Distance Estimation for DNA-Based Molecular Communication

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***Abstract*—DNA is a promising information carrier for Molecular Communication (MC) links. Therefore, accurate distance estimation between transmitters and receivers is crucial for optimized communication. Existing methods rely solely on receiver-side signals, limiting transmitter adaptability. This study proposes a novel two-way DNA-based MC system using Strand Displacement Reactions (SDRs) for bidirectional communication, enabling transmitters to estimate distance via their own signals. Simulation results confirm its effectiveness in diffusion-based environments.**

***Index Terms*—Diffusion, DNA, Molecular Communication, Strand Displacement Reaction, Two-Way Communication**

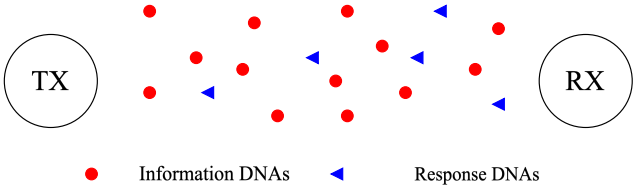
I. Introduction

MOLECULAR Communication (MC) enables nanoscale data transmission using molecules, offering advantages in liquid environments for applications in the Internet of Bio-Nano Things (IoBNT) like disease detection, smart drug delivery, and neural interfaces. DNA is an ideal information carrier due to its specificity, programmability, and stability, supporting precise information processing in biomedical settings [1]. A key challenge in DNA-based MC is accurate transmitter-receiver distance estimation, which is crucial for reliable communication and dynamic network configurations. Existing methods focus on receiver-side information, limiting transmitter adaptability.

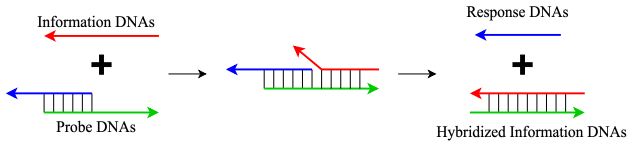
We propose a two-way DNA-based MC system leveraging SDRs for efficient, transmitter-aware distance estimation to address this. Our contributions include: 1) A novel SDR-based communication and estimation framework, 2) A low-complexity transmitter-side distance estimation algorithm, and 3) Monte Carlo validation demonstrating robustness in diffusion-based environments.

II. System Model

The two-way DNA-based MC system, cf. Fig. 1(a), consists of a spherical transmitter (TX), a Three-Dimensional (3D) unbounded diffusion channel, and a spherical receiver (RX). The transmitter releases information DNA molecules, which diffuse through the channel and hybridize irreversibly with probe DNA molecules at the receiver. Successful hybridization triggers a SDR [2], releasing response DNA molecules, cf.Fig. 1(b), that diffuse back to the transmitter, enabling recognition via complementary DNA sequences. Information and response DNA molecules move independently, with diffusion coefficient $D = 4.9 \times 10^{-10}\,\mathrm{m^2/s} \cdot [\mathrm{bp}]^{-0.72}$, where bp denotes base pair length [3].



(a) Illustration of a two-way DNA-based MC system.



(b) Illustration of SDRs between probe DNA and information DNA molecules.

Fig. 1. Illustration of a two-way DNA-based MC system and SDRs between probe DNA and information DNA molecules.

The TX and RX are modeled as spheres with radius r^{TX} and r^{RX}, respectively. The distance between their surfaces is denoted as d, where $d \gg r^{\mathrm{TX}}$ and $d \gg r^{\mathrm{RX}}$, allowing the transmitter and receiver to be approximated as point sources for the release of the molecules. Given this configuration, the absorbing receiver model can be employed to describe the MC system [4]. The hitting rate $f_x(t)$ of information DNA and response DNA molecules can be expressed as follows:

$$f_x^i(t) = \frac{r^i}{r^i + d} \frac{d}{\sqrt{4\pi D_x t^3}} \exp\left(-\frac{d^2}{4D_x t}\right), \tag{1}$$

