

Comparison of Amplitude Detection Techniques for Passive Receivers in Molecular Communications

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Abstract—Amplitude detection is based on observations of the information carrying molecules made at the receiver and can be enhanced by optimizing the timing and the number of them. In this paper, a diffusion-based molecular communications system with a passive receiver is analysed under two different amplitude based detection techniques. In particular, low complexity detectors utilizing a single or multiple observations are evaluated and compared in terms of the achievable mean error probability, when external noise and interference are considered.

Index Terms—Amplitude detection, passive receiver, single threshold detector, diffusion-based molecular communications.

I. INTRODUCTION

Nanotechnology has recently attracted the interest of the scientific community, while its achievements have paved the way for new research areas, such as communication between nano-scale devices. Molecular communication (MC) utilizes molecules to transfer information between nano-machines [1]. Information carrying molecules diffuse freely and randomly in the communication medium and may reach the receiver at a later time than expected, thus creating intersymbol interference (ISI) [2]. Moreover, MC systems suffer from external noise, when molecules of the same type as the information carrying ones exist in the communication environment [2]. Noise and interference, together with the need for low complexity and energy consumption of the receiver, enlist the detection process among the main concerns in MC [1].

In [3], passive receivers that do not interact with the information carrying molecules are presented, along with a detection technique based on the number of molecules observed within the receiver. The detection process in [2] is based on multiple observations of the receiver during a symbol duration. Besides, more complex detection techniques have been suggested [4]–[6], but they are not easily applicable. Interestingly, a comparison between different amplitude based techniques in the presence of ISI and noise does not exist in the literature. To this end, in this paper, a diffusion-based MC system with a passive receiver is analysed in terms of the error probability, while two different amplitude detection techniques based on a single or multiple observations of the receiver are compared, when ISI and external noise are taken into account.

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II. SYSTEM MODEL

The communication system under consideration is depicted in Fig. 1 and consists of a transmitter and a receiver communicating via information molecules, referred to simply as molecules in the rest of the paper. The communication environment is considered three-dimensional, stationary and unbounded, while it is filled with a fluid of certain viscosity and uniform temperature. The transmitter behaves as a zero-dimensional point source and accurately controls the emission of identical molecules that carry the information. Placed at a distance r_d from the center of the receiver, the transmitter emits instantaneously a predefined number of molecules for each different symbol of the utilized constellation at the beginning of the symbol duration T . In this paper, we assume ON/OFF keying, which implies that M molecules are emitted for bit-1 and nothing (i.e., zero molecules) for bit-0, while both transmissions are considered equiprobable, i.e., $\Pr\{x_i = 1\} = \Pr\{x_i = 0\} = \frac{1}{2}$.

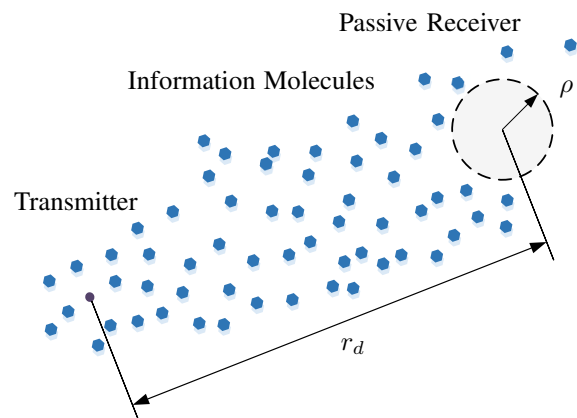


Fig. 1. Diffusion-based molecular communication system

The receiver is spherical with radius ρ and volume V , and works as a passive observer, i.e., it does not react with the information molecules neither does it affect the diffusion process. Moreover, we assume that it is perfectly synchronized with the transmitter. Due to the fact that the information is encoded as the number of transmitted molecules, their number is considered as the amplitude. Therefore, we refer to the detection process as *amplitude detection*, because it is based on the observations of the receiver on the number of received

molecules at predefined time instants. More precisely, the receiver counts the number of molecules that are within its volume at specified time and utilizes this information for the detection process.

