Decode and Forward Relaying in Diffusion-based Molecular Communication Between Two Populations of Biological Agents

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***Abstract*—Molecular communication allows bio nodes to communicate and cooperate in an aqueous environment. We recently proposed an m-ary modulation scheme in which the information is encoded into the concentration of molecules emitted by the bio nodes. The performance of such scheme, among other factors, is limited by the maximum concentration of molecules that can be induced by the transmitter at the receiver. This paper investigates relaying to improve the reliability of such molecular communication. We consider the case that nodes consist of a population of biological agents and study the scenario in which the relay node decodes the incoming information symbol and forwards it to the destination using the same or a different type of molecules as the transmitter. We show how the use of relaying in molecular communication can increase the effective range of molecular concentration induced at the receiver and also can help with achieving diversity at the receiver. We use a generalized form of Maximum Ratio Combining (MRC) and show as to how the probability of error is improved using the optimal relaying. We also compare this scenario with the case that the relay node uses the same type of the molecule.**

I. Introduction and Background

Diffusion-based molecular communication between biological entities is a new paradigm in communications. Recent advances in synthetic biology have encouraged the applications of engineered bacteria as the basic components of communication networks. Molecular communication is the primary method these biological agents can exchange information and hence, cooperate with each other. Such networks of engineered bacteria may enable future medical applications when other forms of wireless communication may not be feasible. For example, these networks can be used for sensing the environment for the density of a particular particle and sending that measurement reliably to the destination. Biocompatible environments like the human body are among the most promising scenarios for molecular communication [1]–[3]. Molecular communication already exists in nature in the form of the quorum sensing observed among bacteria. It has been understood that bacteria use concentration of small molecules that are exchanged among them to understand the state of their population density and to synchronize their actions [4]. This process enables bacteria to behave collaboratively for performing the tasks that would be impossible otherwise. As such, molecular communication has recently received a great deal of attention from several researchers both in biology and communication [5], [6].

There are several ways by which bio agents can communicate. We consider a particular form of molecular communication called diffusion-based molecular communication (DbMC) where the information is embedded in the concentration of molecules. This is different from other forms of molecular communication in which the information is contained in timing of the molecules [7], [8]. Relaying and multi-user DbMC have been previously discussed briefly in some different contexts. The design of repeaters in Calcium junction channels is discussed in [9]. Authors in [10] considered the multi-user problem in DbMC and compared it to its conventional counterparts.

This paper, as in [11], assumes that every communication node consists of a population of biological agents such as synthetic bacteria. Our analysis in [12] suggests that forming reliable communication between two individual bacteria is nearly impossible due to high randomness in the behavior of a single bacterium. As such, we form a reliable node out of a population of unreliable biological agents (i.e., bacteria). Therefore, the collective behavior of the bacteria population influences the node output as a transmitter as well as a receiver. In [11], the information sensing capacity of such a node (formed by a population of bacteria) is studied and it was concluded that the sensing capacity increases by using a larger number of bacteria in a node. In [12], we studied the reliable communication between two such nodes and obtained the capacity and reliability of such a system. We also showed that the achievable rates of information increases by both increasing the maximum range of the concentration of molecules induced at the receiver and a larger number of bacteria in the receiver node.

In molecular communication, however, attenuation of the molecular concentration as it travels in the environment via the diffusion process is a major problem. At the steady state, the concentration of molecules is inversely proportional to the distance between the transmitter and the receiver. Therefore,

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reliable communication to the long distances remains a challenge especially whenever other types of molecules are present at the environment, making the molecular signal sensing even more difficult in the lower concentration regime. On the other hand, due to the restrictions on food availability and also waste disposal at a node, we are constrained to use as few number of bacteria as possible inside a node. Using a smaller number of bacteria limits the maximum range of the molecular concentration output by the transmitter. Therefore, we resort to use relaying to mitigate this problem and improve the communication range.

In [13], the sense and forward relaying problem in DbMC is introduced. In that scenario, the relay node simply senses the received concentration and forwards it to the receiver (comparable to amplify and forward in classical wireless communications). The sense and forward relaying is shown to result in either increasing the range of the concentration of molecules at the receiver or increasing the effective number of bacteria in the receiver node.

