Performance Comparison of Message Encoding Techniques for Bacterial Nanonetworks

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***Abstract*—Utilizing bacteria as information carriers is a promising technique for *molecular communication* to establish connections and networking capabilities between micro- and nanoscale devices. A particular process, that is of interest in this paper, and vital to achieve reliable networking performance in bacterial nanonetwork, is conjugation. Conjugation is a process where bacteria come within close range to form physical connections to allow plasmids to be transferred. However, there are a number of processes that could cause loss or damage during the transfer process, such as external vibrations. Message encoding techniques are envisioned as a promising technique to mitigate these effects. In this study we first define the concept of optimal message encoding for bacterial nanonetworks providing the upper bound on the message delivery time and the probability of message delivery within the specified time. We then investigate the effect of encoding on the performance of these metrics by proposing and numerically comparing several feasible encoding techniques. The performance comparison has been done using a specifically developed simulation environment capturing bacteria movement and interactions. Numerical results demonstrate that even the simple encoding strategies allow to significantly improve the performance compared to the baseline system.**

I. Introduction

The promising approach to enabling communications at the micro- and nanoscales in a biological environment is to rely on nature inspired paradigms. One of such approaches is to use bacteria for information transport between artificial micro- and nanomachines. Indeed, in addition to information delivery via swimming the bacteria offer a number of features required for end-to-end communications. Pertaining to information capacity, a bacterium contains a DNA molecule known as the plasmid having millions of base pairs that can potentially be used for data storage [1]. Recent developments in information encoding into DNA chains demonstrated that density of almost 2 bits per base pair can be achieved [2]. Theoretically, it gives us an opportunity to transfer gigabytes of data for distances of up to several millimeters (mm), which could be sufficient for many forthcoming applications for bacterial nanonetworks.

Establishing a reliable link between two nanomachines using bacteria is a non-trivial task. Aside from technological difficulties of reliable encoding and decoding at micro and nano scales there are inherent shortcomings due to random movement of bacteria. The basic approach to overcome randomness in bacterial nanonetworks is to release significant amount of bacteria with identical messages and, thus, let at least one of them reach the destination point with tolerable probability. Meanwhile, there are considerable drawbacks of this approach, such as non-efficient resource (bacteria) utilization and extensive flooding. One could also rely on the effect of chemotaxis to change the movement of a bacterium to the biased motility towards the source of the chemoattractant emitted by the receiver nanomachine [3]. However, this raises the questions of timely injection of the chemoattractant and its further effective removal from the environment. The third approach is to use the process of exchange of genetic information between emitted bacteria and those available in the environment, called conjugation [4]. In our recent study [5] we showed that this process may substantially improve the metrics pertaining to message delivery in bacterial nanonetworks including the message delivery time and delivery probability within the specified time. However, the conjugation process can face premature breakage that can result from environmental vibrations resulting in only the recipient with partially copied chromosome [4], [6].

One of the possible solutions to improve performance of the conjugation-enabled system is to use channel coding process. There are a number of error correction codes proposed to date that have proven their efficiency in modern communications systems. However, even the simplest ones such as capacity-approaching low-density parity-check codes are still not directly applicable to bacterial nanonetwork as their decoding complexity is still too high for prospective nanomachines. For these systems we have to develop unique codes that are (i) simple to decode and (ii) exploit natural properties of the bacterial nanonetworking environment.

In this paper we study the process of channel encoding for bacterial nanonetworks. To quantify the gain of the encoding process in conjugation-enabled environment we first construct the theoretical upper bound on the performance of optimal message encoding in bacterial nanonetworks. We propose a number of simple encoding schemes that are feasible for such systems including repetition-based, forward/reverse and cyclic shift encoding strategies. We then thoroughly evaluate the performance of the abovementioned encoding methods in terms of successful message decoding at the receiver and the average delay in a broad range of scenarios using our system-

