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Joint Optimization of Molecular Resource Allocation and Relay Positioning in Diffusive Nanonetworks

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ABSTRACT We consider a realistic two-hop diffusion-based molecular communication (DbMC) system with spherical absorbing receivers in the presence of molecular degradation and noises. We address the problem of joint optimization of molecules allocation and relay location for the given detection thresholds in order to minimize the error probability of budget limited DbMC system. Numerical and simulation results reveal the improvement in error performance when molecules distribution and relay placement are in accordance with their joint optimal value. Moreover, it is found that as the relay detection threshold increases, more molecules are needed to be allocated to the source while relay need to be placed closer to the destination in order to satisfy the optimization criteria. Eventually, we demonstrate the effectiveness of our optimization solution through 3D and contour plots illustrating the convergence time.

INDEX TERMS Nanonetworks, molecular communication, diffusion, error performance, molecules allocation, relay positioning, joint optimization.

I. INTRODUCTION

Molecular communication (MC) is a bio-inspired approach for establishing communication in nanonetworks over fluidic environments using chemicals as the information carriers [1]. Owing to its biocompatibility in general, MC finds importance in the cutting-edge *in vivo* biomedical applications [2] such as targeted drug delivery, continuous health monitoring by using Internet of Bio-Nano Things (IoBNT) [3] enabled bio-nanosensors, and so on.

Among the various forms of MC described in [4], the diffusion-based molecular communication (DbMC) has emerged as an effective and energy-efficient method for exchanging information among nanomachines (NMs). In DbMC system, information is encoded in quantity, type or emission frequency of the released molecules. Due to the concentration gradient, these information-bearing molecules traverse across the diffusive medium from the transmitter nanomachine (T_xN) to the receiver nanomachine (R_xN) according to the Brownian motion. On reaching the R_xN ,

molecular wave interact with the sensors to be decoded and interpreted as the received signal. The performance of DbMC system depends on various design parameters such as molecules allocation, T_xN releasing rate, relay nanomachine (RN) location, detection timing, reception delay, symbol interval, detection threshold, weight values of the detector, path between the NMs, which need to be optimized to achieve the minimum error rate. In [5], optimal number of released molecules for the given detection thresholds was derived in order to minimize the error probability of each hop in a multi-hop DbMC system. A game-theoretic approach has been presented in [6] for the distributed resource allocation in nanoscale MC systems. Salehi *et al.* [7] have derived optimal releasing rate of the T_xN for molecular drug delivery system (DDS) with limited resources. Ntouni *et al.* [8], [9] have specified optimal time for the observation process to minimize the error probability. A symbol interval optimization algorithm has been proposed in [10] and the optimal reception delay to minimize the inter-symbol interference in DbMC system has

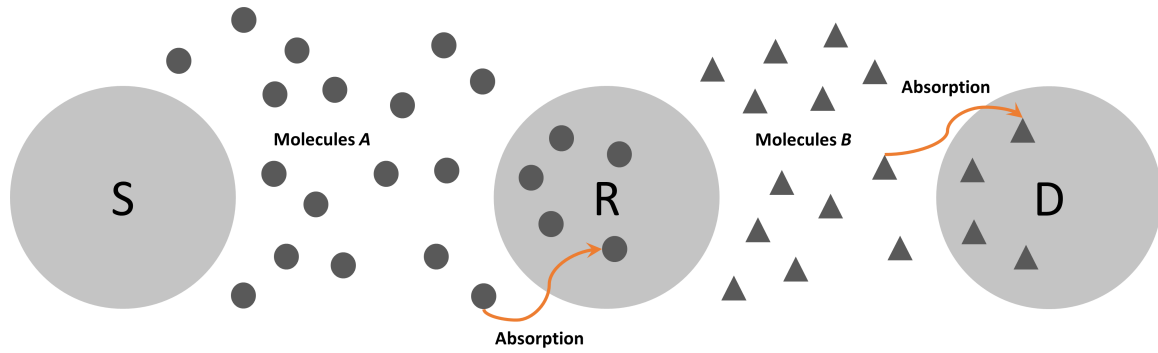


FIGURE 1. Schematic diagram of a two-hop DbMC system with absorbing receivers.