The information molecules diffuse independently from each other via Brownian motion in the communication medium. Their motion is affected by the diffusion coefficient D of the fluid medium, which is considered constant and identical for all the information molecules. Besides, there exists no flow and the molecules diffuse freely without being impeded by other molecules that may be present in the fluid medium. However, it has been assumed that molecules of the same type as the information molecules exist in the communication environment and reach the receiver, acting as an external noise. Finally, molecules that correspond to a previous transmission may be observed within the receiver at a later time. Therefore, these systems suffer from intersymbol interference.

Due to the fact that the molecules diffuse randomly in the communication medium, the number of molecules observed within the receiver each time is considered as a random variable (RV) following Poisson distribution with a proper mean value [2]. The probability that an information molecule is inside the passive receiver at the time instant t , assuming that it was emitted at time $t = 0$, is [7]

$$p(t) = \frac{V}{(4\pi Dt)^{3/2}} \exp\left(-\frac{r_d^2}{4Dt}\right). \quad (1)$$

Denoting as $N^i(t)$ the number of observed molecules at the receiver at $t \in [0, T]$ after the i -th transmission, we have

$$N^i(t) = N_c^i(t) + N_{\text{isi}}^i(t) + N_n^i(t), \quad (2)$$

where $N_c^i(t)$, $N_{\text{isi}}^i(t)$ and $N_n^i(t)$ stand for the number of received molecules corresponding to the current transmission, to previous transmissions and to external noise, respectively. Hereby, we note that $N_n^i(t)$ can also be characterized as a Poisson RV with mean μ_n [2], while the sum of independent Poisson RVs is also a Poisson RV with mean equal to the sum of the means. Therefore, if we denote as x_i the bit transmitted in the i -th transmission, i.e., $[(i-1)T, iT]$, we have that

$$N^i(t) \sim \text{Poisson} \left(Mx_i p(t) + \sum_{j=1}^I [Mx_{i-j} p(t + jT)] + \mu_n \right), \quad (3)$$

where $t \in [0, T]$ and I stands for the number of the previous transmissions that are taken into account in the analysis and, thus, are considered as ISI to the current transmission.

III. AMPLITUDE DETECTION TECHNIQUES

In amplitude detection, the receiver counts the received molecules in one or more time instants within the symbol duration and, depending on the utilized technique, constructs a variable denoted as N_R^i . Afterwards, due to the ON/OFF keying modulation, a *single threshold detector* compares N_R^i

with an appropriate threshold τ in order to detect the transmitted symbol as follows

$$\hat{x}_i = \begin{cases} 1, & \text{if } N_R^i \geq \tau \\ 0, & \text{otherwise.} \end{cases} \quad (4)$$

For the selection of the symbol duration T , we consider a single transmission and denote α as the fraction of the number of molecules that have already entered the receiver till T , divided by the total number of molecules that would enter the receiver till infinite time. Consequently, the selection of T is based on α and can be calculated using the formula [3]

$$T = \frac{r_d^2}{4D[\text{erfc}^{-1}(\alpha)]^2}. \quad (5)$$

In order to validate and compare the detection techniques, a molecular communication system with diffusion coefficient equal to $D = 10^{-9}$ m²/sec and $\alpha = 0.4$ has been simulated. Moreover, we assume that $M = 50000$ molecules are transmitted for bit-1, while the external noise molecules have a mean value that equals $\mu_n = 50$. The receiver's radius is set equal to $\rho = 0.4$ μm and its center is placed $r_d = 3$ μm away from the transmitter. Finally, it should be mentioned that for each implemented scenario the optimal threshold value has been found numerically and utilized.