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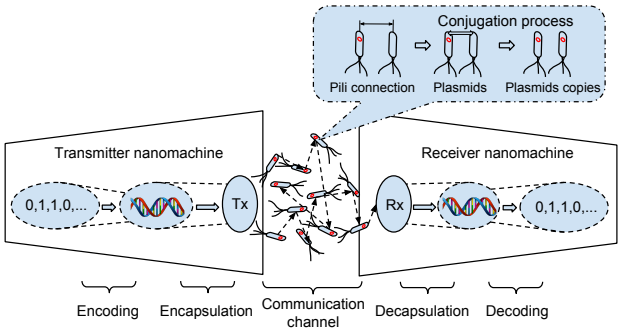


Fig. 1. End-to-end communication model.

level simulator for bacterial nanonetworks.

The rest of the paper is organized as follows. In Section II we present the communication model for bacterial nanonetworks and discuss the most important processes involved. The notion of optimal message encoding is defined in Section III. We also introduce practical encoding schemes there. In Section IV we describe our performance assessment framework and introduce our metrics of interest. Numerical results are provided in Section V. Conclusions are drawn in the last section.

II. Bacterial nanonetworks

The communication model for a single link of a bacterial nanonetwork is presented in Fig. 1. To establish communications between two nanomachines we use a number of bacterial properties. These are (i) message encoding into a DNA, (ii) picking up a DNA molecule by a bacterium, (iii) mobility of the bacteria, and (iv) conjugation. Below, we describe a set of operations and processes that could be considered as *channel coder* and *communication mechanism*.

A. Bacterial Mobility

A number of bacteria have capabilities of mobilizing themselves. An example is the *Escherichia coli (E.coli)*, which is the bacteria that we utilize for our nanonetworks. The motility process is through the flagella, which are tail-like structure that protrude from the body of the bacterium. When the flagella groups into a single body and rotates in an anticlockwise motion, this will lead to forward movement of the bacteria. According to the studies of E.Coli movement [7], [8] we know that in absence of external stimulus (i.e., attraction via chemiotaxis) the bacteria moves in the repetitive process between runs and tumbles. During the tumbling process the bacterium first chooses a direction angle a uniformly between 0 and 2π by swirling around and then moves along the straight line for exponentially distributed time T with mean $E[T] = 3.5$s. at constant speed $v = 20$mcm/s. The latter implies that the distance between two stopping points, D, is exponentially distributed with parameter $\lambda = 1/vE[T]$.

From the mathematical point of view, the bacterium swimming process is a modification of a classic Pearson-Rayleigh random walk [9]. Although the structure of the model is relatively simple, it is surprisingly difficult to analyze. Up to date only first-order properties, e.g. probability density of a position at the nth epoch have been obtained. As we will see in what follows, for bacterial nanonetworking applications the most important metric is the first passage time (FPT) distribution. Since no explicit analytical results are available for FPT distribution of this random movement model, it is often simulated in applied studies.