been found recently in [11]. In [12], swarm intelligence algorithm has been implemented in order to evaluate the weight values for the weighted sum detector of a passive receiver in a DbMC system. The ant colony optimization approach has been used in [13] to find the optimal path between the NMs. In [14], an optimization problem for detection threshold has been formulated as quasi-convex and then solved using the bisection method. Whereas, the work in [15] and [16] uses logarithmic barrier, Karush-Kuhn-Tucker conditions and Newton Raphson method sequentially to find the optimal detection threshold. Further, a joint convex optimization problem has been addressed for a cooperative DbMC system to obtain suboptimal detection thresholds using MATLAB-based interior-point algorithm [17]. Tavakkoli *et al.* [18] have proposed a joint RN positioning and R_xN detection threshold optimization problem for the given number of molecules released by the T_xN and the RN, and solved using an iterative algorithm.

However, to the best of our knowledge, the joint optimization of molecules allocation and RN positioning for the given predetermined detection thresholds has not been yet investigated. Note that molecules are limited resource because of the finite availability of molecule synthesizing energy and limited storage capabilities of the reservoir. In fact, such investigation in the context of bio-nanosensor networks [19] is essential for their practical implementation of local DDS [7] where drug molecules may be expensive and their large amount can have ill effects on healthy parts of the body. Above all, the emission of an arbitrary number of molecules would increase multi-source interference for other NMs present in the medium. Therefore, optimal allocation of these molecules and RN placement for the given detection thresholds would reduce the network error without increasing much the complexity of the NMs (i.e., NMs neither need to update their detection thresholds nor require high computational cost involved with the maximum likelihood (ML) detection).

Motivated by above, we investigate the problem of joint optimization of molecules allocation and RN location for a RN-assisted DbMC system that employs spherical absorbing receivers under the influence of molecular degradation and

pertinent noises. To this end, we derive an expression for the end-to-end error probability by assuming a decode-and-forward (DF) relaying strategy at the RN. Thereafter, we solve the optimization problem by using an iterative algorithm based on the block coordinate descent algorithm (BCDA). Numerical and simulation results demonstrate that the error performance improves significantly by jointly optimizing the molecular resource allocation and RN location. Moreover, our results highlight the effect of detection thresholds on the joint optimal solution.

II. SYSTEM MODEL

In this paper, we consider a static¹ DbMC system, as illustrated in Fig. 1, wherein communication between a T_xN (node S) and a R_xN (node D) occurs over an unbounded 3-dimensional fluidic environment having uniform temperature and viscosity. The RN (node R) is placed linearly in-between the nodes S and D. We assume node S to be a point source while nodes R and D to be fully absorbing [20] spherical receivers each having radius r . Further, node R is assumed to be a point object (whenever it transmits) and is located at distance $d_{pq} + r$ from end nodes, where d_{pq} is the distance between the center of transmitting node $p \in \{S, R\}$ and the nearest point on the surface of receiving node $q \in \{R, D\}$. We assume that the transmitting nodes S and R respectively use different types of molecules A and B for information transmission. Nodes R and D have sensors only for the intended molecules A and B respectively. As such, self-interference at node R gets avoided. Moreover, node R employs DF strategy with full-duplex transmission protocol. All nodes are supposed to be synchronized in time, utilizing the strategy mentioned in [21]. We rely on the on-off keying modulation in which N_A and N_B number of molecules are released by the nodes S and R, respectively, for conveying the information bit 1, whereas for bit 0, no molecules are released by them at the beginning of the symbol duration T . These molecules propagate

¹NMs can be immobilized in the medium in certain scenarios where they get anchored to larger objects or bound to fixed molecules [18].

