Mutual Information Rate of Gaussian and Truncated Gaussian Inputs on Intensity-Driven Signal Transduction Channels

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Abstract—In this letter, we investigate the mutual information rate (MIR) achieved by an independent identically distributed (IID) Gaussian input on the intensity-driven signal transduction channel. Specifically, the asymptotic expression of the continuoustime MIR is given. Next, aiming at low computational complexity, we also deduce an approximately numerical solution for this MIR. Moreover, the corresponding lower and upper bounds that can be used to find the capacity-achieving input distribution parameters are derived in closed-form. Finally, simulation results show the accuracy of our analysis.

Index Terms—MIR, signal transduction channel, IID Gaussian input, numerical solution, bound, molecular communication.

I. INTRODUCTION

Signal transduction, a typical form of molecular communication in nature, can support the communication between living cells. Examples of such systems include: binding of the acetylcholine (ACh) neurotransmitter to its receptor protein [1], modulation of the channel opening transition by light intensity in the channelrhodopsin (ChR) protein [2], and so on.

At present, there are two main branches of signal transduction research in the communication field. One is to construct a stochastic model for the signal transduction system, while the other is to provide insights into these systems from the information-theoretic perspective. In the first branch, stochastic modeling of signal transduction as a communication channel has considered the chemical reactions in terms of Markov chains [3] and in terms of the "noise" inherent in the binding process [4]. Further, a linear noise approximation was developed for signal transduction channels in [5]. In the second branch, Shannon capacity or mutual information of some typical signal transduction processes has been analyzed based on the above stochastic model. In particular, when considering a single receptor and multiple independent receptors, the Shannon capacity of two-state Markov signal transduction under arbitrary inputs was derived in [6] and [7], respectively. Calculation of the mutual information rate (MIR) and capacity for individual receptors with ChR-2 (ChR2),

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Andrew W. Eckford is with the Department of Electrical Engineering and Computer Science, York University, Toronto M3J 1P3, Canada (Email: aeckford@yorku.ca). ACh, and calmodulin (CaM) was performed in [8], where the states considered in the Markov chain are more diverse.

Notably, the previous work on the mutual information or channel capacity analysis of the signal transduction channel only considered the channel input to be independent and identically distributed (IID) discrete symbols, especially IID binary symbols [6]-[8]. However, when it comes to the input of the target system, continuous-valued variables are often used: the concentration of a ligand, the intensity of a light source, the potential difference across a cell membrane, etc. In nature, the above input can be easily modeled as a Gaussian distribution, due to the central limit theorem. For example, the spatial intensity distribution for the LED (such as Laser TEM00 beam) can be approximated by a Gaussian profile (> 95%) [9]. Against this background, in this paper, we propose to exploit the MIR achieved by an IID Gaussian or truncated Gaussian continuous input on the intensity-driven signal transduction channel. For ease of analysis, the approximate solution for the MIR is theoretically studied, and the corresponding bounds are also derived in closed-form. Finally, Monte Carlo simulations are carried out to verify the analysis.

II. SYSTEM MODEL

In this paper, we consider a typical signal transduction process, which can be regarded as a Markov chain model first, and then as a communication model. The complete equivalent process will be detailed in the sequel.

A. Markov Chain Model of Signal Transduction

The finite-state Markov chain model is first employed to describe the signal transduction process for a single receptor. Assuming a receptor with k discrete states, there exists a k-dimensional vector of state occupancy probabilities $\mathbf{p}(t)$, i.e.,

$$\mathbf{p}(t) = [p_1(t), p_2(t), \dots, p_k(t)], \qquad (1)$$

where $p_i(t)$ denotes the probability that the receptor is in state i at time t with i = 1, 2, ..., k. It is well known that this probability evolves according to the master equation [8], i.e.,

$$\frac{d\mathbf{p}(t)}{dt} = \mathbf{p}(t) \mathbf{Q}(x(t)).$$
(2)

Here, $\mathbf{Q}(x(t))$ is a $k \times k$ matrix of rate constants, where the element at the *i*-th row and *j*-th column of $\mathbf{Q}(x(t))$, $q_{ij}(x(t))$, is the instantaneous rate at which receptors starting in state *i* enter state *j* under the input x(t). Here, we define a discrete time step as Δt to analyze the Markov chain [10]. When $\Delta t \rightarrow 0$, the master equation in (2) can be approximated as