In this paper, we study another strategy, namely the decode and forward relaying. In this scenario, the relay node decodes the incoming m-ary information symbol sent by the transmitter and then forwards it to the receiver (destination node). We will investigate two different strategies for relaying: 1. same-type relaying via the same or another type of molecules (i.e., the relay uses the same type of the molecules as the transmitter node) and 2. heterogeneous relaying ((i.e., the relay employs a different type of the molecules used by the transmitter). The incoming information symbols from the direct path (i.e., from the transmitter to the receiver node) and from the relay path (i.e., from the relay node to the receiver node) form the concentration of molecules at the receiver node. In the case of same-type relaying, the molecules from the relay and direct paths are superimposed and form a single output. In contrast, in the hetero-type relaying case, two different outputs are generated at the receiver node. As such, we use a generalized form of Maximum Ratio Combining (MRC) to optimally combine the received symbols at the receiver. We compare the above two scenarios and investigate the resulting probability of error at the receiver node.

The rest of the paper is as follows. In Section. II, we briefly review the two-node m-ary DbMC. Section. III introduces the decode and forward relaying in the context of m-ary DbMC. Section. IV, discusses the case when only one type of molecules is used in the relay setup. Finally, Section. V concludes the paper.

II. Channel model

In this section, we briefly explain the channel model for m-ary DbMC between a single transmitter and receiver. This will then be extended to the relaying scenario. The information is encoded in the concentration of Acyl homoserine lactone (AHL) molecules molecular signals emitted by the transmitter. As we can see in Fig. 1, the produced molecules by the transmitter node (namely type I molecules[1]) are diffused freely in all directions into the environment to reach the receiver. The receiver node then decodes the information from the induced AHL concentration.

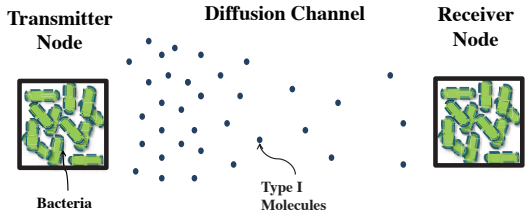


Fig. 1. Molecular communication setup:the transmitter, the diffusion channel and the receiver.

Upon the reception of molecules at the receiver, as in Fig. 1, the received molecules probabilistically bind to the ligand receptors of the bacteria [14]. By binding of the molecules to the bacteria's receptors, a chain of chemical processes is triggered at each corresponding bacterium of the receiver node. The details regarding the communication between the transmitter and receiver nodes via AHL molecular signal in a 3-D environment is discussed in [15]. The final output of each bacterium is determined by the type of the synthetic bacteria; via the program placed in its plasmid. The output can be in the form of fluorescence, in particular Green Fluorescent Protein (GFP), or the production of another type of molecules and so on [16]. Here, the output of each bacterium is considered to be GFP. The output of each individual bacterium depends on the level of concentration of molecules that it senses. The level of the total GFP output by the receiver node is the aggregate of all the GFP outputs by all the bacteria within the node. Ideally, by measuring this output, we can decode the concentration of molecular signals at the receiver and hence, decode the transmitted information. Note that since the decoding process contains huge delays, the concentration of molecules at the receiver should remain constant until it is decoded. Hence, we are only interested in the steady-state behavior of the diffusion channel. As we have shown in [12], the dominant factor contributing to the communication noise is due to the probabilistic nature of the molecular signal sensing by each bacterium at the receiver. We denote by A the concentration of the received molecules (i.e., the receiver input) and by P the corresponding ideal probability of the activation of individual receptors in bacteria. Using [14], we have

$$P = \frac{A\gamma}{A\gamma + \kappa}, \tag{1}$$

where γ and κ are parameters due to synthetic bacteria which may vary slightly from one bacterium to another in a node. The parameters γ and κ can be viewed as random variables varying around their averages, γ_0 and κ_0, by zero-mean Gaussian noises ϵ_γ and ϵ_κ with variances σ_γ^2 and σ_κ^2, respectively. Since the probability P is a one-to-one function of A, we can consider P as the input in the reception process. Then,

[1]Throughout this paper, we use type I molecules as a generic reference to the chemical molecular signal (i.e., AHL molecules.)