where $x \in \{\mathrm{info}, \mathrm{resp}\}$ and $i \in \{\mathrm{TX}, \mathrm{RX}\}$. The fraction of information DNA and response DNA molecules until a point in time t, by integrating Eq. (1) from 0 to t, follows:

$$F_x^i(t) = \int_0^t f_x^i(t')\,\mathrm{d}t' = \frac{r^i}{r^i + d} \mathrm{erfc}\left(-\frac{d^2}{4D_x t}\right), \tag{2}$$

where $\mathrm{erfc}(\cdot)$ is the complementary error function. According to the characteristic of SDRs, the number of information DNA molecules hybridized with the probe equals the response DNA

This work was supported by the German Research Foundation (DFG) as part of Germany's Excellence Strategy – EXC 2050/1 – Cluster of Excellence "Centre for Tactile Internet with Human-in-the-Loop" (CeTI) of Technische Universität Dresden under project ID 390696704 and by the Federal Ministry of Education and Research (BMBF) in the program of "Souverän. Digital. Vernetzt." Joint project 6G-life, grant number 16KISK001K. This work was also supported by the project IoBNT, funded by the German Federal Ministry of Education and Research (BMBF) under grant number 16KIS1994.

molecules. The hitting rate of the response DNA molecules propagating back to the transmitter can be described as:

$$f'_{\text{resp}}(t) = \int_0^t f^{\text{TX}}_{\text{info}}(t') f^{\text{RX}}_{\text{resp}}(t - t')\, \mathrm{d}t'. \tag{3}$$

The fraction of response DNA molecules propagating back to the transmitter by integrating Eq. (3) from 0 to t, follows:

$$F'_{\text{resp}}(t) = \int_0^t f'_{\text{resp}}(t')\, \mathrm{d}t'. \tag{4}$$

Assuming the release of a number of Q information DNA molecules at $t = 0$, the concentration of the total absorbed response DNA molecules at t is $N(t) = QF'_{\text{resp}}(t)$.

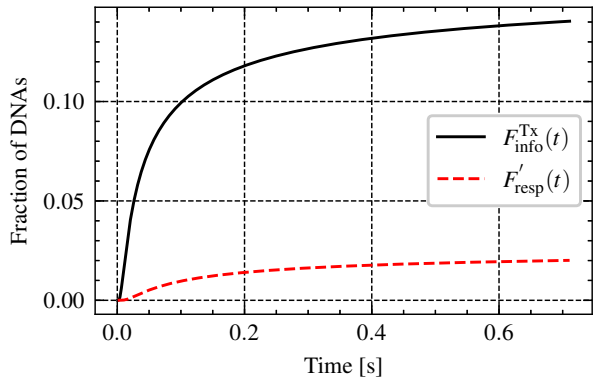


Fig. 2. Fraction of information DNA and response DNA molecules. Simulation parameters following Table I.

III. Distance Estimation

Here, we present a low-complexity distance estimation algorithm based on the way DNA-based MC system. When the transmitter releases Q information DNA molecules at $t = 0$, these molecules diffuse to the receiver. Over time, the fraction of absorbed molecules, as shown in Fig. 2, asymptotically approaches a threshold value denoted as Ω_{info}. This threshold can be expressed as the limit of the absorbed fraction as time approaches infinity, derived from Eq. (2):

$$\Omega_{\text{info}} = \lim_{t \to +\infty} F^{\text{RX}}_{\text{info}}(t) = \frac{r^{\text{RX}}}{r^{\text{RX}} + d}. \tag{5}$$