Fig. 1. State transition diagram for ChR2. Sensitive transitions are depicted with bold arrows. States are labeled by their channel state: $\{C, O\}$ for closed and open, respectively; the state number is in subscript. Dashed lines surround all states in either the closed or open state.

$$\mathbf{p}(t + \Delta t) = \mathbf{p}(t)(\mathbf{I} + \mathbf{Q}\Delta t) + o(\Delta t), \quad (3)$$

where **I** is the identity matrix and $\mathbf{Q}(x(t))$ is simplified as **Q**. Neglecting the high-order terms $o(\Delta t)$, the channel state can be represented as a discrete-time Markov chain with the transition probability matrix

$$\mathbf{P} = \mathbf{I} + \mathbf{Q}\Delta t,\tag{4}$$

where \mathbf{P} is given by using p_{ij} as the *i*-th row and *j*-th column element, which indicates the probability of receptors moving from state *i* to state *j* in one time step. Note that \mathbf{P} (and \mathbf{Q}) is dependent on x(t), and thus the Markov chain described via \mathbf{P} is not generally time-homogeneous if x(t) is known.

For clarity, we take the ChR2 receptor as an example to detail the state transition process. As shown in Fig. 1, the ChR2 receptor has three states, namely C_1 , O_2 , and C_3 . Specifically, the $C_1 \rightarrow O_2$ transition is sensitive to the input x(t), while the $O_2 \rightarrow C_3$ and $C_3 \rightarrow C_1$ transitions are insensitive. Here, the rate matrix for ChR2 can be written as

State 1 2 3

$$\mathbf{Q} = \begin{array}{c} 1 \\ 2 \\ 3 \end{array} \begin{pmatrix} R_1 & q_{12}x(t) & 0 \\ 0 & R_2 & q_{23} \\ q_{31} & 0 & R_3 \end{pmatrix}, \quad (5)$$

where $R_1 = -q_{12}x(t)$, $R_2 = -q_{23}$, and $R_3 = -q_{31}$. By observing (5), we define S (or S') as a set where the state transition is dependent (or independent) on x(t). For the ChR2 receptor, we have $S = \{C_1 \rightarrow C_1, C_1 \rightarrow O_2\}$, while S' includes all transitions except S.

B. Communication Model of Signal Transduction

Here, the signal transduction will be regarded as a communication system with Markov channels, consisting of the input, output, and conditional input-output probability function.

- Input: The input x (t) is the concentration or intensity in the environment at time t. When x (t) is discretized in time, the input is x (iΔt) for integers i. For clarity, let x_i = x (iΔt) in the rest of this paper.
- *Output*: The output y(t) means the state of receptors at time t. For simplicity, we employ the state number given

by the subscript of the state label in Fig. 1 to mark the state of receptors. Therefore, for the ChR2 receptor, we have y(t) = 1, 2, 3, corresponding to states $\{C_1, O_2, C_3\}$, respectively. Similarly, y(t) can be discretized in time as $y_i = y(i\Delta t)$.

• Input-output relationship: As a Markov channel, y_i , the state of the receptor at time *i*, depends on the current input x_i and the previous channel output y_{i-1} . Here, we can write the conditional input-output probability as

$$p_{Y_1^n|X_1^n}\left(y_1^n | x_1^n\right) = \prod_{i=1}^n p_{Y_i|X_i, Y_{i-1}}\left(y_i | x_i, y_{i-1}\right), \quad (6)$$

where $x_1^n = [x_1, x_2, \dots, x_n]$, $y_1^n = [y_1, y_2, \dots, y_n]$, and $p_{Y_1|X_1, Y_0}(y_1 | x_1, y_0) = p_{Y_1|X_1}(y_1 | x_1)$. From (4), we can further obtain $p_{Y_i|X_i, Y_{i-1}}(y_i | x_i, y_{i-1}) = p_{y_{i-1}y_i}$.

In particular, we will omit the subscripts for probability functions where unambiguous, e.g., $p_Y(y)$ becomes p(y).