the noisy probability of the receptor activation at the receiver is obtained by [12] as

$$\hat{P} = P + P(1-P)\left(\frac{\epsilon_\gamma}{\gamma_0} + \frac{\epsilon_\kappa}{\kappa_0}\right). \quad (2)$$

By obtaining the probability of activation P, one can use (1) to obtain the corresponding A. Hereafter, we refer to the symbols by the probabilities. It was shown in [12] that due to the low-pass nature of the chemical processes inside the bacteria, i.e., the averaging operations that happen due to the collective reception of molecules by the bacteria, the last stage noise due to the probabilistic reception of molecules by the receiver dominates the other noises (e.g., the transmitter noise) accumulated by the previous stages. The noisy probability of receptor activation in (2) translates into a noisy GFP production (the output Y) as described above. The output Y at the receiver is a linear function of $\hat{P}$. The normalized value of the output can be described by [12]:

$$\begin{cases} \mathbf{E}[Y] &= p \\ \mathbf{Var}(Y) &= p^2(1-p)^2\frac{\sigma_0^2}{n}. \end{cases} \quad (3)$$

where n is the number of bacteria in each node and $\sigma_0^2 = \frac{\sigma_\gamma^2}{\gamma_0^2} + \frac{\sigma_\kappa^2}{\kappa_0^2}$.

In the m-ary scenario, the information is encoded in m levels of concentrations in the range $[0, A_{\max}]$. Note that the maximum level of concentration of molecules induced at the receiver $A_{\max}$ depends on the transmitter functionality and its distance from the receiver. Note that since we are only interested in the steady-state behavior of the response, $A_{\max}$ decreases inversely with the distance between the transmitter and the the receiver [17]. Equivalently, one may imagine the m information symbols being chosen from the interval $[0\ p_{\max}]$ where $p_{\max} = \frac{A_{\max}\gamma}{A_{\max}\gamma+\kappa}$. One can obtain the optimal distribution of the symbols such that it minimizes the probability of the decoding error for a direct communication from the transmitter to the receiver [12]. At the receiver node, the thresholds for decoding the m symbols are set by the Maximum Likelihood (ML) decoding of the symbol [12].

We analyzed the information rate and probability of error for such a setup in [12]. We showed that how increasing either $A_{\max}$ or n increases the reliability of the communication. In particular, we showed that for a fixed number of bacteria in the nodes n, reliable communication is not possible for m larger than a threshold. In the next section, we study how relaying can improve the reliability of communication and allow to use larger values of m.

III. Decode and Forward Relaying in m-ary Molecular Communication

The schematic for a relay setup is shown in Fig. 2. In this setup, the relay node forms another path to the receiver node to help the receiver (from now on called the destination) in decoding the information. We assume that nodes are able to produce as well as decode m levels of concentration of molecules. The transmitter broadcasts the information symbols

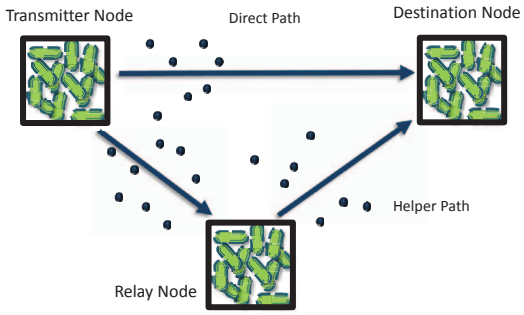


Fig. 2. Communication via molecular relaying.

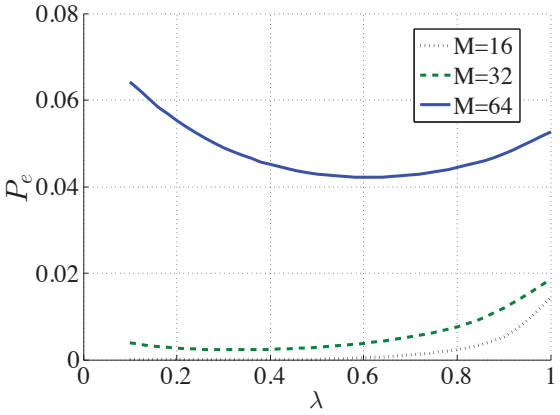


Fig. 3. Average probability of error vs λ for different m-ary schemes.

through type I molecules to both the relay and the destination nodes. The received symbol by the relay node is decoded and forwarded to the destination alongside with the symbol from the direct path.

