

Receiver Design Using Genetic Circuits in Molecular Communication

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Abstract—Understanding the dynamics of molecular communications between cells and intracellular response is crucial to create predictable cellular applications. When the propagation mechanism is diffusion based, the arrival histogram of molecules becomes heavy tailed and the stray molecules create interference for the following symbol slots. Here, we present a model-based framework to design diffusion-based systems using computer simulations. To overcome interference problems, we utilize two different signals with two different molecule types to carry a single bit of data. While the first signal is the actual data carrier, the latter acts as an antagonist to cancel out the heavy tail of the former signal. At the receiver side, these signals are used to control cellular behaviour via a synthetic genetic circuit, which eliminates the effect of stray molecules. This holistic and model-driven design approach combines both intracellular and intercellular dynamics to create novel applications.

Index Terms—Synthetic biology, molecular communications, diffusion, genetic circuits, model-driven design, automation.

I. INTRODUCTION

In molecular communications (MC), transferring information via messenger molecules (MM) is widely studied. However, processing of the received information that is transferred through MC channels is often not coupled with intracellular signalling dynamics, which is key to understand receiver characteristics. In MC studies, the encoding and decoding processes are oversimplified. Using diffusion dynamics and synthetic genetic circuits, we aim to make the design processes of MC channels and receivers more realistic by considering and integrating intercellular and intracellular processes. We develop a complex workflow, for a molecular communication via diffusion (MCvD) system with pre-equalizer [1], building upon model-driven design methodologies in synthetic biology and MC. We consider a 3D molecular channel propagation [2] and bacterial genetic circuits for decoding information for the intercellular and the intracellular processes, respectively.

II. SYSTEM MODEL

Here, genetic circuit designs were represented using the Synthetic Biology Open Language (SBOL) [3], [4], a data standard that has emerged as a computational exchange format for genetic circuits. SBOL was used to computationally represent the order and composition of genetic circuits, trans-

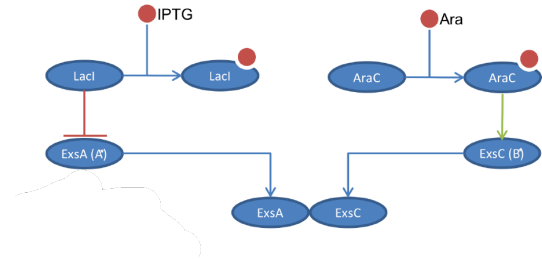


Fig. 1. An overall diagram of the genetic circuits showing protein-protein relationships only.

relationships such as the regulation of gene expression, and protein-protein interactions. SBOL designs were then utilised to derive computational models to create a model-driven design workflow.

Fig. 1 displays the genetic circuit of the receiver node (Rx) when a pre-equalizer is used. For reducing the effects of interference, the transmitter node (Tx) first emits MMs and then emits antagonist molecules after a short delay, which will be referred to as A and B . Here IPTG and Arabinose signals are used to represent A and B respectively. In summary, the main aim of the pre-equalizer is to reduce the level of stray molecules at the Rx [1]. The cellular representation of A and B inside the Rx are referred as A' and B' (i.e., ExsA and ExsC). When IPTG is sensed ExsA (A') is produced. Similarly, when Ara is sensed, ExsC (B') is produced.

A. Intercellular Processes

Assuming a simple MCvD channel without flow, the expected number of MMs that will reach and be absorbed by the Rx in a certain time frame can be calculated by using the analytic model introduced in [2]. Expected number of received molecules for type- A in a certain time frame t_k can be calculated as

$$E[N_A^{Rx}(t_k)] = N_A^{Tx} \{F^{Rx}(t_k^+) - F^{Rx}(t_k^-)\} \quad (1)$$

where $E[\cdot]$ is the expectation operator, N_A^{Tx} is the number of emitted molecules, $F(t)$ is the cumulative arriving function [2], t_k^- is the start and t_k^+ is the end of the time frame t_k .

TABLE I
SIMULATION PARAMETERS

Parameter	Value
Radius of the receiver	2 μm
Distance between Tx and Rx (d)	200 μm
Diffusion coefficients for IPTG and Ara	{600, 870} $\mu\text{m}^2/\text{s}$
Symbol duration (t_k)	1080 s
Length of bit sequence	18 bits
Bit sequence	11 01 11 00 11 11 10 11 11
Signal shift between A and B (t_{shift})	630 s

The activation of the genetic circuit inside the Rx requires a specific level of intercellular signalling molecules for a certain amount of time and is affected by several parameters such as channel properties, absorption rate, biochemical kinetic rates.

