

Noise properties of linear molecular communication networks

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Abstract

Molecular communication networks consist of transmitters and receivers distributed in a fluid medium. The communication in these networks is realised by the transmitters emitting signalling molecules, which are diffused in the medium to reach the receivers. This paper investigates the properties of noise, or the variance of the receiver output, in molecular communication networks. The noise in these networks come from multiple sources: stochastic emission of signalling molecules by the transmitters, diffusion in the fluid medium and stochastic reaction kinetics at the receivers. We model these stochastic fluctuations by using an extension of the master equation. We show that, under certain conditions, the receiver outputs of linear molecular communication networks are Poisson distributed. The derivation also shows that noise in these networks is a nonlinear function of the network parameters and is non-additive. Numerical examples are provided to illustrate the properties of this type of Poisson channels.

Keywords: Molecular communications; nano communication networks; noise; stochastic reaction kinetics; master equations; Poisson distribution;

1. Introduction

A molecular communication network consists of transmitters and receivers distributed in a fluid medium. A transmitter communicates with the receiver

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by sending one or more signalling molecules, which are diffused in the fluid medium. Molecular communication networks are ubiquitous in living organisms and have been extensively studied in biology. There is a growing interest in *engineering* synthetic or artificial molecular communication networks in disciplines such as synthetic biology [1] and nano communication networks [2, 3, 4]. These synthetic molecular communication networks have applications in areas such as nano-sensor networks [2], nano-medicine [5] and so on. In order to be able to engineer synthetic molecular communication networks, one needs to understand the properties of these networks. Some example of properties of interest include the noise characteristics at the receivers, signal detection performance and capacity of the communication channel. The aim of this paper is to understand the *noise* properties in a specific class of molecular communication networks.

The noise characteristics of molecular communication networks have recently been studied in [6]. The work is based on analysing the molecular dynamics of the transmitters and receivers. It shows that the noise at the transmitters and receivers can be modelled as, respectively, sampling and counting noise. The sampling noise at the transmitter is due to random emission of signalling molecules while the counting noise at the receiver is due to random ligand-receptor binding and unbinding.

Instead of molecular dynamics, we take a different approach in [7] and propose an extension to the reaction-diffusion master equation (RDME) for modelling molecular communication networks. We call our extension reaction-diffusion master equation with exogenous input (RDMEEX) where the exogenous input is used to model the emission of signalling molecules by the transmitters. We show in [7] that RDMEEX can readily be used to model molecular communication networks with multiple transmitters and receivers. The work in [7] is focused on understanding the mean receiver outputs. In this paper, we use RDMEEX to understand the noise properties of a specific class of molecular communication networks, namely *linear* molecular communication networks.

In a linear molecular communication network, the reactions at the receivers are restricted to those reactions whose reaction rates are linear functions of the

quantity of the reactants. Linear molecular reactions have been extensively studied in bio-mathematics and bio-physics because they can model some chemical reactions in living organism and can be used to approximate higher order reactions whose reaction rates are nonlinear functions [8]. We show in [7] that linear molecular communication networks can be used to approximate the behaviour in their nonlinear counterparts.

In this paper, our aim is to study the noise properties of linear molecular communication networks. We present two key results. First, we derive an efficient method to compute the covariance of the receiver outputs of these networks (Section 3). Second, we prove that, under certain assumptions, the receiver outputs of these networks are Poisson distributed. For those networks where these assumptions do not hold, we use simulation and statistical tests to investigate whether Poisson distribution may still hold. An insight from this result is that the noise in linear molecular communication networks is *non-additive* and nonlinear. This is discussed in Section 4. As an application of these results, we investigate the capacity of a discrete memoryless channel formed by linear molecular communication networks in Section 5. Related work and conclusions can be found in Sections 6 and 7, respectively. We begin the core component of this paper by presenting an overview of the RMDEX model in Section 2.

2. The RMDEX model

This section reviews the RMDEX model, which is proposed in our recent work [9], for modelling molecular communication networks. The inclusion of this review is to make this paper self-contained. The review covers model assumptions, notation, and results on the computation of mean and variance of receiver outputs. We will use RMDEX to study the noise properties of molecular communication networks in later sections.

2.1. Model assumptions and notation

2.1.1. Framework and transmission medium

The RMDEX model is an extension to the RDME [10, 11] which is commonly used in physics to model systems with both diffusion and reactions. The RMDEX model assumes that time is continuous while the space is discrete. We consider a 3-dimensional volume of dimension $X \times X \times X$. Each dimension is divided into N_v equal parts of length $\Delta = \frac{X}{N_v}$. This results in N_v^3 voxels of volume Δ^3 each. We will refer to the voxel by a triple (x, y, z) where x , y and z are integers in the range $[1, N_v]$ or a single index $\xi \in [1, N_v^3]$ where $\xi(x, y, z) = x + N_v(y - 1) + N_v^2(z - 1)$.

We assume all the transmitters in the molecular network use the same type of signalling molecule (or chemical species) L for communication. The medium is assumed to be homogeneous with the diffusion coefficient for L in the medium is D . Define $d = \frac{D}{\Delta^2}$. The mean rate that a molecule of L will diffuse from a voxel to a neighbouring (resp. non-neighbouring or outside the medium) voxel is d (resp. 0).

2.1.2. Transmitters

We assume the network consists of N_t transmitters and N_r receivers. For simplicity, we assume a transmitter or a receiver occupies exactly one voxel. However, it is straightforward to generalise to the case where a transmitter or a receiver occupies multiple voxels. We further assume that the voxels occupied by the transmitters and receivers are all distinct. The a -th transmitter ($a = 1, \dots, N_t$) is assumed to be located at the voxel with index T_a . The h -th receiver ($h = 1, \dots, N_r$) is assumed to be located at the voxel with index R_h .

In RMDEX, a transmitter is modelled by a sequence which specifies the number of molecules emitted by the transmitter at a certain time. We assume that, at time t_b (where $b = 1, 2, \dots$), the a -th transmitter emits $k_{a,b}$ signalling molecules. This is identical to viewing the arrival of the signalling molecules to the system as an exogenous input; this is what ‘‘X’’ in RMDEX stands for. In this section, we assume the number of molecules emitted is deterministic, we will generalise to the probabilistic case in later sections.

2.1.3. Receivers

When a signalling molecule L arrives at the receiver, it may react, via one or more chemical reactions, to produce one or more *output molecules*. The output signal of a receiver is the number of output molecules at the receiver over time. For example, a signalling molecule L reacts with a receptor R to form a complex C (the output molecule), via the reaction:



In this paper, we will focus on linear molecular communication networks. In such networks, the reactions at the receivers have the property that their reaction rates are linear functions of the quantity of reactants in the reactions. The classes of reactions that are linear include: $S_i \rightarrow S_j$ (conversion), $S_i \rightarrow \phi$ (degradation), $S_j \rightarrow S_j + S_k$ (catalytic) and $S_i \rightarrow S_j + S_k$ (splitting) where S_i , S_j and S_k denote chemical species, and ϕ denotes chemicals that we are not interested in keeping track in our model.

For illustration purpose, in this section, we assume that at the receivers, signalling molecules L are converted to complexes C (output molecules) reversibly via the following conversion reaction:



where k_+ and k_- are, respectively, the macroscopic rate constant for the forward and reverse reactions. This means that at a receiver voxel, the complexes are formed at a rate of $\frac{k_+}{\Delta^3}$ times the number of signalling molecules in the voxel. We assume that the complex C does not diffuse. For simplicity, we assume all receivers have the same structure but RMDEX can be applied to heterogenous receiver structures too.

We use the number of complexes at a receiver as the output of the receiver. This is motivated by using the number of complexes at the receiver to detect the symbols that the transmitter has sent. Note that the number of complexes at a receiver is a stochastic process. The stochastic fluctuations come from three sources: (1) The emission by the transmitter is a probabilistic event; (2) The

diffusion of the signalling molecule being probabilistic; and (3) The stochastic nature of the reaction at the receiver. Since we assume that the number of molecules emitted by the transmitters is deterministic in the section, we will not consider the effect of (1) here, but it will be studied in the later sections.