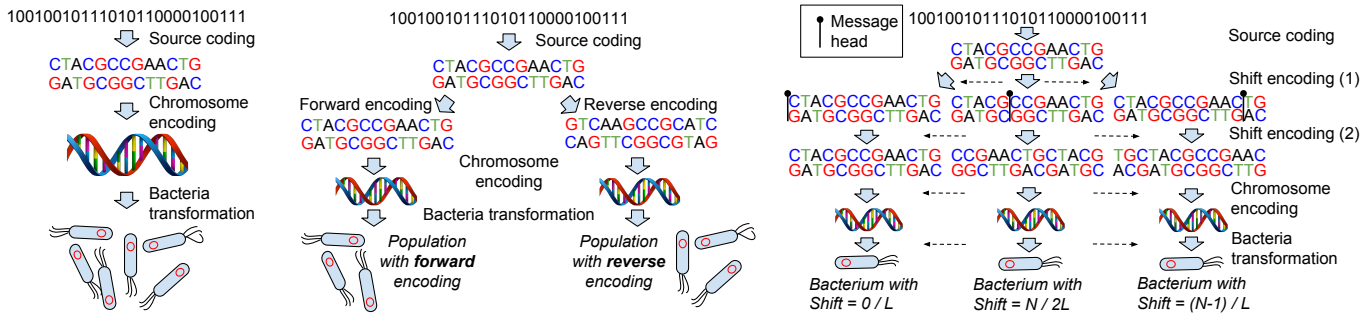
B. Bacterial conjugation

Due to the random movement, there is a non-zero probability of message not being delivered to the destination within a specified time. To decrease this probability one may (i) release a number of bacteria with identical messages encoded and/or (ii) utilize the effect called *conjugation* [4]. Bacterial conjugation is the unidirectional transfer of single stranded DNA (i.e. plasmid or chromosome) from a donor to a recipient cell using a transmembrane pore. Once the bacteria are within range of few millimeters from each other, the connection is formed to enable the DNA transfer. Naturally, the conjugation process helps the bacteria to exchange various genes, and one of these examples if the resistance genes to antibiotics.

We utilize the conjugation for developing artificial communication systems as follows. The message encoded into the plasmid is marked such that it is transmitted during the conjugation process to any bacteria that does not have the message yet. This increases the population of bacteria with particular message swimming in the environment and, consequently, improves the probability that one of these bacteria will reach the destination nanomachine within a given time. In a stable environment, the transfer speed achieves values of around 800 base pairs a second, which enables the whole chromosome to be copied within tens of minutes (full plasmid copying can take up to half an hour). However, the connection between bacteria performing conjugation is unstable and can be interrupted by mechanical stress or environmental vibrations (e.g., ultrasounds) resulting in partial message copying. Since the transfer of a message in conjugation starts at the prescribed point known as the *origin of Transfer* (*oriT*)and proceeds in one direction only the probability that the whole message is copied decreases with the message length.

C. Message decoding

Before we proceed describing the proposed encoding schemes we state our assumptions regarding the decoding process. Once a bacterium having full or partial copy of the plasmid reaches the nanomachine, the encoded message it carries is considered delivered. Although there is a number of technical questions how could this process be performed, in this paper we will assume the decoding is error-free, i.e. once a bacterium is picked up, the message encoded into the chromosome could be successfully decoded with probability one. Note that a particular bacterium may or may not have the whole message. The latter happens when a part of the original message have been copied during the conjugation process. Without channel coding, delivery of partial information to the receiver does not increase the probability of decoding of the whole message within a given time. In other words, the process of message delivery is said to be complete once one



(a) Replication encoding (b) Forward reverse encoding (c) Shift encoding

Fig. 2. Three message encoding techniques analyzed in the paper.

of the original bacterium or a bacterium that has successfully received the whole message during the conjugation with original bacterium reaches the destination nanomachine.

In real conditions a large quantity of partial messages could be received before the bacterium with the whole message arrives. Without channel coding, the delivery of partial information to the receiver does not assist the decoding process. Trying to benefit from the partial message delivery leads to the idea of selecting a proper message encoding technique.

III. Message Encoding Techniques

Throughout this section we assume that an informational message is encoded into the plasmid. The encoding process could be based on techniques proposed in [10] using the principle described in [2], where the information may contain the address of the source nanomachine as well as the type of condition (e.g., disease) that has been sensed.

A. Optimal encoding

The optimal encoding we consider is an upper bound on the encoding process that can be performed at the transmitter nanomachine. Let us assume that the transmitter nanomachine sends L bits of data using N bacteria, where storage of each bacterium is greater or equal to L. In case of an ideal source coder, the message entropy is close to L bits implying that at least L bits have to be delivered to the receiver nanomachine to get the message decoded. We define an optimal encoding as a technique that results in message being successfully decoded once L or more bits are received irrespective of what part of the message these bits belong to. Thus, the probability of successful decoding is $P_s = Pr\{\sum_{i=1}^{N} L_i^*(t) \geq L\}$, where $L_i^*(t)$ denotes the length of data segments received within a time period t, and N is the total number of bacteria, released by the transmitter nanomachine.