independently² through the molecular channel and may degrade [20] before hitting the receiver nanosensors. As soon as molecules hit the nanosensors, they are removed from the medium and contribute only once to the signal. This activity is described by the first hitting probability function and is derived in [20, eq. (9)] for a spherical absorbing receiver in a 3-dimensional molecular degraded diffusive channel, between nodes p and q , as

$$h_f^{pq}(t) = \frac{r}{d_{pq} + r} \frac{d_{pq}}{\sqrt{4\pi D_f t^3}} \exp\left(-\frac{d_{pq}^2}{4D_f t}\right) \phi(\lambda, t), \quad (1)$$

where D_f is the diffusion coefficient of type, $f \in \{A, B\}$, molecules in the given medium and $\phi(\lambda, t) = \exp(-\lambda t)$ is the survival probability of a molecule, until time t , with degradation rate λ . Hence, the expected fraction of node p transmitted molecules absorbed at node q , at time t , before getting degraded can be calculated by integrating (1) as

$$H_f^{pq}(t) = \int_0^t h_f^{pq}(\tau) d\tau = \frac{r}{2(d_{pq} + r)} \times \left[\exp(\psi) \operatorname{erfc}\left(\varphi + \sqrt{\lambda t}\right) + \exp(-\psi) \operatorname{erfc}\left(\varphi - \sqrt{\lambda t}\right) \right], \quad (2)$$

where $\psi = d_{pq}\sqrt{\lambda/D_f}$ and $\varphi = d_{pq}/\sqrt{4D_f t}$. Consequently, the arrival probability, at node q in the current symbol duration, for a molecule released by node p in the i th previous symbol duration is given by

$$P_{i,f}^{pq} = H_f^{pq}((i+1)T) - H_f^{pq}(iT). \quad (3)$$

Besides the residual molecules from prior emissions, molecular signal is also corrupted by the emission from other NMs prevailing in the diffusive medium and the counting error induced at the reception node. As such, the total sensed molecules in the j th symbol duration at node q can be represented as

$$N_{c,f}^{pq}[j] = N_{c,f}^{pq}[j] + N_{nr,f}^{pq}[j] + N_{no,f}^{pq}[j] + N_{nc,f}^{pq}[j], \quad (4)$$

where $N_{c,f}^{pq}[j]$ and $N_{nr,f}^{pq}[j]$ amount to the respective number of molecules received from the current and prior transmissions. For large N_f , the binomial distributions of $N_{c,f}^{pq}[j]$ and $N_{nr,f}^{pq}[j]$ can be approximated by the Gaussian distributions $\mathcal{N}(a_j^p N_f P_{0,f}^{pq}, a_j^p N_f P_{0,f}^{pq} (1 - P_{0,f}^{pq}))$ and $\sum_{i=1}^I \mathcal{N}(a_{j-i}^p N_f P_{i,f}^{pq}, a_{j-i}^p N_f P_{i,f}^{pq} (1 - P_{i,f}^{pq}))$ respectively [14], [15], where a_j^p and $a_{j-i}^p \in \{0, 1\}$, are the j th current and $(j-i)$ th previous transmitted bits respectively by node p , and I symbolizes the number of previous transmissions. Furthermore, $N_{no,f}^{pq}[j]$ denotes the sensed number of molecules that were emitted by the other prevailing NMs of the medium and $N_{nc,f}^{pq}[j]$ signifies the induced counting error at node q , conforming the distributions $\mathcal{N}(\mu_{no}^{pq}, \sigma_{no}^{2,pq})$ and $\mathcal{N}(0, \sigma_{nc}^{2,pq})$

²This assumption holds good for sufficiently dilute suspension of the information-carrying molecules.

respectively [14], [15], where $\sigma_{nc}^{2,pq}$ depends on the expected number of molecules sensed by node q .

