Carrier Allocation in Mobile Bacteria Networks

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Abstract—We propose a transmission model for bacteria networks inspired by *ad hoc* wireless mobile networks. Using bacteria as a message transmission medium has been proposed as a promising way in molecular communication. The expected message delivery delay is derived for single source-destination pair and can be approximated by a convex function of the number of available carriers in the environment. In the scenario with multiple source-destination pairs, bacteria serving as the medium of message transmission are viewed as a limited resource, since each source-destination pair requires unoccupied carriers to transfer messages. We show that optimal resource allocation can be achieved while satisfying a priority requirement by controlling the release probability of messages at the source nodes. This suggests a guideline for communicating prioritized tasks in ad hoc bacteria networks

Index Terms—molecular communication, Markov processes, convex functions, mobile ad hoc networks

I. INTRODUCTION

Communication between nanomachines is an ongoing research area with two main approaches: electromagnetic (EM) and molecular transmission [1]. Due to the size of nanomachines, traditional communication structures and techniques are not directly applicable. Hence, EM approaches [2] mainly focus on novel materials such as graphene or carbon nanotubes to implement nano-scale transceivers. Molecular approaches are inspired by biological systems and can send information in either passive or active modes [3].

The development of efficient and reliable communication scheme, however, is still an area of active research. A number of solutions in molecular communication have been proposed, such as calcium signaling, neuron-based nanomachines, carbon nanotubes, and bacteria networks. Bacteria networks have been proposed as a promising communication method in nanonetworks thanks to biased motility of bacteria and highthroughput message transfer potential of DNA molecules.

The nanonetwork architecture for medium-range communication using flagellated bacteria was described in [4]. An analytic model was studied in [5] and showed to be a highthroughput transmission scheme compared to other molecular communication approaches. The network performance in terms of capacity and end-to-end delay is also considered in their work. In [6], an opportunistic routing approach for multi-hop message transfers through bacteria conjugation is considered. These investigations provide great background and understanding of the benefits and challenges of bacteria nanonetworks.

This work extends previous work by considering the mobile node network rather than fixed topology. To the best of the authors' knowledge, this is the first work in the literature that combines the notion of bacteria networks with *ad hoc* mobile nodes. The message delivery delay performance is derived based on a cell-based i.i.d. model as in [7]. For the multi-pair scenario, we consider different priorities for source-destination pairs and propose a transmission scheme that approximating the optimal allocation of available carriers.

The rest of the paper is organized as follows. In section II, we introduce biological background for bacteria nanonetwork and state the model assumptions used in this work. Section III presents the analysis for single source-destination pair that shows expected delay is a convex function. We extend the analysis to multiple pairs in Section IV, where we view message transmission as a resource allocation problem and propose strategy to approximate the optimal allocation of carriers for prioritized tasks. In Section V, we draw the conclusions and discuss future work.

II. NANONETWORK SYSTEM MODEL

A. Biological Background

A bacteria network (BN) consists of nodes and carriers, which are roaming in a fluid medium as shown in Fig. 1. Nodes are considered to be bio-hybrid nanomachines that can perform either computing, sensing and/or actuation [8]. Information carriers are bacteria that can carry DNA packets. As in wireless communication, where information is carried via electromagnetic waves, nanomachines in BN communicate by exchanging DNA molecules via bacteria carriers, which take DNA packets from the transmitter to the receiver [4], [5].

Serving as information carriers, the mobility of bacteria is crucial to facilitate the communication process. Bacteria are capable of moving in the liquid by flagella, a tail-like appendage to propel them in a certain direction. The *chemotaxis* process, is the characteristic movement of a bacterial cell along a chemical concentration gradient [9]. Usually, the bacteria swim toward higher concentrations of beneficial chemicals called attractants. Consider *E. Coli* for example. It can sense at least 12 different attractants using different chemoreceptors that give independent chemotactic responses [9].

The genetic information transfer between bacterial cells is accomplished by bacterial *conjugation* process. It is a process involving direct contact of the bacteria to perform genetic materials transfer [10] and to pass on beneficial information to the recipient cells. The conjugation duration depends on the amount of information in the gene, the longer the gene, the longer the conjugation process [6].