B. Replication-based encoding

The replication-based encoding, illustrated in Fig. 2(a), does not use any special transformations at the sender side. The whole message is divided into blocks of data of a certain sufficiently small and equal size, B_i, and the population having N bacteria is supplied with these blocks in the forward order. That is the message is $B_1, B_2, \ldots, B_M$. The bacteria are then released into environment.

C. Forward/Reverse encoding

Although the conjugation allows plasmids to be copied from one bacterium to another, environmental effects such as shaking or ultrasound may result in partial transfer of encoded information. Since multiple conjugations are allowed the size of the delivered message decreases as the number of conjugation grows. This effect is more profound when the size of the initial population is rather small compared to the number of free bacteria in the environment. To deal with this situation an intelligent but simple message encoding is needed.

The first scheme we proposed is the so-called forward/reverse message encoding illustrated in Fig. 2(b). According to this approach, the sender nanomachine creates two populations having $N/2$ bacteria each. Bacteria in the first population are supplied with a message having forward encoding $B_1, B_2, \ldots, B_M$ while the bacteria in the second population – with reversed order of blocks, i.e. $B_M, B_{M-1}, \ldots, B_1$. Since the conjugation process is assumed to start from the first block and may result in partial message transfer the dissemination of blocks in the environment increases resulting in more unique blocks arriving to the receiver nanomachine in a specified time.

D. Shift encoding

Shift encoding is another variant of the encoding process exploiting the fact that the transfer of data between the bacteria during the conjugation process starts from the beginning of the message. Here, the whole population of bacteria is divided into n groups each having N/n species, see Fig. 2(c). Each group receives a message shifted by a block with respect to the previous group, that is, species in group one have the message $B_1, B_2, \ldots, B_{M-1}, B_M$, species of the second group - $B_2, B_3, \ldots, B_M, B_1$ and so on until the last group having the message $B_M, B_1, \ldots, B_{M-1}$. This encoding process ensures that during the conjugation process the first block to read is not always the same but random among the whole number of blocks in a message.

IV. Performance Assessment Framework

A. System model description

We aim to evaluate the link-level performance in bacterial nanonetwokrs considering a single pair of nanomachines, source and destination. As envisioned by the end-to-end

TABLE I
PARAMETERS OF THE SIMULATED SCENARIO.

Parameter	Value
Bacteria swimming speed, ν	20μm/s [7], [8]
Bacteria run duration, exp. distributed, $1/\lambda$,	3.5s [7], [8]
Transfer speed during conjugation, f	833 bp/s [6]
Area of interest size, X^2	1cm^2
Destination nanomachine size, $2r$	100μm
Distance between the nanomachines, d	0-10mm
Number of released bacteria with message, N	10
Total number of bacteria in the area, M	0-1000
Message lengths, L	10Kbp
Conjugation Probability, ρ	1
Vibration stress, exp. distributed, λ_{Stress}	0-1Hz
Maximum delay bound, T	up to 24h

communication model described in Section II, the following system model is used. There is an area of interest with a number of bacteria swimming in it. None of them originally contains any message implying that all are technically capable to conjugate to receive one. Bacteria mobility model follows the mobility pattern described by Wang et. al [7], [8]. Source and destination nanomachines are deployed in the center of the area of interest, $d$mm distance each other.

At time $t = 0$, the source nanomachine releases N bacteria with the pre-encoded messages towards the destination nanomachine. These bacteria swim with the same pattern as others and, eventually, transfer their messages to other bacteria through the conjugation process. The active conjugations can be interrupted by an external vibrations process. We model external vibrations using the homogeneous Poisson process with intensity λ_{Stress}. When the vibration occurs, all the active conjugation links are terminated resulting in partial message copying to the recipient bacterium in each of the conjugations. Both released bacteria and the original bacteria that have a partial of full copy of the message, if captured by the destination nanomachine, unloads their data to the decoder. The destination nanomachine combines the received data with those received prior to this moment aiming to assemble and decode the original message. The scenario is over once the decoding process successfully finishes or, depending on the metric of interest, after the maximum delay bound is reached. Table I summarizes the values of input parameters.