Additionally, we assume that the input x_i follows an IID Gaussian distribution, and then x_i can be simplified as x. In this work, the input x denotes the intensity, which should be in a certain range without reaching infinity. To the best of our knowledge, the truncated Gaussian distribution, in which the range of definition is made finite at both ends of the interval, is employed to avoid extreme values. Therefore, we suppose that x has a Gaussian distribution with mean $\bar{\mu}$ and variance $\bar{\sigma}^2$ and lies within the interval [a, b] with $0 \le a < b < +\infty$. Then xconditional on [a, b] obeys the truncated Gaussian distribution, whose probability density function can be given by [11]

$$p(x) = \begin{cases} 0 & \text{if } x < a \\ \frac{\phi(\bar{\mu}, \bar{\sigma}^2; x)}{\Phi(\bar{\mu}, \bar{\sigma}^2; b) - \Phi(\bar{\mu}, \bar{\sigma}^2; x)} & \text{if } a \le x \le b \\ 0 & \text{if } x > b \end{cases}$$
(7)

where

$$\phi\left(\bar{\mu}, \bar{\sigma}^2; x\right) = \frac{1}{\sqrt{2\pi\bar{\sigma}^2}} e^{\left(-\frac{(x-\bar{\mu})^2}{2\bar{\sigma}^2}\right)}$$
$$\Phi\left(\bar{\mu}, \bar{\sigma}^2; b\right) = \frac{1}{2} \left(1 + \operatorname{erf}\left(\left(x-\bar{\mu}\right)/\sqrt{2\bar{\sigma}^2}\right)\right),$$

where $\operatorname{erf}(\cdot)$ is the error function. For the considered x, its mean and variance will be updated as

$$\mu = \bar{\mu} - \frac{\phi(0,1;\beta) - \phi(0,1;\alpha)}{\Phi(0,1;\beta) - \Phi(0,1;\alpha)}\bar{\sigma}$$
$$\sigma^{2} = \bar{\sigma}^{2} \left\{ 1 - \frac{\beta\phi(0,1;\beta) - \alpha\phi(0,1;\alpha)}{\Phi(0,1;\beta) - \Phi(0,1;\alpha)} - \left(\frac{\phi(0,1;\beta) - \phi(0,1;\alpha)}{\Phi(0,1;\beta) - \Phi(0,1;\alpha)}\right)^{2} \right\}$$

where $\alpha = \frac{a-\bar{\mu}}{\bar{\sigma}}$ and $\beta = \frac{b-\bar{\mu}}{\bar{\sigma}}$. Under the above assumption, the receptor states Y_1^n can form a time-homogeneous Markov chain [10], i.e.,

$$p(y_1^n) = \prod_{i=1}^n \int_x p(x) p(y_i | x, y_{i-1}) dx = \prod_{i=1}^n \bar{p}_{y_{i-1}y_i}, \quad (8)$$

where $\bar{p}_{y_{i-1}y_i}$ is the y_{i-1} -th row and y_i -th column element of $\bar{\mathbf{P}}$ and $\bar{\mathbf{P}}$ is the transition probability matrix of Y_1^n , written as

$$\bar{\mathbf{P}} = E\left[\mathbf{P}\right] = \mathbf{I} + E\left[\mathbf{Q}\right]\Delta t. \tag{9}$$

Recalling (4) and (5), we can replace x (or x(t)) in these terms with E[x] to form $E[\mathbf{P}]$ and $E[\mathbf{Q}]$, respectively, since the sensitive terms in \mathbf{P} and \mathbf{Q} are assumed to be linear in x.

III. MIR OF SIGNAL TRANSDUCTION

In this section, we first give an asymptotic expression for the MIR in continuous time, i.e., obtaining $\lim_{\Delta t \to 0} \frac{\mathcal{I}(X;Y)}{\Delta t}$. Next, we derive an approximately numerical solution for the continuous-time MIR. Finally, its lower and upper bounds are deduced.