B. Related Work

A mathematical model for characterizing the delay from forming a message at the source node to interpret the message at the receiver node is presented in [5]. In particular, the delay is decomposed into the encoding delay, encapsulation delay, propagation delay, decapsulation delay, and decoding delay. In our work, we mainly consider the propagation delay, i.e., the time required by bacteria to move from the transmitter node to the receiver node. The delay can be shortened if nodes can emit attractants to create concentration gradient of chemicals to facilitate the *chemotaxis* process of bacteria. Therefore, transmitter nodes (source nodes) emit transmission attractants (TA) and receiver nodes (destination nodes) emit reception attractants (RA) [5], which only combine with the chemoreceptors on bacteria without and with messages, respectively.

In [4], the framework of using flagellated bacteria as message carriers is proposed, and the physical channel characterization is provided in [11]. Priorly designed message can be encoded and embedded into a DNA plasmid used for information transfer [12]. The transmitter nodes can carry the constructed commands or synthesized messages that are referred to as DNA packets. They are set to be actively sending commands to react to the observations of the environment. The receiver nodes are assumed to be capable of decoding messages and responding accordingly based on the received DNA packets.

Since the bacteria and the nodes are both continuously moving, we propose to combine the notion of bacteria network with mobile *ad hoc* networks in the wireless literature. In this work, we apply the cell partitioned i.i.d. mobility model as studied in [7], which will be explained in section II.C. Other alternate mobility models can be found in [13].

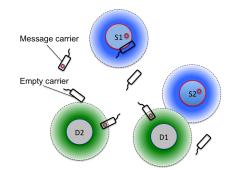


Figure 1: Illustration of the bacteria network. The blue and green regions refer to the effective regions of transmission attractants (TA) and releasing attractants (RA), respectively. Empty carriers are attracted by the TA while message carriers are attracted by the RA.

C. System Model

We model the environment with N equally-partitioned cells as shown in Fig. 2. The system has n pair of nodes and Mbacteria serving as carriers in the network. Time is slotted so that the message transfer process can be accomplished within one time-slot if nodes and carriers are within the same cell. Similar to [7], we apply the *i.i.d.* mobility model, which means that each node or carrier roams to a different cell in each timeslot, independently of its cell in the previous time-slot, and independently across nodes and carriers. Nodes and carriers remain in their current cells for one time-slot and move to a new cell at the end of the time-slot. Carriers within the same cell as the nodes are assumed to be within attractant's effective range, while they are insensitive to attractants outside their current cells.

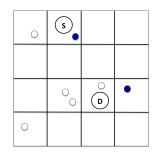


Figure 2: Illustration of single source-destination pair (n = 1) with N = 16 and M = 7 (5 empty carriers and 2 message carriers) in the network.

Throughout the rest of this paper, we refer to the bacteria as *message carriers* for those currently containing message, while as *empty carriers* for those not carrying messages. After the reception of a message at a destination node, we assume that the message carried in the message carrier is destroyed and the message carrier becomes an empty carrier that is sensitive to the TA.

The DNA message transfer process between bacterial carriers and nanomachines are assumed to be similar to the *conjugation* process. Also, one node is allowed to interact with a single bacterial carrier one at a time, i.e., if there are two empty carriers within the TA range of the source node, only one of the empty carriers will perform *conjugation* with the node and become a message carrier. Another empty carrier will remain in the empty status. To simplify the analysis, we limit the bacterial carriers to at most carrying one set of messages from a source node.

III. SINGLE SOURCE-DESTINATION PAIR

In this section, we consider the case where we have only single S-D pair in the network. We use m = 0, 1, ..., M to denote the number of message carriers carrying information for the source S. The number of empty carriers is thus M-m. At a particular time-slot, the probability of having at least one empty carriers within the same cell as S is

$$p_m = 1 - \left(1 - \frac{1}{N}\right)^{M-m}$$
. (1)

The probability that at least one message carrier is within the same cell as D is

$$q_m = 1 - \left(1 - \frac{1}{N}\right)^m$$
. (2)

A. Stationary Distribution

In the steady state, we can model the dynamics of the number of message carriers in the environment as a Markov chain. The state transition diagram is shown in Fig. 3.