B. Metrics of interest

We focus on two metrics as part of our analysis:

- *Propagation delay, D*, refers to the time interval between the bacteria that are released from the source nanomachine until the entire message is delivered and assembled at the destination.
- *Link reliability, ρ*, refers to the probability of a message being successfully delivered from the source nanomachine to the destination nanomachine within the specified time. With respect to the system model, assuming a single message to be transmitted, the link reliability is equal to the probability of successful message decoding at the destination nanomachine.

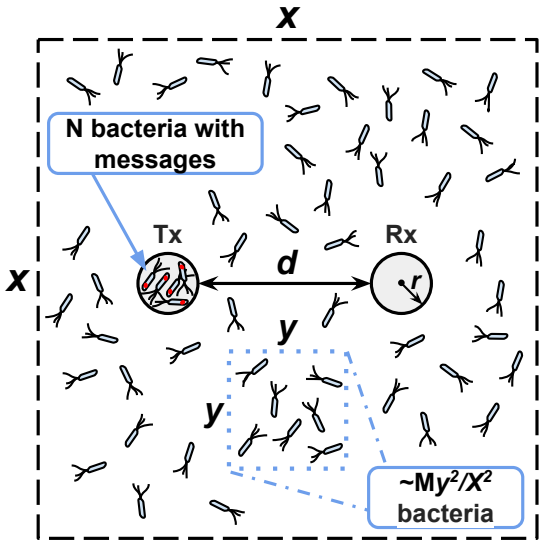


Fig. 3. Simulated scenario.

Both metrics depend on the characteristics of bacteria propagation process through the medium and encoding schemes being used. In the following section we propose an appropriate simulation methodology to derive these metrics.

C. Simulator description

In order to analyze the performance of the encoding techniques in the environment described above, we developed our own simulation environment. There are a number of simulators available for molecular communication and, particularly, bacterial nanonetworks, e.g., BNSim [11], NFsim [12] and BioNetGen [13] to name a few. Most of these simulators, however, abstracts the bacteria motility process by a biased movement model. For example, the movement incorporated in BNSim by default assume chemoattractant available in the environment and use the Berg and Brown [3] data to model the biased version of the Pearson-Rayleign random walk by fitted Gamma distribution. Since the movement process of bacteria is of special interest in the context of the introduced metrics we have to model it explicitly to achieve the desired accuracy. On top of this, the cited simulation environment are too concentrated on specific features they have been developed for making them inefficient for encoding analysis.

The utilized simulation tool, NCSim [14], is a comprehensive time-driven system-level simulation framework, that supports typical deployment policies (manual/regular/random), for several simultaneous links between the nanomachines, and all the abovementioned message encoding techniques. NCSim incorporates the stochastic model for bacteria mobility by Wang et al. [7], [8] and the plasmid/chromosome transfer between bacteria through the conjugation process. The tool also has an adjustable vibration generator to model different levels of stability of the environment. The major features of this software are high detail levels combined with reasonable

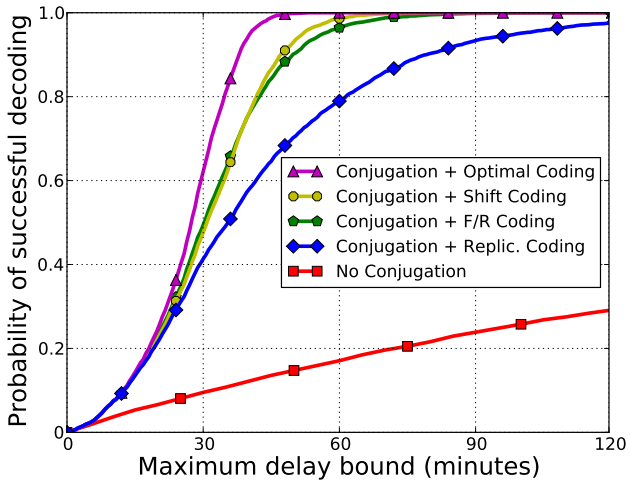


Fig. 4. Delivery probability as a function of time.

performance. The accuracy of the produced metrics in major scenarios has been confirmed via comparison with analytical results in simplified scenarios in [5], [15]. The tool is optimised for multi-core PC and is cross-platform supporting Windows, Linux and OS X operating systems.