A. Calculation for the Continuous-time MIR

For any communication system with input x and output y_i , the MIR can be given by [8]

$$MIR = \frac{\mathcal{I}(X;Y)}{\Delta t}$$

= $\lim_{n \to \infty} \frac{1}{n\Delta t} I(Y_1^n; X_1^n)$
= $\lim_{n \to \infty} \frac{1}{\Delta t} \{H(Y_n | Y_{n-1}) - H(Y_n | X_n, Y_{n-1})\}.$ (10)

Note that $\mathcal{I}(X; Y)$ in (10) is the mutual information exchanged between X and Y per channel use with a duration Δt . Correspondingly, the unit of the MIR is bits/s, when $\log_2(\cdot)$ is used for the entropy calculation. With the aid of (8), we have

$$H(Y_n | Y_{n-1}) = -E\left[\log p\left(y_n | y_{n-1}\right)\right]$$

= $-\sum_{\{y_{n-1}, y_n\}} \pi_{y_{n-1}} \bar{p}_{y_{n-1}y_n} \log \bar{p}_{y_{n-1}y_n},$ (11)

and

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$$H(Y_{n} | X_{n}, Y_{n-1})$$

$$= \int_{x} p(x) H(Y_{n} | X_{n} = x, Y_{n-1}) dx$$

$$= -\int_{x} p(x) E[\log p(y_{n} | x, y_{n-1})] dx$$

$$= -\sum_{\{y_{n-1}, y_{n}\} \in \mathcal{S}} \pi_{y_{n-1}} \int_{x} p(x) p_{y_{n-1}y_{n}} \log p_{y_{n-1}y_{n}} dx$$

$$-\sum_{\{y_{n-1}, y_{n}\} \in \mathcal{S}'} \pi_{y_{n-1}} p_{y_{n-1}y_{n}} \log p_{y_{n-1}y_{n}}, \quad (12)$$

where $\pi_{y_{n-1}}$ is the steady-state marginal probability that the receptor is in state y_{n-1} , which is the solution to the following system of equations:

$$\begin{cases} \pi \overline{\mathbf{P}} = \pi \\ \sum_{y_{n-1}} \pi_{y_{n-1}} = 1 \end{cases}$$
 (13)

It is clear from (9) and (13) that $\pi_{y_{n-1}}$ is only dependent on E[x] and q_{ij} . Besides, since the transition in S' is independent on x, we have $\bar{p}_{y_{n-1}y_n} = p_{y_{n-1}y_n}$ for $\{y_{n-1}, y_n\} \in S'$. Here, substituting (11) and (12) into (10) yields

$$\frac{\mathcal{I}(X;Y)}{\Delta t} = \frac{1}{\Delta t} \sum_{(y_{n-1},y_n)\in\mathcal{S}} \pi_{y_{n-1}} \left(\int_x p\left(x\right)\phi\left(p_{y_{n-1}y_n}\right) dx -\phi\left(\int_x p\left(x\right)p_{y_{n-1}y_n}dx\right) \right),$$
(14)

and

$$\phi(p) = \begin{cases} 0, & p = 0\\ p \log p, & p \neq 0 \end{cases} .$$
 (15)

Further, we will compute an asymptotic expression for the MIR in continuous time, i.e., $\lim_{\Delta t \to 0} \frac{\mathcal{I}(X;Y)}{\Delta t}$. First, we have

$$\lim_{\Delta t \to 0} \frac{\mathcal{I}(X;Y)}{\Delta t} = \sum_{\{y_{n-1},y_n\} \in \mathcal{S}, y_{n-1} \neq y_n} \iota_{(y_{n-1},y_n)} + \sum_{\{y_{n-1},y_n\} \in \mathcal{S}, y_{n-1} = y_n} \iota_{(y_{n-1},y_n)}, \quad (16)$$

where

$$\iota_{(y_{n-1},y_n)} = \lim_{\Delta t \to 0} \pi_{y_{n-1}} \left(\frac{\int_x p(x) \phi\left(p_{y_{n-1}y_n}\right) dx}{\Delta t} - \frac{\phi\left(\int_x p(x) p_{y_{n-1}y_n} dx\right)}{\Delta t} \right).$$
(17)