2.1.4. State vector and state transition

We define the state vector of the molecular communication network to consist of the number of signalling molecules in each voxel and the number of complexes at each receiver. The state vector $Q(t)$ contains $N_q = N_v^3 + N_r$ elements. We define

$$Q(t) = \left[n_{L,1}(t) \quad \dots \quad n_{L,N_v^3}(t) \quad n_{R,1}(t) \quad \dots \quad n_{R,N_r}(t) \right] \quad (3)$$

where $n_{L,\xi}(t)$ represents the number of signalling molecules in voxel with index ξ at time t and $n_{R,h}$ is the number of complexes in the h -th receiver at time t . Let the set \mathcal{Q} denote the set of all possible states. At each time t , we have $Q(t) \in \mathcal{Q}$. We will use q to denote an element from \mathcal{Q} , i.e. $q \in \mathcal{Q}$.

The aim of the RDDEX is to describe how the probability $\text{Prob}(Q(t) = q)$ evolves over time. State transitions can be caused by four different types of **events**:

1. The emission of signalling molecules by a transmitter
2. The diffusion of a signalling molecule from one voxel to another
3. The conversion of a signalling molecule to a complex in a receiver
4. The conversion of a complex to a signalling molecule in a receiver

We first discuss the last three types of events. Each of these events is characterised by a state transition vector r (which has the same dimension as q) and a transition rate $W(q)$. We will illustrate this by using two examples.

In the first example, a state transition is caused by the diffusion of a signalling molecule from voxel $(1, 1, 1)$ (equivalent to index 1) to voxel $(2, 1, 1)$ (equivalent to index 2). If $n_{L,1}$ and $n_{L,2}$ are the number of signalling molecules in voxels 1 and 2 before this state transition, then after the state transition, the number of signalling molecules in these voxels will be $n_{L,1} - 1$ and $n_{L,2} + 1$.

We can capture this by using a state transition vector r . If the state before the transition is q , then the state after transition is $q + r$. For the diffusion of a signalling molecule from voxel 1 to voxel 2, the state jumps from q to $q + r$ where

$$r = \begin{bmatrix} -1 & 1 & 0 & 0 & \dots & 0 \end{bmatrix}.$$

This state transition occurs at a rate of $W(q) = \frac{d}{\Delta^2} n_{L,1}$ which is a linear function of n_{L,R_1} .

In the second example, consider the conversion of a signalling molecule to a complex at receiver 1 located at voxel R_1 . The state transition vector r has only two non-zero elements. The R_1 -th element of r is -1 and the $(N_v + 1)$ -th element of r is 1 . Note that the R_1 -th element of q is the number of signalling molecules in the voxel occupied by receiver 1 and $(N_v + 1)$ -th element of q is the number of complexes in receiver 1. Hence, the state transition vector r captures the conversion of a signalling molecule to a complex at receiver 1. The transition rate is $W(q) = \frac{k_+}{\Delta^3} n_{L,R_1}$ which is linear in n_{L,R_1} .

In this paper, we assume that the event types 2 – 4 can be modelled by J transitions with state transition vectors r_j and rate $W_j(q)$ where $j = 1, \dots, J$. For linear molecular communication networks, all transition rates $W_j(q)$ are linear functions.

2.2. RDMEX model and its properties

The RDMEX model for the molecular communication network is:

$$\begin{aligned} \frac{dP(q,t)}{dt} &= \sum_{a=1}^{N_t} \sum_{b=1}^{\infty} \{P(q - k_{a,b} \mathbf{1}_{T_a}) - P(q,t)\} \delta(t - t_{a,b}) \\ &\quad + \sum_{j=1}^J W_j(q - r_j) P(q - r_j, t) - \sum_{j=1}^J W_j(q) P(q,t) \end{aligned} \quad (4)$$

where $P(q,t)$ is a shorthand for $\text{Prob}(Q(t) = q)$, $\delta(t)$ denotes the Dirac delta function and $\mathbf{1}_g$ is vector whose g -th element is 1 but zero otherwise.

The second term in equation (4) models the diffusion of signalling molecules and the reactions at the receivers, or in other words, events of types 2–4 men-

tioned in section 2.1.4. If the first term in (4) is absent, then (4) is the RDME in the literature [11, 10].

The first term in (4) models the emission of signalling molecules by the transmitters, or the first type of events mentioned in section 2.1.4. Consider the example that $k_{a,b}$ molecules are emitted by the a -th transmitter at time $t_{a,b}$ and if the state just before time $t_{a,b}$ is q , then the state just after time $t_{a,b}$ is $q + k_{a,b}\mathbb{1}_{T_a}$ because $k_{a,b}$ signalling molecules are added to the T_a -th voxel. This state transition is modelled by the first term in (4).

It is well known that RDME models a Markov process [11]. However, RD-MEX is no longer a Markov process due to the presence of exogenous arrivals, i.e. the first term in (4). It can be shown that RDMEX is a piece-wise Markov process in the sense that RDMEX is only a Markov process between two consecutive arrivals. Define the mean and covariance of $Q(t)$ as:

$$\langle Q(t) \rangle = \sum_q q \text{Prob}(Q(t) = q) = \sum_q q P(q, t) \quad (5)$$

$$\Sigma(t) = \sum_q (q - \langle Q(t) \rangle)(q - \langle Q(t) \rangle)^T P(q, t) \quad (6)$$

where $\langle \bullet \rangle$ will be used in this paper to denote the mean operator.

The following proposition is proved in [9].

Proposition 1. *For the RDMEX model in (4), assuming that $W_j(q)$ is a linear function of q . Let $\sum_{j=1}^J r_j W_j(q) = Aq$, then*

$$\frac{d\langle Q(t) \rangle}{dt} = A\langle Q(t) \rangle + \sum_{a=1}^{N_t} \mathbb{1}_{T_a} \underbrace{\sum_{b=1}^{\infty} k_{a,b} \delta(t - t_{a,b})}_{k_a(t)} \quad (7)$$

$$\frac{d\Sigma(t)}{dt} = A\Sigma(t) + \Sigma(t)A^T + \sum_{j=1}^J r_j r_j^T W_j(\langle Q(t) \rangle) \quad (8)$$

The above proposition shows that given the emission patterns of the transmitters, we can compute the mean and variance of the output signals. Our previous work [9] has focused on solving equation (7). We will study how equation (8) can be efficiently solved in the next section.

- Remark 1.** 1. *The choice of linear reactions at the receiver may not be a severe limitation. We show in [9] that some higher order reactions, such as Michaelis-Menten, can be approximated by linear reactions.*
2. *If the reactions at the receiver are not linear, it is still possible to write down the RDME model and the form is identical to (4). However, the transition rates $W(q)$ are no longer linear functions. We leave the analysis of such RDME models for future work.*

3. Variance of the output signal at receivers

In section 2, we show that we can compute the mean and covariance of the receiver output signal by solving two coupled ordinary differential equations (ODEs) (7) and (8). Note that the dimensions of these ODEs are high: (7) and (8) have a dimension of N_q and N_q^2 , respectively. Recall that $N_q = N_v^3 + N_r$ where N_v^3 is the number of voxels, which is likely to be a large number. In our previous work [9], we present a method to compute the mean number of complexes at the receivers. Let $c_h(t)$ denote the mean number of complexes at h -th receiver at time t and define the input signal of the a -th transmitter as $k_a(t) = \sum_{b=1}^{\infty} k_{a,b} \delta(t - t_{a,b})$. The paper [9] derives the transfer function from $k_a(t)$ to $c_h(t)$. The transfer function allows us to directly compute $c_h(t)$ from $k_a(t)$ without having to compute the mean number of signalling molecules in the voxels, thus lowering the complexity of the computation. In this section, we focus on solving the covariance equation (8) efficiently.

3.1. Solving equation (8) via a reduced dimension ODE

In order to explain the method for solving equation (8) efficiently, we first examine the matrix $\Sigma(t)$ and the forcing function term $W_j(\langle Q(t) \rangle)$. The matrix $\Sigma(t)$ contains covariances of the form $\text{cov}(n_{L,\xi_1}(t), n_{L,\xi_2}(t))$, $\text{cov}(n_{L,\xi_1}(t), n_{R,h_1}(t))$ and $\text{cov}(n_{R,h_1}(t), n_{R,h_2}(t))$ where $n_{L,\xi_1}(t)$ denotes the number of signalling molecules in voxel ξ_1 at time t , and $n_{R,h_1}(t)$ denotes the number of complexes at h_1 -th receiver at time t etc. The dimension of $\Sigma(t)$ is N_q^2 , which can be a large number.

