Diversity Combining in diffusion-based Molecular Communication Systems

Charitha, Aravind

I. INTRODUCTION

Molecular communication (MC) is an emerging idea that takes inspiration from nature to make communication using molecules possible. The significance of this technique lies in areas where communication using conventional resources like electromagnetic or acoustic energy fails either partially or completely. Examples of such scenarios could be communication in media with high permittivity or electrical conductivity, like saline water or blood, where electromagnetic signals attenuate quickly. Molecular communication enables nano-scale devices to communicate over short distances using molecules. Some literature also exist on using Molecular Communication for macro-scale communication. In MC, the transmitter devices encode information into molecules called information molecules (IMs), which are then released into the surrounding medium. These IMs can propagate through various mechanisms. A common example is diffusion-based molecular communication, where IMs undergo random Brownian motion. Through either passive or active means (as per the receiver type), the receiver detects and measures the count of IMs, allowing for the estimation of the transmitted information. MC holds great potential due to its bio-compatibility and energy efficiency and has garnered interest among researchers for applications such as nano-communication, targeted drug delivery, and molecular computing. Studies have shown that it can also be integrated with THz-based systems to create hybrid systems for more efficient healthcare applications.

The molecular communication channel can be characterized by the fraction of IMs being sensed by the receiver or, equivalently, the probability that the intended receiver senses an IM. Based on the obtained channel information, optimal receivers can be designed. Molecular

communication is typically characterized by its slow and probabilistic nature, which can lead to substantial decoding errors. To address this issue, deploying an array of multiple receiving nodes at the receiver can be advantageous due to the benefits of spatial diversity, and this approach could enhance the communication capability of the system. The utilization of multiple receivers enables the establishment of both single-input multiple-output (SIMO) and multiple-input multiple-output (MIMO) communication links, offering improved reliability and performance. SIMO configurations increase diversity by incorporating multiple receivers, while MIMO setups facilitate spatial multiplexing, allowing for higher data rates.

This work focuses primarily on a diffusion-based molecular communication system with a point transmitter and one receiver device with multiple receiver ports (RxPs). We analyze the system for effects owing to diversity, considering the cases for both; with Inter Symbol Interference (ISI) and without ISI. RxPs in molecular communication can be assumed to be similar to antennas in wireless communication and can be located arbitrarily. We characterize the joint channel between the transmitter and RxPs and propose an optimal maximum a posteriori (MAP) decoding for this system when all ports can share complete received signal information. We also discuss various hard combining schemes and evaluate their performance in terms of the error probability. Additionally, we consider a Poisson channel approximation and demonstrate that weighted linear combining with weights based on average channel values is an optimal decoding scheme. Furthermore, we examine a SIMO system with a uniform circular array (UCA) of RxPs at the receiver and show that the decoding error decreases as the number of RxPs increases.

II. SYSTEM MODEL

Here, the system under consideration is a multiple time slot SIMO diffusion-based MC system with a point transmitter and K RxPs (Receiver Ports) in a three-dimensional medium. Since the system is diffusion-based, We assume that any IM released by the point transmitter propagates in the medium via random Brownian motion. We consider On/Off keying (OOK) modulation, in which the transmitter sends N molecules for bit 1 and does not release any molecule into the medium for bit 0 transmission. Let b represent the bit value to be sent. The signal transmitted

into the medium is thus $x = Nb$. A RxP detects the IM when it enters its detection region. We assume that the molecules transmitted have some expiry/life expectancy before which they can interfere with the future molecules which are going to be sent. Or in other words, we assume that the molecules sent upto M time slots prior to the current time slot (or slot l) can interfere with the molecules sent in the current slot (or l^{th} slot), to create Inter Symbol Interference (ISI). Let the received signal at the kth RxP in l^{th} slot be:

$$r_k[l] = s_k[l] + I_k[l] + n_k[l], \tag{1}$$

where we define $I_k[l] = \sum_{m=1}^{M} i_k[l; m]$ as the number of interfering molecules arriving at the current slot (l) that were transmitted in the previous slots (starting from the 1st (immediate previous slot) to the Mth previous slot). Further, individual $i_k[l; m]$ denotes the number of molecules that reach the kth RxP in l^{th} slot due to transmission in m^{th} previous slot, $r_k[l]$ denotes the total number of molecules sensed at the kth RxP in the lth time slot, $s_k[l]$ denotes the contribution due to the transmitted signal in the lth slot and $n_k[l]$ denotes the noise due to unintended or freely roaming molecules.

We assume the noise to be Poisson distributed and in particular, the noise variables at different RxPs $n_k[l]$ are taken as independent Poisson distributed random variables with mean λ and so their PMF is given by $q_z = \mathbb{P}[n_k[l] = z] = \exp(-\lambda)\lambda^z/z!$.

Stacking the above variables from all the K receiver ports gives the received vector $\mathbf{r}[l] = [r_1[l], r_2[l], \cdots, r_k[l]]$. Let the stacked vector $\mathbf{s}[l] = [s_1[l], s_2[l], \cdots, s_k]$ denote the IMs received corresponding to desired signal. Let $\mathbf{i}[l; m] = [i_1[l; m], i_2[l; m], \cdots i_k[l; m]]$ denote the total number of molecules received at each RxP due to the transmission in the previous m^{th} slot which represents the inter-symbol-interference between the lth and m^{th} slots, and $\mathbf{n}[l] = [n_1[l], n_2[l], \cdots, n_K[l]]$ represent the noise molecules received across all K ports at time slot l. We denote the total number of ISI molecules from all of the M previous slots as $\mathbf{I}[l] = \sum_{m=1}^{M} \mathbf{i}[l; m]$. Thereby, the received signal at each port can be compactly given as,

$$\mathbf{r}[l] = \mathbf{s}[l] + \mathbf{I}[l] + \mathbf{n}[l]. \tag{2}$$

3

III. CHANNEL CHARACTERIZATION

Let $p_k(T)$ denote the probability that an IM is sensed by the kth RxP for sampling time T, which depends on the RxP's sensing mechanism. For a passive RxP, $p_k(T)$ denotes the probability that an IM is inside k^{th} RxP *at* sampling time T. D denotes the diffusion coefficient of IM in the medium through which it moves and v_k is the volume of the kth RxP. Assuming the dimension of the RxP is very small compared to its distance d_k from the transmitter, the probability is given by:

$$p_k(T) = \frac{v_k}{\sqrt{4\pi DT^3}} \exp\left(-\frac{d_k^2}{4DT}\right).$$

Similarly, for a fully absorbing RxP, $p_k(T)$ refers to the probability that an IM is absorbed by the kth RxP *till* time T. Note that here we neglect the mutual influence of other RxPs by assuming that the transmitter is far away, at a distance larger than the size of RxPs. If each RxP is spherical with radius a, then the probability $p_k(T)$ in this case is given by:

$$p_k(T) = \frac{a}{d_k} \operatorname{erfc}\left(\frac{d_k - a}{4DT}\right),$$

Now, the probability that an IM emitted at the mth previous slot is sensed by the kth RxP in the current (l^{th}) slot is given by,

$$\text{Passive} : h_k[m] = p_k\left(mT_s + T\right)$$

$$\text{Absorbing} : h_k[m] = p_k\left((m+1)T_s\right) - p_k\left(mT_s\right).$$

An IM can only be sensed by one RxP in MC because they can only be present in one place at a time. This causes a correlation between the number of IMs detected by various RxPs. Further, the number of signal IMs sensed at the lth slot by individual RxPs due to the transmission of $Nb[l]$ molecules in l^{th} slot is jointly distributed as multinomial distribution [1], given as

$$\mathsf{P}_{\mathbf{S}}\left(\mathbf{s}[\mathbf{l}]\right) = \binom{Nb[l]}{s_1, s_2, \ldots s_K, s_0} \prod_{k=0}^{K} h_k[0]^{s_k}, \tag{3}$$

4

where $h_0[0] = 1 - \sum_{k=1}^{K} h_k[0]$ gives the probability that an IM is not received at any of the K RxPs, s_k is the kth element of s and $s_0 = Nb[l] - \sum_{k=1}^{K} s_k$ denotes the number of IMs not sensed at any of the K RxPs in the current slot.

The number of interfering molecules sensed at the RxPs in the lth slot due to the transmission of $Nb[l-m]$ molecules in m^{th} previous slot is jointly distributed as multinomial distribution, given by

$$\mathsf{P_I}\left(\mathbf{i}[\mathbf{l}; \mathbf{m}]\right) = \begin{pmatrix} Nb[l-m] \\ i_1, i_2, \ldots i_k, i_0 \end{pmatrix} \prod_{k=0}^{K} (h_k[m])^{i_k}, \tag{4}$$

where $h_0[m] = 1 - \sum_{k=1}^{K} h_k[m]$ gives the probability that no molecule transmitted in the previous m^{th} slot is received at any of the K RxPs in the current slot, i_k is the kth element of i which represents the number of molecules transmitted in the previous m^{th} slot is received at the kth RxPs in the current slot and $i_0 = Nb[l-m] - \sum_{k=1}^{K} i_k$ denotes the number of molecules transmitted in the mth previous slot but not received by any of the K RxPs in the current slot.

Theorem 1: In the SIMO molecular communication channel with finite length (M) ISI, the joint distribution of number of molecules sensed at individual RxPs in the lth slot $r_k[l]$ is given as

$$\mathsf{P_R}\left(\mathbf{r}[l]|b[l] = 0\right) = \sum_{A(\mathbf{r},N)} \left[\left(\prod_{m=1}^{M} \mathsf{P_I}\left(\mathbf{i}[l; m]\right) \right) \prod_{k=1}^{K} q_{r_k[l] - I_k[l]} \right],$$

$$\mathsf{P_R}\left(\mathbf{r}[l]|b[l] = 1\right) = \sum_{\mathcal{M}(\mathbf{r},N)} \mathsf{P_S}\left(\mathbf{s}[l]\right) \left[\sum_{A(\mathbf{r}-\mathbf{s},N)} \left(\left(\prod_{m=1}^{M} \mathsf{P_I}\left(\mathbf{i}[l; m]\right) \right) \prod_{k=1}^{K} q_{r_k[l] - s_k - I_k[l]} \right) \right], \tag{5}$$

where

$$A(\mathbf{r}, N) = \left\{ \begin{array}{l} \mathbf{i}[l; m] : I_k[l] \leq r_k[l], \forall k \in [0, K] \text{ and} \\ \sum_{k=1}^{K} i_k[l; m] \leq Nb[l-m] \forall m \in [1, M] \end{array} \right\}$$

$$\text{and } \mathcal{M}(\mathbf{r}, N) = \left\{ \begin{array}{l} \mathbf{s}[l] : s_k \leq r_k[l] \forall k \in [0, K] \\ \text{and } \sum_k s_k \leq N \end{array} \right\}.$$

Proof: When $b[l] = 0$, there are no IMs transmitted in the current slot, hence the event that $r_k[l]$ molecules are received at k^{th} RxP is purely due to the finite length interference and noise.

Out of the $r_k[l]$ received molecules, $i_k[l; m]$ would be the number of molecules received at the kth RxP which were transmitted in the mth previous slot. So in total due to the interference $I_k[l]$ are the molecules received at the kth RxP and the remaining $(r_k[l] - I_k[l])$ molecules would be due to the noise with probability $\prod_{k=1}^{K} q_{r_k[l]-I_k[l]}$. Here $0 \leq i_k[l; m] \leq Nb[l - m]$ and $\sum_{k=1}^{K} i_k[l; m] \leq Nb[l - m]$. According to equation (4), $\mathsf{P}_I(\mathbf{i}[l; m])$ is the probability that $\mathbf{i}[l; m]$ out of $\mathbf{r}[l]$ molecules at the receiver are caused by interference from the mth slot. Since the number of molecules received from each of the M interfering slots are independent, the total probability of interference is $\prod_{m=1}^{M} \mathsf{P}_I(\mathbf{i}[l; m])$.