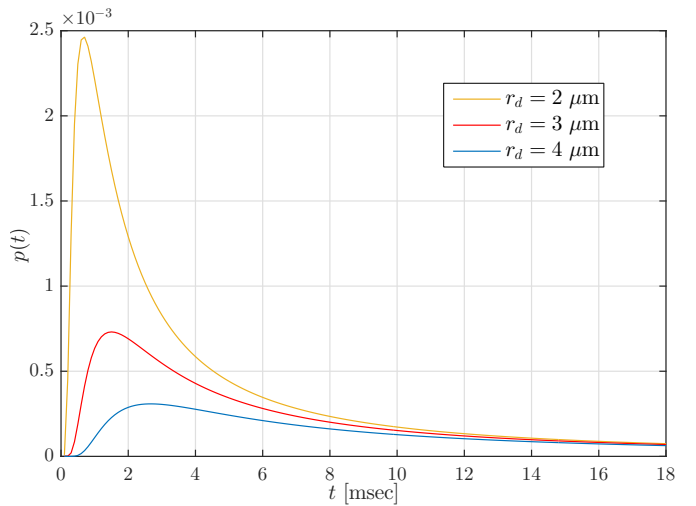


Fig. 2. Probability of a molecule being within the receiver versus time

A. Single sample detector (SSD)

In molecular communications, it is critical the detector to be of the least possible complexity. To this end, the *single sample detector (SSD)* utilizes a single observation of the receiver for the detection. Observing Fig. 2, it can be easily inferred that the optimal sampling time, t_{opt} , would be the time instant when the probability that a molecule is inside the receiver reaches its global maximum, which equals [3]

$$t_d = \frac{r_d^2}{6D}. \quad (6)$$

However, this holds true only if the ISI is ignored, i.e., $I = 0$. In the presence of ISI and choosing $\alpha < 0.6$ to achieve

an acceptable transmission rate, a sampling time, t_s , greater than t_d is preferable in order to mitigate the effect of ISI, which decreases as the time increases.

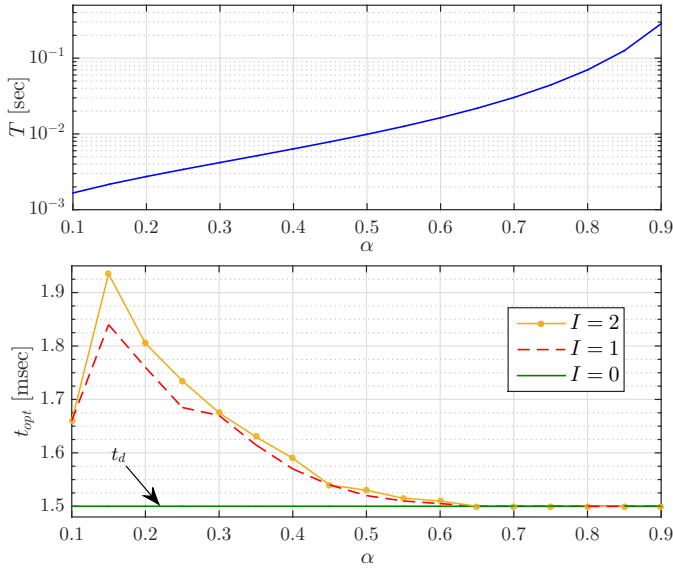


Fig. 3. Symbol duration T and optimal sampling time t_{opt} versus α

The symbol duration with respect to α is illustrated in the first subplot of Fig. 3, which reveals that the symbol duration increases significantly for high α values. Meanwhile, the optimal sampling time t_{opt} , depicted in the second subplot of Fig. 3 for different I values, corresponds to the sampling time value that minimizes the probability of error for various α and accordingly T values. We note that t_{opt} for $\alpha = 0.1$ takes the maximum possible value that equals T .

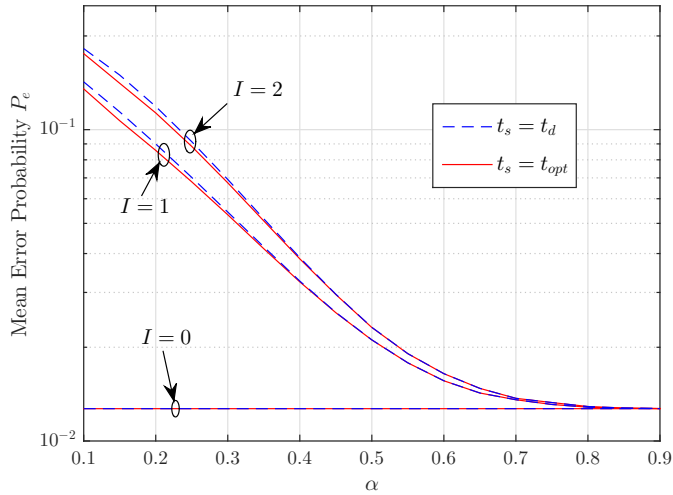


Fig. 4. Mean error probability P_e versus α

A closed-form expression for the mean error probability, P_e , can be derived by utilizing the approximation of the Poisson distribution with a Gaussian distribution, and an appropriate