By using the L'Hôpital's rule for (17), we find $\iota_{(y_{n-1},y_n)} = 0$ when $\{y_{n-1}, y_n\} \in S$ and $y_{n-1} = y_n$ [10]. Hence, (16) can be further re-written as

$$\lim_{\Delta t \to 0} \frac{\mathcal{I}(X;Y)}{\Delta t} = g_{y_{n-1},y_n} \left(\int_x p(x) x \ln(x) \, dx - \mu \ln \mu \right), \quad (18)$$
where

where

$$g_{y_{n-1},y_n} = \sum_{\{y_{n-1},y_n\}\in\mathcal{S}, y_{n-1}\neq y_n} \frac{\pi_{y_{n-1}}q_{y_{n-1}y_n}}{\ln 2}.$$
 (19)

So far, the derivation for $\lim_{\Delta t \to 0} \frac{\mathcal{I}(X;Y)}{\Delta t}$ has been finished.

B. Approximately Numerical Solution for $\lim_{\Delta t \to 0} \frac{\mathcal{I}(X;Y)}{\Delta t}$

In this subsection, we provide an approximately numerical solution for (18). By observing (18), we need to focus on the item with $\int_x p(x) x \ln(x) dx$, since the other items in (18) are given for the target system. According to the McLaughlin formula, $\ln(x)$ can be approximately expressed as [10]

$$\ln(x) = \ln(1 + (x - 1)) = \sum_{k=1}^{\infty} (-1)^{k-1} \frac{(x - 1)^k}{k}.$$
 (20)

It is worth noting that when $0 < x \le 2$, the McLaughlin series of $\ln (1 + (x - 1))$ holds and successfully converges to $\ln (1 + (x - 1))$. Therefore, we assume $0 < x \le 2$ in this paper.¹Substituting (20) into $\int_x p(x) x \ln(x) dx$, we can have

$$\int_{x} p(x) x(\ln(x)) dx$$

$$= \sum_{k=1}^{\infty} \frac{(-1)^{k-1}}{k} \int_{x} p(x) x(x-1)^{k} dx$$

$$= -1 + E[x] + \sum_{k=2}^{\infty} \frac{(-1)^{k}}{k(k-1)} E[(x-1)^{k}]$$

$$= -1 + E[x] + \sum_{k=2}^{\infty} \sum_{m=0}^{k} \frac{(-1)^{m} C(k,m)}{k(k-1)} E[x^{m}], \quad (21)$$

where $C(\cdot, \cdot)$ is the binomial coefficient and $E[x^m]$ denotes the *m*-th moment. According to the description in [11], $E[x^m]$ for the truncated Gaussian distribution can be calculated as:

¹This assumption can easily hold for the considered system. For a truncated Gaussian random variable, its product with a constant still obeys a truncated Gaussian distribution. For example, when $x \sim \mathcal{N}(\mu, \sigma^2 | x \in [a, b])$, we have $qx \sim \mathcal{N}(q\mu, (q\sigma)^2 | qx \in [qa, qb])$ for any possible q [11]. Herein, the value range of x can be adjusted via q.

$$E[x^{m}] = \sum_{i=0}^{m} C(m,i) \,\bar{\sigma}^{i} \bar{\mu}^{m-i} L_{i}, \qquad (22)$$

$$L_{0} = 1$$

$$L_{1} = -\frac{\phi(0,1;\beta) - \phi(0,1;\alpha)}{\Phi(0,1;\beta) - \Phi(0,1;\alpha)} \qquad . (23)$$

$$L_{i} = -\frac{\beta^{i-1}\phi(0,1;\beta) - \alpha^{i-1}\phi(0,1;\alpha)}{\Phi(0,1;\beta) - \Phi(0,1;\alpha)} + (i-1)L_{i-2}$$

Finally, the limit of the continuous-time MIR in (18) can be numerically expressed as

$$\lim_{\Delta t \to 0} \frac{\mathcal{I}(X;Y)}{\Delta t} = g_{y_{n-1},y_n} \left(\sum_{k=2}^{\infty} \sum_{m=0}^{k} \frac{(-1)^m C(k,m)}{k(k-1)} E[x^m] - E[x] \ln \frac{E[x]}{e} - 1 \right).$$
(24)