The forcing functions in the ODE (8) are $W_j(\langle Q(t) \rangle)$. From the definition of $Q(t)$, it follows that the forcing functions $W_j(\langle Q(t) \rangle)$ are of the form $v_\xi \langle n_{L,\xi}(t) \rangle$ or $v_h \langle n_{R,h}(t) \rangle$, where v_ξ and v_h are some proportional constants. The number of forcing functions is N_q which can be a large number. Note that our previous work provides efficient algorithm to compute $\langle n_{R,h}(t) \rangle$ but computing $\langle n_{L,\xi}(t) \rangle$ for all voxels can be prohibitive.

In order to reduce the complexity of solving (8), we assume that the number of complexes $n_{R,h}$ in the h -th receiver, whose location is the voxel with index R_h , depends only on the number of signalling molecules in the voxels close to voxel R_h . This simplification means that we can set up a lower dimensional ODE with terms involving only those voxels that are close to the receivers. In order to formally describe the method, we define the distance function $\text{dist}(\xi_1, \xi_2)$, where ξ_1 and ξ_2 are indices for voxels (x_1, y_1, z_1) and (x_2, y_2, z_2) , as

$$\text{dist}(\xi_1, \xi_2) = \max\{|x_1 - x_2|, |y_1 - y_2|, |z_1 - z_2|\} \quad (9)$$

The proposed method takes a positive integer U as the input parameter. The method is to construct a reduced-dimension ODE from (8) that contains *only* the following variables and forcing functions (note: ξ and h below are, respectively, indices for voxels and receivers):

1. Variables:

- (a) All $\text{cov}(n_{L,\xi_1}(t), n_{L,\xi_2}(t))$ such that $\text{dist}(\xi_1, R_{h_1}) \leq U$ for some h_1 and $\text{dist}(\xi_1, R_{h_2}) \leq U$ for some h_2 where $h_1, h_2 = 1, \dots, N_r$
- (b) All $\text{cov}(n_{L,\xi_1}(t), n_{R,h_1}(t))$ and $\text{cov}(n_{R,h_1}(t), n_{L,\xi_1}(t))$ such that $\text{dist}(\xi_1, R_{h_1}) \leq U$ for some $h_1 = 1, \dots, N_r$
- (c) All $\text{cov}(n_{R,h_1}(t), n_{R,h_2}(t))$ for $h_1, h_2 = 1, \dots, N_r$

2. Forcing functions

- (a) All $\langle n_{L,\xi}(t) \rangle$ such that $\text{dist}(\xi, R_h) \leq U$ for some $h = 1, \dots, N_r$
- (b) All $\langle n_{R,h}(t) \rangle$ for $h = 1, \dots, N_r$

In other words, all the variables and forcing function that are not retained are assumed to be zero.

The input parameter U can be chosen as follows. We begin with an initial choice of U_0 and solve the reduced dimension ODE. We can solve the ODE again with input parameter U_1 greater than U_0 . If the solutions given by these two input parameters are similar, we stop; otherwise, we increase the input parameter U until two consecutive choices give similar solutions.

3.2. Numerical examples

In this section, we give two numerical examples to illustrate our proposed method to solve (8).

3.2.1. 1-transmitter 1-receiver network

This section considers a molecular communication network with one transmitter and one receiver in a fluid medium with $D = 0.05$. Since the parameters in a reaction-diffusion system can be scaled to some dimensionless quantities [12, Section 8.2], we do not specify the units for the parameters here. The fluid medium is divided in 30^3 voxels with the transmitter locating at voxels $[0, 0, 0]$ and $[3, 0, 0]$ respectively. The transmitter emits 10 molecules every 10^{-4} time units for a duration of 0.2 time units and then stops the emission. The reaction at the receiver is conversion type in (2) with parameters are $k_+ = 2.5 \times 10^{-3}$ and $k_- = 8$.

We first solve the reduced dimension ODE using input parameter $U = 3$. For verification, we use τ -leaping [13] to simulate the RDME model 120 times and compute the empirical variance of the receiver output. Note that the simulation keeps track of the number of signalling molecules in all voxels, i.e. 30^3 voxels, while our proposed method uses only the information in the $(2U + 1)^3$ voxels centred around the receiver voxel.

Figure 1 shows the variance of the number of complexes at the receiver computed by the reduced ODE (our proposed method) as well as empirical variance from simulation. The figure shows that the variance computed by the reduced order ODE is fairly accurate. We have increased the input parameter U of our proposed method to 5 and it gives almost the same result. The result is not showed in the figure in order not to clutter the graph.

We will discuss the curve with the label *Mean of output* in Figure 1 in Section 3.2.3.

3.2.2. 2-transmitter 2-receiver network

This section considers a molecular communication network with two transmitters and two receivers in a fluid medium with $D = 0.05$. The transmitters are located at $(0, 0, 0)$ and $(-2, -2, -2)$. Receivers 1 and 2 are located at $(3, 0, 0)$ and $(2, -2, -2)$ respectively. Both transmitters have the same emission pattern of emitting 20 molecules every 10^{-4} time units for a duration of 0.1 time units and then stops the emission. Both receivers use conversion type reaction (2) with $k_+ = 1.25 \times 10^{-4}$ and $k_- = 0.05$.

We use our proposed method with input parameter $U = 3$ to compute the variance of the output of both receivers. For verification, we use τ -leaping to simulate the system 270 times and compute the empirical variance. The results are plotted in Figures 2 and 3, for, respectively, receivers 1 and 2. It can be seen that the variance computed by our proposed method is accurate. We have used a larger value of $U = 5$ and the results are similar. The curves with label *mean of output* in Figures 2 and 3 will be discussed next.

3.2.3. Comparing mean of output and variance of output

In Figures 1 (for the receiver output of the 1-transmitter 1-receiver network), and 2 and 3 (for the receiver outputs of the 2-transmitter 2-receiver network), we have plotted the mean number of complexes at the receivers as well as the variance of the number of the complexes. An observation that we can make from these three figures is that the mean number of complexes are almost the same as the variance of the number of complexes. These observations suggest that the number of complexes at the receiver may be Poisson distributed. We will investigate this further in Section 4.

4. Probability distribution of receiver output

The RDME model that we have considered so far assumes that the number of signalling molecules emitted by a transmitter at a given time is a deterministic

quantity. In this section, we extend the RDMEX model so that the number of signalling molecules emitted by a transmitter at a given time is probabilistic. In particular, we will show that, if the number of signalling molecules emitted is Poisson distributed and the reactions at the receivers are limited to a few specific types, then the receiver output of a linear molecular communication network is also Poisson distributed.

4.1. RDMEX with random emissions at the transmitters

The RDMEX model (4) assumes that the a -th transmitter emits exactly $k_{a,b}$ molecules at time $t_{a,b}$. In this section, we instead assume that at time $t_{a,b}$, the a -th transmitter emits $K_{a,b}$ molecules where $K_{a,b}$ is a random variable. Under this revised assumption, the RDMEX model becomes:

$$\begin{aligned} \frac{dP(q,t)}{dt} &= \sum_{a=1}^{N_t} \sum_{b=1}^{\infty} \sum_{k_{a,b}=0}^{\infty} \{P(q - k_{a,b} \mathbf{1}_{T_a}) - P(q,t)\} P(K_{a,b} = k_{a,b}) \delta(t - t_{a,b}) \\ &\quad + \sum_{j=1}^J W_j(q - r_j) P(q - r_j, t) - \sum_{j=1}^J W_j(q) P(q, t) \end{aligned} \quad (10)$$

where $P(K_{a,b} = k_{a,b})$ is the probability that the random variable $K_{a,b}$ takes the value $k_{a,b}$ with $k_{a,b}$ being a non-negative integer.

Under this revised model, the evolution of the mean and covariance of the state vector $Q(t)$ is given in the following proposition.