continuity correction, as follows

$$P_e^{SSD} = \left(\frac{1}{2}\right)^{I+1} \sum_{l=1}^{2^I} \left[Q\left(\frac{\mu(l,1) - \tau + 0.5}{\sqrt{\mu(l,1)}}\right) + Q\left(\frac{\tau - 0.5 - \mu(l,0)}{\sqrt{\mu(l,0)}}\right) \right], \quad (7)$$

where $Q(x) = (1/\sqrt{2\pi}) \int_x^\infty \exp(-u^2/2) du$ is the Gaussian Q-function, l corresponds to each of the 2^I possible bit sequences $\{u_1, u_2, \dots, u_I\}$ that stand for the I previous transmissions, and the mean value $\mu(l, x_i)$ equals

$$\mu(l, x_i) = Mx_i p(t_s) + \sum_{j=1}^I [Mu_j p(t_s + jT)] + \mu_n. \quad (8)$$

From Figs. 3 and 4, it can be inferred that the increase of the symbol duration with increasing α enhances the performance in terms of the error probability, as the ISI effect decreases with the increase of the symbol duration. Moreover, utilizing the optimal sampling time instead of t_d is proved advantageous for $I \neq 0$, as expected. Finally, for $\alpha = 0.8$ the error probability approximates very well its lower possible value corresponding to $I = 0$, but the resulting high symbol duration induces a tremendous decrease to the transmission rate, i.e. $R = 1/T$ for the ON/OFF keying.

B. Multiple samples detector (MSD)

A receiver that utilizes more than one observations has been analyzed in [2]. Assuming that K samples are taken by the receiver at time instants given by $g(k) = kt_s$, where $k = 1, 2, \dots, K$, and they are summed up before the single threshold detection, we have

$$N_R^i \sim \text{Poisson} \left(\sum_{k=1}^K \left[Mx_i p(g(k)) + \sum_{j=1}^I [Mx_{i-j} p(g(k) + jT)] + \mu_n \right] \right) \quad (9)$$

and the average error probability can be computed as

$$P_e^{MSD} = \left(\frac{1}{2}\right)^{I+1} \sum_{l=1}^{2^I} \left[Q\left(\frac{\sum_{k=1}^K \mu_k(l,1) - \tau + 0.5}{\sqrt{\sum_{k=1}^K \mu_k(l,1)}}\right) + Q\left(\frac{\tau - 0.5 - \sum_{k=1}^K \mu_k(l,0)}{\sqrt{\sum_{k=1}^K \mu_k(l,0)}}\right) \right], \quad (10)$$

where the mean value $\mu_k(l, x_i)$ equals

$$\mu_k(l, x_i) = Mx_i p(g(k)) + \sum_{j=1}^I [Mu_j p(g(k) + jT)] + \mu_n. \quad (11)$$

In the simulations, uniform sampling has been assumed where the K samples are equally spaced in time, i.e., $t_s =$

T/K , as suggested in [2]. Utilizing a high number of samples increases the complexity of the receiver without being always beneficial in terms of error performance, as it can be observed in Fig. 5. In general, the number of samples that need to be considered in order to minimize the error probability depends on the value of α and r_d .