C. Bounds for $\lim_{\Delta t \to 0} \frac{\mathcal{I}(X;Y)}{\Delta t}$

In this subsection, we will provide lower and upper bounds to estimate the possible range of the continuous-time MIR. It is clear from (18) that $(\int_x p(x) x \ln(x) dx - \mu \ln \mu)$ is a Jensen gap of $x \ln(x)$. According to the description in [12], we can calculate a bound for the considered Jensen gap. First, we define $f(x) = x \ln(x)$. Next, assuming that $E|x - \mu|^s < \infty$ holds for $s = 2m, m = 1, 2, 3 \dots$ and f(x) is a (s + 1)-times differentiable function on $\forall x \in (a, b)$, we further have

$$h^{(s)}(x;\mu) = \frac{f(x) - f(\mu)}{(x-\mu)^s} - \sum_{i=1}^{s-1} \frac{f^{(i)}(\mu)}{i!(x-\mu)^{s-i}},$$
 (25)

where $f^{(i)}(x) = \frac{d^i}{dx^i} f(x)$. Based on Theorem 2.1 in [12], we have

$$E[f(x)] - f(E[x]) \ge \sum_{i=1}^{s-1} r_i + \inf_{x \in (a,b)} \{h^{(s)}(x;\mu)\} \mu_s$$

$$E[f(x)] - f(E[x]) \le \sum_{i=1}^{s-1} r_i + \sup_{x \in (a,b)} \{h^{(s)}(x;\mu)\} \mu_s , \quad (26)$$

where $r_i = \frac{\mu_i}{i!} f^{(i)}(\mu)$ and $\mu_i = E[x - \mu]^i$ is the *i*-th central moment of x with i = 1, 2, ..., s, which can be solved via (22). Besides, it is obvious from Lemma 2.3 of [12] that if $f^{(s-1)}(x)$ is strictly convex (concave), $h^{(s)}(x;\mu)$ strictly increases (decreases) with respect to x. Assuming that $f^{(s-1)}(x)$ is concave for $\forall x \in (a,b)$, (26) can be re-written as

$$E[f(x)] - f(E[x]) \ge \sum_{\substack{i=1\\s-1}}^{s-1} r^i(\mu) + h^{(s)}(b;\mu)\mu_s$$

$$E[f(x)] - f(E[x]) \le \sum_{i=1}^{s-1} r^i(\mu) + h^{(s)}(a;\mu)\mu_s$$
 (27)

Following the example given in [12], in this paper, we consider s = 2 and s = 4 to derive the bounds for the target MIR.

1) s = 2: From the second derivative of $f^{(1)}(x)$ with respect to x, i.e., $f^{(3)}(x) = -\frac{1}{x^2}$, it is clear that $f^{(1)}(x)$ is concave. Therefore, $h^{(2)}(x;\mu)$ is monotonically decreasing with respect to x. Based on the aforementioned, (26) can be rewritten as

$$E[f(x)] - f(E[x]) \ge \left\{ \frac{b \ln b - u \ln u}{(b-u)^2} - \frac{1 + \ln u}{b-u} \right\} \sigma^2$$

$$E[f(x)] - f(E[x]) \le \left\{ \frac{a \ln a - u \ln u}{(a-u)^2} - \frac{1 + \ln u}{a-u} \right\} \sigma^2 \quad .$$
(28)

Substituting (28) into (18) yields

$$\lim_{\Delta t \to 0} \frac{\mathcal{I}(X;Y)}{\Delta t} \ge g_{y_{n-1},y_n} \left\{ \frac{b \ln b - u \ln u}{(b-u)^2} - \frac{1 + \ln u}{b-u} \right\} \sigma^2$$

$$\lim_{\Delta t \to 0} \frac{\mathcal{I}(X;Y)}{\Delta t} \le g_{y_{n-1},y_n} \left\{ \frac{a \ln a - u \ln u}{(a-u)^2} - \frac{1 + \ln u}{a-u} \right\} \sigma^2 \quad .$$
(29)

2) s = 4: Similarly, $h^{(4)}(x; \mu)$ is monotonically decreasing with respect to x, due to $f^{(3)}(x) = -\frac{6}{x^4} < 0$ for $\forall x \in (a, b)$. Here, (26) can be rewritten as

$$E[f(x)] - f(E[x]) \ge \frac{\sigma^2}{2\mu} - \frac{\mu_3}{6\mu^2} + h^{(4)}(b;\mu)\mu_4$$

$$E[f(x)] - f(E[x]) \le \frac{\sigma^2}{2\mu} - \frac{\mu_3}{6\mu^2} + h^{(4)}(a;\mu)\mu_4$$
(30)

Here, the bounds for $\lim_{\Delta t \to 0} \frac{\mathcal{I}(X;Y)}{\Delta t}$ can be obtained by substituting (30) into (18).

