An Efficient MIMO Detection Algorithm Employed in Imperfect Noise Estimation

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Abstract: - An efficient multiple-input multiple-output (MIMO) detection (MD) algorithm includes novel, low-complexity, near-optimal and robust scheme is proposed in wireless communications when imperfect noise estimation is considered. By using MIMO technique, capacity increases proportionally as the number of antennas is increased, but the introduced inter-antenna interference (IAI) degrades system performance. To better mitigate IAI, we propose a two-stage procedure to achieve maximum likelihood (ML) performance while keeping at acceptable level of computational complexity. A novel two-stage procedure is proposed as follows that is suitable for either in an overdetermined or an underdetermined MIMO system. In an overdetermined system, interference cancellation is first processed at Stage-1 using sorted QR decomposition (SQRD) followed by Stage-2 that performs a genetic algorithm (GA). In terms of computational complexity, this procedure provides three significant advantages: 1) The SQRD scheme provides excellent interference cancellation so as to largely improve initial setting of GA. 2) By using QRD, fitness value evaluation of GA involves less complexity due to reducing the matrix multiplication. 3) In aspect of diversity knowledge, lately decoded sub-streams expect to have lower error probabilities by using SQRD. In this paper, each mutated gene is decoded from the various diversity gains, termed as a diversity mutation (DM) scheme. To achieve the fore-mentioned three significant advantages in an underdetermined system, on the other hand, we propose zero forcing (ZF) assisted SQRD GA-MD (ZF-SQRD GA-MD) to achieve ML performance. Beside, the proposed two-stage detection procedure is quite robust as it does not rely on noise information. Simulation results show that the proposed two-stage detection procedure can achieve a near-ML performance, but at a low-complexity level.

Key-Words: multiple-input multiple-output, inter-antenna interference, maximum likelihood detector, sorted QR decomposition, genetic algorithm, underdetermined.

1 Introduction

In future wireless communications [1]-[3], to make sure a reliable and efficient transmission, the multiple-input multiple-output (MIMO) technique is often employed [4]-[5]. However, MIMO technique calls for a reliable data detection scheme to mitigate the introduced inter-antenna interference (IAI) caused by the mutual interference between the different transmitting antennas. Moreover, detection complexity becomes an issue especially at detector when the number of employed antennas and/or modulation order is increased. In this study, an efficient MIMO detection (MD) algorithm includes novel, low-complexity, near-optimal and robust scheme is proposed in wireless communications when imperfect noise estimation is considered.

To reduce IAI, the maximum likelihood (ML) detector [6] can achieve remarkable performance; however, it suffers from high computational complexity in practice especially when we intend to improve transmission capacity by increasing the number of antennas. Various near-optimal MIMO detection (MD) techniques have been proposed in open literatures including those based on zero forcing (ZF) [7], minimum mean-squared-error (MMSE) [7], successive interference cancellation (SIC) [8], parallel interference cancellation (PIC) [9] and ordered SIC (OSIC) [10]-[11]. Unfortunately, they all can not approach performance of an ML detector. To achieve the ML performance, sphere decoder (SD) [12]-[20] has been investigated by using reliable radius. However, it relies heavily on the accuracy of noise power estimation [13]-[14]. In practical outdoor environments, however, noise power estimation

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may be error-prone, leading to complexity increase in SD when inaccurate radius is estimated. As a result, an excessive complexity is required for cases that the initial radius is over-estimated [16]. If the initial radius is under-estimated, on the other hand, SD might choose to restart the search procedure again by gradually increasing radius or terminate the search procedure. As such, SD always cannot guarantee optimal performance. To enhance robustness without utilizing noise information [21]-[30], Jiang, Ng and Hanzo [27] give contributions to propose a two-stage procedure that employs a genetic algorithm (GA) aided MMSE MD (MMSE GA-MD) to achieve ML performance. However, MMSE GA-MD requires both complicated full matrix inversion [31] for inherent "MMSE" operation and costly full matrix multiplication for fitness value evaluation in GA. In this paper, we propose a novel two-stage procedure that outperforms conventional detectors at quite low complexity as follows.

When the number of receiving antennas (*M*) is larger than or equal to the number of transmitting antennas (*N*) (for overdetermined MIMO system), Stage-1 performs interference cancellation using sorted QR decomposition (SQRD) followed by Stage-2 that performs GA to further refine the accuracy of all data substreams [32]-[34]. In terms of computational complexity, this procedure provides three significant advantages: 1) The SQRD scheme provides excellent interference cancellation so as to largely improve initial setting of GA [23], [30]. 2) By using QRD, fitness value evaluation of GA involves less complexity due to reducing matrix multiplication [35]-[37]. 3) In aspect of diversity knowledge [32], lately detected sub-streams tend to have lower error probabilities by using SQRD. In this paper, each mutated gene [38] is decoded from the various diversity gains, termed as a diversity mutation (DM) scheme.

With $N > M$ (for underdetermined MIMO system), the SQRD detector fails because the MIMO channel matrix is not in full column rank. To achieve the fore-mentioned three significant advantages, we propose a ZF detector assisted SQRD (ZF-SQRD) to realize the OSIC scheme. Based on column-reordering strategy in ZF-SQRD, the ZF detector is employed in Stage-1 to detect partial transmitted signals. By successively nulling the interference of the previously detected signal in the followed SQRD detection procedure, the remainder of the transmitted signals can be well detected. At the end of Stage-1, all the detected signals will be treated as chromosome for initial setting in GA-MD of Stage-2. The two-stage procedure is called ZF-SQRD GA-MD in this paper. Extensive simulations show that, at the same level of bit error rate performance, the proposed two-stage procedure can largely save the required computational complexity comparing to other existing schemes when inaccurate noise power estimation is employed [35]-[37].

This paper is organized as follows. In Section 2, conventional GA-MD consists of initial population, fitness value evaluation and mutation is depicted. In Section 3, the proposed QR-based GA-MD consists of initial population, fitness value evaluation and mutation is developed. In Section 4, we analyze the computational complexity of the GA-based detectors in multiplications. In Section 5, we conduct computer simulation to confirm the effectiveness of the proposed algorithms. Finally, we conclude the contributions in this paper and suggest future work in Section 6. The proposed algorithm is a convex optimization problem that is relegated to the appendix.

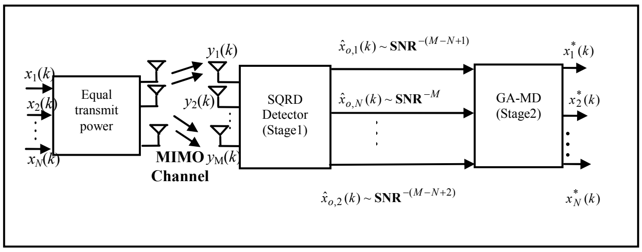


Fig. 1. The proposed SQRD GA-MD for interference cancellation and performance optimization based on the sorted QR decomposition technique when $M \geq N$ (assume the detected layer is from N to 1).

2 Conventional detection in MIMO system

In this section, we will introduce several conventional MIMO detectors as follows: A) ML B) conventional MD C) SQRD and D) sphere decoder (SD).