Proposition 2. *For the RDMEX model in (10), assuming that $W_j(q)$ is a linear function of q . Let $\sum_{j=1}^J r_j W_j(q) = Aq$, then*

$$\frac{d\langle Q(t) \rangle}{dt} = A\langle Q(t) \rangle + \sum_{a=1}^{N_t} \mathbf{1}_{T_a} \sum_{b=1}^{\infty} \langle K_{a,b} \rangle \delta(t - t_{a,b}) \quad (11)$$

$$\begin{aligned} \frac{d\Sigma(t)}{dt} &= A\Sigma(t) + \Sigma(t)A^T + \sum_{j=1}^J r_j r_j^T W_j(\langle Q(t) \rangle) \\ &\quad + \sum_{a=1}^{N_t} \sum_{b=1}^{\infty} \text{cov}(K_{a,b}) \mathbf{1}_{T_a}^T \mathbf{1}_{T_a} \delta(t - t_{a,b}) \end{aligned} \quad (12)$$

where $\langle K_{a,b} \rangle$ and $\text{cov}(K_{a,b})$ are respectively the mean and covariance of $K_{a,b}$. One can readily observe that equations (7) and (8) are special cases of equations (11) and (12).

4.2. Poisson distribution property

The following proposition gives the key result of this section on the probability distribution of the state $Q(t)$ for RDMEX model (10).

Proposition 3. *Consider the RDMEX model (10), assuming*

- (a) *The random variable $K_{a,b}$ is Poisson distributed;*
- (b) *The initial state $Q(0)$ is either zero or Poisson distributed;*
- (c) *The reactions at the receiver are composed of conversion or degradation types;*

then the state $Q(t)$ is Poisson distributed at any time t . Furthermore, the mean of the Poisson distributed state vector $\langle Q(t) \rangle$ evolves according to equation (11).

Proof: Let $t_0 = \min_a t_{a,1}$ be the time at which the first transmitter emission occurs in the network. Let also $\tilde{a} = \arg \min_a t_{a,1}$, i.e. the first molecule is emitted by \tilde{a} -th transmitter.

We first consider the case where the initial state $Q(0)$ is Poisson distributed. We know from [11, 14] that for a system consisting of the stated types of reactions and whose master equation is

$$\frac{dP(q, t)}{dt} = \sum_{j=1}^J W_j(q - r_j)P(q - r_j, t) - \sum_{j=1}^J W_j(q)P(q, t), \quad (13)$$

if the initial state $Q(0)$ is Poisson distributed, then the system state $Q(t)$ is Poisson distributed with mean of $\langle Q(t) \rangle$ evolving

$$\frac{d\langle Q(t) \rangle}{dt} = A\langle Q(t) \rangle \quad (14)$$

where A is again defined by $\sum_{j=1}^J r_j W_j(q) = Aq$. Note that equations (13) and (14) are special cases of (10) and (11) where transmitter emissions are *absent*.

Consider time $t \in [0, t_0)$, i.e. before the first transmitter emission occurs. In the absence of transmitter emissions during $t \in [0, t_0)$, RDMEX (10) and master equation (14) are identical. Hence the results in [11, 14] apply to $t \in [0, t_0)$. This means, if the initial state $Q(0)$ is Poisson distributed, then for $t \in [0, t_0)$,

the state $Q(t)$ is Poisson distributed with mean given by (11), which takes the form of (14) in this time interval.

Let us consider what happens at time t_0 . Let t_0^- denote the time just before t_0 . We know that the state $Q(t_0^-)$ is Poisson distributed. At time t_0 , $K_{\tilde{a},1}$ signalling molecules are added to the voxel occupied by the \tilde{a} -th transmitter. Therefore the system state at time t_0 is the random variable $Q(t_0^-) + \mathbb{1}_{T_a} K_{\tilde{a},1}$. Since $K_{\tilde{a},1}$ is Poisson distributed and sum of two independent Poisson distributed random variables is also Poisson, this implies that the state $Q(t_0)$ is Poisson distributed. It also means that $\langle Q(t_0) \rangle = \langle Q(t_0^-) \rangle + \mathbb{1}_{T_a} \langle K_{\tilde{a},1} \rangle$ which is also the result given by equation (11).

We can now repeat the above arguments for the time interval from t_0 till the next transmitter emission. The time t_0 is considered to be the initial time and since $Q(t_0)$ is Poisson distributed, the assumptions required for the above arguments hold. Therefore, by repeating these arguments, we can prove that the proposition holds for all time t if the initial state $Q(0)$ is Poisson distributed.

For the case where the initial state $Q(0)$ is zero, we know that the state at time t_0 is $\mathbb{1}_{T_a} K_{\tilde{a},1}$, which is Poisson distributed. We now can repeat the above arguments to prove the proposition for this case. \square

The above proposition shows that for certain receiver structures, the states (which also include the receiver outputs) of linear molecular communication networks are Poisson distributed with mean of the distribution evolving according to (11). Such networks have the following properties:

1. The variance of receiver output equals to the mean receiver output.
2. The mean (or variance) of receiver output is a *nonlinear* function of the receiver parameters and diffusion coefficient D of the fluid medium.
3. The mean transmitter input $\sum_{b=1}^{\infty} \langle K_{a,b} \rangle \delta(t - t_{a,b})$ and the mean state are related by a linear time-invariant (LTI) dynamical system. The transfer function of this LTI system can be computed by taking the Laplace transform of (11), see [9] for derivation. This statement also applies to variance of system state because variance and mean are identical for Poisson dis-

tribution.

If we consider the receiver noise as the variance of receiver output, then the noise in linear molecular communication networks is neither of constant amplitude (in fact it is a nonlinear function of system parameters) nor additive.

4.3. What happens if the input is not Poisson distributed?

Proposition 3 shows that if the number of molecules emitted by the transmitter is Poisson distributed, then the state of the linear molecular communication networks (10) is also Poisson distributed. However, no analytical results on the probability distribution of the state are available if these assumptions do not hold. In our numerical study in Section 3.2, where the number of molecules emitted by the transmitter is deterministic, we find that the variance of the receiver output is equal to its mean. This observation suggests that the probability distribution of the receiver outputs may be Poisson. In this section, we use statistical tests to study whether the receiver output may have Poisson distribution.

We first consider the 1-transmitter 1-receiver molecular network studied in Section 3.2.1. We use the same set of parameters and simulate the network 120 times using τ -leaping. The simulation duration is 1.6 time units with a time interval of 10^{-4} time units. This gives 120 output trajectories, each with the number of complexes at the receivers at 16000 time points. We apply three different statistical tests — Neyman-Scott statistic, Poisson dispersion test, Likelihood ratio test [15, Chapter 4] — to determine whether the Poisson distribution may hold at each time point, with a significance level of 95%. The results of the statistical tests are plotted in Figure 4. It appears that the receiver output is Poisson distributed for most of the time points with high probability.

We next consider the 2-transmitter 2-receiver molecular network studied in section 3.2.1. We use the same set of parameters and simulate the network 270 times using τ -leaping. Each simulation spans 0.5 time units and gives the number of complexes at the two receivers at 5000 time points. We apply the same statistical tests as before. The results are plotted in Figures 5 and 6 for the

two receivers. The figures show that the receiver outputs are Poisson distributed with a high probability.

5. Application to communications

In this section, we present an application of the results to communications. We consider single-transmitter single-receiver linear molecular communication networks. In particular, we investigate the impact of receiver structures and receiver parameters on the communication performance in these networks.

We consider two different receiver structures. The first receiver structure consists of reversible conversion in (2). We will refer to this as **c+c** because both the forward and reverse reactions are of conversion type. The second receiver structure consists of two reactions:



Reaction (15) converts the signalling molecules L to a complex C at a rate of k_+ and in reaction (16), the complex C degrades at a rate of k_- . We will refer to this type of receiver as **c+d**. Note that we use the same k_+ and k_- values in **c+c** and **c+d** for fair comparison. Both types of receivers satisfy the conditions of Proposition 3.

We consider two molecular communication networks. Each network has a transmitter located at voxel $(0, 0, 0)$ and one receiver at $(3, 0, 0)$. The transmitter parameters for both networks are identical, but one network uses **c+c** receiver structure while the other uses **c+d**.

