Diffusion-Based Nanonetworking: A New Modulation Technique and Performance Analysis

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***Abstract*—In this letter, a new molecular modulation scheme for nanonetworks is proposed. To evaluate the scheme, a system model based on the Poisson distribution is introduced. The error probability of the proposed scheme as well as that of two previously known schemes, the concentration and molecular shift keying modulations, are derived for the Poisson model by taking into account the error propagation effect of previously decoded symbols. The proposed scheme is shown to outperform the previously introduced schemes. This is due to the fact that the decoding of the current symbol in the proposed scheme does not encounter propagation of error, as the decoding of the current symbol does not depend on the previously transmitted and decoded symbols. Finally, fundamental limits on the probability of error of a practical set of encoders and decoders are derived using information theoretical tools.**

***Index Terms*—Nanonetworking, molecular communication, modulation, Poisson distribution.**

I. Introduction

NANONETWORKING promises new solutions for many applications in the biomedical and industrial fields. This new paradigm utilizes various methods to communicate information between nano-scale machines [1]. A promising communication method at this scale is *molecular communication*. Different molecular communication schemes have been proposed that can be categorized based on their effective range of communication, namely short, medium or large [2].

In this paper, we focus on a diffusion-based communication system for short and medium range nanonetworks. In this system, molecule concentration represents information. The transmitter emits molecules whose type and intensity depend on the current input symbol. These molecules propagate through the environment, with a part hitting the receiver's surface. Receptors located on receiver's surface form chemical bonds with incoming molecules, initiating a process that eventually results in the decoding of the transmitted information.

Different channel models for molecular communication have been developed and their related channel capacities have been evaluated in [3]-[8]. Authors in [9] have proposed two modulation schemes called Concentration Shift Keying (CSK) and Molecular Shift Keying (MOSK). In these schemes, information is encoded in molecule diffusion rate and molecule type, respectively. Both CSK and MOSK suffer from interference caused by molecules from previous transmissions, which hit the receiver after a long delay. To control this interference in CSK (where only one molecule type is used), the decoding of the current symbol is adapted to the last decoded symbol. Although this helps to manage the interference, it results in an error propagation to the current symbol if the last symbol is decoded incorrectly. Using multiple molecule types, MOSK is more resistant to interference than CSK but it requires complex molecular mechanisms at both the transmitter and the receiver for message synthesis and decoding [9].

In this paper we propose a new modulation scheme based on using distinct types of molecules for consecutive slots at the transmitter, thus effectively suppressing the interference. Although simple in its formulation, the scheme outperforms the existing ones. To evaluate our schemes as well as the CSK and MOSK schemes, we propose a new system model for the molecule propagation process based on the Poisson distribution. This model is more realistic and amenable to analysis than the one proposed in [9] based on the binomial distribution. We evaluate and formulate the probability of error for our proposed scheme as well as the previous ones and compare the results. Specially, we take into account the dependency of decoding of the current symbol on the last transmitted and decoded symbols to compute these metrics. Numerical results indicate our scheme has a lower probability of error compared to CSK and MOSK. To understand the efficiency of our proposed scheme, we use information theoretical tools to derive a fundamental limit on the minimum probability of error of any arbitrary scheme. A comparison indicates that although our scheme outperforms the existing ones, its error exponent (in terms of transmission power) is larger than our fundamental lower bound, suggesting room for further improvement.

The rest of the paper is organized as follows. The proposed modulation scheme and system model are described in Section II. In Section III, the performance of different modulation techniques are discussed. Also, in this section a more general molecular communication system is introduced for which a lower bound on the probability of error is computed. Lastly, numerical results are presented in Section IV.

II. Proposed Modulation Scheme and System Model

A. Previously introduced modulation schemes

The Concentration Shift Keying (CSK) scheme [9] is inspired by the Amplitude Shift Keying (ASK) used in the classical communication. In this scheme, symbols are encoded in the number of molecules that the transmitter diffuses per time slot; this is called *diffusion rate* or *transmission power*. For example, to represent b bits, 2^b different molecule diffusion rates are utilized. At the receiver, the concentration (the number of the received molecules) is compared with decision thresholds in order to decode the transmitted symbol. The molecules from the previous symbol in the last time slot may hit the receiver in the current time slot and contribute to the interference signal. Thus, to reduce the effect of the interference in this scheme, decision thresholds for the current symbol need to be adapted to the last decoded symbol.