2.1 ML detector in MIMO System

We consider a communication system with *N* transmitting and *M* receiving antennas ($M \geq N$) over the MIMO channel. The sampled basedband received signals are given by [9]

$$\mathbf{y}(k) = \mathbf{H}(k)\mathbf{x}(k) + \mathbf{v}(k), \tag{1}$$

where $\mathbf{y}(k) \sim C^{M\times 1}$ is the received signal vector, $\mathbf{x}(k) \sim C^{N\times 1}$ is the transmitted signal vector and $\mathbf{H}(k) \sim C^{M\times N}$ is the MIMO channel matrix and the noise vector $\mathbf{v}(k) \sim C^{M\times 1}$ has an *i.i.d.* complex Gaussian entries and noise power is σ_v^2 . Consider optimization problem under the assumption of equally probable transmitted symbols, the ML detection with the additive white Gaussian noise (AWGN) channel model is given as [6]-[7], [35]-[37]:

$$\begin{aligned}\mathbf{x}^*_{\mathrm{ML}}(k) &= \arg\max_{\mathbf{x}(k)} p(\mathbf{x}(k) \mid \mathbf{y}(k)) \\ &= \arg\max_{\mathbf{x}(k)} p(\mathbf{y}(k) \mid \mathbf{x}(k)), \qquad (2)\end{aligned}$$

where $p(\mathbf{y}(k) \mid \mathbf{x}(k))$ is the conditional probability as

$$p(\mathbf{y}(k) \mid \mathbf{x}(k)) = \frac{1}{(2\pi\sigma_v^2)^N} \exp\left(-\frac{\|\mathbf{y}(k) - \mathbf{H}\mathbf{x}(k)\|^2}{2\sigma_v^2} \right), \qquad (3)$$

and therefore maximization of (3) equals the minimization of $\|\mathbf{y}(k) - \mathbf{H}\mathbf{x}(k)\|^2$, the ML estimation can be denoted as

$$\mathbf{x}^*_{\mathrm{ML}}(k) = \arg\min_{\mathbf{x}(k)\in C^{N\times 1}} \|\mathbf{y}(k) - \mathbf{H}\mathbf{x}(k)\|^2 . \qquad (4)$$

where $\mathbf{x}^*_{\mathrm{ML}}(k)$ is the optimum decision of the ML detector invoking exhaustive search for all possible symbol vectors, especially in a large solution space.

2.2 Conventional MD

To avoid the ML complexity, we will introduce several detectors when low-complexity is considered as follows:

1) GA-MD: GA-MD has been introduced in [35]-[37], where the analysis was based on an MIMO channel given as

$$\mathbf{x}^*_{\mathrm{GA}}(k) = \arg\min_{\mathbf{x}(k)\in\Omega} \|\mathbf{y}(k) - \mathbf{H}\mathbf{x}(k)\|^2 , \qquad (5)$$

where $\mathbf{x}^*_{\mathrm{GA}}(k)$ is the detected signal vector of GA and Ω denotes the feasible set containing the possible symbol vector $\mathbf{x}(k)$ in the evolution of GA. The conventional GA evaluates potential solutions to solve an optimization problem in terms of population, selection, mutation, and crossover. For fitness value evaluation, the full MIMO channel matrix (**H**) of (5) is used for multiplying possible candidates to obtain the fitness values given as [21]-[30]

$$S(\mathbf{x}_i(k)) = \|\mathbf{y}(k) - \mathbf{H}(k)\mathbf{x}_i(k)\|^2 , \qquad (6)$$

where $S(\mathbf{x}_i(k))$ is the fitness value (score) at the i^{th} candidate $\mathbf{x}_i(k)$.

2) ZF MD: This ZF detector invokes the inverse operation [27], [31] which estimated signal is given by

$$\tilde{\mathbf{x}}_{\mathrm{ZF}}(k) = (\mathbf{H}^H(k)\mathbf{H}(k))^{-1}\mathbf{H}^H(k), \qquad (7)$$

where $(\cdot)^{-1}$ is the inverse operation.

3) ZF-OSIC MD: In this detector, the ordered SIC algorithm is incorporated to the ZF detector, in which the optimal detection order at each layer is determined by the associated channel gain [7]-[10].
4) ZF GA-MD: In this detector, a two-stage procedure involving ZF detection and GA-MD is employed [6]. The ZF detector is executed as a pre-processor for a better initial point to improve GA-MD evolution. Furthermore, in this paper, considering the low-complexity detector via QR-based detection, we will introduce the SQRD detector, SD detector and proposed GA-MD in next.

2.3 SQRD detector in the MIMO System

To realize the OSIC scheme under considering the low complexity in Stage-1, in Fig. 1, we introduce the SQRD detector which is the QR-based successive cancellation detector with an optimal ordered detection via (1) as follows

$$\begin{aligned}\mathbf{y}(k) &= \mathbf{H}(k)\mathbf{x}(k) + \mathbf{v}(k) \\ &= \mathbf{H}(k)\mathbf{F}(k)\mathbf{F}^{-1}(k)\mathbf{x}(k) + \mathbf{v}(k)\end{aligned}$$

$$= \mathbf{H}(k)\mathbf{F}(k)\mathbf{x}^{o}(k) + \mathbf{v}(k), \tag{8}$$

where $\mathbf{x}^{o}(k) = \mathbf{F}^{-1}(k)\mathbf{x}(k)$ is the re-ordering signal vector with inverse matrix $\mathbf{F}^{-1}(k)$, and $\mathbf{F}(k)$ is the permutation matrix [32]-[34] that involves re-ordering the sub-streams given by

$$\mathbf{f}_i = \underset{l=1,\ldots,N}{\arg\min}\left\|\mathbf{h}_l\right\|^2,\ \ i = 1,2,\ldots,N\,, \tag{9}$$

where $\mathbf{F} = [\mathbf{f}_1, \mathbf{f}_2,\ldots, \mathbf{f}_N]$ is achieved by minimizing the norm of the column of the channel from left to right. Therefore, the $M\times N$ MIMO channel matrix involves the re-ordering method in (9) where the SQRD method can be expressed as follows [32]:

$$\mathbf{HF} = [\mathbf{Q}_1, \mathbf{Q}_2]\begin{bmatrix}\mathbf{R}\\ \mathbf{0}\end{bmatrix} = \mathbf{QR}, \tag{10}$$

where $\mathbf{Q} = [\mathbf{Q}_1 \in C^{N\times N}, \mathbf{Q}_2 \in C^{N\times(M-N)}]$ is an $M\times N$ unitary matrix so $\mathbf{Q}^{H}\mathbf{Q} = \mathbf{I}$ and $\mathbf{R}$ is an $N\times N$ upper triangular matrix as [32]

$$\mathbf{R} = \begin{bmatrix} r_{1,1} & r_{1,2} & \cdots & r_{1,N} \\ 0 & r_{2,2} & \cdots & r_{2,N} \\ \vdots & \vdots & \cdots & \vdots \\ 0 & \cdots & 0 & r_{N,N} \end{bmatrix} \in C^{N\times N}, \tag{11}$$

