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► **To cite this version:**

Trang C Mai, Malcolm Egan, Trung Q Duong, Marco Di Renzo. Event Detection in Molecular Communication Networks with Anomalous Diffusion. *IEEE Communications Letters*, 2017, 21 (6), pp.1249 - 1252. 10.1109/LCOMM.2017.2669315 . hal-01671181

HAL Id: hal-01671181

<https://hal.science/hal-01671181v1>

Submitted on 22 Dec 2017

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Event Detection in Molecular Communication Networks with Anomalous Diffusion

Trang C. Mai¹, Malcolm Egan², Trung Q. Duong¹ and Marco Di Renzo³

Abstract—A key problem in nanomachine networks is how information from sensors is to be transmitted to a fusion center. In this paper, we propose a molecular communication-based event detection network. In particular, we develop a detection framework that can cope with scenarios where the molecules propagate according to anomalous diffusion instead of the conventional Brownian motion. We propose an algorithm for optimizing the network throughput by exploiting tools from reinforcement learning. Our algorithms are evaluated with the aid of numerical simulations, which demonstrate the tradeoffs between performance and complexity.

I. INTRODUCTION

Networks consisting of a large number of nanomachines, which are able to sense, communicate, and actuate at the nanoscale, have been proposed for applications ranging from intrabody health monitoring to pollution control [1]. A key component of these networks is the detection of events such as the presence of undesirable chemicals in the atmosphere or the malfunction of cells in biological systems. In a network of distributed nanomachines, this information must then be sent to a fusion nanomachine (FN), which can take action to mitigate the effect of the event.

Molecular communication forms one approach to support communication among sensing nanomachines (SNs) and a FN, where unlike conventional electromagnetic-based communication, each SN encodes information in the release time, number, or type of molecules emitted by each SN [1]–[3]. Molecular communication raises new challenges, due to the low energy and limited computational resources available at each nanomachine. Moreover, the achievable throughput of molecular communication systems is limited by the noise introduced from the random diffusion time of each molecule.

In existing works, the diffusion is typically modeled according to Brownian motion. In this case, it is possible to derive closed-form expressions for the first passage time distribution and the impulse response for reasonable boundary conditions. Under the assumption of Brownian motion, capacity characterizations [4], [5], practical receiver designs [6], [7] and intersymbol interference mitigation strategies [8] have been proposed.

However, Brownian motion cannot capture *anomalous diffusion*, where the growth of the mean square displacement

is much faster or slower as it usually occurs in scenarios with turbulence [9]. A key class of models for anomalous diffusion are the Lévy walks, which introduce challenges for the design of reliable molecular communication systems, as the first passage time and the impulse response are not generally available in closed-form. Moreover, the diffusion process cannot be encapsulated in a small number of parameters in Lévy walk models, as is the case in Brownian motion. These challenges are exacerbated in the context of event detection, where the large number of SNs lead to a corresponding number of diffusion channels, each with a different distance and fluid properties between the transmitting and receiving nanomachines. In particular, existing molecular communication techniques for Brownian motion and a single transmitting SN cannot be directly applied.

In this paper, we propose a molecular communication system for event detection which can cope with anomalous diffusion. Our system consists of an event detector and a training phase to optimize the time slot duration and tune the detection rule. In particular, we design the training phase to estimate the parameters required for reliable detection based on one bit messages from each SN. To design the training phase, we introduce a reinforcement learning-based algorithm for optimizing the time slot duration. In the proposed algorithm, the duration of each time slot is chosen in order to maximize the throughput and is applicable to any diffusion process with stationary increments and an independent first passage time for each link between a SN and the FN. In particular, it can be applied to the Lévy walks. To evaluate the performance of the system, we derive a tractable expression for the probability of error and numerically investigate tradeoffs between performance and complexity.

The remainder of this paper is organized as follows. In Section II, the system model is described. In Section III, the detection rule and the error probability are introduced. In Section IV, the training phase design is provided. In Section V, the numerical results are given. Finally, Section VI concludes this paper.