Once the receiver absorbs the information DNA molecules, it releases corresponding response DNA molecules. Similarly, over time, the fraction of absorbed response molecules approaches a threshold, denoted as Ω_{resp}. This threshold is obtained by taking the limit as time approaches infinity in Eq. (4):

$$\Omega_{\text{resp}} = \lim_{t \to +\infty} F'_{\text{resp}}(t) = \frac{r^{\text{TX}}}{r^{\text{TX}} + d} \frac{r^{\text{RX}}}{r^{\text{RX}} + d}. \tag{6}$$

The distance d between the transmitter and receiver can be determined as:

$$d = \frac{-\Omega_{\text{resp}} x + \sqrt{\Omega^2_{\text{resp}} x^2 + 4\Omega_{\text{resp}}(1 - \Omega_{\text{resp}}) y}}{2\Omega_{\text{resp}}}, \tag{7}$$

where $x = r^{\text{TX}} + r^{\text{RX}}$ and $y = r^{\text{TX}} r^{\text{RX}}$. An estimated threshold value $\hat{\Omega}_{\text{resp}}$ can be obtained using $\hat{\Omega}_{\text{resp}} = \frac{\hat{N}(t_e)}{Q}$.

TABLE I
Summary of the Simulation Parameters.

Parameters	Symbol	Value	Unit
Number of released information DNA molecules	Q	1×10^3	
Diffusion coefficient of information DNA molecules	D_{info}	1.78×10^{-11}	m^2/s
Base pair size of information DNA molecules	bp_{info}	100	
Diffusion coefficient of response DNA molecules	D_{resp}	2.93×10^{-11}	m^2/s
Base pair size of response DNA molecules	bp_{resp}	50	
Radius of the transmitter	r^{TX}	2×10^{-7}	m
Radius of the receiver	r^{RX}	2×10^{-7}	m

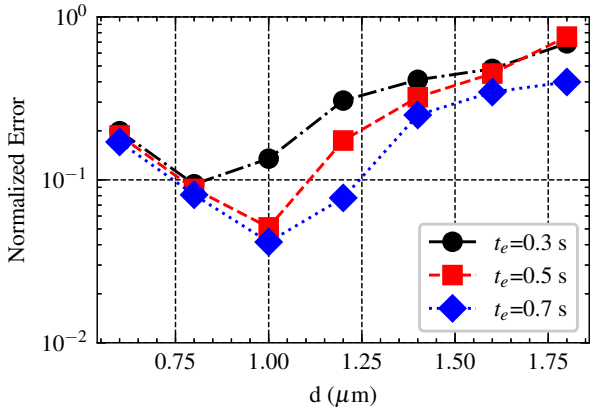


Fig. 3. Normalized error versus transmitter-receiver distance d for different estimation times t_e.

IV. Simulation Results and Discussion

Finally, we evaluate the proposed two-way DNA-based MC model with SDRs for efficient distance estimation. Monte Carlo simulations validate its performance, demonstrating low normalized errors, where $(\hat{d} - d)/d$ measures accuracy. The simulation parameters follow Table I.

Fig. 3 shows the normalized error variation with d for different estimation times t_e. As t_e increases, the estimated threshold $\hat{\Omega}_{\text{resp}}$ converges to Ω_{resp}, improving accuracy. The error is initially high at $d = 0.6\,\mu$m, decreases to a minimum at an optimal range, then rises again. The lowest error occurs at $d = 0.8\,\mu$m for $t_e = 0.3\,$s and at $d = 1\,\mu$m for $t_e = 0.5\,$s and $t_e = 0.7\,$s. This trend is influenced by molecular diffusion and hybridization dynamics. At short distances, unsatisfied conditions $d \gg r^{\text{TX}}$ and $d \gg r^{\text{RX}}$ lead to sub-optimal performance. Optimal estimation occurs within a specific range where model assumptions hold, while at larger distances, diffusion losses reduce arriving response DNA molecules, increasing error. Enhancing DNA release can mitigate these effects, improving long-distance estimation.

Future research could optimize the distance estimation range for the proposed distance estimation algorithm and evaluate the scalability of the two-way MC system in larger networks.

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