where $r_{N,N}$ achieves the largest signal-to-noise ratio (SNR) in the lowest layer (layer N) and the detected step is from $r_{N,N}$ to $r_{1,1}$ [32]. By pre-multiplying (1) with $\mathbf{Q}^{H}(k)$, the modified received signal vector is given by

$$\mathbf{z}(k) = \mathbf{Q}^{H}(k)\mathbf{y}(k) = \mathbf{R}(k)\mathbf{x}^{o}(k) + \tilde{\mathbf{v}}(k), \tag{12}$$

where $\tilde{\mathbf{v}}(k)$ is given by

$$\tilde{\mathbf{v}}(k) = \mathbf{Q}^{H}(k)\,\mathbf{v}(k). \tag{13}$$

Because $\mathbf{Q}(k)$ is a unitary matrix, the statistics of the noise term $\mathbf{Q}^{H}(k)\mathbf{v}(k)$ remain unchanged and noise power is $\sigma^2_{\tilde{v}}(k)$. Then, the modified received signal at the l^{th} layer of the SQRD detector can be written as [35]-[37]

$$z_l(k) = r_{l,l}(k)x^{o}_{l}(k) + \tilde{v}(k) + \text{interference} + x^{o}_{l+1}(k), x^{o}_{l+2}(k),\ldots, x^{o}_{N}(k). \tag{14}$$

Assuming the decisions of $x_i(k)$ for $i = l+1,\ldots, N$ are correct, so their effects can be perfectly removed from the l^{th} layer signal $z_l(k)$, we have the cleaned received signal at the l^{th} layer:

$$\tilde{z}_l(k) = r_{l,l}(k)x^{o}_{l}(k) + \tilde{v}(k)\,. \tag{15}$$

Then, the symbol decision at the l^{th} layer is given by

$$\hat{x}_l(k) = Decision(\tilde{z}_l(k)), \tag{16}$$

where l is from 1 to N and $\hat{\mathbf{x}}^{o}(k) = [\hat{x}_{o,1}(k), \hat{x}_{o,2}(k),\ldots,\hat{x}_{o,N}(k)]$ is the symbol decision vector and $Decision(\cdot)$ stands for mapping to the nearest symbol in the symbol constellation. Therefore, the SQRD detector with (8)-(16) is proposed in Stage-1 of hybrid GA-MD [35]-[37]. Especially, the unsorted QR (or called QR) is similar to SQRD when the permutation matrix of (8) is the identity matrix.

2.4 Sphere decoder (SD)

To compare computational complexity between SD and GA-based detector; we thus introduce SD with desired radius involving the accuracy of the noise power estimation to achieve the near-ML performance as follows [16]. We consider SD with a "list" of candidate symbol vectors, and find the minimum in the list instead of the exhausted search. Consider $M \geq N$ in the QR factorization, the solution of (4) satisfies the following bound as [12]-[16]

$$\left\|\mathbf{y}(k) - \mathbf{H}(k)\mathbf{x}(k)\right\|^2 = (\hat{\mathbf{x}}_{\mathrm{ZF}}(k) - \mathbf{x}(k))^{H}\,\mathbf{H}^{H}(k)\mathbf{H}(k)(\hat{\mathbf{x}}_{\mathrm{ZF}}(k) - \mathbf{x}(k)) + \hat{\mathbf{x}}^{H}_{\mathrm{ZF}}(k)(\mathbf{I} - \mathbf{H}(\mathbf{H}^{H}\mathbf{H})\mathbf{H}^{H})\hat{\mathbf{x}}_{\mathrm{ZF}}$$

$$\cong (\hat{\mathbf{x}}_{\mathrm{ZF}}(k) - \mathbf{x}(k))^{H}\,\mathbf{H}(k)^{H}\,\mathbf{H}(k)(\hat{\mathbf{x}}_{\mathrm{ZF}}(k) - \mathbf{x}(k))$$

$$= (\hat{\mathbf{x}}_{\mathrm{ZF}}(k) - \mathbf{x}(k))^H \mathbf{R}(k)^H \mathbf{R}(k)(\hat{\mathbf{x}}_{\mathrm{ZF}}(k) - \mathbf{x}(k)) \le d^2 , \tag{17}$$

where *d* is the desired radius given as [13]

$$d^2 = \alpha M \sigma_v^2 , \tag{18}$$

where $\alpha \ge 1$ is a constant factor. For SD, the search process for seeking candidate symbols can be written as [13]-[14]

$$\sum_{i=1}^{N}\left(r_{i,i}^2(k)\left|\hat{x}_{\mathrm{ZF},i}(k) - x_i(k)\right|^2 + \sum_{j=i+1}^{N} r_{i,j}^2(k)\left|\hat{x}_{\mathrm{ZF},i}(k) - x_i(k)\right|^2 \right) \le d^2 . \tag{19}$$

Specifically, based on (19), we start from $i = N$ and accumulate the distance, layer by layer. If the distance of one branch is smaller than the desired radius, we continue to calculate the branch distance extending from this branch. If the distance is larger than the desired radius, we prune this branch. In the QAM transmission, we can transform the original complex-value problem to the real-value problem with $2 \cdot N$ dimensions as

$$\underset{\mathbf{x}(k)\in C^{N\times 1}}{\arg\min}\ (\dot{\mathbf{x}}_{\mathrm{ZF}}(k) - \dot{\mathbf{x}}(k))^H \dot{\mathbf{R}}(k)^H \dot{\mathbf{R}}(k)(\dot{\mathbf{x}}_{\mathrm{ZF}}(k) - \dot{\mathbf{x}}(k)) , \tag{20}$$

where

$$\dot{\mathbf{x}}_{\mathrm{ZF}}(k) = \left[\mathrm{Re}\{\hat{\mathbf{x}}_{\mathrm{ZF}}(k)\} \quad \mathrm{Im}\{\hat{\mathbf{x}}_{\mathrm{ZF}}(k)\}\right]^T , \tag{21}$$

$$\dot{\mathbf{x}}(k) = \left[\mathrm{Re}\{\mathbf{x}(k)\} \quad \mathrm{Im}\{\mathbf{x}(k)\}\right]^T , \tag{22}$$

$$\dot{\mathbf{R}}(k) = \begin{bmatrix} \mathrm{Re}\{\mathbf{R}(k)\} & -\mathrm{Im}\{\mathbf{R}(k)\} \\ \mathrm{Im}\{\mathbf{R}(k)\} & \mathrm{Re}\{\mathbf{R}(k)\} \end{bmatrix} . \tag{23}$$