II. SYSTEM MODEL

We consider a synchronized and time-slotted nanoscale network, where N_S SNs monitor the state of a system. The duration of each time slot is \mathcal{T}_S . When a SN observes an event, it emits a molecule at the beginning of the next transmission slot. The intended receiver of the message is the FN, which processes the messages from the SNs. For example, the FN might be the head of a cluster of SNs which sends the detection of an event to an actuator nanomachine.

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Events occur with probability p_E and we assume that each SN detects an event with probability p_D . The molecule transmitted by each SN diffuses to the FN according to a Lévy walk [10]. We assume that the FN perfectly absorbs any detected molecule. As we will see in further text, our system design is applicable to any network of SNs where the diffusion process is stationary and the first passage time of each SN-FN link is independent. In particular, the proposed design applies both to Brownian motion and to Lévy walks under a wide range of boundary conditions. As Lévy walks form a very general class of diffusion processes, to make our description concrete, we assume that the FN is an absorbing boundary, the Lévy walk is one-dimensional, and the distance that a molecule travels within time t is given by

$$d_t = \sum_{j=1}^{n_t} v D_j, \quad (1)$$

where n_t is the number of jumps within time t , $D_j \in \mathbb{R}$ is the duration and direction of the j -th jump, and v is the fixed velocity. We assume that D_j is an α -stable random variable with exponent $1 < \alpha < 2$, scale parameter $\sigma \in \mathbb{R}_{>0}$, skewness $\beta = 0$, and shift $\delta = 0$.

Molecules that are emitted in earlier time slots and that are not absorbed by the FN persist. As a consequence, there is inter-symbol interference and the number of molecules observed by the FN in time slot j is given by $\sum_{k=1}^j Y_k^j$, where $Y_k^j = \sum_{i=1}^{N_S} Y_{k,i}^j$ is the number of molecules that are transmitted in time slot k and that arrive in time slot j . In particular, the random variable $Y_{k,i}^j$ is Bernoulli distributed with success occurring when an event occurs and the molecule sent from the i -th SN in slot k arrives at the FN in slot j . Let $F(t)$ be probability that a molecule transmitted at time 0 is absorbed before time t . Then the success probability is equal to

$$P_{j-k,i} = F((j+1-k)\mathcal{T}_S) - F((j-k)\mathcal{T}_S), \quad (2)$$

where $P_{j-k,i}$ is the probability that $(j-k)$ time slots for the molecule from SN i to diffuse to the FN are needed. Based on these assumptions, the inter-symbol interference is given by $\sum_{k=1}^{j-1} Y_k^j$ and the desired signal is Y_j^j .

III. DETECTION RULE AND ERROR PROBABILITY

To determine whether or not an event has occurred, the FN solves a hypothesis-testing problem based on the number of observed molecules. Let H_1 be the hypothesis that an event occur and H_0 be the hypothesis that an event did not occur. The number of molecules that arrive in time slot j under each hypothesis is given by

$$\begin{aligned} H_0 : R_{H_0} &= \sum_{k=1}^{j-1} Y_k^j \\ H_1 : R_{H_1} &= Y_j^j + \sum_{k=1}^{j-1} Y_k^j, \end{aligned} \quad (3)$$

For an observation of r molecules, the detection rule is given by the likelihood ratio test [11]

$$\frac{\Pr(r|H_1)}{\Pr(r|H_0)} \underset{H_0}{\overset{H_1}{\geq}} \eta, \quad (4)$$

where $\eta = (1-p_E)/p_E$ and the costs are $C_{00} = C_{11} = 0$ and $C_{01} = C_{10} = 1$.

As observed in [6], $Y_{k,i}^j$, which is the event that the molecule emitted in time slot k by SN i that arrive in time slot j , is a Bernoulli random variable with success probability $P_{j-k,i}$. It then follows that $Y_k^j = \sum_{i=1}^{N_S} Y_{k,i}^j$ is binomial distributed. For finite j , R_{H_0} and R_{H_1} , which are sums of independent binomial distributions, are Poisson-binomial distributed. Moreover, for systems operating for long periods of time corresponding to $j \rightarrow \infty$, it follows from the law of rare events [12], [13] that R_{H_0} and R_{H_1} converge in distribution to a Poisson random variable. The large j approximation also forms a worst case scenario for short system run times.