As discussed in the previous section, the m symbols are placed uniformly in the interval $[0\ \ p_{\max}]$. Hence, the i^{th} symbol corresponds to $p_i = \frac{i}{m-1}p_{\max}$ for $i = 0, 1..., m-1$. In the setup shown in Fig. 2, the direct distances from the transmitter to the destination, from the transmitter to the relay and from the relay to the destination are assumed r_1, r_2 and r_3, respectively. Note that since the distances may not be equal, each symbol would correspond to a different concentration of molecules at the nodes. Hence, in order to obtain the proper symbols, nodes must know the distances and scale the concentration of molecules accordingly. Here, without loss of generality, we assume that $r_1 = r_2 = r_3$. We assume that the relay node behaves according to the same model we described for the reception and decoding in Sec. II. As discussed there, the output of the bacteria can be altered by manipulating the corresponding genes. Hence, the only difference between the relay and receiver nodes is that the output of the relay node, instead of GFP, is a molecular signal. Using (3), the output Y at the relay due to the transmission of the symbol p where

$p \in p_0, p_2, \ldots, p_{m-1}$, would be equal to

$$Y = p + p(1-p)\epsilon \tag{4}$$

where ϵ is a zero-mean Gaussian noise with the variance $\frac{\sigma_0^2}{n}$. Upon the reception of the molecules, the relay forwards the decoded symbol p_{R} by using type II molecules (i.e., hetero-type relaying). Note that due to noisy decoding at the relay, p_{R} is not necessarily equal to p. The two types of molecules arriving from both the direct path and from the relay are then used at the destination to decode the transmitted symbol.

The two types of molecules at the receiver would result in two different outputs such as GFP and YFP, i.e., the Green and Yellow Fluorescent Proteins. We neglect the subtle interference between the two different types of molecules at the receiver and assume that they act independently. The rationale is that the reception and production of molecules at the relay incur huge amounts of delay. As a result, we have two different time slots for the reception of type I and II molecules at the destination node. We assume that the reception process is the same for the two types of molecules but only differs in the noise attribute σ_0^2 in (3). We denote by Y_{D} and Y_{R} the outputs due to the direct and relay paths, respectively. Hence, we have

$$\begin{cases} Y_{\mathrm{D}} &= p + p(1-p)\epsilon_{\mathrm{D}} \\ Y_{\mathrm{R}} &= p_{\mathrm{R}} + p_{\mathrm{R}}(1-p_{\mathrm{R}})\epsilon_{\mathrm{R}} \end{cases} \tag{5}$$

where ϵ_{D} and ϵ_{R} are zero-mean noises with variances $\frac{\sigma_{\mathrm{D}}^2}{n}$ and $\frac{\sigma_{\mathrm{R}}^2}{n}$, respectively. Note that σ_{D}^2 and σ_{R}^2 correspond to the noises in the reception of type I and II molecules, respectively. Moreover, p_{R} would not be the same as P if an error occurs in decoding of the sent symbol at the relay node.

In [13], we studied the performance of Maximum Likelihood (ML) decoding when there was only one type of molecule at the receiver node. Since, in this case, the noise depends on the input signal and moreover error may incur at the relay node, the maximum likelihood decoding would be complicated at the receiver node. Therefore, we consider a linear combination of the outputs $Y = w_{\mathrm{D}}Y_{\mathrm{D}} + w_{\mathrm{R}}Y_{\mathrm{R}}$ in order to decode the transmitted symbol. In a collocated multiantenna setup [18], Maximum Ratio Combining (MRC) employs the optimal weights $w_i = \frac{h_i}{\bar{n_i}^2}$, where h_i is the attenuation of the i^{th} channel and $\bar{n_i}^2$ is the average power of the corresponding channel noise. Likewise, adapting MRC in our setup, the optimal weights are given by $w_{\mathrm{R}} = \frac{1}{\sigma_{\mathrm{R}}^2}$ and $w_{\mathrm{D}} = \frac{1}{\sigma_{\mathrm{D}}^2}$. However, since the relaying node may have a decoding error (i.e., $p_{\mathrm{R}} \neq p$), the performance of MRC would not be optimal for our setup.