When $b[l] = 1$, N IMs are transmitted, out of the $\mathbf{r}[l]$ received molecules, $\mathbf{s}[l]$ would be the number of IMs received at the receiver with probability $\mathsf{P}_S(\mathbf{s}[l])$ as given in equation (3), and remaining molecules would be due to interference and noise. Therefore, the noise and interference probability would be same as when $b[l] = 0$, except that they would only account for $r_k[l] - s_k$ molecules at the kth RxP. ∎

For a special case, 1×2 SIMO MC channel with N = 1 IM and only one interfering slot (M=1), the joint distribution of $\mathbf{s}[l]$ is

$$\mathsf{P}_S(s_1, s_2) = \begin{cases} 1 - h_1(l; 0) - h_2(l; 0) & (s_1, s_2) = (0, 0) \\ h_1(l; 0) & (s_1, s_2) = (1, 0) \\ h_2(l; 0) & (s_1, s_2) = (0, 1) \end{cases}$$

The distribution of the number of interfering molecules from the previous slot(M=1) is, (assuming bit 1 is transmitted)

$$\mathsf{P}_I(i_1, i_2) = \begin{cases} 1 - h_1(l; 1) - h_2(l; 1) & (i_1, i_2) = (0, 0) \\ h_1(l; 1) & (i_1, i_2) = (1, 0) \\ h_2(l; 1) & (i_1, i_2) = (0, 1) \end{cases}$$

Hence, the SIMO channel transition probabilities assuming bit is 1 in the previous slot are given

as

$$p_R\left(r_1, r_2 \mid b = 0\right) =$$

$$\begin{cases} \left(h_0(l;1)\right) q_0^2 & r = (0,0) \\ h_1(l;1)q_0^2 + \left(h_0(l;1)\right) q_1 q_0 & r = (1,0) \\ h_2(l;1)q_0^2 + \left(h_0(l;1)\right) q_0 q_1 & r = (0,1) \quad \text{and} \\ h_1(l;1)q_0 q_1 + h_2(l;1)q_1 q_0 + \left(h_0(l;1)\right) q_1^2 & r = (1,1) \\ h_1(l;1)q_{r_1-1}q_{r_2} + h_2(l;1)q_{r_1}q_{r_2-1} + \left(h_0(l;1)\right) q_{r_1}q_{r_2} & r_1, r_2 > 1 \end{cases}$$

$$p_R\left(r_1, r_2 \mid b = 1\right) =$$

$$\begin{cases} \left(h_0[0]\right)\left(h_0(l;1)\right) q_0^2 & r = (0,0) \\ h_1(l;0)\left(h_0(l;1)\right) q_0^2 + \left(h_0[0]\right)\left(h_1(l;1)q_0^2 + \left(h_0(l;1)\right) q_1 q_0\right) & r = (1,0) \\ h_2(l;0)\left(h_0(l;1)\right) q_0^2 + \left(h_0[0]\right)\left(h_2(l;1)q_0^2 + \left(h_0(l;1)\right) q_0 q_1\right) & r = (0,1) \\ \begin{aligned} &h_1(l;0)\left(h_2(l;1)q_0^2 + h_0(l;1)q_0 q_1\right) + h_2(l;0)\left(h_1(l;1)q_0^2 + h_0(l;1)q_1 q_0\right) \\ &+ \left(h_0(l;1)\right)\left(h_1(l;1)q_0 q_1 + h_2(l;1)q_1 q_0 + h_0(l;1)q_1^2\right) \end{aligned} & r = (1,1) \\ \begin{aligned} &h_1(l;0)\left(h_1(l;1)q_{r_1-2}q_{r_2} + h_2(l;1)q_{r_1-1}q_{r_2-1} + \left(h_0(l;1)\right) q_{r_1-1}q_{r_2}\right) \\ &+ h_2(l;0)\left(h_1(l;1)q_{r_1-1}q_{r_2-1} + h_2(l;1)q_{r_1}q_{r_2-2} + \left(h_0(l;1)\right) q_{r_1}q_{r_2-1}\right) \\ &+ \left(h_0[0]\right)\left(h_1(l;1)q_{r_1-1}q_{r_2} + h_2(l;1)q_{r_1}q_{r_2-1} + \left(h_0(l;1)\right) q_{r_1}q_{r_2}\right) \end{aligned} & r_1, r_2 > 1 \end{cases}$$

(6)

Soft Combining

Theorem 2: The MAP decoder 1 in a SIMO MC system with finite length ISI having K RxPs is given as,

Choose bit 1 if:

$$N![h_0[0]]^N \sum_{\mathcal{M}(r,N)} \sum_{\mathcal{A}(r-s,N)} \frac{1}{s_0!} \prod_{k=1}^{K} \lambda^{-s_k - I_k[l]}$$

$$\frac{\prod_{m=1}^{M} \frac{1}{i_0(m)!} \begin{pmatrix} r_k[l] \\ s_k, i_k[l;m] \end{pmatrix} \left[\frac{h_k[0]}{h_0[0]}\right]^{s_k} \left[\frac{h_k[m]}{h_0[l;m]}\right]^{i_k[l;m]}}{\sum_{\mathcal{A}(r,N)} \prod_{k=1}^{K} \lambda^{-I_k[l]} \prod_{m=1}^{M} \frac{1}{i_0(m)!} \begin{pmatrix} r_k[l] \\ i_k[l;m] \end{pmatrix} \left[\frac{h_k[m]}{h_0[l;m]}\right]^{i_k[l;m]}} > \frac{\rho_0}{\rho_1} \qquad (7)$$

where ρ_0 and ρ_1 are the bit probabilities.