To derive the parameter of the Poisson random variable, we note that an event occurs and is detected by SN i with probability $p_E p_D$. Moreover, $\sum_{k=0}^j P_{j-k,i} = 1$ when $j \rightarrow \infty$. This means that the inter-symbol interference due to SN i is a Poisson random variable with expected value $p_E p_D (1 - P_{0,i})$, where $P_{0,i}$ is the probability that a single time slot is needed for a molecule emitted by SN i to reach the FN. Since the sum of Poisson random variables is Poisson, it follows that

$$\begin{aligned} R_{H_0} &\sim \text{Poisson} \left(p_E p_D \sum_{i=1}^{N_S} (1 - P_{0,i}) \right) \\ R_{H_1} &\sim \text{Poisson} \left(\sum_{i=1}^{N_S} P_{0,i} + p_E p_D \sum_{i=1}^{N_S} (1 - P_{0,i}) \right). \end{aligned} \quad (5)$$

We are now in the position to derive a decision rule. Let

$$\begin{aligned} \lambda_0 &= p_E p_D \sum_{i=1}^{N_S} (1 - P_{0,i}) \\ \lambda_1 &= \sum_{i=1}^{N_S} P_{0,i} + p_E p_D \sum_{i=1}^{N_S} (1 - P_{0,i}). \end{aligned} \quad (6)$$

By using the probability density function of the Poisson distribution in (4), we obtain the decision rule

$$r \underset{H_0}{\overset{H_1}{\geq}} \Theta, \quad (7)$$

where

$$\Theta = \frac{\log \eta + \lambda_1 - \lambda_0}{\log(\lambda_1) - \log(\lambda_0)}. \quad (8)$$

Under the Poisson approximation, the average probability of detection error is given by

$$P_e = p_E F(\lambda_1; \lfloor \Theta \rfloor) + (1 - p_E)(1 - F(\lambda_0; \lceil \Theta \rceil)), \quad (9)$$

where $F(\lambda; x)$ is the CDF of the Poisson distribution. Since Poisson-binomial random variables converges in distribution to a Poisson random variable under the conditions [12] satisfied by our model, it follows that the probability of error converges to (9).

A key observation is that the decision rule and hence the error probability are completely determined by the parameter

$$A = \sum_{i=1}^{N_S} P_{0,i}. \quad (10)$$

We remark that if Brownian motion is considered, it is possible to obtain an analytical expression for $P_{0,i}$, under appropriate boundary conditions, and perfect knowledge of the fluid diffusion coefficient as well as the distances between each SN and the FN. However, in the case of Lévy walks, a closed-form expression for the first passage time is not available. Moreover, due to the large number of SNs, it is unlikely that the FN will have access to the necessary information on the fluid properties and locations of all the SNs throughout the network. In the next section, we explore the effect of the training phase on the estimate of A and the decision rule.

IV. TRAINING PHASE DESIGN

Due to the unknown diffusion process, the training phase plays a crucial role in obtaining the parameters that are required for the decision rule. In this section, we design the training phase to ensure that the probability of error lies within a known confidence interval. We then exploit the confidence interval to develop an online algorithm inspired by reinforcement learning [14], to optimize the time slot duration. By exploiting reinforcement learning, our approach optimizes the time slot duration by exploiting observations from sensor signals without having a complete characterization of the channel. As the first passage time and the impulse response in our model are not available in closed-form, such a learning-based approach is highly desirable.

To develop an online algorithm, we assume that after each time slot in the training phase, the network can remove the transmitted molecules from the system. This can be achieved by the introduction of reactants, such as the enzyme-based approach in [8], which reduce the lifetime of the information molecules, only necessary during the training phase to reduce the energy consumption at the FN while achieving accurate parameter estimation.