With $N > M$, SD fails because **H** is not full column rank and thus cannot be decoded by the QR factorization [17]-[19]. To solve this underdetermined MIMO system in generalized sphere decoding (GSD), the augment **H** is extended to full column rank as [19]

$$\widetilde{\mathbf{H}}_{N\times N} = \begin{bmatrix} a\mathbf{I}_{N-M} & \mathbf{0}_{(N-M)\times M} \\ \multicolumn{2}{c}{\mathbf{H}} \end{bmatrix} , \tag{24}$$

where *a* is either a small real of complex value with various modulation schemes and **I** is the identity matrix. Therefore, the pseudo received vector is given as [19]

$$\begin{bmatrix} \mathbf{0}_{(N-M)\times 1} \\ \mathbf{y}_{M\times 1}(k) \end{bmatrix} = \widetilde{\mathbf{H}}(k)\mathbf{x}(k) + \widetilde{\mathbf{v}}(k) = \begin{bmatrix} ax_1(k) \\ \vdots \\ ax_{N-M}(k) \\ \sum_{i=1}^{N} h_{1,i}(k)x_i(k) + v_1(k) \\ \vdots \\ \sum_{i=1}^{N} h_{M,i}(k)x_i(k) + v_N(k) \end{bmatrix} + \begin{bmatrix} -ax_1(k) \\ \vdots \\ -ax_{N-M}(k) \\ v_1(k) \\ \vdots \\ v_M(k) \end{bmatrix} . \tag{25}$$

With (25), $\widetilde{\mathbf{H}}$ is full column rank and therefore GSD can be employed in standard QR factorization algorithms at (19). Further, the desired radius of GSD is given as [19]

$$d^2 = \alpha(\phi(N - M)|a|^2 + M\sigma_v^2) , \tag{26}$$

where ϕ is a constant value for various modulation orders. Like SQRD in this paper, we consider SD and GSD involve column-reordering of (9) in the following simulations, respectively.

3 The proposed efficient near-ML algorithms in MIMO system

In this section, a novel, low-complexity, near-optimal and robust SQRD GA-MD is proposed to achieve a near-ML performance as follows: A) SQRD aided GA-MD (SQRD GA-MD) is proposed to realize the ML performance when $M \ge N$. B) ZF-SQRD aided GA-MD (ZF-SQRD GA-MD) is proposed to realize the ML performance when $N > M$. Finally, the proposed pseudo-procedure will be presented.

3.1 Proposed SQRD GA-MD for $M \ge N$

In this subsection, with $M \ge N$, the proposed SQRD GA-MD has three significant advantages for initial population, fitness value evaluation and mutation. First, for the initial population, GA is employed to refine the accuracy of the data substreams (by removing the residual IAI) after the SQRD detection. Therefore, according to (5) and (12), the optimization problem can be expressed as

$$\mathbf{x}_{\mathrm{o,GA}}^{*}(k)=\underset{\mathbf{x}^{o}(k)\in\Omega}{\arg\min}\left\|\mathbf{z}(k)-\mathbf{R}(k)\mathbf{x}^{o}(k)\right\|^{2},\ M\geq N\cdot \tag{27}$$

where $\mathbf{x}_{\mathrm{o,GA}}^{*}(k)$ is the detected signal vector in the evolution of GA and shows that (27) is a convex optimization problem in appendix. Obviously, the feasible set in (5) and (27) is a critical issue significantly influencing the complexity of GA-MD. The feasible set which is too large leads to the evolution of GA containing a very high number of hypotheses and therefore detection complexity. Selecting a feasible set is too small that may involve a less diverse search in the GA evolution. The aim of this work is to show, for this two-stage procedure, which QR-based MDs (SQRD, QR and ZF-SQRD) of the MIMO channel may be equivalently used. Note, using QR-based MDs may be advantageous for carrying transmitted signals information in the initial setting of GA-MD. In this paper, we examine the initial setting criteria in the process of GA, and derive an approximation to (27) as

$$\mathbf{x}_{\mathrm{o,GA}}^{*}(k)=\underset{\mathbf{x}^{o}(k)\in\overline{\Omega},\overline{\Omega}\subset\Omega}{\arg\min}\left\|\mathbf{z}(k)-\mathbf{R}(k)\mathbf{x}^{o}(k)\right\|^{2},\ M\geq N\cdot \tag{28}$$

In the above, $\overline{\Omega}$ denotes a set involving information of transmitted signals generated by the detected signals with the SQRD (QR and ZF-SQRD) detector to reduce the complexity of the search process in (28). Then, the detected signals of (28) will be processed by the reorder strategy to approach the original transmitted signals which can be given as

$$\mathbf{x}_{\mathrm{GA}}^{*}(k)=\mathbf{F}(k)\mathbf{x}_{\mathrm{o,GA}}^{*}(k)\,. \tag{29}$$

Also, for the initial setting of the SQRD (ZF, QR and ZF-SQRD) GA-MD, the transmitted information about any given symbol $\hat{x}_l(k)$ is possibly contained in the l^{th} layer of the candidate $\hat{\mathbf{x}}(k)$. To achieve this, in this paper, this initial setting of (28) means transmitted signals information can be represented as

$$G_d^l(k)=[b_1^l(k),b_2^l(k),\ldots,b_D^l(k)]\ \mathit{or}\ (2^{d-1})_2,\ b(k)\in\{0,1\}\ \text{and}\ d=1,2,\ldots,D, \tag{30}$$

where $G_d^l(k)$ is a bit string of symbol of the l^{th} layer that is modified by the inverse at the d^{th} position, "*or*" is an operator in the Boolean arithmetic, $(\cdot)_2$ is a binary number system and D denotes the modulation order. Specifically, the proposed population for the initial setting in the process of GA that creation can be depicted as

$$\begin{gathered}
\hat{\mathbf{x}}_0(k)=[\hat{x}_1(k),\hat{x}_2(k),\ldots,\hat{x}_N(k)]\\
\hat{\mathbf{x}}_{1,d}(k)=[\mathrm{mod}(G_d^1(k)),\hat{x}_2(k),\ldots,\hat{x}_N(k)]\\
\hat{\mathbf{x}}_{2,d}(k)=[\hat{x}_1(k),\mathrm{mod}(G_d^2(k)),\ldots,\hat{x}_N(k)]\\
\vdots\\
\hat{\mathbf{x}}_{N,d}(k)=[\hat{x}_1(k),\hat{x}_2(k)\ldots,\mathrm{mod}(G_d^N(k))]\\
\hat{\mathbf{x}}_{N+1,d}(k)=[\mathrm{mod}(G_d^1(k)),\mathrm{mod}(G_d^2(k)),\ldots,\hat{x}_N(k)]\\
\vdots
\end{gathered} \tag{31}$$

where $\{\hat{\mathbf{x}}_0(k),\hat{\mathbf{x}}_{1,d}(k),\ldots,\hat{\mathbf{x}}_{1,d}(k),\hat{\mathbf{x}}_{2,d}(k),\ldots,\hat{\mathbf{x}}_{2,d}(k),\ldots,\hat{\mathbf{x}}_{N,1}(k),\ldots\hat{\mathbf{x}}_{N,d}(k),\hat{\mathbf{x}}_{N+1,d}(k),\ldots\}\subset\overline{\Omega}$ and $\mathrm{mod}(\cdot)$ is the modulation operator converting bit strings to a symbol is proposed set for the initial population by (31). Thus, with the aid of transmitted signals information, better initial populations are produced to enhance the performance of GA's convergence, this is called the bit flipping (BF) strategy in this paper.