We first investigate the impact of the receiver parameter k_+ on the output signal of these networks. We assume that the transmitter emits on average 10^2 molecules per 10^{-4} time units according to Poisson distribution, for 0.2 time units and then stop the emission. According to Proposition 3, the number of complexes at the molecular networks is Poisson distributed with mean evolving according to equation (11). We use two different values for k_+ : 2.5×10^{-4} and

7.5×10^{-4} . The k_- is 5 for both networks. Figure 7 shows the mean receiver output for both receiver structures and both choices of k_+ . If $k_+ = 2.5 \times 10^{-4}$, the mean receiver outputs for both **c+c** and **c+d** are similar. However, if $k_+ = 7.5 \times 10^{-4}$, the mean receiver output for **c+c** is higher than that of **c+d**. The difference can be explained as follows. In **c+c** networks, if a complex C is converted to a ligand L (the reverse reaction), the resulting ligand may diffuse to a neighbouring voxel or reacts to form a complex again. The *re-uptaking* of the ligand accounts for the difference in the results. When k_+ is sufficiently large, the rate of the forward reaction is higher than diffusion; this increases re-uptaking of ligand molecules. However, if k_+ is small, re-uptaking rate is low and ligand molecules tend to diffuse to a different voxel; this has almost the same effect as degradation.

In our second investigation, we consider the communication performance of these two networks as discrete memoryless channels. The transmitter uses the same pulse waveform considered before but it can vary the emission rate. The emission rate can be varies from 10 to 100 molecules per 10^{-4} time units. We assume the resolution in emission rate is 1. This results in 91 different emission rates or input symbols. The output is the number of molecules at the receiver at 0.25 time units after the beginning of the pulse. This particular sampling time is indicated by the vertical line in Figure 7. We also assume that consecutive symbols are well separated in time so that inter-symbol interference can be neglected.

We consider the receiver structures **c+c** and **c+d**, and vary the parameter k_+ from 2.5×10^{-4} to 2.3×10^{-3} . We use the Blahut algorithm [16] to calculate the capacity of the discrete memoryless channel for both receiver structures and for different k_+ . The results are shown in Figure 8. It shows that for both receiver structures, the capacity is an increasing function of k_+ . In fact, for these networks, the capacity is an increasing function of a *gain* parameter g . The gain g is defined as the ratio of the mean receiver output at sample time to the mean (non-zero) emission rate of the pulse input. Due to the linearity between the mean receiver output and mean transmitter emission rate (see the

discussion in Section 4), the gain g is a constant for a given network and sample time. The computation shows that capacity is an increasing function of g which is in turn an increasing function of k_+ .

6. Related work

Molecular communication networks are investigated in the area of nano communication networks. Recent reviews on this topic can be found in [2, 3, 4].

The characterisation of noise in molecular communication networks is important in understanding the communication performance of these networks. Pioneering work has been done in [17] and [18, 19] to understand the mean behaviour and noise properties of molecular communication networks. These models are based on modelling molecular communication networks using discrete molecular particle dynamics.

An alternative approach to modelling molecular systems, but with coarser granularity compared to molecular dynamics, is the master equation approach [20, 10]. Master equations have been used to model systems with chemical reactions alone, which results in chemical master equation (CME) [10], as well as systems with both reactions and diffusion, which results in RDME.

The work in [19] uses the CME to study the stochastic dynamics of ligand-receptor at the receiver. This model covers only the receiver, and does not consider the transmitter and the diffusion channel. Another stochastic model for molecular communication is proposed in [21]. The model gives the probability distribution of the number of signalling molecules arriving at the receiver through the fluid channel. This model covers the transmitter and fluid medium, but does not consider the receivers.

In our earlier work in [9], we propose the RDMEX model for molecular communication networks. The model covers the transmitter, the fluid medium and the receiver. In particular, RDMEX can be used to model networks with multiple transmitters and multiple receivers. The work in [9] focus on understanding the behaviour of the mean output signal at the receivers. In this paper, we

consider linear molecular communication networks and investigate the variance and distribution of the output signal.

The fact that one of the solutions for an RDME has a Poisson distributions is shown in [22]. This article also shows the connection between Poisson distribution and grand canonical ensemble in statistical physics. This paper extends this result to RDMEX model. Note that RDME models a Markov process but RDMEX is piece-wise Markov.

The capacity of the photon channel is studied in [23, 24, 25]. The receiver signal of a photon channel is Poisson distributed, and is given by the sum of a noise-free and a noisy Poisson distribution. Although the receiver signals of linear molecular communication networks are also Poisson distributed under certain conditions, the noise in molecular communication is *not* additive.

7. Conclusions

In this paper, we investigate the properties of the variance of the receiver outputs of linear molecular communication networks. We show that, under certain conditions, the output signals of these networks are Poisson distributed. The derivation also shows that the variance of the receiver output, which can be considered to be the receiver noise, is a nonlinear function of the network parameters and is non-additive. Our future work is to investigate more complicated receiver structures.

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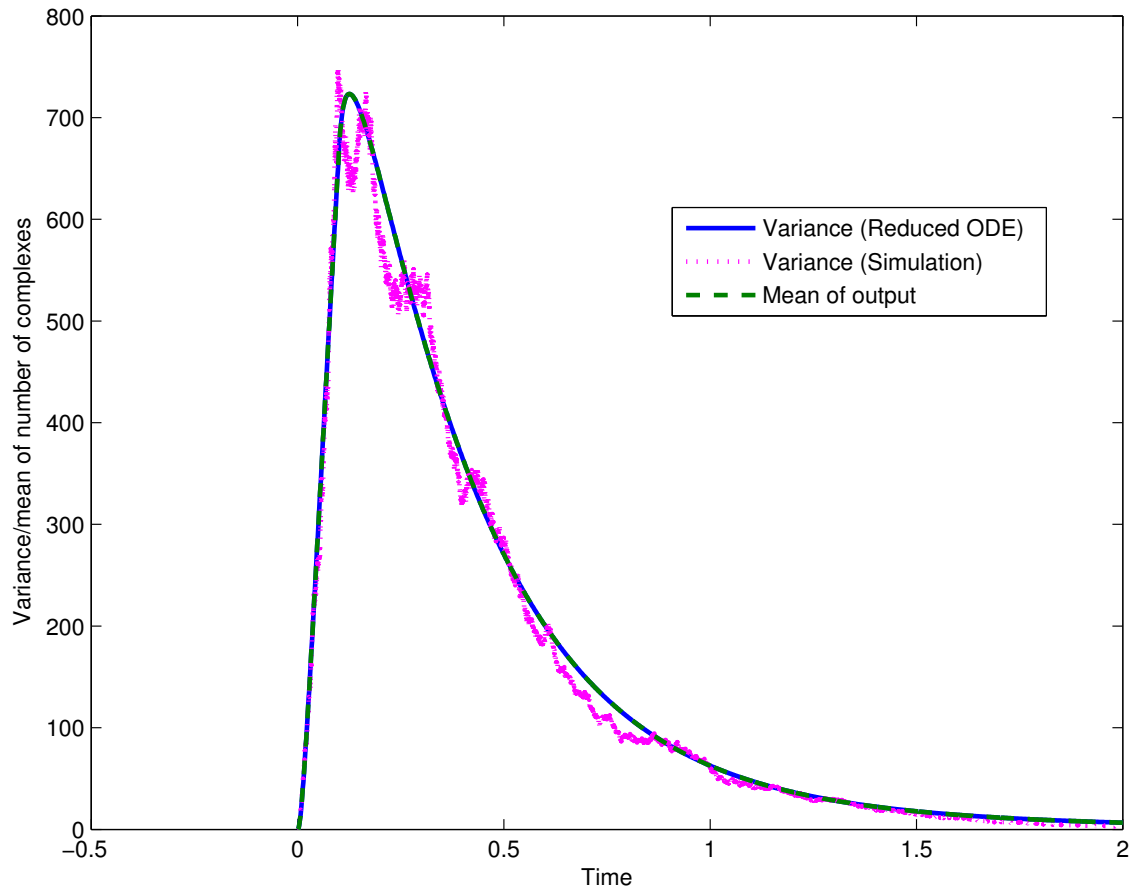


Figure 1: The variance and mean number of complexes in the 1-transmitter 1-receiver network.