In our case study (i.e., in an MCvD system with pre-equalizer [1]), to comply with the processing rate of the Rx 's genetic circuit, a specific level of MM concentration should be maintained. Moreover, in order to eliminate the heavy tail of A' at the Rx side, B is emitted at the Tx side t_{shift} seconds after A is released.

B. Intracellular Processes

The eventual effect of the diffusing MMs is to trigger a desired cellular activity within the Rx (i.e., to convert the molecular signal into a cellular signal). Afterwards, using signalling cascades on the cellular signal, different logical computations can be performed. Here, we adopt transcriptional activation and repression processes to control the production of proteins in response to the sensing of A and B signalling molecules. Interactions of these proteins form the basis of our biological program to evaluate $A' - B'$.

In our model, after receiving A and B the resulting proteins inside the Rx , (i.e., A' and B' respectively) can bind together. Therefore B' can eliminate MM's heavy tail after symbol duration. If A' exceeds a certain level of concentration (λ) in time slot t_k , the Rx interprets the received symbol as (sym_1) and (sym_0) otherwise. This process can be represented as

$$S[t_k] = \begin{cases} sym_1 & N_{A'}^{Rx}[t_k] \geq \lambda \\ sym_0 & N_{A'}^{Rx}[t_k] < \lambda \end{cases}$$

where $S[t_k]$ is the received symbol in the time slot t_k .

III. NUMERICAL RESULTS AND DISCUSSION

Here, we used the Virtual Parts Repository (VPR) framework [5], [6] to computationally model the genetic circuit in this work. The main aim of the VPR framework is to provide modular and reusable modular models of biological systems. The resulting models can be simulated and hence simulations can be used while exploring the space of solutions heuristically for complex biological systems. Parameters for time course simulation can be seen in Table I.

Simulation results are shown in Fig. 2 and 3 for the systems without and with pre-equalizer. In Fig. 2, lack of a pre-equalizer causes inter-symbol interference (ISI) and accumula-

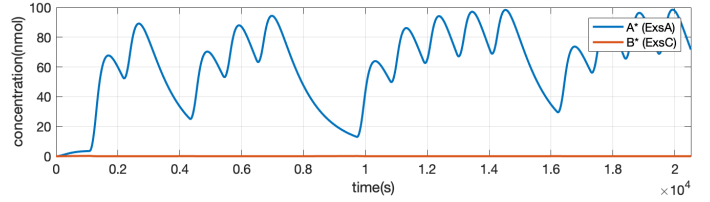


Fig. 2. Rx response without using pre-equalizer (i.e., B and B' are not used).

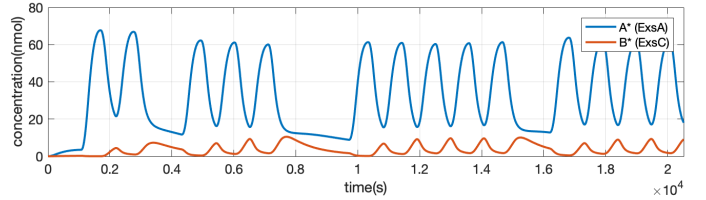


Fig. 3. Rx response with using pre-equalizer.

tion of stray molecules. On the other hand (Fig. 3), introducing another molecule and a genetic circuit for pre-equalizer improves the received response of the Rx node drastically. In Fig. 3, the effects of interference are eliminated and for $\lambda = 40$ nmol, symbol decoding is less error prone compared to the system without pre-equalizer. ExsC (B') reduces the concentration of ExsA (A') drastically right before the next time slot, which eliminates the accumulation of molecules and consequently the interference for the next symbol.

IV. CONCLUSION AND FUTURE WORK

In this work, we have focused on the utilisation of a genetic circuit for an MCvD system in order to improve the channel response by designing and integrating a pre-equalizer and its genetic circuit. A pre-equalizer eliminates ISI and the accumulation of molecular signal in the MCvD systems. Future work for this research is the optimization and improvement of the proposed system's parameters. We aim to design more complex and robust MCvD systems using synthetic biology.

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