III. ERROR PROBABILITY ANALYSIS

This section derives the error probability expression for the considered DbMC system. If the detection is erroneous at either of the receiving nodes, error occurs at the destination node. Hence, the j th bit error probability can be evaluated as

$$P_e[j] = \Pr(a_j^S=1) \times [\Pr(\hat{a}_j^R=0 | a_j^S=1) \times \Pr(\hat{a}_{j+1}^D=0 | a_{j+1}^R=0)] + \Pr(a_j^S=1) \times [\Pr(\hat{a}_j^R=1 | a_j^S=1) \times \Pr(\hat{a}_{j+1}^D=0 | a_{j+1}^R=1)] + \Pr(a_j^S=0) \times [\Pr(\hat{a}_j^R=1 | a_j^S=0) \times \Pr(\hat{a}_{j+1}^D=1 | a_{j+1}^R=1)] + \Pr(a_j^S=0) \times [\Pr(\hat{a}_j^R=0 | a_j^S=0) \times \Pr(\hat{a}_{j+1}^D=1 | a_{j+1}^R=0)] \quad (5)$$

and is given by

$$P_e[j] = \frac{1}{2} \left(1 + g(N_A, d_{SR}) g(N_B, d_{RD}) \right), \quad (6)$$

for the equally likely binary information bits, where \hat{a}_j^R and \hat{a}_{j+1}^D are the detected information bits at nodes R and D respectively in the j th and $(j+1)$ th symbol durations, and $\hat{a}_j^R = a_{j+1}^R$. The functions $g(N_A, d_{SR})$ and $g(N_B, d_{RD})$ are calculated as

$$g(N_A, d_{SR}) = Q\left(\frac{\eta_R - \mu_0^{SR}}{\sqrt{\sigma_0^{2,SR}}}\right) - Q\left(\frac{\eta_R - \mu_1^{SR}}{\sqrt{\sigma_1^{2,SR}}}\right), \quad (7)$$

and

$$g(N_B, d_{RD}) = Q\left(\frac{\eta_D - \mu_1^{RD}}{\sqrt{\sigma_1^{2,RD}}}\right) - Q\left(\frac{\eta_D - \mu_0^{RD}}{\sqrt{\sigma_0^{2,RD}}}\right), \quad (8)$$

respectively, where $Q(x) = \frac{1}{\sqrt{2\pi}} \int_x^\infty \exp(-\frac{x^2}{2}) dx$. Moreover, the involved statistics are computed as

$$\mu_0^{SR} = \frac{N_A}{2} \sum_{i=1}^I P_{i,A}^{SR} + \mu_{no}^{SR}, \quad (9)$$

$$\mu_1^{SR} = \frac{N_A}{2} \sum_{i=1}^I P_{i,A}^{SR} + N_A P_{0,A}^{SR} + \mu_{no}^{SR}, \quad (10)$$

$$\sigma_0^{2,SR} = \frac{N_A}{2} \sum_{i=1}^I P_{i,A}^{SR} (1 - P_{i,A}^{SR}) + \frac{N_A^2}{4} \sum_{i=1}^I (P_{i,A}^{SR})^2 + \sigma_{no}^{2,SR} + \sigma_{nc}^{2,SR} |_{a_j^S=0}, \quad (11)$$

and

$$\sigma_1^{2,SR} = N_A P_{0,A}^{SR} (1 - P_{0,A}^{SR}) + \frac{N_A}{2} \sum_{i=1}^I P_{i,A}^{SR} (1 - P_{i,A}^{SR}) + \frac{N_A^2}{4} \sum_{i=1}^I (P_{i,A}^{SR})^2 + \sigma_{no}^{2,SR} + \sigma_{nc}^{2,SR} |_{a_j^S=1}, \quad (12)$$

where $\sigma_{n_c}^{2,SR}|_{a_j^S=0} = \mu_0^{SR}$ and $\sigma_{n_c}^{2,SR}|_{a_j^S=1} = \mu_1^{SR}$. Further, $\mu_0^{RD}, \mu_1^{RD}, \sigma_0^{2,RD}$ and $\sigma_1^{2,RD}$ are calculated likewise. Eventually, η_R and η_D are the predetermined detection thresholds at nodes R and D respectively.