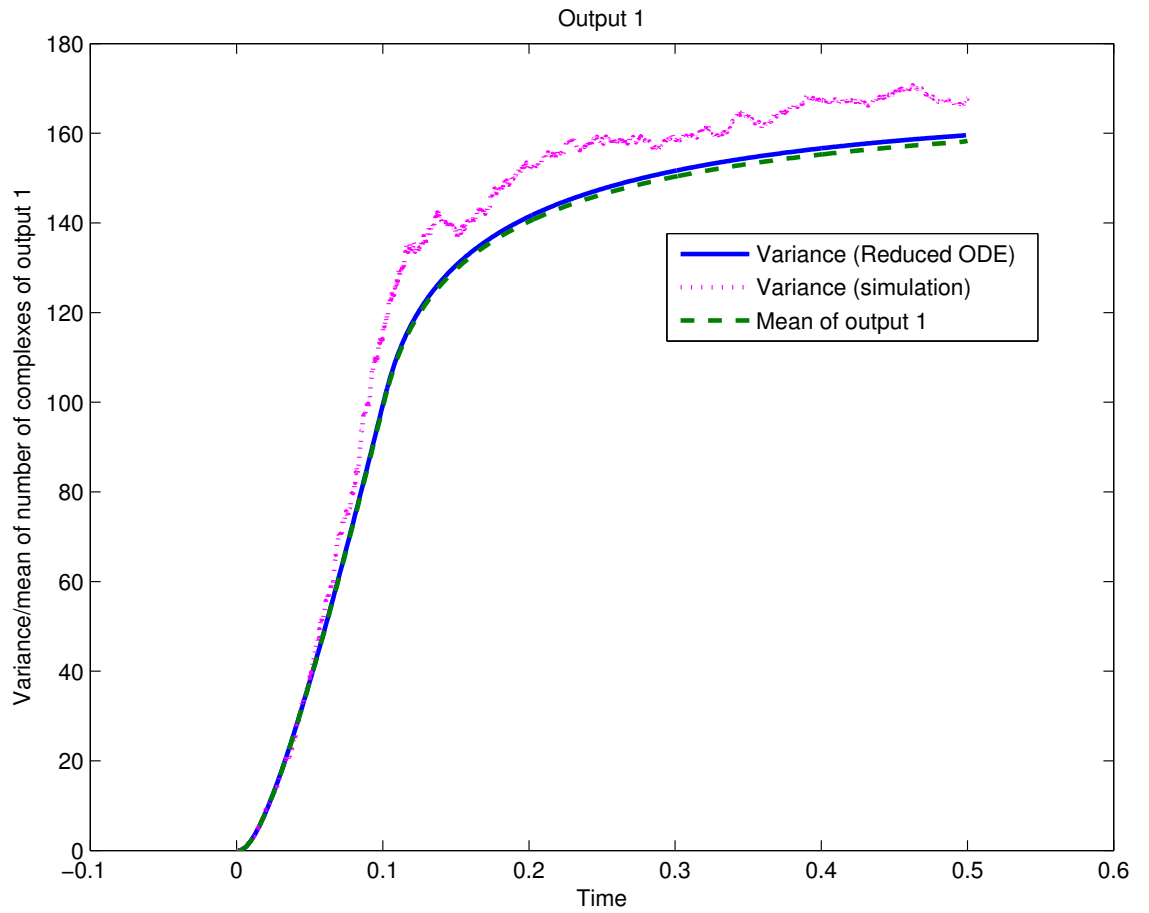


Figure 2: The variance and mean number of complexes of output 1 of the 2-transmitter 2-receiver network.

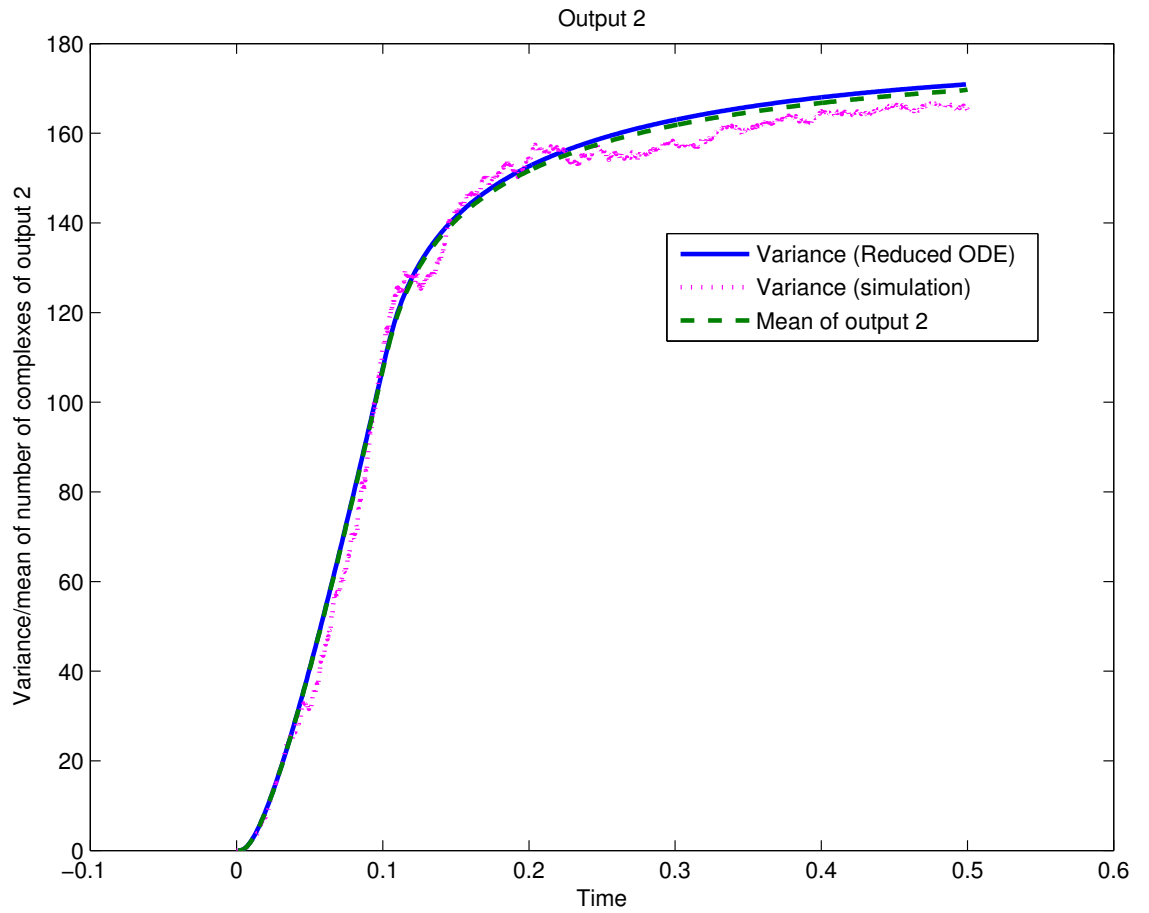


Figure 3: The variance and mean number of complexes of output 2 in the 2-transmitter 2-receiver network.