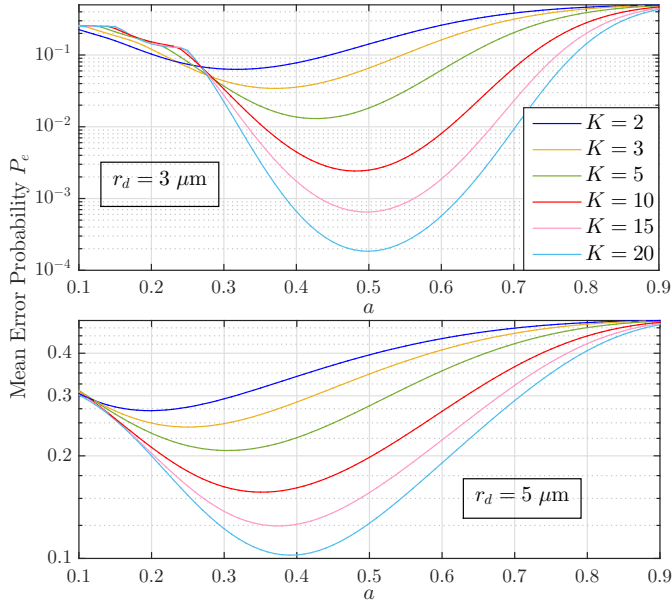


Fig. 5. Mean error probability versus α for different number of samples K and r_d , $t_s = T/K$ and $I = 2$

More precisely, for low α and r_d where the MC system suffers from high ISI due to small T given by (5), the number of samples that need to be used is small. Furthermore, for a high value of α and accordingly T , the MSD with uniform sampling results in some observations where most of the molecules correspond to external noise and not to information carrying ones, as can be inferred from Fig. 2. This increased presence of external noise reduces the efficiency of the MSD for high α . To this end, the number of samples that will be utilized has to be selected together with a proper α value in order to enhance the system reliability. Interestingly, the MSD has been proved to significantly increase the error performance of MC systems for $\alpha \in [0.4, 0.6]$ and proper K values depending on the acceptable complexity.

In Fig. 6, SSD and MSD are compared for different α values. It can be observed that the MSD outperforms the SSD when proper K and α values are considered. The SSD performs better as α increases due to the decrease of the experienced ISI, while the MSD is mostly advantageous for α values close to 0.5. This preference of the MSD regarding α is also advantageous for the achievable transmission rate as smaller α values result in higher rate values. Moreover, for $\alpha = 0.2$ the error probability is not tremendously decreased when MSD with $K = 2$ is utilized. Besides, MSD with $K = 5$ and $\alpha = 0.4$ can achieve the same error probability as an SSD with $\alpha = 0.7$, ensuring a higher transmission rate with the countereffect of an increase in the complexity of the receiver.

Therefore, the selection of the most appropriate detector to utilize among SSD and MSD highly depends on the MC system parameters and the application requirements.

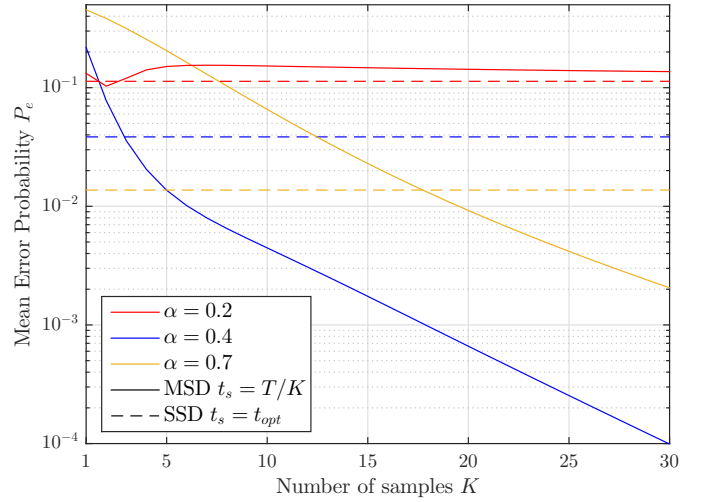


Fig. 6. Comparison of SSD and MSD in terms of mean error probability for different α and $I = 2$

IV. CONCLUSION

Diffusion-based molecular communication systems that suffer from ISI and noise have been analysed in terms of the achievable error probability for amplitude based detectors utilizing one or multiple samples. It has been proved that the MSD significantly enhances the system performance both in terms of error performance and transmission rate, when $\alpha \in [0.4, 0.6]$ and $t_s = T/K$. The SSD may be utilized for low or high α values for its acceptable performance with low complexity, while its optimal sampling time depends on the ISI. Finally, it has been inferred that optimizing the sampling timing may further enhance the performance of MSD, which will be considered in future work.

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