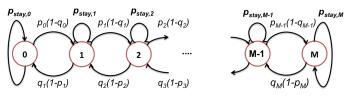


Figure 3: The state transition diagram of the number of message carriers in the steady state.

The probabilities of increasing one message carrier, reducing one message carrier, and remaining at the same number of message carrier in the next time-slot are defined as following respectively,

$$p_{right} = p_i(1 - q_i),\tag{3}$$

$$p_{left} = (1 - p_i)q_i, \tag{4}$$

$$p_{stay,i} = 1 - p_{right} - p_{left}.$$
(5)

Note that in the steady state, the rate of generating empty carriers and message carriers in the system will be the same. Therefore, the stationary distribution of the number of message carriers is expected to be centered at half of the total available carriers M. The intuition is verified by numerical computation and system simulation histogram as shown in Fig. 4.

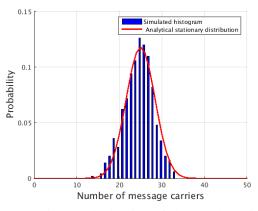


Figure 4: Stationary distribution of the number of message carriers. The smooth (red) curve represents the result obtained by numerical computation of stationary distribution. The histogram is obtained by simulation for the case of N = 125, M = 50.

B. Expected Delay

It is of great interest to know the delay for a newly generated message at the source node to arrive at the destination node. Let t_0 be the time when a new message is generated at S, and t_1 be the time when one of the message carriers carrying the new message passes it to D. The quantity of interest is therefore $E[t_1 - t_0]$. Note that in the steady state, there are often some occupied carriers before the new message generated. Let $E[\sigma|m, n]$ be the average message delay remaining given that there are m message carriers carrying the "new" message and n message carriers carrying the "old" messages. By definition, we have

$$E[t_1 - t_0] = E_n \left[E\left[\sigma | m = 0, n \right] \right].$$
(6)

In the future, we will use the notation $E_M [\sigma | m = 0]$ to denote the quantity in (6). We first compute $E [\sigma | m, n]$. In each time-slot, we consider three possible events:

- A: At least one of the message carriers carrying the "new" message meets D. The "new" message is delivered to D in the current time-slot.
- **B:** At least 1 of the message carriers carrying the "old" msg meets D. Therefore, *n* decreases by 1.
- C: At least 1 of the empty carriers meets S. Therefore, m increases by 1.

Considering the possible events at each time-slot, we can form the recursive equation,

$$E[\sigma|m,n] = 1 \cdot P(A) + (E[\sigma|m,n-1]+1) \cdot P(\bar{A} \cap B \cap \bar{C}) + (E[\sigma|m,n]+1) \cdot P(\bar{A} \cap \bar{B} \cap \bar{C}) + (E[\sigma|m+1,n]+1) \cdot P(\bar{A} \cap \bar{B} \cap C) + (E[\sigma|m+1,n-1]+1) \cdot P(\bar{A} \cap B \cap C).$$
(7)

Note that the events A, B, and C are independent with each probability given as follows,

$$P(A) = 1 - \left(1 - \frac{1}{N}\right)^m,$$
 (8)

$$P(B) = 1 - \left(1 - \frac{1}{N}\right)^n,$$
(9)

$$P(C) = 1 - \left(1 - \frac{1}{N}\right)^{M - m - n}.$$
 (10)

Since the maximum number of message carriers is M, and the expected message delivery time when we have M message carriers is the mean of a geometric random variable with parameter $1 - \left(1 - \frac{1}{N}\right)^M$, we have

$$E[\sigma|m = M, n = 0] = \frac{1}{1 - \left(1 - \frac{1}{N}\right)^M}.$$
 (11)

We can therefore obtain $E[\sigma|m,n]$ for every m,n = 0, 1, ..., M recursively by (7). $E_M[\sigma|m=0]$ is computed for each particular M by

$$E_n [E[\sigma|m=0,n]] = \sum_n E[\sigma|m=0,n]p[n],$$
(12)

where p[n] is the stationary distribution as explained in previous section.