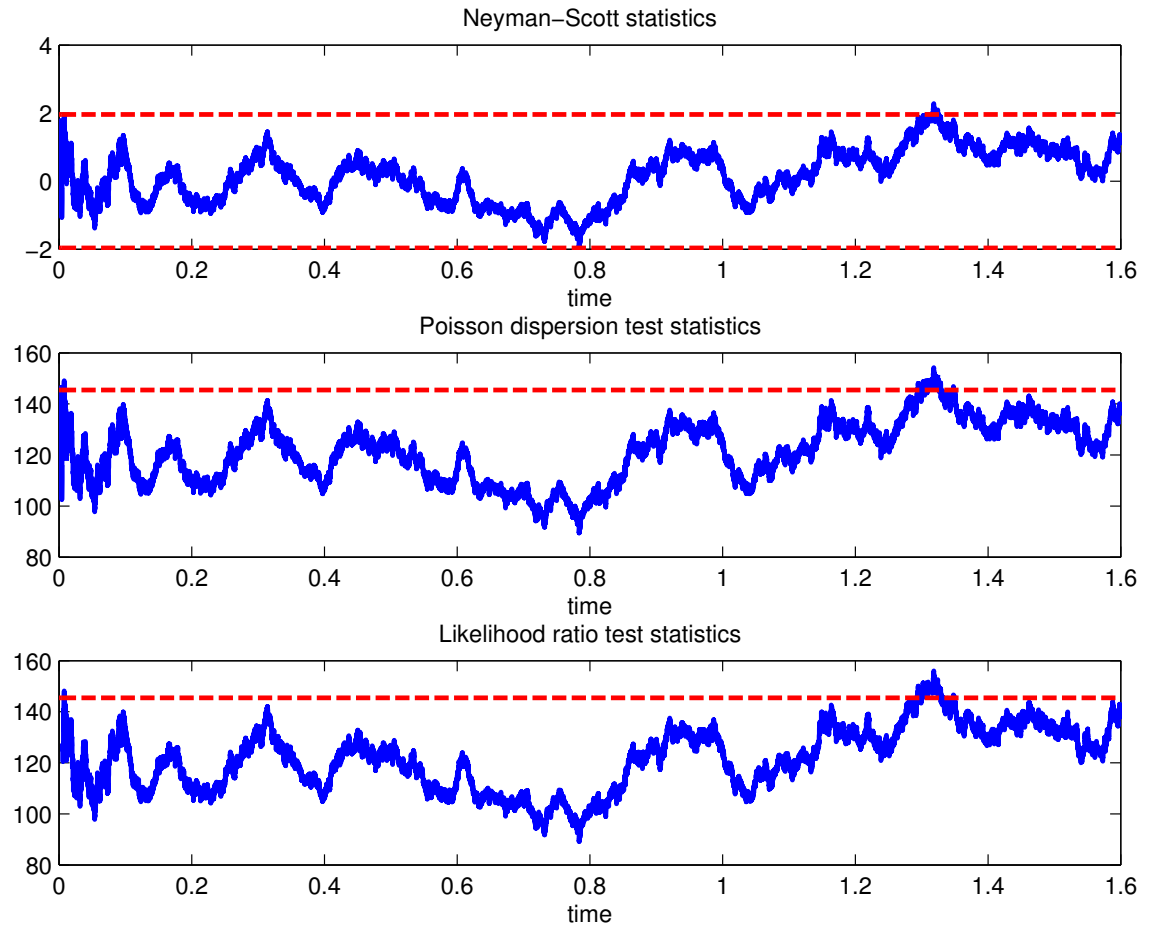


Figure 4: Poisson statistical tests on the receiver output of the 1-transmitter 1-receiver network.

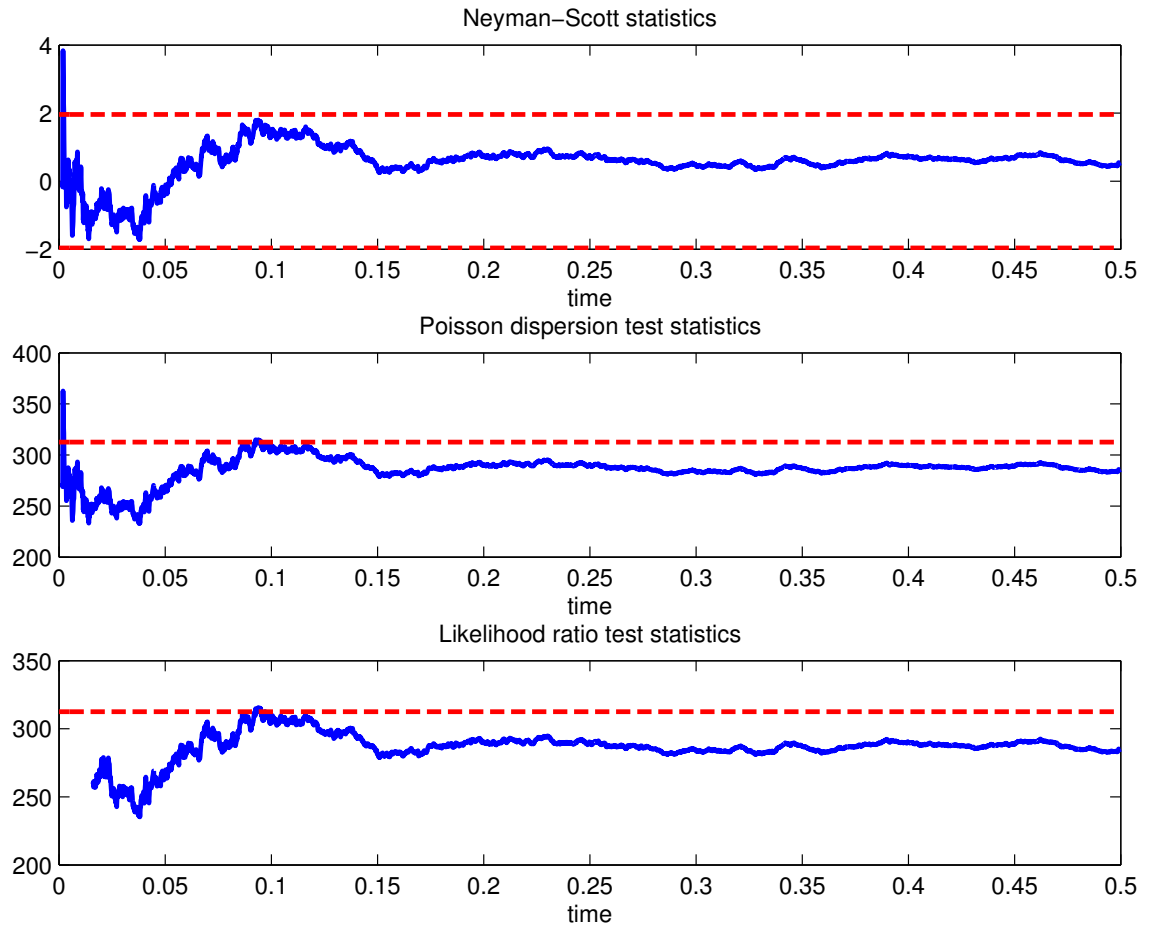


Figure 5: Poisson statistical tests on output of receiver 1 of the 2-transmitter 2-receiver network.