Second, to analyze the low computational complexity of the fitness value evaluation, in Fig. 2, we assume the number of transmit antennas is four and the number of receive antennas is five. Based on using QR decomposition (10), the figure describes the MIMO channel matrix which has been reduced to a triangle matrix (**R**), which reduces the computational complexity of the fitness value evaluation for (6) in the evolution of GA [35]-[37]. Thus, the computational complexity of (27) and (28) are much less than (6) due to reducing the matrix multiplication, which involves a lot of zeros. In this analysis, a triangular matrix (**R**) is used for multiplying the possible candidates to obtain the fitness values given as

$$S(\mathbf{x}_i^o(k)) = \left\| \mathbf{z}(k) - \mathbf{R}(k)\mathbf{x}_i^o(k) \right\|^2, \tag{32}$$

where $S(\mathbf{x}_i^o(k))$ is the fitness value at the i^{th} candidate $\mathbf{x}_i^o(k)$.

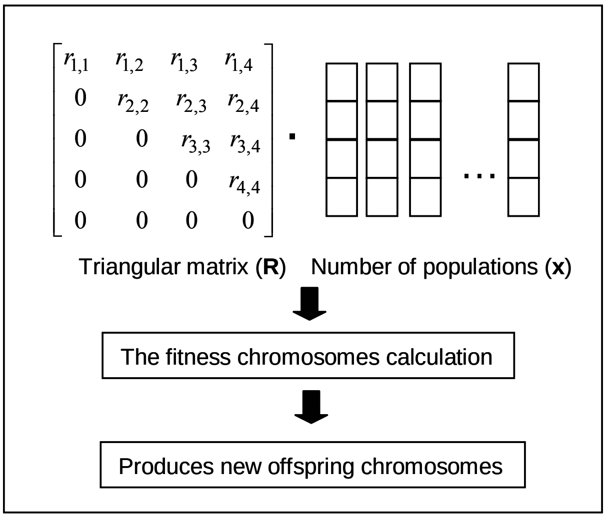


Fig. 2. Matrix multiplication reduction for fitness value evaluation in GA-MD with the triangle matrix operation.

Third, to derive the reliable mutation scheme in QR-based GA-MDs, the diversity gain is derived from QR-based detection as follows. Based on (16), the pairwise error probability (PEP) of the l^{th} layer $P(x_l(k) \to \hat{x}_l(k))$ is the probability that the decoder decides as its output $\hat{x}_l(k)$, when the transmitted symbol of the l^{th} layer was in fact $x_l(k)$. This scenario occurs if

$$\left|\tilde{z}_l(k) - r_{l,l}x_l(k)\right|^2 \ge \left|\tilde{z}_l(k) - r_{l,l}\hat{x}_l(k)\right|^2, \tag{33}$$

or equivalently, it can be rewritten as

$$\begin{aligned} 2\,\mathrm{Re}\{\tilde{v}_l(k) r_{l,l}(x_l(k)-\hat{x}_l(k))\} &\ge \left|r_{l,l}(x_l(k)-\hat{x}_l(k))\right|^2 \\ &:= d^2(x_l(k),\hat{x}_l(k)), \end{aligned} \tag{34}$$

For a given **H** (or equivalently the matrix **R**), the left hand side of (34) is a Gaussian random variable with zero mean. As a result, applying the Chernoff bound ($Q(x) \le \frac{1}{2}e^{-x/2}, x \ge 0$), the conditional PEP for a given **H** is upper-bounded by

$$\begin{aligned} P(x_l(k) \to \hat{x}_l(k)\,|\,\mathbf{H}) &\le \frac{1}{2}\exp(-d^2(x_l(k),\hat{x}_l(k))\frac{E_s}{4N_0}) \\ &\le \exp(-|r_{l,l}|^2 |x_l(k)-\hat{x}_l(k)|^2 \frac{E_s}{4N_0}), \end{aligned} \tag{35}$$

where E_s is the energy per symbol at each transmit antenna, $\frac{E_s}{N_0}$ is the average symbol energy to noise power spectral density ratio and $|r_{l,l}|^2$ is a sum of $2(M - l)$ Gaussian random variable with zero-mean and variance 0.5. That is, $|r_{l,l}|^2$ is chi-square distribution with $2(M - l)$ degree of freedom which probability density function (PDF) is given by [29]

$$f(t = |r_{l,l}|^2) = \frac{t^{D-1}e^{-t/2}}{2^D\Gamma(D)}, \tag{36}$$

where $\boldsymbol{\Gamma}(D) = (D- 1)!$ is a gamma function and $D = M- l$ is a integer variable. The average PEP can be expressed in term of the moment generating function (MGF) of t which is denoted as $M_t(s)$ and $M_t(s)$ is given by

$$M_t(s) = E_t[\exp(st)] = \int_0^\infty \exp(st) f(t)dt = \frac{1}{(1-2s)^D}. \tag{37}$$

Then, we can obtain the average PEP of (35) via (36) and (37) is given as

$$\begin{aligned} P(x_l(k) \to \hat{x}_l(k)) &:= E_t\{P(x_l(k) \to \hat{x}_l(k))|\mathbf{H}\} \\ &\le E_t\{\exp(-|r_{l,l}|^2 |x_l(k)-\hat{x}_l(k)|^2 \frac{E_s}{4N_0}))\} \\ &= \{1+|x_l(k)-\hat{x}_l(k)|^2 \frac{E_s}{8N_0})\}^{-(M-l)}. \end{aligned} \tag{38}$$

Equation (38) shows that the average PEP of the first layer detection in the SIC process is inversely proportional to the $(M - N + 1)^{\text{th}}$ power of SNR, and the M^{th} power SNR for last layer. This implies that different layer has different diversity order in the SIC detection, ranging from $M - N + 1$ to M (from the first layer to the last layer), which mean that a diversity order for a later detection stage is more than that for an earlier one. Therefore, the error probability for the l^{th} detected substream can be approximated as [32]

$$P_{e,l}(\mathrm{SNR}) \propto \mathrm{SNR}^{-(M-l+1)}, \quad 1 \le l \le M. \tag{39}$$

Based on (39), in this paper, a mutation scheme based on the diversity technique is proposed; it is also called diversity mutation (DM). That is, the proposed mutation rate for each layer ($1 \le l \le M$) can be approximated as

$$P_{m,l} \cong \kappa \cdot P_{e,l}(\text{SNR}), \tag{40}$$

where $\kappa \ge 0$ is a real constant to realize a suitable mutation rate. Equation (40) shows a different gene (layer) that has a different mutation rate in the GA processes.