C. Approximating the Delay by a Convex Function

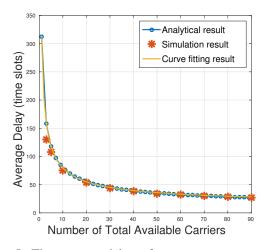


Figure 5: The average delay of a new message versus the number of total available carriers is derived and verified by simulation results. Here we have the number of cells N = 125.

The expected delay has the appearance of a convex function with respect to the number of available carriers M in the environment as shown in Fig. 5. We can approximate the function in the form of a convex cost function

$$f(M) = -w_s \frac{M^{1-\alpha}}{1-\alpha} + c,$$
 (13)

where w_s and α are scaling parameters, and c is the offset of the curve. By least-square curve fitting approach, we obtain the parameters to be $\alpha = 1.646$, $w_s = 193.53$, c = 11.93 for the case N = 125. Based on this approximation, we formulate a convex problem and solve for the optimal available carriers for multiple source-destination pairs as shown in the next section.

IV. MULTIPLE SOURCE-DESTINATION PAIRS

In this section, we discuss the design problem in this case of multiple source-destination pairs. Since the number of available carriers to carry information in the environment is fixed, we can view carriers as a limited resource that is shared by all S-D pairs. The problem now is: how can we allocate the resource among all the pairs to have overall minimum delivery time in the system?

To simplify the analytical solution, we first consider partitioned multiple S-D pairs scenario. That is, we form the optimization problem of minimizing the total system delay by using the weighted sums of single S-D pair delays. We later simulate the practical situation using the result from the simplified math model and show that it gives a satisfactory result and provides useful intuition for system designing.

A. Resource allocation: the homogeneous Case

Let M_i be the number of carriers allocating to pair *i*. Then we can form the partitioned multiple S-D pair problem as,

$$\begin{array}{ll} \underset{M_{i}}{\text{minimize}} & \sum_{i=1}^{n} E_{M_{i}}[\sigma | m = 0] \\ \text{subject to} & \sum_{i=1}^{n} M_{i} \leq M. \end{array}$$

$$(14)$$

By approximating $E_{M_i}[\sigma|m=0]$ by (13), the solution is

$$M_i^* = \frac{M}{n}$$
, for $i = 1, 2, ..., n.$ (15)

This is an intuitive solution due to the diminishing return property in the improvement of average delay with the number of available carriers. Specifically, the reduction of the average delay for increasing one more available carriers in one pair is less than the increase in the average delay of another pair. Hence, the optimal solution is obtained by averaging the total available carriers equally to all the pairs needed.

B. Different Pair Priorities

The message delay requirement may not be the same for different S-D pairs. For example, some pairs of nodes are responsible for communications that require quick responses to detected malicious events. We would like those pairs to stimulate the immune system more quickly to react, i.e. shorter delay. In such scenarios, we modify (14) by introducing weighting factors $w_i \ge 0$ before the expected delay for each S-D pair i,

$$\begin{array}{ll} \underset{M_{i}}{\text{minimize}} & \sum_{i=1}^{n} w_{i} E_{M_{i}}[\sigma | m = 0] \\ \text{subject to} & \sum_{i=1}^{n} M_{i} \leq M. \end{array}$$

$$(16)$$

Note that a larger w_i indicates higher priority for pair *i*. The optimal allocated number of carriers for pair *i* is given by

$$M_i^* = M\left(\frac{w_i^{1/\alpha}}{\sum_{i=1}^n w_i^{1/\alpha}}\right), \text{ for } i = 1, ..., n.$$
 (17)

C. Approximating the Optimal Resource Allocation

In Sections IV.A and IV.B, we have assumed that the carriers are partitioned in such a way that there is a dedicated subset of carriers for each source-destination pair. In practice, such partitioning may not be feasible. Next, we consider an alternate scenarios where carriers are not partitioned. Consider any one of the M carriers. Its state transition diagram is shown in Fig. 6, where the state 0 represents it being an empty carrier, and the state k represents that the carrier is carrying messages for pair k. The probability of a message carrier switching to state 0 at the next timeslot is $\gamma \simeq 1/N$, while the probability of staying at its current state is $1 - \gamma$. We will control the values of β_k below to achieve a desired allocation of carriers. Note that here we assume that $N \gg M$ so that the probability of having two nodes or two carriers in the same cell at a particular

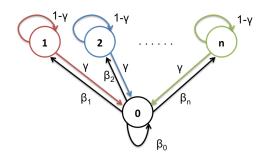


Figure 6: Approximated state transition diagram of a single carrier for estimating the number of message carriers for each S-D pair. We assume $N \gg M$.

timeslot is negligible. Thus, the state transitions of different carriers can be taken as independent.