Molecular Shift Keying (MOSK) scheme [9] resembles the Frequency Shift Keying (FSK) in the classical communications. To transmit b bits per time slot, 2^b different molecule types are utilized. The transmitter releases a specified number

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of molecules of the type corresponding to the current input symbol. To decode the transmitted signal at a certain time slot, the receiver looks for a unique molecule type whose concentration exceeds a certain threshold τ. An error occurs if the concentration of none of the molecule types or more than one molecule type exceeds τ. Although interference due to the previous transmission in MOSK is less than that in the CSK, it still exists. Also, using different molecule types complicates the hardware structure at both the transmitter and the receiver, since the number of molecule types increases exponentially with b.

B. Proposed modulation scheme

Our scheme borrows ideas from CSK and MOSK. Having molecules of types A_1 and A_2, the transmitter uses type A_1 in odd time slots, and type A_2 in even time slots. The use of two molecule types resembles MOSK but the difference is that the molecule type is not used for signaling. To convey information in each time slot, different diffusion rates are used (similar to CSK). Thus, to match each symbol to b bits, 2^b different propagation rates are utilized in each time slot. As the molecule types are different in two subsequent time slots, (i) the previous symbol interference is drastically reduced (ii) the decision threshold of the current symbol is independent of the last decoded symbol. Since the data is not encoded in the molecule types (but in the concentrations), the number of molecule types (and as a result the complexity), does not increase with b. We refer to this scheme as Molecular-Concentration Shift Keying (MCSK).

C. A Poisson model for molecular communication

In this section, we develop a model for a general molecular transmission. Later, we use this model to compare probabilities of error of MOSK, CSK and MCSK. It is assumed that the symbols are transmitted in equal time slots called symbol duration, t_s. Generally the signal is decoded based on the concentration of molecule types received during a time slot. We assume that in a time slot three sources contribute to the received molecules of a specific type: (i) molecules due to transmission in the current time slot (ii) the residue molecules due to transmission in the last time slot (the residue molecules from two or more earlier time slots are ignored) (iii) the molecules from other sources as the noise of environment. Validity of the assumption of ignoring two and more earlier time slots depends on the symbol duration, t_s. Let the molecule hitting probabilities in the current, next and two and more earlier time slots be $P_1, P_2, P_3, ...$ respectively ($P_1+P_2+P_3+... \leq 1$). We assume sufficiently large t_s such that $P_3, P_4, \cdots$ can be ignored compared with P_1. We assume inter-molecule collisions have little effect on the molecule's movement.

For each molecule type, the transmitter has a storage. Every storage has an outlet whose size controls how many molecules can exit the storage to be diffused in the environment. The distribution of the number of molecules that exit from the storage in a time slot is expressed as a Poisson. This follows from the fact that the number of molecules in the storage is large and probability of each passing through the outlet is small. We use $Poisson(X)$ to denote the number of molecules exiting the storage (and diffused in the environment). The parameter X is called the diffusion rate and is determined by the size of the opening of the outlet. Parameter X itself is a random variable that is decided by the transmitter based on the message it wishes to transmit.

Assume that the transmitter chooses diffusion rates X_1 and X_2 of a molecule type like A in two consecutive time slots in a modulation scheme. Also, consider an environment noise, independent of the source signal, and following a Poisson distribution with parameter λ_0 (see [8] for a Poisson model of the environmental noise). Considering hitting probabilities P_1 and P_2, and using the thinning property of Poisson and the fact that sum of independent Poisson rv's is itself a Poission, the number of type A molecules received within the current time slot (denoted by $Y^{(A)}$) follows a Poisson distribution with parameter λ where $\lambda = P_1X_1 + P_2X_2 + \lambda_0$. This Poisson model has advantages over the binomial model considered in [9]: (i) The Poisson model is more realistic and practical in comparison with the binomial model. For instance, in binomial model the transmitter needs to count the number of molecules that it diffuses in comparison with the Poisson model in which the size of the storage's outlet is controlled (without counting the exact number of molecules passing through the outlet). (ii) The Poisson model is easier to work with analytically because of the nice properties of Poisson (e.g. thinning property, etc.).

D. Decoding probabilities for CSK, MOSK and MCSK

In the CSK scheme, only one type of molecule A is used in all time slots. So, the decoding is made by comparing the number of received molecules, i.e. $Y^{(A)}$, with the thresholds determined based on the last decoded symbol.

