaborative sensors, in the presence of the noisy channel between the FCs and the GW.

A. Collaborative Sensors

Each FC obtains $K$ independent samples, amplifies and forwards the observed signals with $K$ different markers. Focusing on the $k$th type of markers, the number of released markers from FC$i$ is $\alpha Y_i^k$, where $\alpha \in \mathbb{N}$ is the amplification factor. The probability of a marker released by FC$i$ observed after the duration of $T_{G,obs}$ in GW’s receptor volume is $8^3$ [31]

$$
\hat{\mu}(d_{FG}, T_{G,obs}) = \frac{V_G}{4\pi D_2 T_{G,obs}} \exp \left( -\frac{d_{FG}^2}{4D_2 T_{G,obs}} \right). \quad (20)
$$

Then, the number of markers observed by the GW is an RV as $W_i^k \sim \text{Binomial}(\alpha Y_i^k, \hat{\mu}(d_{FG}, T_{G,obs}))$. Since the number of released markers, $\alpha Y_i^k$, is large enough, the Binomial distribution can be approximated by Gaussian as [32, p. 105]

$$
W_i^k \sim \mathcal{N}(\alpha Y_i^k \hat{\mu}(d_{FG}, T_{G,obs}), \alpha Y_i^k \hat{\mu}(d_{FG}, T_{G,obs})). \quad (21)
$$

The best observing time for the GW is the peak time of the markers concentration in (20), which is obtained as $T_{G,obs} = (d_{BG}^2/4D_2)$. Defining $m_G(d_i) \triangleq \alpha Y_i^k \hat{\mu}(d_{FG}, (d_{FG}^2/2ND_2))$, (21) results in

$$
W_i^k \sim \mathcal{N}(m_G(d_i), m_G(d_i)). \quad (22)
$$

8We assume that the volume $V_G$ is small enough, such that the concentration of markers in this volume is uniform.
Due to (4) and (21), RVs \(d_i, Y_k^i, \) and \(W_k^i\) form a Markov chain \(d_i \rightarrow Y_k^i \rightarrow W_k^i\). Note that the mean number of observed markers at the GW [i.e., \(m_G(d_i)\)] is an RV and \(W_k^i\) is a doubly stochastic RV. The ML decision rule at GW is

\[
\hat{d}_i = \arg \max_d P(W_i | d) = \arg \max_d \prod_{k=1}^K P\left(W_k^i | d\right)
\]

where

\[
P\left(W_k^i | d\right) = \int_{0}^{\infty} P\left(W_k^i | Y_k^i = y, d\right) P\left(Y_k^i = y | d\right) dy
\]

\[
P\left(W_k^i = w | Y_k^i = y, d\right) = \left(2\pi \left(m_G(d_i) | Y_k^i = y\right)\right)^{-\frac{1}{2}} \exp\left(-\frac{(w - m_G(d_i) | Y_k^i = y)^2}{2(m_G(d_i) | Y_k^i = y)}\right)
\]

\[
P\left(Y_k^i = y | d\right) = \left(2\pi N_{th} \mu \left(d, \frac{w^2}{4N}\right)^{-\frac{1}{2}} \exp\left(-\frac{(y - N_{th} \mu \left(d, \frac{w^2}{4N}\right))^2}{2N \mu \left(d, \frac{w^2}{4N}\right)}\right) \times \right.
\]

\[
= \left(2\pi N_{th} \mu \left(d, \frac{w^2}{4N}\right)^{-\frac{1}{2}} \exp\left(-\frac{(y - N_{th} \mu \left(d, \frac{w^2}{4N}\right))^2}{2N \mu \left(d, \frac{w^2}{4N}\right)}\right) \right)
\]

\[
\text{as } Y_k^i = m(d_i). \text{ Thus, the decision rule and probability of error are obtained as (18) and (19) by substituting } m(d_i) \text{ with } m_G(d_i) \simeq \alpha m(d_i) \mu(d_{FG}, T_{G,obs}).
\]

\section{VI. NUMERICAL AND SIMULATION RESULTS}

\textbf{System Parameters:} The system parameters are shown in Table II. To have a fair comparison of both types of sensors, we assume that at stop time, \(T_h\), the number of activated noncollaborative sensors is \(N_{th}\) (i.e., \(N_r = N_{th}\)). Thus, for both types of collaborative and noncollaborative sensors, the number of activated sensors, which release molecules, is equal. Note that in the case of noncollaborative sensors, the FCs do not know the number of activated sensors. As mentioned above, we do not simulate sensors movements. For the simulation of the proposed system, it is not feasible to use the particle-based simulation (PBS), which considers the movements of each molecule in very short time intervals, since our considered metric is the probability of error and the required number of iterations will be very high. We simulate Phases (2) and (3), molecules/markers movements to reach the FCs/GW, by generating \(N_{th} / \alpha Y_k^i\) independent identical Binomial RVs, where their mean is described in (1)/(20), and \(Y_k^i\) is an RV obtained through simulations.

First, we define the localization resolution as the inverse of the subregion area in Fig. 2 as \((w/L)^{-2}\). The probability of localization error versus the resolution is shown in Fig. 4. Note that for collaborative and noncollaborative sensors, two and three FCs are used, respectively. As can be seen, if the number of released molecules is \(N_{th} M = 10^6\), the performance of collaborative sensors is better than noncollaborative ones. Also, we can see that for a higher number of molecules \((N_{th} M = 2 \times 10^6, 3 \times 10^6)\), the noncollaborative sensors perform better than the collaborative ones for the medium resolutions, as it uses one more FC for deciding the location. It is also observed that the probability of error decreases if the total number of molecules increases. The simulation results are also provided in Fig. 4 for the case of \(N_{th} M = 10^6\), which perfectly validate the numerical results for collaborative sensors. The gap between the numerical and simulation results for noncollaborative sensors is due to the approximation used in Section IV for the ratio of two normal RVs.