3.2 Proposed ZF-SQRD GA-MD for $N > M$

Consider $N > M$, the SQRD detector fails because **H** is not full column rank. To achieve the fore-mentioned three significant advantages in this underdetermined system, we propose the ZF detector assisted SQRD (ZF-SQRD) to realize the OSIC operation. Based on column-reordering strategy in ZF-SQRD, the ZF detector is employed in Stage-1 to estimate transmitted signals from $x_M(k)$ to $x_N(k)$. Then, by applying these estimated signals to realize OSIC, the interference of these signals is subsequently nulled and therefore the remainder transmitted signals are estimated. After Stage-1, to achieve the ML performance, these estimated signals will be a chromosome of initial setting in GA-MD of Stage-2; it is called ZF-SQRD GA-MD in Fig. 3. In this ZF-SQRD GA-MD, there are three processes are described as follows. First, by applying the SQRD operation, (1) can be expressed as

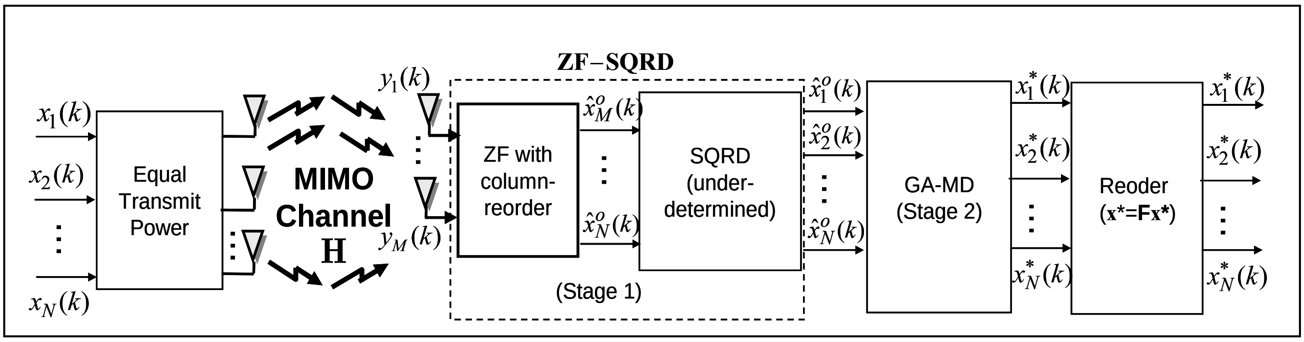


Fig. 3. The proposed ZF-SQRD GA-MD for achieving the ML performance when $N > M$.

$$\begin{aligned}\mathbf{z}(k) &= \mathbf{Q}^H(k)\mathbf{H}(k)\mathbf{F}(k)\mathbf{F}^{-1}(k)\mathbf{x}(k) + \mathbf{Q}^H(k)\mathbf{v}(k)\\ &= \mathbf{Q}^H(k)\mathbf{Q}(k)\mathbf{R}(k)\mathbf{x}^o(k) + \tilde{\mathbf{v}}(k)\\ &= \mathbf{R}(k)\mathbf{x}^o(k) + \tilde{\mathbf{v}}(k),\end{aligned} \tag{41}$$

where **R** is an $M \times N$ triangular matrix is given as

$$\mathbf{R} = \begin{bmatrix} r_{1,1} & r_{1,2} & \cdots & \cdots & \cdots & r_{1,N} \\ 0 & r_{2,2} & \cdots & \cdots & \cdots & r_{2,N} \\ \vdots & \vdots & \cdots & \cdots & \cdots & \vdots \\ 0 & \cdots & 0 & r_{M,M} & \cdots & r_{M,N} \end{bmatrix} \in C^{M \times N} \cdot \tag{42}$$

Second, by applying the ZF detector in Stage-1, $\hat{x}_M^o(k),\ldots,\hat{x}_{N-1}^o(k),\hat{x}_N^o(k)$ of the reordering signals can be estimated by (7). Therefore, in Stage-1, the SQRD-based detector realizes the OSIC operation by sequential signal detection can be expressed as

for $i = M - 1 : -1 : 1$

$$\hat{x}_i^o(k) = Decision\left[\frac{\left(z_i(k) - \sum_{j=i+1}^{N} r_{i,j}(k)\hat{x}_j^o(k)\right)}{r_{i,i}(k)}\right] \tag{43}$$

end.

Third, by obtaining $\hat{\mathbf{x}}^o(k) = [\hat{x}_1^o(k),\ldots,\hat{x}_{N-1}^o(k),\hat{x}_N^o(k)]^T$ from Stage-1, these estimated signals can be a chromosome of initial setting of GA-MD of Stage-2. Therefore, in Stage-2, ZF-SQRD GA-MD can be expressed as

$$\mathbf{x}_{\text{GA}}^*(k) = \underset{\mathbf{x}^o(k) \in \overline{\Omega}, \overline{\Omega} \subset \Omega}{\arg\min} \left\| \mathbf{z}(k) - \mathbf{R}(k)\mathbf{x}^o(k) \right\|^2, \quad N > M \cdot \tag{44}$$

With (43), remember the initial setting of (28) in $\overline{\Omega}$ and therefore the optimum solution can be achieved efficiently in (43). Like (29), the detected signals of

(44) will be processed by the reorder strategy to approach original transmitted signals, depicted in Fig. 3.

Finally, based on these contributions, the proposed QR-based GA-MDs consisting of the initial population, selection, fitness value evaluation, crossover, mutation and elitism is described as follows.

1) *Population Initialization*: The population method strongly depends on the initial setting knowledge [21]-[30]. In the proposed two-stage procedure, the single seed chromosome from the output of the SQRD detector (or ZF-SQRD) carries the transmitted signal information. This transmitted signal information will be inserted into the initial population to generate the parent chromosomes for enhancing the evolution of GA. Consider the BF strategy in this paper, the first chromosome is the same as the seed chromosome. The second chromosome randomly changes one gene from the seed chromosome. The third and fourth chromosomes also change one gene from the seed chromosome. In addition, other chromosomes are created randomly when large populations are considered. For example, we have $N = M = 2$, 4-QAM modulation, and the seed chromosome (1, j). Thus, based on the BF strategy, the chromosomes (1, j), (1, –1), (1, 1), (–j, 1) and (j, 1) can be selected to the set in population initialization.

2) *Fitness Value Evaluation*: The fitness value evaluation evaluates the fitness value for each chromosome. The fitness value can be seen as an indication of how well each chromosome adapts to its current environment. Based on these values, the target chromosomes can be identified. In this research, the evaluation of GA is based on (28) and (30) to obtain the fitness value. Then, the GA's task is to find the optimum individual chromosomes using the objective function to yield the high-fitness values [21]-[30].

3) *Selection*: After a fitness value evaluation for each chromosome is obtained, a selection operation is used to select chromosomes from the existing population and to breed the next generation. There are many selection schemes, such as ranking selection, roulette wheel selection, and tournament selection. The ranking method selects chromosomes with the rule of first-rate score [21]. The roulette wheel selection method gives each chromosome a different chosen rate [21]. In contrast, the tournament selection chooses several pairs of chromosomes and selects the better one of each pair. In this paper, the tournament selection for popular parent selection [21] in GA's evolution is used.

4) *Crossover*: Crossover operation combines subparts of two selected parent chromosomes to generate the fitness offsprings containing some parts of both parents' genetic material. In this paper, a single-point crossover with [21] is applied to generate offsprings.