NCSim consists of three modules: (i) physical (PHY) layer of bacterial nanonetworks, including deployment, bacteria mobility and conjugation, and messages encoding/decoding, (ii) scenarios generator and simulation monitor and (iii) plotting tool, intended to post-processing of raw simulation data and plots generation. The most computationally intensive PHY module is implemented in C++ with a number of technical enhancements to speed up the bacteria mobility and conjugation simulations. The later two modules are written in Python for maintenance and extension simplicity.

A number of special enhancements allow NCSim to simulate up to one million of different high-dense scenarios within 12 hours on 8-cores Intel Core i7 CPU. This level of performance makes it possible to thoroughly and accurately estimate our metrics of interest for bacterial nanonetworks.

V. Numerical Results and Discussion

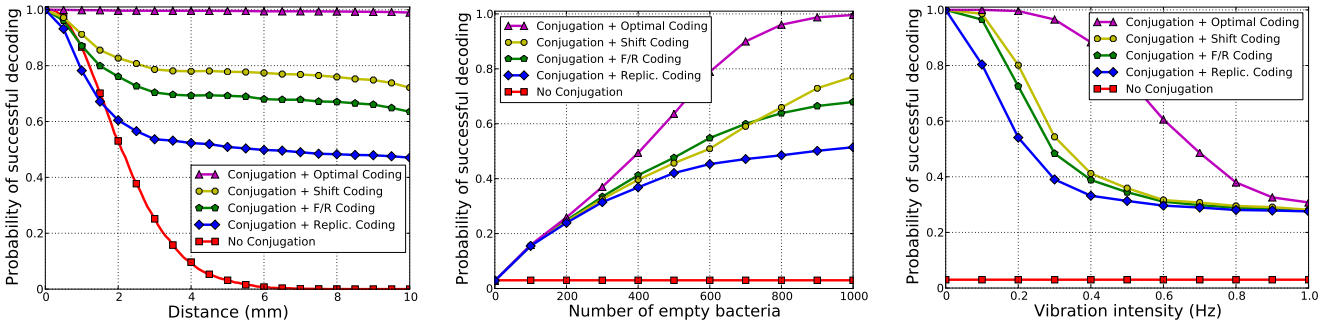
In this section, we compare the performance of selected encoding schemes to that of optimal encoding. In addition, we add as the baseline an extra scenario with no conjugations occurring in the environment. The comparison to this scenario gives insights about the benefit of utilizing the conjugation feature of bacteria regardless of the selected message encoding technique. The input parameters are the distance between two nanomachines, the maximum delay bound, the vibration intensity, and the concentration of the bacteria in environment.

Fig. V demonstrates the probability of successful delivery as a function of time for 5mm distance between the nanomachines, fixed concentration of bacteria in the environment, 1000 bacteria per square centimeter, and constant vibration intensity of 0.2Hz. When the delay bound is rather small, i.e. up to 5 minutes, the performance of all the considered schemes are similar. However, this region is of no interest, as the probability of successful delivery is extremely small. Increasing the delay bound further, we emphasize the gap between the optimal encoding defined and conventional repetition coding, where all the bacteria have identical copies of the message. The effect of both forward/reverse coding and shift coding techniques is noticeable and gets more evident as the delay bound increases.