In MOSK, as information is encoded in molecule type, if two subsequent symbols are the same, only one molecule type for instance A_1 is received, otherwise two molecule types A_1 from the current symbol and A_2 type from the previous symbol are received. In the former case, the symbol is decoded correctly if the total received molecules in the current time slot, i.e. $Y^{(A_1)}$, exceeds the threshold τ. In the latter, the decision is made based on $Y^{(A_1)}$, $Y^{(A_2)}$ and the threshold τ.

In the proposed MCSK scheme, as stated above, 2 different types of molecules in 2 subsequent time slots are used. As the receiver knows the type of the current symbol, it needs only to compare the number of the molecules of this type with the thresholds to decode the current symbol. We now compute the average probabilities of error for CSK, MOSK and MCSK.

As in [9], we only consider the class of simple symbol-by-symbol decoders that are practically appealing. Comparisons are made consistently for decoders in this class with the same transmission powers.

For binary CSK (BCSK) using molecules of type A, if the current input symbol is $s_c = 0$ and the last transmitted and decoded symbols are s_p and $\widehat{s}_p$ respectively, the probability of successful decoding is computed as

$$P_{\widehat{S}_c|S_c,S_p,\widehat{S}_p}(\widehat{s}_c = 0|s_c = 0, s_p, \widehat{s}_p) = P(Y^{(A)} < \tau_{\widehat{s}_p}), \quad (1)$$

where $\widehat{s}_c$ is the decoded current symbol and $\tau_{\widehat{s}_p}$ is the decision threshold corresponding to the value of $\widehat{s}_p$. Note that in this equation, $\widehat{s}_p$ is not necessarily equal to the previous transmitted symbol, i.e. s_p. In fact, the decision threshold for the current symbol is determined based on the previous decoded symbol regardless of being decoded correctly or not.

For binary MOSK (BMOSK), assume molecules type A_1 and A_2 are sent for 0 and 1, respectively. For the current transmitted symbol of $s_c = 0$, probability of successful decoding for $s_p = 0$ and $s_p = 1$ are computed as follows:

$$P_{\widehat{S}_c|S_c,S_p}(\widehat{s}_c = 0|s_c = 0, s_p = 0) = P(Y^{(A_1)} > \tau), \quad (2)$$
$$P_{\widehat{S}_c|S_c,S_p}(\widehat{s}_c = 0|s_c = 0, s_p = 1) = P(Y^{(A_1)} > \tau)P(Y^{(A_2)} \leq \tau).$$

For the proposed binary MCSK (BMCSK), if the molecules of type A is used in the current slot, the probability of successful decoding can be computed as follows:

$$P_{\widehat{S}_c|S_c}(\widehat{s}_c = 0|s_c = 0) = P(Y^{(A)} < \tau). \quad (3)$$

These probabilities for the case $S_c = 1$ and also quaternary and higher modulation levels can be calculated similarly.

III. Performance Analysis

A. Probability of error

Let $E = \mathbf{1}\{\hat{S}_c \neq S_c\}$ be the error event. For BCSK, the average probability of error is equal to $P_e = 0.5P(E|S_c = 0) + 0.5P(E|S_c = 1)$. As the decoding of the current symbol is dependent on both the last transmitted and decoded symbols in BCSK, we have:

$$\begin{aligned} P(E|S_c = 0) &= \sum_{s_p,\widehat{s}_p} P_{S_p,\widehat{S}_p|S_c}(s_p, \widehat{s}_p|S_c = 0)P(E|S_c = 0, s_p, \widehat{s}_p) \\ &= \sum_{s_p,\widehat{s}_p} P_{S_p}(s_p)P_{\widehat{S}_p|S_p}(\widehat{s}_p|s_p)P(E|S_c = 0, s_p, \widehat{s}_p), \\ P(E|S_c = 1) &= \sum_{s_p,\widehat{s}_p} P_{S_p,\widehat{S}_p|S_c}(s_p, \widehat{s}_p|S_c = 1)P(E|S_c = 1, s_p, \widehat{s}_p) \\ &= \sum_{s_p,\widehat{s}_p} P_{S_p}(s_p)P_{\widehat{S}_p|S_p}(\widehat{s}_p|s_p)P(E|S_c = 1, s_p, \widehat{s}_p). \end{aligned} \quad (4)$$

When $\widehat{s}_p \neq s_p$, $P_{\widehat{S}_p|S_p}(\widehat{s}_p|s_p)$ is the probability that the previous symbol s_p is falsely decoded to $\widehat{s}_p$ and can be substituted by $P(E|s_p)$. So when $\widehat{s}_p = s_p$, $P_{\widehat{S}_p|S_p}(\widehat{s}_p|s_p)$ will be equal to $1 - P(E|s_p)$. Therefore, $P(E|0)$ and $P(E|1)$ can be computed recursively from (4) which is a system of linear equations. For quaternary CSK (QCSK) and higher levels, the probability of error can be computed similarly.