The probability of localization error versus the total number of molecules \(K N_{th} M\) is shown in Fig. 5, in the presence of an ideal communication channel between the FCs and GW. As can be seen, the noncollaborative sensors perform better than the collaborative ones when the number of released
molecules increases. Since the normal distribution used for the ratio of GW observations is more accurate when the number of molecules increases. Also, we can see that the error probability increases for higher resolutions (higher values of $L$). Similar to Fig. 4, the simulation results validate the numerical results.

In Fig. 5, we have also plotted the performance of noncollaborative sensors assuming that the FCs know the exact value of $m_1(d_2)$ and they do not use the MSE minimizer in (16). We provide both numerical and simulation results, which confirm the accuracy of the approximation of $m_1(d_2)$ given in (16). For this figure, the approximation does better at a higher value of $N_{th}M$, as expected.

Now, we investigate the performance of the proposed model in the presence of a nonideal (noisy) communication channel between the FCs and GW. The probability of localization error is plotted versus the amplification factor $\alpha$ for different distances between the FCs and GW. As shown in Fig. 6, the probability of localization error is decreasing versus the amplification factor. The performance of collaborative sensors is better for lower amplification factors. The error is higher for longer distances $d_{FG}$ and the simulation results validate the numerical results. Also from Figs. 5 and 6, it can be seen that the effect of $\alpha$ on the probability of error is similar to the effect of the number of molecules ($N_{th}M$). Because the decision rules and the probabilities of error depend on $m(d_1)$ for the case of ideal channel between the FCs and GW, and $m_G(d_1)$ for the case of nonideal communication channel. Reminding that $m(d_1)=N_{th}M\mu(d_1, (w^2/4ND))$ and $m_G(d_1) \approx \alpha m(d_1)\tilde{\mu}(d_{FG}, T_{G,obs})$, so the effects of $N_{th}M$ and $\alpha$ on $P_e$ would be similar.

In Fig. 7, we plot the histogram and the approximated PDF of the number of markers observed at the GW, for different values of amplification factor $\alpha$. The PDF is obtained by approximating the number of molecules observed at the FC with its mean value. As can be seen, two results are close to each other, that confirms the accuracy of the mean-value approximation used in Section V.

VII. CONCLUSION

In this article, we consider a general setup to perform joint sensing, communication, and localization of a silent abnormality with MC. We investigate the abnormality localization problem in a 2-D medium, with no physical access to the abnormality point, with three types of devices: 1) mobile sensors; 2) FCs; and 3) a GW. We consider two types of collaborative and noncollaborative sensors and study both cases of the ideal and noisy communication channel between the
FCs and GW. For the collaborative sensors, we obtain the ML decision rule and suboptimum thresholds and derive the probability of error. For the noncollaborative sensors, we face doubly stochastic RVs, which make our analyses difficult. To overcome this problem, we use the ratio of GW observations and obtain the ML decision rule and probability of error in a closed form. In the case of noisy communication channel between the FCs and GW, we use mean-value approximations for doubly stochastic RVs to obtain the decision rules and probabilities of error. It is observed that the noncollaborative sensors perform better than collaborative ones when the number of molecules increases. The proposed model can be extended into a 3-D environment easily by utilizing one more FC.

APPENDIX

LEMMA 1 AND 2

Lemma 1 [36, p. 262]: If we have $K$ independent RVs $X_i \sim N(\mu_i, \sigma_i^2)$, $i = 1, \ldots, K$, then the RV $Z_i = \sum_{k=1}^{K}(X_i/\sigma_i)^2$ has a noncentral chi-squared distribution with the following cumulative distribution function (CDF):

$$P[Z_i < x] = 1 - Q_\nu(\sqrt{x}, \sqrt{\lambda})$$

where $\lambda = \sum_{k=1}^{K}(\mu_i/\sigma_i^2)$, and $Q_\nu(a, b)$ is the Marcum Q-function, defined as follows [37]:

$$Q_\nu(a, b) = \int_{b}^{\infty} x^{\nu - 1} e^{-x/2} I_{\nu - 1}(ax) dx$$

where $I_{\nu - 1}$ is modified Bessel function of order $\nu - 1$.

Lemma 2 [38]: Let $V_1$ and $V_2$ be two independent RVs as $V_i \sim N(\mu_i, \sigma_i^2)$, $i = 1, 2$, such that $0 < \sigma_1/\mu_1 < \lambda < 1$ and $0 < \sigma_2/\mu_2 < \sqrt{\lambda^2 - (\sigma_1/\mu_1)^2}$, where $\lambda$ is a known constant. For any $Z$ that belongs to the interval $[\beta - (\sigma_2/\mu_2)\lambda, \beta + (\sigma_1/\mu_1)\lambda]$, where $\beta = \mu_1/\mu_2$, and $\sigma_1 = \sqrt{(\sigma_1/\mu_1)^2 + (\sigma_2/\mu_2)^2}$, satisfies that $|G(z) - F_Z(z)| < \epsilon$, for every $\epsilon > 0$, where $G(z)$ is the distribution function of a normal RV with mean $\beta$ and variance $\sigma_1^2$, and $F_Z(z)$ is the distribution function of $Z = V_1/V_2$.

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