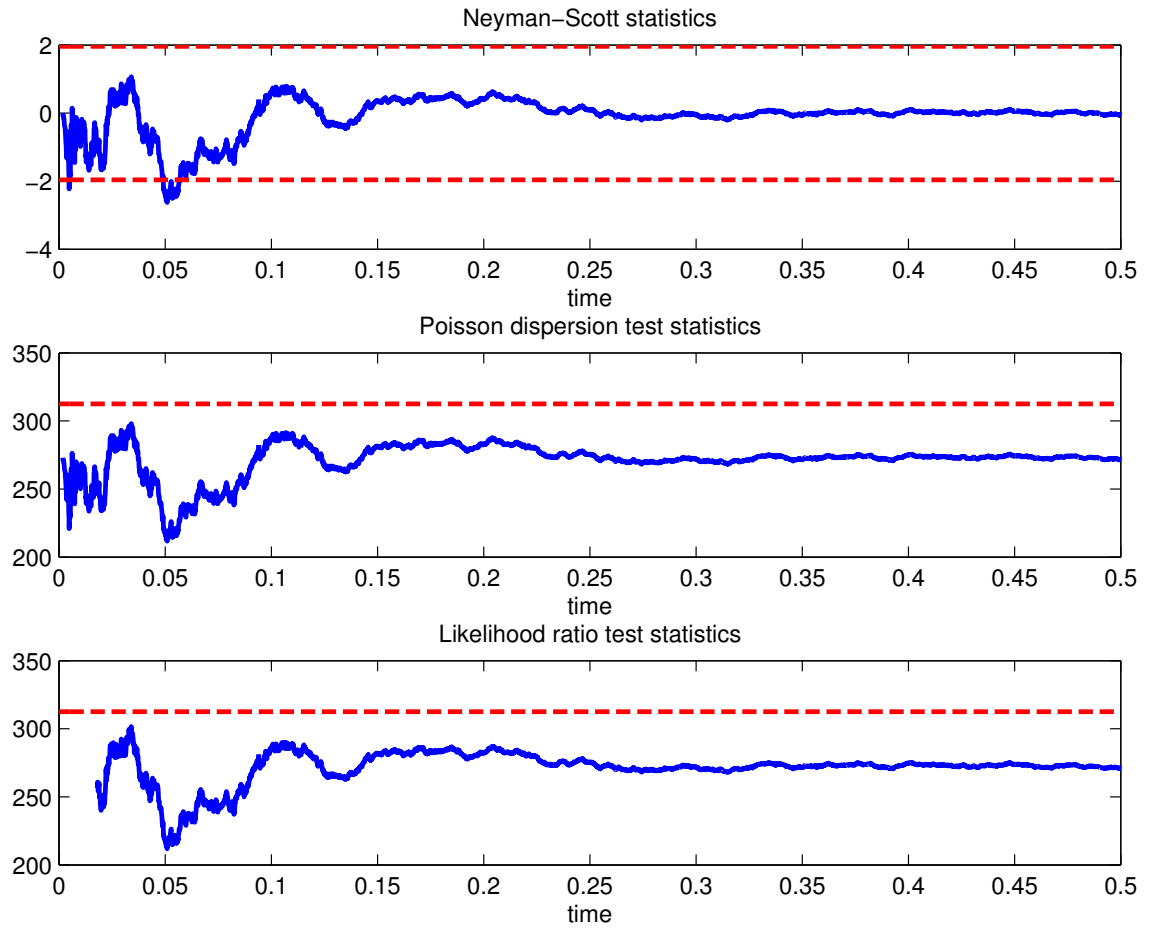


Figure 6: Poisson statistical tests on output of receiver 2 of the 2-transmitter 2-receiver network.

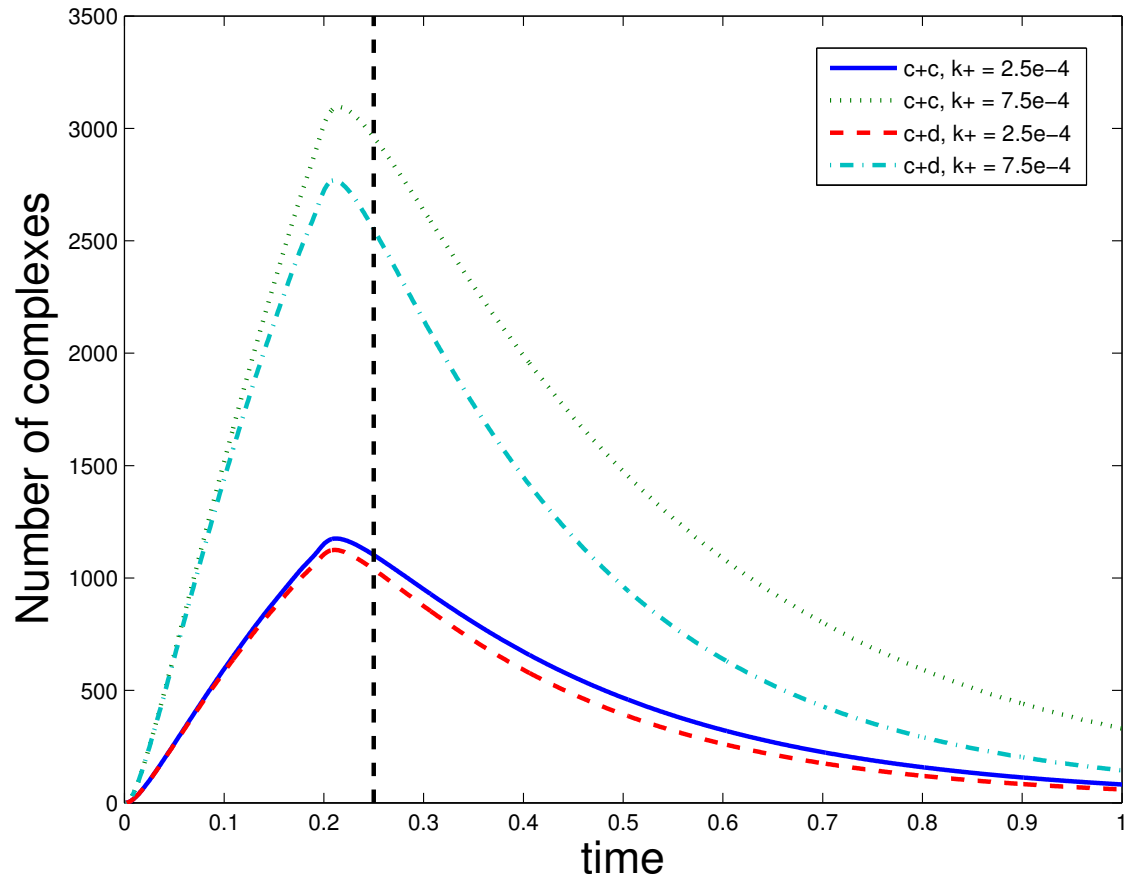


Figure 7: The mean number of complexes for c+c and c+d receivers for two different values of k_+ .

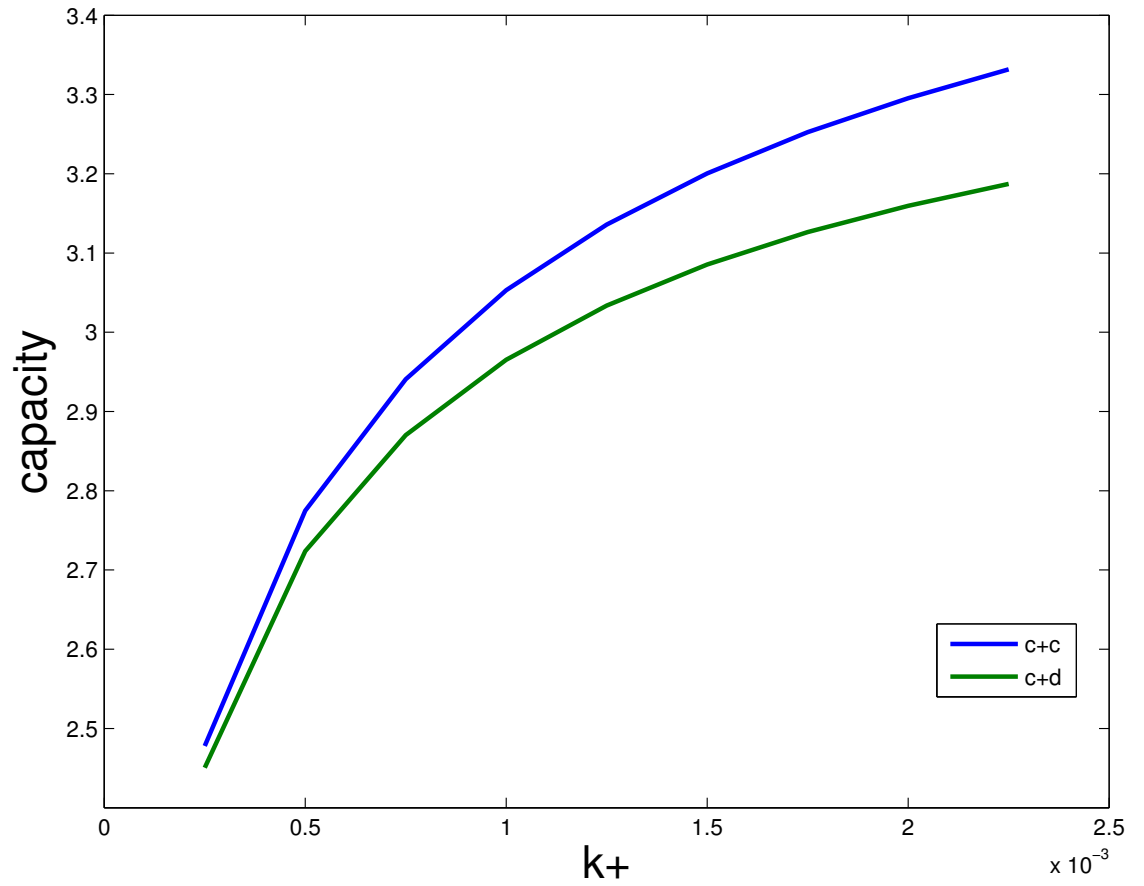


Figure 8: The influence of k_+ on capacity for c+c and c+d receivers.