IV. JOINT OPTIMAL MOLECULES ALLOCATION AND RELAY POSITIONING

As evident from (6), the error probability expression depends on the transmitted number of molecules N_A and N_B , and distances d_{SR} and d_{RD} . Hence, we show interest in the optimal molecules allocation and RN placement that minimizes error probability derived in the previous section. To this end, we formulate a joint optimization problem as

$$\min_{m,n} P_e[j], \tag{13}$$

where $m = d_{SR}/(d_{SR} + d_{RD})$ represents relay positioning factor and $n = N_A/(N_A + N_B)$ denotes the fraction of molecular budget allocated to node S. Then, we solve the optimization problem (13) by using BCDA which relies on the concept of fixing all the parameters except one and finding its optimal value that minimizes the objective function. This process is repeated until all the parameters converge [22].

At first, using BCDA, we consider problem (13) for the fixed value of n as

$$\min_m P_e[j]. \tag{14}$$

Then, we determine convexity of (14) from the numerical results presented in Section V since calculating the second order derivative of $P_e[j]$ with respect to m is cumbersome. $P_e[j]$ follows Jensen’s inequality for quasiconvexity [23], i.e., the value of the function on a segment does not exceed the maximum of its values at the endpoints. Alternatively, since $P_e[j]$ is nonincreasing till the minimum point and non-decreasing from thereon, $P_e[j]$ is quasiconvex [23]. Thus, the optimization problem (14) can be solved by using the bisection method provided in Algorithm 1 with convex feasibility problem as

$$\begin{aligned} &\text{Find } m \\ &\text{s.t. } P_e[j] - \theta \leq 0. \end{aligned} \tag{15}$$

Algorithm 1 Bisection Method

Choose $\delta \in (0, 1)$ and set $P_e^l = 0, P_e^u = 1;$
 $P_e^l \leq P_e[\text{optimal } m] \leq P_e^u$
Iterate
 1. $\theta = (P_e^l + P_e^u)/2$.
 2. Check the convex feasibility problem (15).
 3. If enforceable then update $P_e^u = \theta$; else $P_e^l = \theta$.
 Until $P_e^u - P_e^l \leq \delta$.

Thereafter, we fix the value of m as the next step of BCDA algorithm and find the optimal n that minimizes the given objective function i.e.,

$$\min_n P_e[j]. \tag{16}$$

Similar to (14), optimization problem (16) is also quasiconvex that can be solved using Algorithm 1 by replacing m with n and using the new convex feasibility problem as

$$\begin{aligned} &\text{Find } n \\ &\text{s.t. } P_e[j] - \theta \leq 0. \end{aligned} \tag{17}$$

Finally, the aforementioned steps are repeated until the values of m and n converge for the optimization problem (13) using the BCDA given in Algorithm 2.

Algorithm 2 BCDA for the Joint Optimization of m and n

Choose $\delta \in (0, 1)$ and set iteration $k = 0$.
 Using bisection method in (14), find m^0 for arbitrary n^0 .
Iterate
 1. For m^{k-1} , find n^k from (16) using bisection method.
 2. Invoking n^k , find m^k from (14) using bisection method.
 3. Update $k = k + 1$.
 Until $\|m^k - m^{k-1}\|$ and $\|n^k - n^{k-1}\| \leq \delta$.

Remark: The addressed problem (13) can be solved by a controller NM [18] having higher computational capability than RN and R_xN . It may use information such as diffusion coefficient and communication distance as the channel state information (CSI) available at the reception nodes. Prior to finding joint optimal molecules allocation and RN location, CSI can be estimated by using training sequence-based channel estimators at the reception nodes. Once the controller node finds the optimal solution, it shares the same with the transmitting nodes each of which are having molecular count limited to $N_A + N_B$ in their reservoirs. This facilitates the release of optimal number of molecules. Moreover, RN may have chemical mechanisms or self-organization capability to move itself towards the optimal position.