The abovementioned effects remain the same when the distance between the nanomachines or the bacteria concentration increases, see Fig. 5(a), where the maximum delay bound is set to one hour, number of empty bacteria – to 1000, and vibration intensity – to 0.2Hz. As expected, when the distance increases, the difference between the optimal encoding and three other methods becomes larger. In fact, for the distance of 1cm, the optimal encoding reliability is higher than 0.99. This implies the message loss rate is less than 10^{-2}, so the link can still be considered reliable enough for delay tolerant communications. At the same time, the probability of the message being successfully decoded at the destination nanomachine with shift, forward/reverse, and repetition encoding, degrades to 0.72, 0.63, and 0.46, respectively. Thus, the nanomachines should emit more bacteria and/or increase the maximum delay bound for longer links, or be aware of possible message losses.

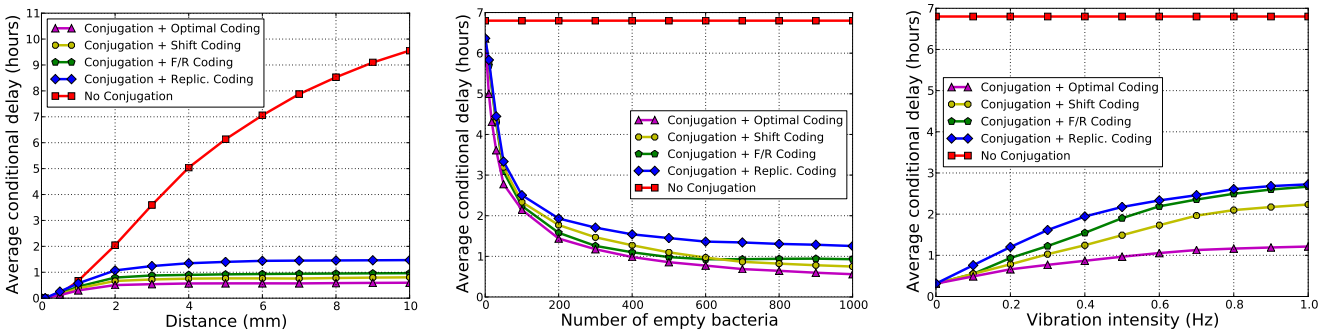
Although the presence of conjugation significantly improves the link performance in bacterial nanonetworks compared to the baseline model with no conjugation, as evident from Fig. V and Fig. 5 and Fig. 6, the gain is more profound when the density of the regular bacteria in the environment is high enough. In Fig. 5(b) and Fig. 6(b), we show the effect of bacteria density in the environment on the performance of the selected message encoding schemes as well as the baseline scenario. The distance between the nanomachines is equal to 5mm, the vibration intensity is set to 0.2Hz, and the maximum delay bound is set to 1h and 24h for reliability and delay studies, respectively. When only 10 bacteria are originally released from the source nanomachine, the difference between ”conjugation” and ”no conjugation” performance is growing extremely fast with the total number of bacteria in the area of interest. The results for forward/reverse and shift encoding schemes are better already from around 200 of bacteria. Finally, the performance of optimal encoding increases even faster and achieves the ultimate value of 0.9997 at 1000 bacteria per cm^2. The latter implies that an reliable link can be established between two nanomachines even at 5mm distance, if an efficient message encoding technique is used.

Considering the effect of vibrations in the environment on the bacterial nanonetwork performance, we concentrate on both the link reliability and the average delay versus the intensity of vibration process. We keep the distance between the nanomachines to 5mm, set the total number of bacteria in the area of interest to 1000, and change the vibration intensity from 0 to 1Hz. The maximum delay bound for reliability and delay figures is again fixed to 1h and 24h, respectively. The results of this study are presented in Fig. 5(b) and Fig. 6(b). We start interpreting the results noticing that in absence of



(a) Distance between the nanomachines (b) Bacteria concentration (c) Vibration intensity

Fig. 5. Probability of successful decoding as a function of distance between the nanomachines, bacteria concentration and vibration intensity.