For the MOSK, the decoding of the current symbol is independent of the previous decoded symbol, i.e. $\widehat{s}_p$. Therefore,

$$P_e = \sum_{s_c,s_p} P(E|s_c, s_p)P_{S_c}(s_c)P_{S_p}(s_p). \quad (5)$$

For the proposed MCSK, since the decoding of the current symbol is independent of both the transmitted and previous decoded symbols, P_e is computed as follows

$$P_e = \sum_{s_c} P_{S_c}(s_c)P(E|s_c). \quad (6)$$

B. Lower bound on probability of error

In order to evaluate the modulation schemes considered above, we examine a general molecular communication system with two molecule types A_1 and A_2 and a memory of only one symbol at the decoder (since we are considering the class of simple and practical symbol-by-symbol decoders only). Let $B_i, 1 \leq i \leq k$ be the i^{th} input symbol (assumed to be i.i.d. and uniform rv's over a set $\mathcal{B}$). The encoder uses $B_1, B_2, ..., B_i$ to determine the diffusion rates $X_i^{(1)}$ and $X_i^{(2)}$ of molecules of type A_1 and A_2 respectively at the i^{th} time slot. Thus the actual number of molecules that are diffused would follow independent Poisson distributions with parameters $X_i^{(j)}$, $j = 1, 2$. Using the thinning property of Poisson, the distribution of the numbers of molecules of type A_j, $j = 1, 2$, received at the receiver in the i^{th} time slot is $Y_i^{(j)} \sim Poisson(P_1X_i^{(j)} + P_2X_{i-1}^{(j)} + \lambda_0)$, where P_1, P_2 and λ_0 are defined in section II-C. The current input symbol is decoded as $\widehat{B}_i$ based on the $Y_i^{(1)}, Y_i^{(2)}$ and $\widehat{B}_{i-1}$ (the previous decoded symbol). The average probability of error is:

$$P_e = \frac{1}{k}\sum_{i=1}^{k} P(\widehat{B}_i \neq B_i). \quad (7)$$

Using the following lemma, a lower bound on P_e is derived.

Lemma 1. $I(B_i, \widehat{B}_i)$ is bounded from above as follows:

$$I(B_i; \widehat{B}_i) \leq I(Y_i^{(1)}; X_i^{(1)}|X_{i-1}^{(1)}) + I(Y_i^{(2)}; X_i^{(2)}|X_{i-1}^{(2)}). \quad (8)$$

Proof: The following chain of inequalities proves (8).