V. NUMERICAL AND SIMULATION RESULTS

In this section, we demonstrate the effectiveness of our joint molecules allocation and relay location optimization solution. We further showcase the effect of detection thresholds on the optimal solution which minimizes the error probability of the considered system. We consider a diffusive medium (like blood) with uniform viscosity of $10^{-3} \text{ kg m}^{-1}\text{s}^{-1}$ at temperature 310°K and the information-bearing molecules (as feasible with human insulin hormone like molecules) of compatible radius 2.56 nm [20]. We choose value of several other parameters from [20] as $r = 10 \mu\text{m}$, $D_A = D_B = 79.4 \mu\text{m}^2\text{s}^{-1}$, $\lambda = 5.41 \text{ s}^{-1}$, and $T = 0.2 \text{ s}$. Furthermore, we select molecular budget $N_A + N_B = 800$, $d_{SR} + d_{RD} = 20 \mu\text{m}$, $\mu_{n_o}^{SR} = \mu_{n_o}^{RD} = \sigma_{n_o}^{2,SR} = \sigma_{n_o}^{2,RD} = 50$, $I = 10$, and $\delta = 10^{-4}$. Results are obtained using Monte Carlo simulation approach (as in [15]) and averaging over 10^4 random realizations of the observations.

Fig. 2 depicts error performance of the considered DbMC system as a function of molecules allocation factor n , for different values of detection thresholds η_R and η_D , when optimal m is chosen. One can visualize Fig. 2 from 3-dimensional

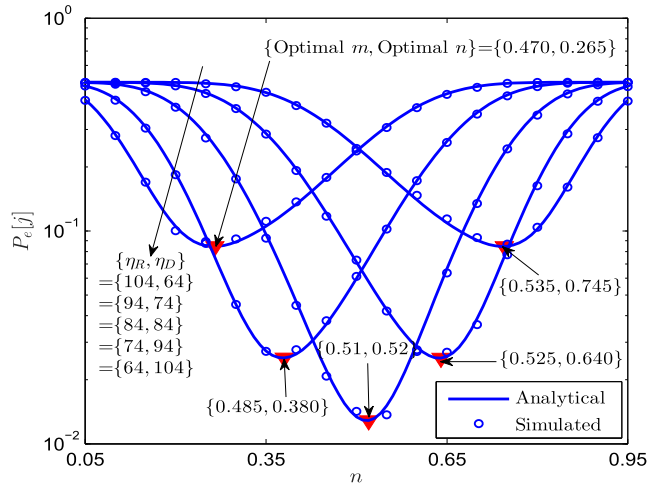


FIGURE 2. $P_e[j]$ as a function of n , with optimal m , for different $\{\eta_R, \eta_D\}$.

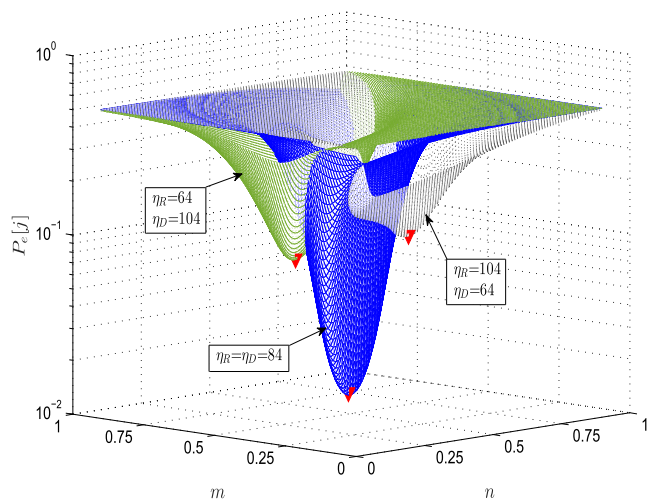


FIGURE 3. $P_e[j]$ as a function of m and n , where \blacktriangledown is the optimal (m, n) .