(a) Distance between the nanomachines (b) Bacteria concentration (c) Vibration intensity

Fig. 6. Average delay as a function of distance between the nanomachines, bacteria concentration and vibration intensity.

any distortion, the performance of all the encoding schemes is equally high. In case of no vibration, all the messages will be fully copied during the conjugation process, thus, there is no need to compensate for any possible partial message copying. The absence of vibration is also advantageous from the delay point of view as the first bacterium with the message captured will lead to successful message decoding.

For nonzero values of vibration intensity, the performance of the encoding techniques, as expected, start to degrade. In the range of 0.1-0.5Hz we see notable gains from the forward/reverse coding in comparison to the repetition coding. However, in case of higher vibration intensity the performance of this scheme does not starts to degrade as the captured front and back parts of the message are often too short to join them into a full-length original message. The proposed shift encoding technique performs better than forward/reverse approach and can tolerate higher vibration intensities. However, comparing to the optimal bound we observe a 40% gap yet to be filled by more sophisticated encoding techniques. Finally, if the vibration intensity is increasing to 1Hz, the performance of all the encoding techniques becomes similar again as none of them, including the theoretical optimal approach, can give any notable gain on top of the conventional repetition coding. Thus, 1Hz vibration for the given set of parameters is the point, starting from which any sophisticated encoding technique would be useless. This limitation of the prospective bacteria nanonetworks is one of the important conclusions of this study.

An interesting effect evident from Fig. 5(b) and Fig. 6(b), is that the performance of forward/reverse coding is slightly better than that of the shift approach at lower values of bacteria concentration, up to $\sim$ 700 bacteria per cm^2. This effect is explained by the following phenomenon. The vibration intensity set for this experiment, 0.2Hz, implies that the average conjugation duration is 5s (the message length is 10Kbp, the rate of copying is 833bp/s). This fact, as well as the natural property of exponential distribution of the interval time of the Poisson vibration process, results in a large quantity of bacteria carrying short messages swimming in the environment and eventually captured by the destination nanomachine. The higher concentration of empty bacteria, the more bacteria with short messages swimming in the environment. The forward/reverse decoder relies mainly on long messages, i.e., in fact, it needs at least one of the messages, either forward or reverse encoded, to be longer than half of the original message. So the high amount of bacteria with very short messages provides almost no support to the forward/reverse scheme. At the same time, the shift decoder can efficiently utilize a large set of short messages and, eventually, combine them into the original message. Thus, it performs better for high concentration of empty bacteria. The same behaviour can be observed for the average delay from Fig. 6(b).

VI. Conclusions

In this paper we studied performance of a number of message encoding techniques for bacterial nanonetworks and

compared their performance to the theoretical upper bound provided by the optimal encoding. Out results demonstrate that the forward/reverse encoding scheme performs better for the lower concentration of empty bacteria in the environment, while for the highly dense scenarios the shift encoding achieves better performance. The gain of shift encoding for high concentration of bacteria holds in a broad range of communication distances and vibration intensities. However, the deign of shift coder and, especially, decoder at the nanoscale is a challenging task. Thus, these two schemes addresses different balance between performance and complexity of implementation. Another major outcome of the performed study is that there is still a huge room for improvement of message encoding/decoding techniques for bacterial nanonetworks, especially to overcome losses at long links, efficiently utilize the higher concentration of present bacteria, and tolerate the highly unstable environments.

Although the optimal encoding presents an attractive upper bound for the link performance in bacterial nanonetworks, it is not constructive, i.e. it does not specify how to achieve it. Nevertheless, this ideal encoding scheme is still useful. First, it provides a strict upper bound for the achievable characteristics of any encoding scheme with respect to network parameters and environment conditions. Secondly, it provides a way to evaluate the performance of any encoding scheme suggested for bacterial nanonetworks, by specifying how close it is to the theoretical limit.

Providing an analytical solution or an accurate approximation for the optimal encoding performance as a function of system parameters is our next goal in this research direction. We also encourage the community to use our simulation framework, available upon request, with all the abovementioned encoding schemes including the optimal bound and scenarios implemented.

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