Proof: The MAP for bit 1 is

$$\rho_0 P_R(r[l] \mid b = 0) < \rho_1 P_R(r[l] \mid b = 1)$$

From theorem 1, we get

$$\frac{\sum_{\mathcal{M}(r,N)} \mathsf{P_S}(\mathbf{s}[l]) \sum_{A(r-s,N)} \prod_{m=1}^{M} P_I(\mathbf{i}[l;m]) \prod_{K=1}^{K} q_{r_k[l]-s_k-I_k[l]}}{\sum_{\mathcal{A}(r,N)} \prod_{m=1}^{M} \mathsf{P_I}(\mathbf{i}[l;m]) \prod_{K=1}^{K} q_{r_k[l]-I_k[l]}} > \frac{\rho_0}{\rho_1}$$

Substituting the values of $\mathsf{P_S}((\mathbf{s}[l])$ and $\mathsf{P_I}(\mathbf{i}[l;m])$,

$$\sum_{\mathcal{M}(r,N)} \begin{pmatrix} N \\ s_1, s_2, \ldots s_K, s_0 \end{pmatrix} \prod_{k=0}^{K} h_k[0]^{s_k} \sum_{A(r-s,N)} \prod_{m=1}^{M} \begin{pmatrix} Nb[l-m] \\ i_1(m), i_2(m), \ldots i_k[l;m], i_0(m) \end{pmatrix}$$

$$\frac{\prod_{k=0}^{K} (h_k[m])^{i_k[l;m]} \prod_{k=1}^{K} q_{r_k[l]-s_k-I_k[l]}}{\sum_{A(r,N)} \prod_{m=1}^{M} \begin{pmatrix} Nb[l-m] \\ i_1(m), i_2(m), \ldots i_k[l;m], i_0(m) \end{pmatrix} \prod_{k=0}^{K} (h_k[m])^{i_k[l;m]} \prod_{k=1}^{K} q_{r_k[l]-I_k[l]}} > \frac{\rho_0}{\rho_1}$$

8

Substituting the value of q_k,

$$\sum_{\mathcal{M}(r,N)} \left(\frac{N!}{s_1! s_2! \cdots s_K! s_0!} \right) \prod_{k=0}^{K} h_k[0]^{s_k} \sum_{A(r-s,N)} \prod_{m=1}^{M} \left(\frac{(Nb[l-m])!}{i_1(m)! i_2(m)! \cdots i_k[l;m]! i_0(m)!} \right)$$

$$\frac{\prod_{k=0}^{K} (h_k[m])^{i_k[l;m]} \prod_{k=1}^{K} \exp(-\lambda) \frac{\lambda^{r_k[l]-s_k-I_k[l]}}{(r_k[l]-s_k-I_k[l])!}}{\sum_{A(r,N)} \prod_{m=1}^{M} \frac{[Nb[l-m]]!}{i_1(m)! i_2(m)! \cdots i_k[l;m]! i_0(m)!} \prod_{k=0}^{K} (h_k[m])^{i_k[l;m]} \prod_{k=1}^{K} \exp(-\lambda) \frac{\lambda^{r_k[l]-I_k[l]}}{(r_k[l]-I_k[l])!}} > \frac{\rho_0}{\rho_1}$$

Simplifying, multiplying and dividing by $r_k[l]!$ we get

$$\sum_{\mathcal{M}(r,N)} \frac{N!}{s_0!} h_0[0]^{s_0} \sum_{\mathcal{A}(r-s,N)} \prod_{k=1}^{K} \frac{1}{s_k!} h_k[0]^{s_k} \lambda^{-s_k-I_k[l]}$$

$$\frac{\prod_{m=1}^{M} \frac{1}{i_0(m)!} (h_0[l;m]))^{i_0(m)} \frac{1}{s_k!} \frac{1}{i_k[l;m]!} (h_k[m])^{i_k[l;m]} r_k[l]!}{\sum_{\mathcal{A}(r,N)} \prod_{k=1}^{K} \lambda^{-I_k[l]} \prod_{m=1}^{M} \frac{1}{i_0(m)!} (h_0[l;m]))^{i_0(m)} \frac{1}{i_k[l;m]!} (h_k[m])^{i_k[l;m]} r_k[l]!} > \frac{\rho_0}{\rho_1} \qquad (8)$$

Using $s_0 = N - \sum_{k=1}^{K} s_k$ for bit1 and $i_0(m) = Nb[m] - \sum_{k=1}^{K} i_k[l;m]$ and further simplifying we get,

$$N![h_0[0]]^N \sum_{\mathcal{M}(r,N)} \sum_{\mathcal{A}(r-s,N)} \frac{1}{s_0!} \prod_{k=1}^{K} \lambda^{-s_k-I_k[l]}$$

$$\frac{\prod_{m=1}^{M} \frac{1}{i_0(m)!} \begin{pmatrix} r_k[l] \\ s_k, i_k[l;m] \end{pmatrix} \left[\frac{h_k[0]}{h_0[0]} \right]^{s_k} \left[\frac{h_k[m]}{h_0[l;m]} \right]^{i_k[l;m]}}{\sum_{\mathcal{A}(r,N)} \prod_{k=1}^{K} \lambda^{-I_k[l]} \prod_{m=1}^{M} \frac{1}{i_0(m)!} \begin{pmatrix} r_k[l] \\ i_k[l;m] \end{pmatrix} \left[\frac{h_k[m]}{h_0[l;m]} \right]^{i_k[l;m]}} > \frac{\rho_0}{\rho_1}$$

Hard Combining

In hard combining, each RxP makes its own decoding of the received signal. The decoding decisions of the RxPs are shared to a central node via some back-haul mechanism. The central node then decodes the bit as 1 or 0 by following various hard combining methods such as OR operation, AND operation and majority combining.

The MAP decoder for individual k^{th} RxP is,

Choose bit as 1 if,

$$\frac{\displaystyle\sum_{s\leq r_k[l]}\binom{N}{s}(h_k[0])^s(1-h_k[0])^{N-s}\sum_{\sum_{m=1}^M i[l;m]\leq r_k[l]-s}\prod_{m=1}^M\frac{1}{i[l;m]!}\frac{1}{(Nb[l-m]-i[l;m])!}}{\displaystyle\sum_{\sum_{m=1}^M i[l;m]\leq r_k[l]}\prod_{m=1}^M\frac{1}{i[l;m]!}\frac{1}{(Nb[l-m]-i[l;m])!}[h_k[m]]^{i[l;m]}}$$

$$\frac{[h_k[m]]^{i[l;m]}[1-h_k[m]]^{Nb[l-m]-i[l;m]}\left[\dfrac{\lambda^{-s-\sum_{m=1}^M(m)}}{(r_k[l]-s-i[l;m])!}\right]}{[1-h_k(m)]^{(Nb[l-m]-i[l;m]}\dfrac{\lambda^{-\sum_{m=1}^M i[l;m]}}{[r_k[l]-i[l;m])!}}>\frac{\rho_0}{\rho_1}$$