Different approaches have been proposed in classical wireless communication literature to find the optimal weights in a decode and forward relaying scenario. In [19], the two consecutive source-relay and relay-destination channels are replaced with an equivalent Gaussian channel. In [20], authors have introduced a generalized form of λ-MRC in which w_{D} is fixed to its MRC value and w_{R} is considered to be λ times its MRC value, where $0 \leq \lambda \leq 1$. Here we use a similar method as the one in λ-MRC. Without loss of generality, we assume $\sigma_{\mathrm{R}}^2 = \sigma_{\mathrm{D}}^2 = \sigma_0^2$. Further, we fix $w_{\mathrm{D}} = \frac{1}{\sigma_0^2}$ and assume $w_{\mathrm{R}} = \frac{\lambda}{\sigma_0^2}$ where $0 \leq \lambda \leq 1$. Hence, by combining the outputs in (5), we have

$$Y = p + \lambda p_{\mathrm{R}} + \epsilon_Y, \tag{6}$$

where ϵ_Y is a zero-mean Gaussian noise with the variance $\frac{\sigma_0^2}{n}(p^2(1-p)^2 + \lambda^2 p_{\mathrm{R}}^2(1-p_{\mathrm{R}})^2)$. We obtain the optimal value of λ such that it minimizes the average probability of error. Note that in the m-ary system introduced in Sec. II, the corresponding error probability depends on the symbol. Hence, we minimize the average probability of error as

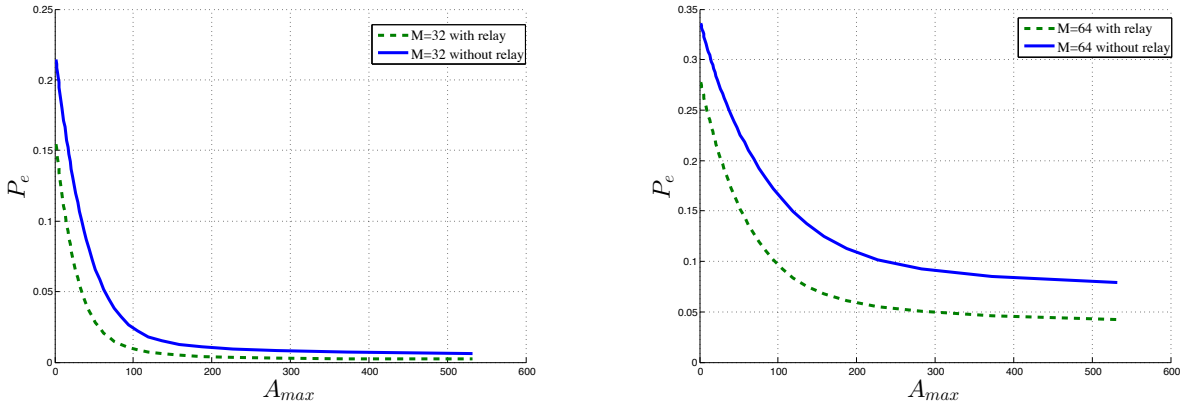
$$P_e = \sum_{i=1}^{M} (P_e|p_i)P(p_i), \tag{7}$$

where the weights $P(p_i)$ corresponding to each symbol are as in [12]. In obtaining P_e, we assume that only transition to the adjacent symbols may result in the error at the relay node. In other words, if the i^{th} symbol is sent, p_{R} would be in $\{p_{i-1}, p_i, p_{i+1}\}$. In Fig. 3, we have plotted P_e vs λ for different values of m. The results are shown for $n = 100$, $p_{\max} = 0.95$ and $\sigma_0^2 = 0.1$. Fig. 3, implies an optimal λ for reliability. The rationale for this behavior is that increasing λ, on the one hand, increases the maximum range of the output and hence, increasing the reliability. On the other hand, the influence of the more noisy symbol from the relay node is increased which decreases the reliability.

In Fig. 4, we have plotted the probability of error versus the maximum concentration of molecules in NanoMolar (nM) with and without using the relay with the optimal choice for λ for $m = 64$ and $m = 32$. As we see in the plots, the effect of relaying diminishes for large values of $A_{\max}$ when the probability of error goes to zero for $m = 32$, but prevails otherwise for $m = 64$. In other words, for $m = 64$ and for $A_{max} > 100$, we would need to increase A_{max} very significantly to achieve the same error rate as relaying.