5) *Mutation*: Mutation operation is responsible for the permanent exploration of the new region's divergent space and preventing a population from collapse and degradation [21], [23], [27], [29]. That is, a mutation operation can prevent the population from converging at any local optima. However, the mutation is low that good individuals may loss and the GA performance will approach a random search. In this paper, considering the proposed mutation scheme, each gene is mutated when a randomly generated value is less than the DM, depicted in (33)-(40). For example, we have $N = M = 2$, BPSK modulation, an original individual (layer 1, layer 2) = (1, –1), a random value 0.2, $P_{m,1} = 0.3$, and $P_{m,2} = 0.2$. Then, after mutation operation, we have a new individual (–1, –1) ((1, –1) → (–1, –1)). In addition, when mutation is occurred, the mutating gene can be replaced by the nearest neighboring symbol as the mutation target candidate.

6) *Elitism*: Among the operational characteristics of GA, elitism can reduce the genetic drift by ensuring the best candidate chromosome(s) is included in the next generation [21]. Based on elitism, some chromosome genes may be more important to the final solution obtained by the minimization strategy [25], [27]. This minimization strategy with (31) is similar to the high-fitness (highest-merit) value invoked in the process of elitism [21]-[30]. Further, the proposed pseudo-procedure is shown in Fig. 4.

```
(G.1) Initialize Population: // (Proposal GA-MD)
(G.2)   PopulationPool ← $\hat{\mathbf{x}}_0$ ; // $\hat{\mathbf{x}}_0$ is obtained by (7) or (43).
(G.3)   for $i = 1$ to $Np - 1$ // Np is the number of populations
(G.4)       $\hat{\mathbf{x}}_i$.Gene is modified by the BF strategy via $\hat{\mathbf{x}}_0$.Gene
(G.5)   end
(G.6)     PopulationPool ← $\hat{\mathbf{x}}_1, \dots, \hat{\mathbf{x}}_{Np-1}$
(G.7) while ( iterations < $N_G$) do
(G.8) Fitness Value Evaluation:
(G.9)         for $i$=0 to $Np$-1
```

```
(G.10)         $Score_{\hat{\mathbf{x}}_i} = \|\mathbf{z} - \mathbf{R}\hat{\mathbf{x}}_i\|^2$ with high-fitness value strategy
(G.11)     end
(G.12) Selection:  // Selection of parents through the tournament.
(G.13)   Push the best candidate of PopulationPool into survivalPool.
(G.14)     for i =1 to ⌈Np/2⌉
(G.15)       ChromosomeA=RandomChoose(PopulationPool);
(G.16)       ChromosomeB=RandomChoose(PopulationPool);
(G.17)       if ChromosomeA.Score < ChromosomeB.Score
(G.18)         Push ChromosomeA into WinnerPool;
(G.19)         Push ChromosomeB into LoserPool;
(G.20)       Else
(G.21)         Push ChromosomeA into LoserPool;
(G.22)         Push ChromosomeB into WinnerPool;
(G.23)       end
(G.24)     end
(G.25) Push candidates of ⌈Np/2⌉ with random strategy into RandomPool.
(G.26) Crossover: // CrossPool is the pool of the crossover operation
(G.27)     for i=1 to ⌈Np/2⌉
(G.28)       ParentA=RandomChoose(WinnerPool);
(G.29)       ParentB=RandomChoose(WinnerPool);
(G.30)       CrossPool=singlecrossover(ParentA, ParentB);
(G.31)     end
(G.32) Mutation: // MutPool is the pool of the mutation operation
(G.33)     for i=1 to Np
(G.34)       ChrM is created from (WinnerPool,CrossPool);
(G.35)       MutationRate=random(0,1);  // random(0,1): 0~1
(G.36)       for j=1 to N
(G.37)         if MutationRate < DM rate (or UM rate)
(G.38)           ChrM.Gene is instead of the nearest neighboring symbol
(G.39)         end
(G.40)       end
(G.41)       Push ChrM into MutPool
(G.42)     end // ChrM is the chromoseome in the mutation process
(G.43)   Update MutPool and RandomPool to survivalPool;

(G.44)     for i=1 to size of survivalPool
(G.45)       $S(\mathbf{x}_i) = \|\mathbf{z}-\mathbf{R}\mathbf{x}_i\|^2$;
(G.46)     end
(G.47) Elitism:
(G.48)   Candidates of Np is selected with Eq. (32) by minimum strategy;
(G.49)   Push candidates into PopulationPool and goto (G.12);

(G.50) end while // CanSelPool is the pool of candidate selection

(G.51) $\bar{\mathbf{x}}_{GA}$ is obtained by optimum detection;
```

Fig. 4. Proposed pseudo code for QR-based GA-MDs.

4 Computational Complexity

The computational complexity of the ML detector is $O(D^N \cdot N \cdot M)$ where D is the modulation order. Though the ML detector can achieve remarkable performance, it suffers from high computational complexity in practical implementation. For the implementation and efficiency consideration, computational complexity is a very important factor. Therefore, we address the comparison of computational complexity with various generations in various GA-based detectors, where SNR and populations are fixed, and therefore a requirement of BER can be denoted as

$$P(x_i \neq x_i^* \mid SNR, N_P) \cong Optimum\ \ Bound, \quad i = 1,2,\dots,N, \tag{45}$$

where optimum bound is the ML bound in this paper and N_P is the population size of GA-MD. Then, for simplicity, the computational complexity is only in terms of the number of complex multiplications [39], the computational complexity of ZF GA-MD can be approximated as [23], [31], [39]

$$Comp_{\text{ZF GA-MUD}} \cong N^3 + N^2 \cdot M + N \cdot M^2 + N \cdot M + 1.5 \cdot N_P \cdot N_G^{ZF} \cdot (N \cdot M + M), \tag{46}$$

where N_G^{ZF} is the generation size of ZF GA-MD. In this work, to reduce the complexity of the inversion of the ZF detector, the QR-based detector is employed because this QR complexity is about $O(2M \cdot N^2 - 2N^3/3)$ [40]. In addition, with (6), it increases the computational complexity of fitness value evaluation in (4) and (5) due to the full MIMO channel matrix. Thus, reducing matrix multiplication in (32), the computational complexity of QR GA-MD can be approximated as [23], [30], [40]

$$Comp_{\text{QR GA-MUD}} \cong 2M \cdot N^2 - \frac{2N^3}{3} + N \cdot M + \frac{N \cdot (N+1)}{2} + 1.5 \cdot N_P \cdot N_G^{QR} \cdot \left(\frac{N^2 + N}{2} + M\right), \tag{47}$$

where N_G^{QR} is the generation size of QR GA-MD. Further, the computational complexity of SQRD GA-MD can be approximated as [23], [30], [40]

$$Comp_{\text{SQRD GA-MUD}} \cong 2M \cdot N^2 - \frac{2N^3}{3} + N \cdot M + \frac{N \cdot (N+1)}{2} + N^2 \cdot M + 1.5 \cdot N_P \cdot N_G^{SQRD} \cdot \left(\frac{N^2 + N}{2} + M\right), \tag{48}$$

where N_G^{SQRD} is the generation size of SQRD GA-MD. Based on (45), assuming possible candidates are large enough and N_P is equal in various GA-based detectors, the computational requirements of ZF GA-MD and SQRD GA-MD are compared by the CE ratio:

$$\mu_{\text{SQRD}} = \frac{Comp_{\text{SQRD GA-MUD}}}{Comp_{\text{ZF GA-MUD}}} \cong \frac{N_G^{SQRD}}{N_G^{ZF}} \cdot \frac{\left(\frac{N+1}{2}\right) \cdot N + M}{N \cdot M + M} < 1, \quad \forall N_G^{SQRD} \le N_G^{ZF}. \tag{49}$$