or

$$\frac{\displaystyle\sum_{s\leq r_k[l]}\binom{N}{s}(h_k[0])^s(1-h_k[0])^{N-s}\sum_{\sum_{m=1}^M i[l;m]\leq r_k[l]-s}\prod_{m=1}^M\binom{Nb[l-m]}{i[l;m]}[h_k[m]]^{i[l;m]}}{\displaystyle\sum_{\sum_{m=1}^M i[l;m]\leq r_k[l]}\prod_{m=1}^M\binom{Nb[l-m]}{i[l;m]}[h_k[m]]^{i[l;m]}[1-h_k(m)]^{(Nb[l-m]-i[l;m]}\dfrac{\lambda^{-\sum_{m=1}^M i[l;m]}}{[r_k[l]-i[l;m])!}}$$

$$\frac{[1-h_k[m]]^{Nb[l-m]-i[l;m]}\left[\dfrac{\lambda^{-s-\sum_{m=1}^M(m)}}{(r_k[l]-s-i[l;m])!}\right]}{}>\frac{\rho_0}{\rho_1}$$

This can be obtained by assuming there is only one RxP in theorem 2.

Since the LHS in the above expression increases with $r_k[l]$, the decoding region for bit 1 can be equivalent written as $D_k(1)=[\eta_k,\infty)$, with

$$\eta_k=\max\left\{r:\frac{\displaystyle\sum_{s\leq r_k[l]}\binom{N}{s}(h_k[0])^s(1-h_k[0])^{N-s}\sum_{\sum_{m=1}^M i[l;m]\leq r_k[l]-s}\prod_{m=1}^M\binom{Nb[l-m]}{i[l;m]}}{\displaystyle\sum_{\sum_{m=1}^M i[l;m]\leq r_k[l]}\prod_{m=1}^M\binom{Nb[l-m]}{i[l;m]}[h_k[m]]^{i[l;m]}}\right.$$

$$\left.\frac{[h_k[m]]^{i[l;m]}[1-h_k[m]]^{Nb[l-m]-i[l;m]}\left[\dfrac{\lambda^{-s-\sum_{m=1}^M(m)}}{(r_k[l]-s-i[l;m])!}\right]}{[1-h_k(m)]^{(Nb[l-m]-i[l;m]}\dfrac{\lambda^{-\sum_{m=1}^M i[l;m]}}{[r_k[l]-i[l;m])!}}\leq\frac{\rho_0}{\rho_1}\right\}$$

POISSON CHANNEL APPROXIMATION

We can approximate s_k's distribution as Poisson with parameter $\mu_k(0) = Nb[l]h_k[0]$ and $i_k[l; m]$ as Poisson distributed with parameter $\mu_k(m) = Nb[l-m]h_k[m]$. The overall interference due to M previous slots $\sum_{m=1}^{M} i_k[l; m]$ will be Poisson distributed with parameter $\sum_{m=1}^{M} \mu_k(m) = \sum_{m=1}^{M} Nb[l-m]h_k[m]$.

Therefore, the total number of molecules sensed at the kth RxP is distributed as

$$r_k[l] \mid b = 1 \sim \text{Poiss}\left(\lambda + \mu_k(0) + \sum_{m=1}^{M} \mu_k(m)\right) \tag{9}$$

$$r_k[l] \mid b = 0 \sim \text{Poiss}\left(\lambda + \sum_{m=1}^{M} \mu_k(m)\right)$$

Similarly from Cor. 3, the total number s of IMs can be approximated as $s = \sum_k s_k \sim \text{Poiss}\left(\sum_k \mu_k\right)$. Hence, the total number of molecules received at any RxPs, $r = \sum_k r_k[l]$ can be approximated as

$$r \mid b = 0 \sim \text{Poiss}\left(\sum_{k=1}^{K}\left(\lambda + \sum_{m=1}^{M} \mu_k(m)\right)\right) \tag{10}$$

$$r \mid b = 1 \sim \text{Poiss}\left(\sum_{k=1}^{K}\left(\lambda + \mu_k(0) + \sum_{m=1}^{M} \mu_k(m)\right)\right)$$

Soft Combining - MAP decoder

Theorem 3: Under Poisson channel approximation, the MAP decoder in a SIMO MC system with K RxPs is given as

Proof:

The MAP decoding rule in general is given as

$$\rho_0 p_R(\mathbf{r} \mid b = 0) \underset{0}{\overset{1}{\lessgtr}} \rho_1 p_R(\mathbf{r} \mid b = 1) \tag{11}$$

$$\rho_0 p_R(r_1, r_2, r_3, ... r_k \mid b = 0) \underset{0}{\overset{1}{\lessgtr}} \rho_1 p_R(r_1, r_2, r_3, ... r_k \mid b = 1)$$

$$\rho_0 \prod_{k=1}^{K} p_R(r_k \mid b = 0) \underset{0}{\overset{1}{\lessgtr}} \rho_1 \prod_{k=1}^{K} p_R(r_k \mid b = 1)$$

11

Substituting Poisson probability from equation 3,

$$\rho_0 e^{-K\lambda - \sum_{k=1}^{K} \sum_{m=1}^{M} \mu_k(m)} \qquad \rho_1 e^{-K\lambda - \sum_{k=1}^{K} \mu_k(0) - \sum_{k=1}^{K} \sum_{m=1}^{M} \mu_k(m)}$$

$$\frac{\prod_{k=1}^{K} \left(\lambda + \sum_{m=1}^{M} \mu_k(m) \right)^{r_k[l]}}{\prod_{k=1}^{K} r_k[l]!} \underset{0}{\overset{1}{\lessgtr}} \frac{\prod_{k=1}^{K} \left(\lambda + \mu_k(0) + \sum_{m=1}^{M} \mu_k(m) \right)^{r_k[l]}}{\prod_{k=1}^{K} r_k[l]!}$$

$$\frac{\rho_0 \left(e^{-\left(\sum_{k=1}^{K} \sum_{m=1}^{M} \mu_k(m) \right)} \right)}{\rho_1 \left(e^{-\sum_{k=1}^{K} \mu_k(0)} \right) \left(e^{-\sum_{k=1}^{K} \sum_{m=1}^{M} \mu_k(m)} \right)} \underset{0}{\overset{1}{\lessgtr}} \frac{\prod_{k=1}^{K} \left(\lambda + \mu_k(0) + \sum_{m=1}^{M} \mu_k(m) \right)^{r_k}}{\prod_{k=1}^{K} \left(\lambda + \sum_{m=1}^{M} \mu_k(m) \right)^{r_k}} \tag{12}$$

$$\ln \left(\frac{\rho_0}{\rho_1} \right) + \sum_{k=1}^{K} \mu_k(0) \underset{0}{\overset{1}{\lessgtr}} \sum_{k=1}^{K} r_k \ln \left(\frac{\lambda + \mu_k(0) + \sum_{m=1}^{M} \mu_k(m)}{\lambda + \sum_{m=1}^{M} \mu_k(m)} \right) \tag{13}$$