IV. Decode and Forward relaying in m-ary DbMC using the same type of molecule

In this section, we study the scenario in which the relay node decodes the incoming information symbol from the transmitter and forwards it via the same type of molecules to the destination. We compare the performance of such a relaying scenario with the hetero-type relaying scenario discussed in the previous section. It is important to note that we assume the production of the same type of molecules by the relay does not affect the relay input coming from the transmitter. The relay output production contains a huge amount of delay and the relay node can be designed such that the production of molecules would shut off the reception of molecules by the relay node. The arriving molecules from both the relay and direct paths would form the concentration of molecules at the receiver. Since the relay employs the same type of molecules as at the transmitter node and also the diffusion process is linear [17], the concentration of molecules at the receiver would be the superposition of the individual concentrations of molecules induced by the transmitter and the relay nodes.



(a) m=32 (b) m=64

Fig. 4. The average probability of error with and without using relaying vs maximum concentration of molecules.

Suppose the transmitter broadcasts the i^{th} symbol resulting the concentration A_i at the receiver node (i.e., corresponding to the probability p_i). Assume the symbol j is decoded at the relay and is forwarded to the receiver. Hence, the concentration of molecules at the receiver is equal to $A_{\text{D}} = A_i + A_j$ where A_j is the concentration of molecules induced by the relay at the receiver node. Note that we again assume that the distances in Fig. 2 are all equal to r. Otherwise, we have to scale the concentration of molecules at the nodes. Hence, the average probability of activation of receptors at the receiver is obtained as

$$p_{\text{D}} = \frac{(A_i + A_j)\gamma}{(A_i + A_j)\gamma + \kappa}. \tag{8}$$

Note that if no error occurs at the relay (i.e., $i = j$), the effect of relaying would have been equivalent to doubling the range of concentration of molecules at the receiver. We again assume that a decoding error at the relay could only occur between the adjacent symbols of the originally transmitted symbol.

We have plotted the probability of error for the same-type relaying scenario in Fig. 5 and compared it to the hetero-type relaying discussed in the previous section. We have used the parameters $n = 100$ and $\sigma_0^2 = 0.1$, as in the previous section. The results are shown for $m = 32$ and $m = 64$. As we see in the plot, the same-type relaying slightly outperforms the hetero-type scenario for mid-level concentration of molecules but it underperforms otherwise. Moreover, by comparing this plot with Fig. 4, we observe that same-type relaying loses its effectiveness for large A_{max}. This is in contrast with hetero-type relaying which is effective even for large A_{max}. This is due to the fact that hetero-type relaying not only results in the extension of the range of the molecular concentration but also results in the diversity at the receiver.

V. Conclusion

In this paper, we studied the decode and forward relaying in the context of m-ary diffusion-based molecular communication. In such a scenario, the relay node decodes the incoming symbol from the transmitter and forwards it to the destination using the same or different type of molecules as the transmitter. In the case of using two types of molecules, we showed as to how the optimal combining of the outputs results in improving the reliability of the communication. We also compared the results with the same-type relaying scenario. We showed that except for the mid-range values of maximum concentration of molecules, the hetero-type relaying outperforms the same-type relaying.

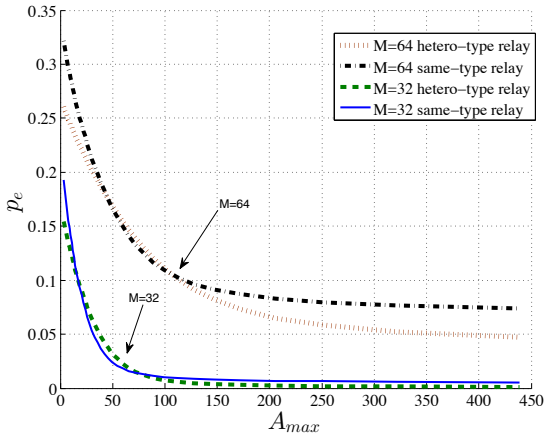


Fig. 5. Comparison between relaying using one and two types of molecules.

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