$$\begin{aligned} I(B_i; \widehat{B}_i) &\leq^a I(B_i; B_{i-1}, \widehat{B}_{i-1}, Y_i^{(1)}, Y_i^{(2)}) \quad (9) \\ &\leq I(B_i; B_{i-1}, \widehat{B}_{i-1}, Y_i^{(1)}, Y_i^{(2)}, X_{i-1}^{(1)}, X_{i-1}^{(2)}) \\ &=^b I(B_i; B_{i-1}, Y_i^{(1)}, Y_i^{(2)}, X_{i-1}^{(1)}, X_{i-1}^{(2)}) \\ &=^c I(B_i; Y_i^{(1)}, Y_i^{(2)}|B_{i-1}, X_{i-1}^{(1)}, X_{i-1}^{(2)}) \\ &\leq I(X_i^{(1)}, X_i^{(2)}, B_i; Y_i^{(1)}, Y_i^{(2)}|B_{i-1}, X_{i-1}^{(1)}, X_{i-1}^{(2)}) \\ &\leq I(X_i^{(1)}, X_i^{(2)}, B_i, B_{i-1}; Y_i^{(1)}, Y_i^{(2)}|X_{i-1}^{(1)}, X_{i-1}^{(2)}) \\ &= I(X_i^{(1)}, X_i^{(2)}; Y_i^{(1)}, Y_i^{(2)}|X_{i-1}^{(1)}, X_{i-1}^{(2)}) \\ &\quad + I(B_i, B_{i-1}; Y_i^{(1)}, Y_i^{(2)}|X_{i-1}^{(1)}, X_{i-1}^{(2)}, X_i^{(1)}, X_i^{(2)}) \\ &=^d I(X_i^{(1)}, X_i^{(2)}; Y_i^{(1)}, Y_i^{(2)}|X_{i-1}^{(1)}, X_{i-1}^{(2)}) \\ &= H(Y_i^{(1)}, Y_i^{(2)}|X_{i-1}^{(1)}, X_{i-1}^{(2)}) \\ &\quad - H(Y_i^{(1)}, Y_i^{(2)}|X_{i-1}^{(1)}, X_{i-1}^{(2)}, X_i^{(1)}, X_i^{(2)}) \\ &\leq H(Y_i^{(1)}|X_{i-1}^{(1)}, X_{i-1}^{(2)}) + H(Y_i^{(2)}|X_{i-1}^{(1)}, X_{i-1}^{(2)}) \\ &\quad - H(Y_i^{(1)}|X_{i-1}^{(1)}, X_i^{(1)}) - H(Y_i^{(2)}|X_{i-1}^{(2)}, X_i^{(2)}) \\ &= I(Y_i^{(1)}; X_i^{(1)}|X_{i-1}^{(1)}) + I(Y_i^{(2)}; X_i^{(2)}|X_{i-1}^{(2)}). \end{aligned}$$

Inequality (a) holds because $\widehat{B}_i$ is function of $\widehat{B}_{i-1}, Y_i^{(1)}, Y_i^{(2)}$; (b) holds as $\widehat{B}_{i-1}$ does not provide further information about B_i conditioned on $X_{i-1}^{(1)}, X_{i-1}^{(2)}, B_{i-1}$. Equality (c) holds because B_i is independent of previous message bits. (d) holds because of the Markov chain $(B_i, B_{i-1}) - X_i^{(1)}X_i^{(2)}X_{i-1}^{(1)}X_{i-1}^{(2)} - Y_i^{(1)}Y_i^{(2)}$. ■

Using the well-known technique of taking a random index Q uniformly distributed on $\{1, 2, \cdots, k\}$ and independent of previously defined rv's, one can show $P_e = P(\hat{B}_Q \neq B_Q)$, and the statement of lemma 1 for random index Q instead of fixed index i. Considering constraints $0 \leq X_Q^{(j)} \leq r_{max}$ and $\mathbb{E}[X_Q^{(j)}] \leq r_{av}$ using the upper bounds on the discrete Poisson channels derived in [11] if $r_{av}/r_{max} \in [1/3, 1]$ we have:

$$I(X_Q^{(j)}; Y_i^{(j)}|X_{Q-1}^{(j)}) \leq \frac{1}{2}\log_2 P_1r_{max} + \frac{1}{2}\log_2\frac{\pi e}{2} + O_{P_1r_{max}}(1), \quad (10)$$

and if $r_{av}/r_{max} \in (0, 1/3)$

$$\begin{aligned} &I(X_Q^{(j)}; Y_i^{(j)}|X_{Q-1}^{(j)}) \quad (11) \\ &\leq 0.5\log_2 P_1r_{max} - (1 - \frac{r_{av}}{r_{max}})\mu - 0.5\log_2 2\pi e \end{aligned}$$

$$-\log_2 (0.5 - \frac{r_{av}\mu}{r_{max}}) + O_{P_1 r_{max}}(1),$$

where $O_{P_1 r_{max}}(1)$ tends to 0 when $P_1 r_{max}$ tends to infinity and μ is the solution of $r_{av}/r_{max} = \frac{1}{2\mu} - \frac{e^{-\mu}}{\sqrt{\mu\pi}erf(\sqrt{\mu})}$. Denoting the RHS of the upper bound inequality (10) or (11) by G, and using the upper bound in (8) we have,

$$I(B_Q; \widehat{B}_Q) = H(B_Q) - H(B_Q|\widehat{B}_Q) \leq 2G. \quad (12)$$

Using the Fano's inequality, $H(B_Q) = \log_2 |\mathcal{B}|$ and the convexity of entropy function, we obtain:

$$H(P_e) + P_e \log_2 (|\mathcal{B}| - 1) \leq \log_2 |\mathcal{B}| - 2G, \quad (13)$$

where $|\mathcal{B}|$ is the size of the alphabet of variable B_i. This inequality gives a lower bound on the average probability of error. Our analysis also extends to M types of molecules in a straightforward way; it is omitted due to lack of space.