Remark: Note that the derivation in Section III is valid for all \mathbf{Q} , when the IID input x follows any possible distribution within the range of (0, 2]. Therefore, we conclude that all MIR expressions derived in this paper can be extended to arbitrary signal transduction systems under the above condition.

IV. NUMERICAL RESULTS AND ANALYSIS

In this section, we employ the ChR2 receptor and the ACh receptor as examples in our analysis, where their parameters have been listed in Table I and Table II of [8], respectively. Moreover, for analysis, we adjust the input range for these two receptors as $x \in [10^{-5}, 2]$ and $x \in [2 \times 10^{-2}, 2]$.

Fig. 2 shows the continuous-time MIR as well as the corresponding numerical solution and bounds for the ChR2 receptor. For clarity, we employ $\bar{\mu}$ and $\bar{\sigma}$ as variables to study the MIR when defining $x \sim \mathcal{N}(\bar{\mu}, \bar{\sigma}^2)$ and $x \mid x \in [10^{-5}, 2] \sim$ $\mathcal{N}(\mu, \sigma^2)$. One can easily observe from Fig. 2 that the MIR can achieve good performance when x with a small value holds a sizable proportion of all inputs, corroborating the results described in [8]. Further, it can be determined from Fig. 2 that the MIR and its approximately numerical counterparts can accurately match when x is concentrated around large values, and the accuracy performance is proportional to k. Moreover, we can find that the bounds are gradually tighter as s goes large, while the calculation complexity is also increasing. Specifically, when s = 4, the derived bounds can provide a relatively narrow range to estimate the exact MIR. Similar numerical results are attained for the ACh receptor, when varying $\bar{\mu}$ or $\bar{\sigma}$. In summary, the derived numerical solution and bounds for the MIR can give an accurate approximation with low complexity, when obtaining the exact MIR is challenging.

Fig. 3 depicts the MIR and its bounds when simultaneously considering $\bar{\mu}$ and $\bar{\sigma}$ for the ACh receptor. Particularly, given the high calculation complexity from the derived bounds with s = 4, its curves have been removed for the ACh receptor. By comparing Fig. 3(a) and Figs. 3(b)-3(c), we can discover that the trends of the MIR and its bounds near-perfectly match, especially for the capacity-achieving values of $\bar{\mu}$ and $\bar{\sigma}$. Thus, the derived bounds can provide a possible range for $\lim_{\Delta t \to 0} \frac{\mathcal{I}(X;Y)}{\Delta t}$, while predicting its trend with varying parameters. For the receptor with a simple input distribution model, the input distribution reaching the capacity can be approximately calculated via (29) to guide the system design.



Fig. 2. Numerical verification for the ChR2 receptor: the approximately numerical solution and bounds for $\lim_{\Delta t \to 0} \frac{\mathcal{I}(X;Y)}{\Delta t}$, where it is assumed that the input x follows the truncated Gaussian distribution with $x \in [10^{-5}, 2]$.



Fig. 3. Numerical verification for the ACh receptor: the lower and upper bounds for $\lim_{\Delta t \to 0} \frac{\mathcal{I}(X;Y)}{\Delta t}$, where it is assumed that the input x follows the truncated Gaussian distribution with $x \in [2 \times 10^{-2}, 2]$ and s = 2.

V. CONCLUSION

This paper brings new insights into the information theory analysis for the signal transduction channels. Specifically, we first derived an asymptotic continuous-time MIR for the signal transduction channel with the IID Gaussian input. To improve the practicality, the approximate numerical expression for the continuous-time MIR was given. Meanwhile, its lower and upper bounds for the considered MIR were deduced in closedform. Finally, simulation results with the ChR2 and ACh receptors validated our analysis.

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