Fig. 3 by looking along the n axis for the fixed but optimal values of m . Our analytical results, in (6), match well with the simulation points, and the optimal solutions for different $\{\eta_R, \eta_D\}$ coincide with their corresponding minimum error points. Marker ‘ \blacktriangledown ’ illustrates the joint optimal values of m and n calculated using the BCDA presented in Algorithm 2. Evidently, one can see the increase in optimal n for higher values of detection threshold η_R . This is because T_xN need to release more number of molecules in order to decrease the probability of miss detection. Consequently, optimal m also increases for this increased value of n . On the contrary, T_xN need to release less number of molecules to reduce the probability of false alarm for the lower values of η_R . As a result, optimal m also decreases. Intuitively, for the optimal thresholds of [15], Algorithm 2 provided the joint optimal $\{m, n\}$ as $\{0.51, 0.52\}$ suggesting the placement of RN in the middle, releasing half the molecules at the T_xN , and the other half at the RN. Above all, our analysis helps in achieving the same minimum error performance for the interchanged values of $\{\eta_R, \eta_D\}$, when optimal $\{m, n\}$ are chosen.

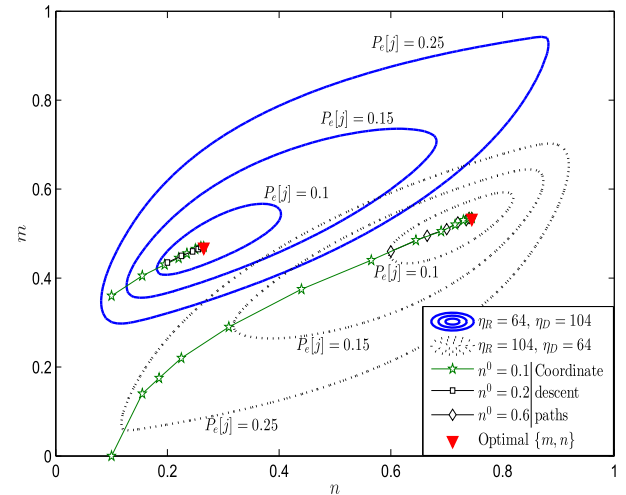


FIGURE 4. Contours or level curves of $P_e[j]$ illustrating coordinate descent paths.

Fig. 4 presents the contours or level curves of $P_e[j]$, for different values of detection thresholds η_R and η_D , along with the coordinate descent paths for different initial values n^0 . Fig. 4 can be generated from Fig. 3 by cutting latter along the mn plane at different heights. Apparently, one can observe that $P_e[j]$ is a quasiconvex function of m and n since the lower contour set is convex for any value of $P_e[j]$ [23]. In other words, $P_e[j]$ is quasiconvex since its value for the level curves increases in the outward direction. Further, one can see the coordinate descent paths (or the sequence of solutions corresponding to each BCDA iterations), for different $\{\eta_R, \eta_D\}$ and n^0 , leading towards their optimal solutions. Note that a single iteration represents minimization for both the optimization parameters. Algorithm 2 takes 8 and 13 iterations, with $n^0 = 0.1$, to provide the joint optimal solutions for $\{\eta_R = 64, \eta_D = 104\}$ and $\{\eta_R = 104, \eta_D = 64\}$ respectively. Moreover, when n^0 is chosen closer to the optimal n then BCDA takes less iterations for convergence. Specifically, Algorithm 2 requires 6 iterations for $\{\eta_R = 64, \eta_D = 104\}$ with $n^0 = 0.2$ and 7 for $\{\eta_R = 104, \eta_D = 64\}$ with $n^0 = 0.6$. Note that an initial value close to 0.5 will result in faster convergence.

VI. CONCLUSION

We performed the joint optimization of molecules allocation and relay location in order to minimize the end-to-end error probability of a RN-assisted DbMC system. Further, we demonstrated that the error performance minimizes for the joint optimal RN placement and molecular resource allocation. Our results showed that as the relay detection threshold gets increased, more molecules would be required at the source while relay should be shifted towards the destination. The proposed analysis helps in designing a reliable and budget limited DbMC system with minimal computational requirements at the receiving NMs.

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