This is essentially same as: $\tag{14}$

$$v \underset{0}{\overset{1}{\lessgtr}} \sum_{k=1}^{K} w_k r_k, \text{ where :}$$

$$v = \left(\ln \left(\frac{\rho_0}{\rho_1} \right) + \sum_{k=1}^{K} \mu_k(0) \right)$$

$$w_k = \ln \left(\frac{\lambda + \mu_k(0) + \sum_{m=1}^{M} \mu_k(m)}{\lambda + \sum_{m=1}^{M} \mu_k(m)} \right)$$

$$w_k = \ln \left(1 + \frac{\mu_k(0)}{\lambda + \sum_{m=1}^{M} \mu_k(m)} \right)$$

The decoding error probability can be computed as

$$P_e = \rho_0 f + \rho_1 m \tag{15}$$

with the false alarm and missed detection probabilities given as

$$f = \sum_{r \in D(1)} p_R(r \mid b = 0), \quad m = \sum_{r \notin D(1)} p_R(r \mid b = 1)$$

and since $r_k[l]$ are Poisson distributed random variables we have

$$\text{f} = \sum_{\mathbf{r}:\sum w_k r_k[l] > v} e^{-\left(K\lambda + \sum_{k=1}^{K}\sum_{m=1}^{M}\mu_k(m)\right)} \prod_k \frac{\left(\lambda + \sum_{m=1}^{M}\mu_k(m)\right)^{r_k[l]}}{r_k[l]!} \tag{16}$$

$$\text{m} = \sum_{\mathbf{r}:\sum w_k r_k[l] \leq v} e^{-\left(K\lambda + \sum_{k=1}^{K}\left(\mu_k(0) + \sum_{m=1}^{M}\mu_k(m)\right)\right)} \prod_k \frac{\left(\lambda + \mu_k(0) + \sum_{m=1}^{M}\mu_k(m)\right)^{r_k[l]}}{r_k[l]!}$$

SISO Case:

$$r_k \underset{0}{\overset{1}{\gtrless}} \frac{\ln\left(\frac{\rho_0}{\rho_1}\right) + \mu_k(0)}{\ln\left(1 + \dfrac{\mu_k(0)}{\lambda + \sum\limits_{m=1}^{M}\mu_k(m)}\right)} \tag{17}$$

UCA (Uniform Circular Array) Case: ($\mu_k(m)$ is same for all K receivers, so suffix k can be omitted for reading simplicity)

$$\sum_{k=1}^{K} r_k \underset{0}{\overset{1}{\gtrless}} \frac{\ln\left(\frac{\rho_0}{\rho_1}\right) + K\mu(0)}{\ln\left(1 + \dfrac{\mu(0)}{\lambda + \sum\limits_{m=1}^{M}\mu(m)}\right)} = \bar{\nu} \tag{18}$$

Since $r = \sum_k r_k[l]$ follows a Poisson distribution, the false alarm and missed detection probabilities are given by,

$$\text{f} = 1 - Q\left(\bar{\nu}; K\left(\lambda + \sum_{m=1}^{M}\mu(m)\right)\right), \quad \text{m} = Q\left(\bar{\nu}; K\left(\lambda + \mu(0) + \sum_{m=1}^{M}\mu(m)\right)\right) \tag{19}$$

where $Q(x,\lambda)$ is the regularized incomplete Gamma function denoting the Cumulative Distribution Function of a Poisson random variable with parameter λ.

Theorem 4: In a SIMO UCA MC system with ISI made of K RxPs, the probability of error varies with the diversity order K as

$$\mathrm{P_e} \leq \rho_0 \left(e^{-\frac{a_K^2}{2\left(\lambda + \sum_{m=1}^M \mu(m) + a_K\right)}} \right)^K + \rho_1 \left(e^{-\frac{b_K^2}{2\left(\lambda + \sum_{m=1}^M \mu(m) + \mu(0) + b_K\right)}} \right)^K$$

with

$$a_K = \frac{\mu(0) + \frac{1}{K}\ln(\rho_0/\rho_1)}{\ln\left(1 + \mu(0)/(\lambda + \sum_{m=1}^M \mu(m))\right)} - \lambda - \sum_{m=1}^M \mu(m),$$

$$b_K = \mu(0) + \lambda + \sum_{m=1}^M \mu(m) - \frac{\mu(0) + \frac{1}{K}\ln(\rho_0/\rho_1)}{\ln\left(1 + \mu(0)/(\lambda + \sum_{m=1}^M \mu(m))\right)}$$

Proof: Upper bounds for poisson tail probabilities are:

$$\mathbb{P}[r \geq K\lambda + \epsilon] \leq e^{-\frac{\epsilon^2}{2(K\lambda + \epsilon)}}, \epsilon > 0, \text{ and}$$

$$\mathbb{P}[r \leq K\lambda + K\mu - \epsilon] \leq e^{-\frac{\epsilon^2}{2(K\lambda + K\mu + \epsilon)}}, 0 < \epsilon < K\lambda + K\mu$$

Therefore, the decoding error probabilities are

$$\mathrm{f} = \mathbb{P}\left[r \geq K\left(\lambda + \sum_{m=1}^M \mu(m)\right) + Ka_K \mid b = 0\right] \leq e^{-\frac{K^2 a_k^2}{2\left(K\left(\lambda + \sum_{m=1}^M \mu(m)\right) + Ka_K\right)}}, \text{ and}$$

$$\mathrm{m} = \mathbb{P}\left[r \leq K\left(\lambda + \sum_{m=1}^M \mu(m)\right) + K\mu(0) - Kb_K \mid b = 1\right] \leq e^{-\frac{K^2 b_k^2}{2\left(K\left(\lambda + \sum_{m=1}^M \mu(m)\right) + K\mu + Kb_K\right)}}$$