From (10), it follows that the probability of error is completely determined by the parameter A in (10). As a consequence, the key step in the training phase is to estimate A . A natural estimator is

$$\hat{A} = \sum_{i=1}^{N_S} \frac{1}{n} \sum_{j=1}^n \mathbf{1}_{\{Y_{i,j}=1\}}, \quad (11)$$

where $Y_{i,j} \in \{0,1\}$ is the number of molecules that are received within a single time slot from the i -th SN in the j -th training slot. Let us define

$$\hat{P}_{0,i} = \frac{1}{n} \sum_{j=1}^n \mathbf{1}_{\{Y_{i,j}=1\}}, \quad (12)$$

which is an empirical distribution function. Thus, it follows that the estimator \hat{A} is consistent [15]. Moreover, we observe that

$$\begin{aligned} \mathbb{P}(|A - \hat{A}| > N_S \epsilon) &\leq \mathbb{P}\left(\sum_{i=1}^{N_S} |P_{0,i} - \hat{P}_{0,i}| > N_S \epsilon\right) \\ &\leq 1 - \prod_{i=1}^{N_S} \left(1 - \mathbb{P}\left(|P_{0,i} - \hat{P}_{0,i}| > \epsilon\right)\right). \end{aligned} \quad (13)$$

Based on these considerations, we can apply the Dvoretzky-Kiefer-Wolfowitz inequality [15], which yields

$$\begin{aligned} \mathbb{P}(|A - \hat{A}| > N_S \epsilon) &\leq 1 - \prod_{i=1}^{N_S} (1 - 2e^{-2n\epsilon^2}) \\ &= 1 - (1 - 2e^{-2n\epsilon^2})^{N_S}. \end{aligned} \quad (14)$$

Let the time slot duration be $\mathcal{T}_S \in \{\mathcal{T}_1, \dots, \mathcal{T}_K\}$. The bound in (14) provides a means of obtaining the confidence intervals for the probability of error and the throughput, which is defined as

$$R_l = \frac{1}{\mathcal{T}_l} (1 - P_{e,l}), \quad (15)$$

for the l -th time slot duration, where $P_{e,l}$ is the probability of error corresponding to a time slot duration \mathcal{T}_l . In particular, given an estimate \hat{A}_l it follows that the probability $A_l \in [\hat{A}_l - N_S \epsilon, \hat{A}_l + N_S \epsilon]$ is bounded by (14). Note that $P_{e,l}$ in (9) is a monotonically decreasing function of A , which is due to the fact that the number of molecules that arrive in a single time slot is increasing as A increases.

Using the fact that $P_{e,l}$ is a monotonically decreasing function of A and (14), the confidence interval bound on R_j

$$\frac{1 - P_{e,l}(\hat{A}_l - N_S \epsilon(\phi))}{\mathcal{T}_l} \leq R_l \leq \frac{1 - P_{e,l}(\hat{A}_l + N_S \epsilon(\phi))}{\mathcal{T}_l}, \quad (16)$$

holds with probability greater than $1 - \phi$, where

$$\epsilon(\phi) = \sqrt{\frac{1}{2n} \log \left(\frac{2}{1 - \sqrt[n_S]{1 - \phi}} \right)}. \quad (17)$$

The confidence interval in (16) bounds the error probability and throughput with n trials, which is useful for providing guarantees on the throughput given a limited training phase. The confidence interval also provides a means for optimizing the time slot duration. Since it is undesirable to obtain tight confidence intervals for every time slot duration, we can use the confidence interval as the basis for an online optimization algorithm. The algorithm can provide guarantees for the probability that the selected time slot duration is suboptimal.

We now present our online algorithm to minimize the probability that a suboptimal time slot duration is selected, as opposed to the time-consuming approach of estimating the throughput for each time slot duration separately. Let $0 < \phi < 1$ be the confidence level in (16) and the stopping criterion is $\delta > 0$. Suppose that the training phase is in the k -th time slot, then:

- 1) If $1 \leq k \leq K$, set $j = k$ and select time slot duration \mathcal{T}_k . Using (11), compute the estimate \hat{A}_k and the confidence interval via (16).
- 2) If $k > K$, select the time slot duration j such that

$$\frac{1}{\mathcal{T}_j} (1 - P_{e,j}(\hat{A}_j + N_S \epsilon(\phi))) \quad (18)$$

is maximized.