IV. Numerical Results

For numerical evaluations, we have assumed the distance between transmitter and receiver and time slot duration are $d = 16\mu m$ and $t_s = 5.9$ sec. respectively and hence the probabilities of hitting as $P_1 = 0.22$ and $P_2 = 0.04$ (unless explicitly stated otherwise as in the description of two of the curves in Fig. 1) [10]. Also, we have considered $\lambda_0 = 20$.

Fig. 1(Top) shows the plots of the probability of error versus the average transmission power (diffusion rate) per bit for binary and quaternary CSK, MOSK and proposed MCSK modulations. This figure shows that BMCSK substantially outperforms the BMOSK, with two types of molecules being employed in the two schemes. As expected, QMOSK with more complicated transmitter and receivers employing four molecule types, yields a better performance compared to the proposed quaternary MCSK (QMCSK) that uses only two molecules types. The same results hold for the radio communication as well, where M-ary FSK substantially outperforms M-ary ASK for $M \geq 4$, at the cost of higher complexity. Also, Fig. 1(Top) shows that MCSK outperforms CSK scheme in binary and higher levels. Further this improvement becomes more significant as we increase the hitting probability P_2. Increasing P_2 results in more interference from the previous symbol, thus degrading the CSK performance. Generally speaking, as the decoding of the current symbol in the MCSK is independent of both the previous transmitted and decoded symbols, this scheme outperforms the CSK and MOSK schemes in a fair comparison. Fig. 1(Bottom) compares the probability of error of the proposed BMCSK and the lower bound derived in (13) versus the maximum transmission power. In the BMCSK, $r_{av}/r_{max} = 0.5$ and 2 molecule types are used. For a fair comparison, the lower bound has been computed for $M = 2$, $r_{av}/r_{max} = 0.5$ and $|\mathcal{B}| = 2$. It is observed that the gap between the lower bound and the proposed scheme increases rapidly. To see how the lower bound changes with increasing $|\mathcal{B}|$, the lower bound has been also plotted for $|\mathcal{B}| = 4, 8, 16$ and $M = 2$.

V. Conclusion

In this letter, a new molecular modulation scheme is proposed and its performance have been evaluated along with the performance of the previously proposed schemes, based on the introduced propagation model. Also, a lower bound on the error probability of a practical set of encoders and decoders has been derived. The proposed scheme is shown to outperform the previously introduced schemes. This is due to the fact that the decoding of the current symbol in the proposed scheme is independent of the previously transmitted and decoded symbols. However, its error exponent is larger than our lower bound, suggesting room for further improvement.

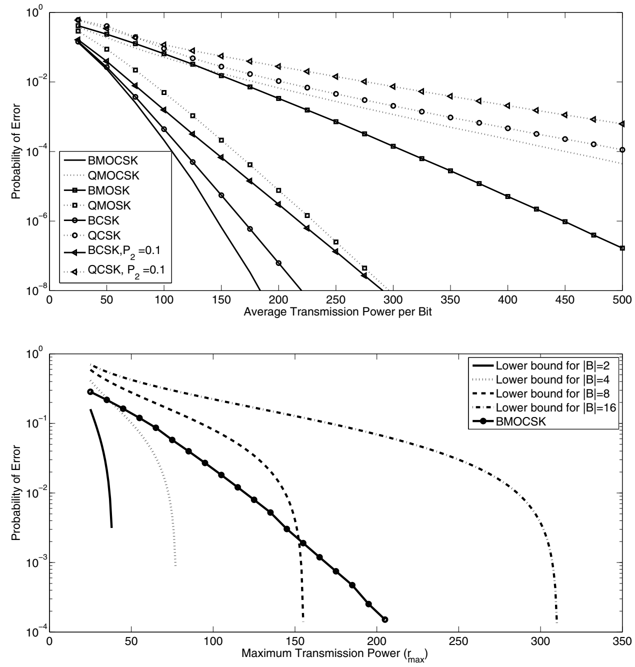

Fig. 1. Top: Average probability of error versus the average transmission power per bit. Bottom: Probability of error of the prposed QMCSK and the lower bound versus the maximum transmission power.

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