IV. WITHOUT ISI

Work till now is a generalization of the system considering ISI. Analysis will be greatly simplified if we do not take ISI into consideration. The received signal at each port will be:

$$r_i = s_i + n_i \tag{20}$$

The total received signal across all K ports will be:

$$\mathbf{r} = \mathbf{s} + \mathbf{n} \tag{21}$$

Lemma. If N number of molecules are released from the transmitter, then numbers of IMs sensed at individual RxPs is jointly distributed as multinomial distribution given by:

$$\mathsf{P_s}\left(\mathbf{s}\right) = \begin{pmatrix} Nb \\ s_1, s_2, \ldots s_K, s_0 \end{pmatrix} \prod_{k=0}^{K} h_k{}^{s_k} = \frac{(Nb)!}{\prod_{k=0}^{K}(s_k)!} \prod_{k=0}^{K} h_k{}^{s_k} \tag{22}$$

Where $\sum_{k=1}^{K} s_k \leq N$, and $s_0 = N - \sum_{k=1}^{K} s_k$ denotes the number of IMs lost (not sensed at any RxP), and $h_0 = 1 - \sum_{k=1}^{K} h_k$ denotes the corresponding probability.

Theorem. The joint distribution of the number of molecules sensed at individual RxPs is given as:

$$p_R\left(r_1, \cdots, r_K \mid b = 0\right) = \prod_{k=1}^{K} q_{r_k} \tag{23}$$

$$p_R\left(r_1, \cdots, r_K \mid b = 1\right) = \sum_{\mathcal{M}(\mathbf{r}, N)} p\left(s_1, \cdots, s_K\right) \prod_{k=1}^{K} q_{r_k - s_k} \tag{24}$$

with $\mathrm{M}(\mathbf{r}, \mathrm{N}) = \{(s_1, \cdots, s_K) : s_k \leq r_k \forall k \in [0, K], \sum_k s_k \leq N\}$

For a special case, 1×2 SIMO MC channel with 2RxPs and N = 1IM, the joint distribution of s is:

$$p\left(s_1, s_2\right) = \begin{cases} 1 - h_1 - h_2 & (s_1, s_2) = (0, 0) \\ h_1 & (s_1, s_2) = (1, 0). \ . \\ h_2 & (s_1, s_2) = (0, 1) \end{cases}$$

Hence, the channel is given as

$$
p_R\left(r_1, r_2 \mid b=0\right) =
\begin{cases}
q_0^2 & r = (0,0) \\
q_1 q_0 & r = (1,0) \text{ or } (0,1) \\
q_1^2 & r = (1,1) \\
q_{r_1} q_{r_2} & r_1, r_2 > 1
\end{cases} ,
$$

and

$$
p_R\left(r_1, r_2 \mid b=1\right) =
$$

$$
\begin{cases}
q_0^2\left(1 - h_1 - h_2\right) & r = (0,0) \\
h_1 q_0^2 + \left(1 - h_1 - h_2\right) q_1 q_0 & r = (1,0) \\
h_2 q_0^2 + \left(1 - h_1 - h_2\right) q_0 q_1 & r = (0,1) \\
h_1 q_0 q_1 + h_2 q_1 q_0 + \left(1 - h_1 - h_2\right) q_1 q_1 & r = (1,1) \\
h_1 q_{r_1-1} q_{r_2} + h_2 q_{r_1} q_{r_2-1} + \left(1 - h_1 - h_2\right) q_{r_1} q_{r_2} & r_1, r_2 > 1
\end{cases} .
$$

Now the molecules reach at the K RxPs and we will see the combining schemes at the receiver for decoding the received signals.

A. Analytical Expressions

For soft combining:

$$
\mathrm{D}(1) = \left\{ \mathbf{r} : h_0^N N! \sum_{\mathcal{M}(\mathbf{r},N)} \frac{1}{s_0!} \prod_{k=1}^{K} \binom{r_k}{s_k} \left(\frac{h_k}{h_0}\right)^{s_k} \lambda^{-s_k} > \frac{\rho_0}{\rho_1} \right\} \tag{25}
$$

For hard combining:

The MAP decoding region for bit 1 for k th RxP is

$$
\mathrm{D}_k(1) = \left\{ r_k : \sum_{s_k \leq r_k, N} \frac{N! r_k!}{(N - s_k)! s_k! (r_k - s_k)!} h_k^{s_k} \left(1 - h_k\right)^{N-s_k} \lambda^{-s_k} > \frac{\rho_0}{\rho_1} \right\}
$$

Since the LHS in the inner term in the above equation increases with r_k, the decoding region can be equivalently written as

$$\mathrm{D}_k(1) = [\eta_k, \infty), \quad \text{with}$$

$$\eta_k = \max \left\{ r : \sum_{s \leq r, N} \frac{N! r! h_k{}^s \left(1 - h_k\right)^{N-s}}{(N-s)! s! (r-s)! \lambda^s} \leq \frac{\rho_0}{\rho_1} \right\}.$$

In other words, each RxP compares r_k with η_k and decodes the bit as 1 if $r_k \geq \eta_k$ and 0 otherwise. Hence, the final decoding region for bit 1 is given as

$$\mathrm{D}(1) = \left\{ \mathbf{r} : \sum_k \mathbb{1}\left(r_k > \eta_k\right) \geq M \right\} \tag{26}$$

B. Poisson channel approximation

$$p_R\left(r \mid b = 0\right) \sim \mathrm{Poiss}(K\lambda)$$

$$p_R\left(r \mid b = 1\right) \sim \mathrm{Poiss}\left(\sum_{k=1}^{K}\left(\lambda + \mu_k\right)\right)$$

For soft combining:

$$\mathrm{D}(1) = \left\{ \mathbf{r} : \sum_{k=1}^{K} w_k r_k > v \right\} \tag{27}$$

where, $\mathrm{w}_k = \ln\left(1 + \frac{\mu_k}{\lambda}\right)$ and $v = \sum_{k=1}^{K} \mu_k + \ln\left(\frac{\rho_0}{\rho_1}\right)$