The training phase is ended if for the selected time slot \mathcal{T}_j , the stopping criterion

$$\frac{1}{\mathcal{T}_j} \left(P_{e,j}(\hat{A}_j - N_S \epsilon(\phi)) - P_{e,j}(\hat{A}_j + N_S \epsilon(\phi)) \right) < \delta \quad (19)$$

is satisfied and the intersection of the confidence intervals defined by (16) is empty. Otherwise, the algorithm continues with $k \leftarrow k + 1$.

Note that the algorithm is based on the confidence interval estimate in (16). Thus, it follows that the probability that the time slot duration \mathcal{T}_j selected by the algorithm is suboptimal based on (9) is upper bounded by ϕK .

We remark that the estimation procedure is based on the estimation of the cumulative distribution function for the first passage time. Hence, our algorithm can be applied to systems with any diffusion process as long as the increments are independent and the first passage times for each SN-FN link are each independent.

V. NUMERICAL RESULTS

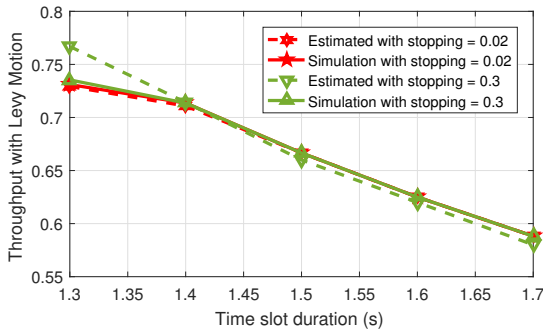


Fig. 1. Throughput with different stopping criteria.

In this section, we show the tradeoffs between performance and complexity of our algorithm by comparing its robustness with time duration spent on the training phase. The system consists of a single FN and $N_S = 100$ transmitting SNs located at equal distance $d = 10^{-2}$ m from the FN. To illustrate the behavior of our algorithm in the presence of anomalous diffusion, we consider a fluid medium with a drift velocity $v = 0.01$ m/s, $p_E = 0.5$, $p_D = 1$, stability exponent $\alpha = 1.2$ and scale parameter $\sigma = 0.01$ for each SN-FN link. We assume that the network can select a time slot duration in the set $\{1.3, 1.4, 1.5, 1.6, 1.7\}$.

Fig. 1 compares the throughput for each time slot duration obtained directly from Monte Carlo simulations and from the estimated parameter \hat{A} using our algorithm for each time slot duration separately with a confidence level $\phi = 0.01$.

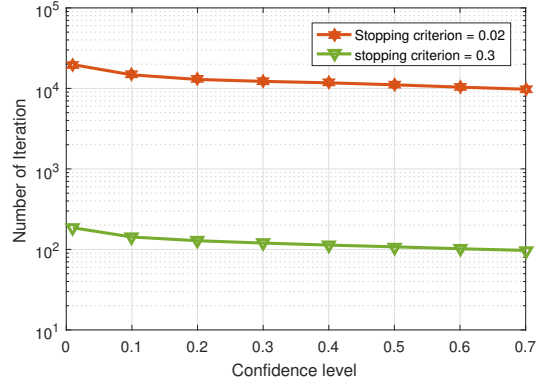


Fig. 2. Number of iterations with different stopping criteria.

We observe that the estimate from our algorithm is in good agreement with the throughput obtained from Monte Carlo simulations. This implies that our algorithm can obtain the optimal throughput with probability dependent on the stopping time.

Fig. 2 plots the complexity in terms of the number of iterations for the training period as the confidence level varies, which determines the probability the selected throughput is suboptimal. We observe that the stopping criterion has a large influence on the number of iterations. Despite this, we can still obtain an accurate estimate of the throughput in our setting with a small number of iterations as observed in Fig. 1.

VI. CONCLUSION

We have proposed an algorithm to optimize molecular communication in nanomachine sensor networks in the presence of a medium with anomalous diffusion. A key feature of our algorithm is that it does not rely on detailed statistical knowledge of the underlying diffusion processes and that it provides a guarantee on the probability that the throughput is optimal. Simulation results suggest that good performance can be obtained with very short training periods.

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