In order to adjust the ratio of the number of message carriers dedicated to different S-D pairs in the steady state, we introduce the parameter a_i to be the release probability at the source node *i*. That is, the source node of pair *i* only passes its message to an empty carrier with probability a_i . Then, the probability β_0 of an empty carrier staying at state 0, and the probabilities β_k of switching to state *k*, at the next timeslot, are, respectively,

$$\beta_0 = \prod_{i=1}^n \left(1 - \frac{1}{N} a_i \right),\tag{18}$$

$$\beta_k \simeq \frac{1}{N} a_k \prod_{i \neq k}^n \left(1 - \frac{1}{N} a_i \right), \quad k = 1, 2, ..., n.$$
 (19)

Note that here we use again the approximation that the probability of having two nodes in the same cell at a particular time slot is negligible. Solving for the stationary distribution, we have

$$\pi_0 = \frac{1}{1 + N \sum_{i=1}^n \beta_i},$$
(20)

$$\pi_k = (N\beta_k)\pi_0, \quad k = 1, 2, ..., n.$$
 (21)

By a similar analysis, we can derive the total number of message carriers being a faction of the total available carriers as follows,

$$\sum m_i^* = \eta M,\tag{22}$$

where $\eta = (1 - \beta_0)/(1 - \beta_0 + \gamma)$ and m_i^* is the number of message carriers of pair *i* in the steady state. We now propose a heuristic way to emulate the partitioned multi-pair model with $\sum M_i^* = M$. Specifically, we set

$$m_i^* = \eta M_i^*. \tag{23}$$

By combining (21) and (23), we have

$$\beta_i = (1 - \beta_0) \left(\frac{M_i^*}{M}\right), \quad i = 1, ..., n.$$
 (24)

This results in n equations for solving n variables, i.e. the $a'_i s$. Let $a_{j_{\text{max}}} = 1$, where $j_{\text{max}} = \arg \max_i w_i$, the rest of the release probabilities can be solved by Newton's method.

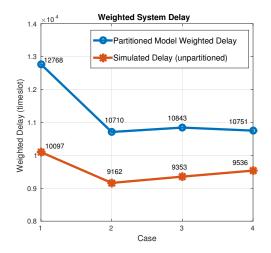


Figure 7: The weighted system delay of four cases with different release probability for 3 S-D pairs with weights $\{1, 25, 50\}$. The four cases of $\{a_1, a_2, a_3\}$ are $\{1, 1, 1\}$, $\{0.17, 0.44, 1.00\}$, $\{0.2, 0.8, 1.0\}$ and $\{0.1, 0.5, 1.0\}$.

D. Simulation Results

We show the simulation with multiple S-D pairs using n = 3, N = 500, and M = 100. The release probabilities are calculated by the method described in the previous section and adopted in the corresponding source nodes. Four cases of different release probabilities are compared and shown in Fig. 7, where Case 2 is the result of using the release probabilities defined in (24). We see that the system indeed achieve smaller weighted delay both in the partitioned model and in our simulation scenarios.

V. CONCLUSION AND FUTURE WORK

This work presents an analysis of bacteria networks based on a mobile *ad hoc* network model. Average message delivery delay is derived for the case of a single source-destination pair and is approximated by a convex function with respect to the number of available carriers in the environment.

In the multi-pair scenario, bacteria carriers can be viewed as a limited resource for each S-D pair since each pair expects minimum delays. We solve the optimal carrier allocation for a partitioned multi-pair model, based on which we design a heuristic transmission strategy. We show by simulation that by controlling the release probability at the source nodes, the system can achieve smaller weighted delay for S-D pairs with different priorities. The exact analytical expression for the delay for the unpartitioned case with multiple S-D pairs is left in our future work.

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