For hard combining:

$$r_k \underset{1}{\overset{0}{\lessgtr}} \frac{\mu_k + \ln\left(\rho_0/\rho_1\right)}{\ln\left(1 + \mu_k/\lambda\right)} \triangleq v_k. \tag{28}$$
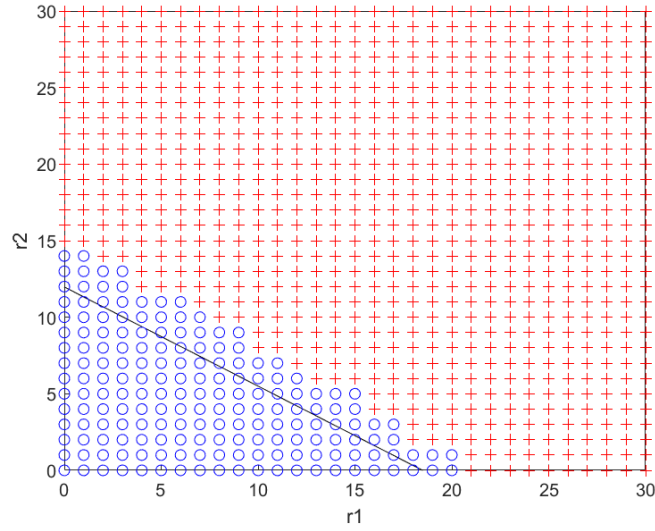
V. SIMULATION RESULTS

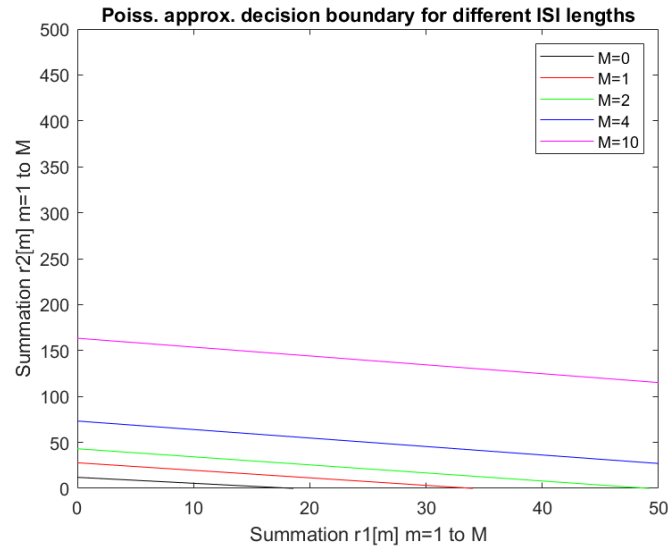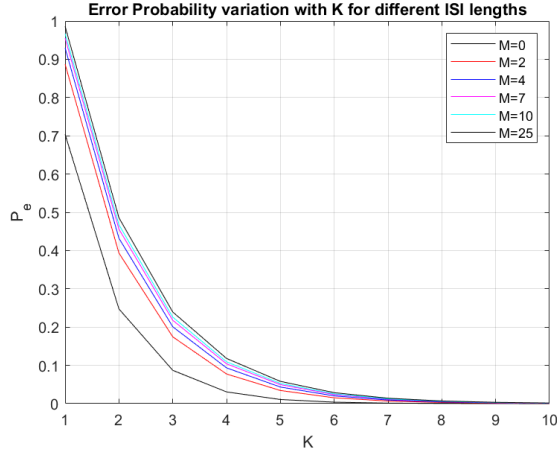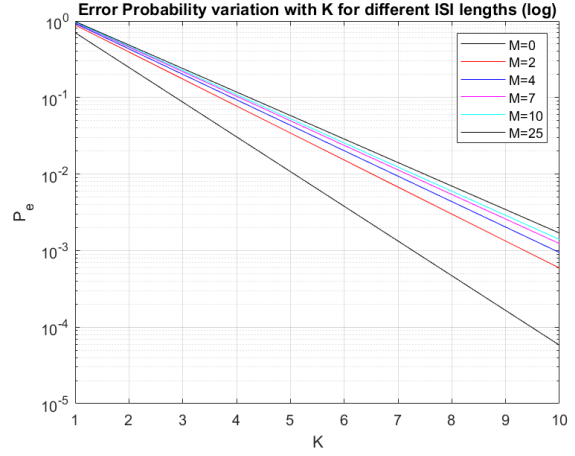Fig. 1: Poisson Approximation vs Analytical (Without ISI)

Fig. 2: Variation of Poisson MAP Decoding with ISI length

(a)

(b)

Fig. 3: Error Probability variation with K for different ISI lengths in log scale. $\mu = 3, \lambda = 0.5$ ($M = 0$ represents no ISI case)
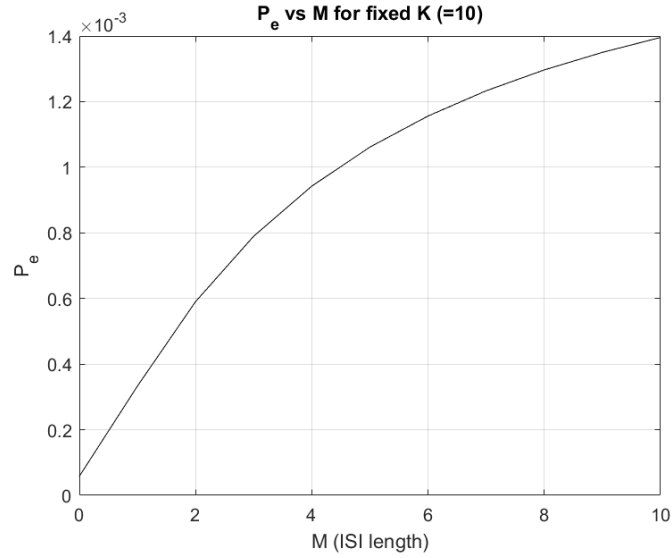

Fig. 4: Error probability vs M for fixed K. $\mu = 3, \lambda = 0.5$

VI. REFERENCES

[1] Will be updated