Indeed, N_G^{SQRD} is less than N_G^{ZF} due to good initial setting [35]-[37]. Next, with $N > M$, the computational complexity of ZF-SQRD GA-MD can be approximated as

$$Comp_{\text{ZF-SQRD GA-MUD}} \cong \frac{1}{3} \cdot N^3 + 3 \cdot N^2 \cdot M + N \cdot M^2 + 2 \cdot N \cdot M + \frac{M^2}{2} + \frac{M}{2} + \ldots$$

$$+1.5 \cdot N_P \cdot N_G^{ZF-SQRD} \cdot \left(\frac{M \cdot (2N - M + 1)}{2} + M \right), \qquad (50)$$

where $N_G^{ZF-SQRD}$ denotes the number of generations in ZF-SQRD GA-MD. Based on (45), assuming possible candidates are large enough and N_P is equal in various GA-based detectors, the CE ratio of ZF GA-MD to ZF-SQRD GA-MD when $N > M$ can be approximated as

$$\mu_{\text{ZF-SQRD}} = \frac{Comp_{\text{ZF-SQRD GA-MUD}}}{Comp_{\text{ZF GA-MUD}}}$$

$$\cong \frac{N_G^{ZF-SQRD}}{N_G^{ZF}} \cdot \frac{\left(\frac{2N - M + 1}{2} \right) \cdot M + M}{N \cdot M + M} < 1, \quad \forall N_G^{ZF-SQRD} \leq N_G^{ZF} \cdot \qquad (51)$$

Clearly, with (49) and (51), by applying QR decomposition, proposal QR-based GA-MD is less computational complexity than the conventional ZF GA-MD [35]-[37] because of the matrix multiplication reduction and less generations.

TABLE I.

SIMULATIONS USING OF VARIOUS PARAMETER TECHNIQUES

Parameter	*Type or values*
GA	
Stage-1	ZF, QR and SQRD
Comparison	Symbol vector
Population creation	Bit flipping (BF)
Fitness evaluation	Minimum value criteria
Selection	Tournament
Crossover	Single-point
Mutation	UM and DM
MIMO system	
Channel impulse response (CIR)	Complex Gaussian channel
Modulation consideration	BPSK and 16QAM
Number of antenna issues	M N or $N > M$

5 Simulation Result

In this section, assuming perfect channel state information (CSI) is given at receiver, computer simulation results are presented to characterize the BER performance of the various detectors described in [35]-[37]. In this MIMO system [41]-[43], the channel coefficient is obtained from the transmitting antenna n ($n = 1, 2, \ldots, N$) to the receiving antenna m ($m = 1, 2, \ldots, M$) as

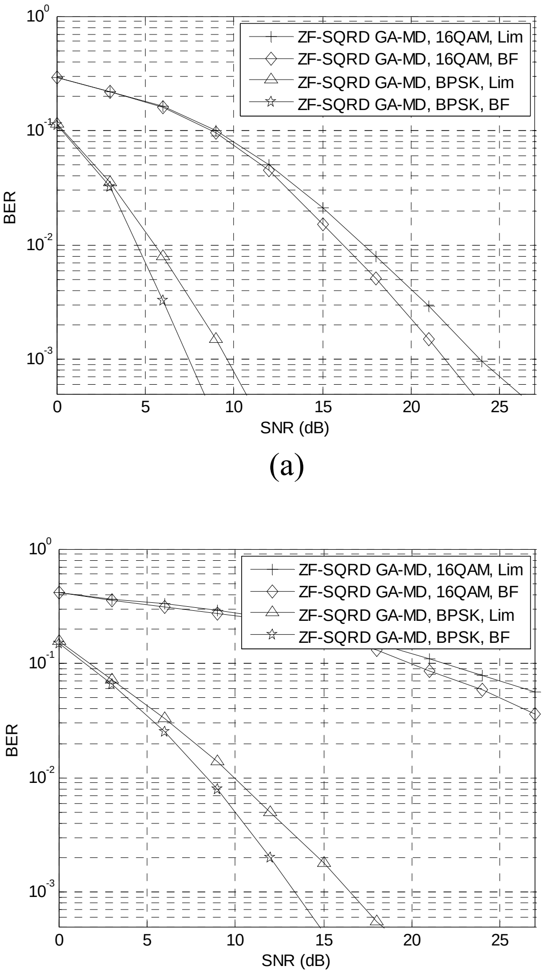
$$h_{m,n}(k) = h_R(k) + jh_I(k), \qquad (52)$$

where $h_R(k)$ and $h_I(k)$ are complex Gaussian random variables with zero mean representing the real part and the image part, respectively. For the GA's setting, the method of single-point crossover in [21] is employed. The scheme for selecting offspring is the Tournament method which is depicted in [21]. Each point on the curves was obtained by averaging over 10^7 trials in the Monte-Carlo simulation. TABLE I shows the proposed QR-based GA-MD schemes evaluating the effects of A) initial setting techniques, B) mutation schemes and C) computational complexity.

A. Effect of Initial Setting techniques

To describe the various creations from the initial setting in each population, the Lim strategy [30] and the BF strategy of (30) are used for the SQRD GA-MD. In this Lim strategy, the detected signals of the SQRD detector are treated as one of the populations and the others are created randomly when the noise information is unknown [30]. In Fig. 5, the simulation results show the proposed BF strategy provides a better performance than the Lim strategy [30] by about 3 dB when BPSK and 16QAM are employed, respectively. This is better because the BF strategy transmits more signal information with which to enhance the performance of GA. Therefore, the BF scheme is considered as follows. For BPSK signals, Fig. 6(a) shows SQRD GA-MD is better than other detectors by 2 dB to 25 dB. For 16QAM signals, Fig. 6(b) shows SQRD GA-MD is better than other detectors by 2 dB to 15 dB. These simulation results show useful knowledge concerning the initial setting can actually enhance the performance of GA. This is better because Stage-1 creates a suitable seed chromosome, which contains the information of the transmitted signal. This information enables GA to achieve a faster convergence. In addition, with $N > M$, Fig. 7(a) shows ZF-SQRD GA-MD is better than other detectors for BPSK signals. For 16QAM in Fig 7(b), the performance of QR-based detectors decays more steeply than others when SNR > 21 dB. Further, the performance of ZF-SQRD MD is worse than the performance of ZF MD when SNR < 21 dB. This worsens because the noise energy dominates the performance of the ZF-SQRD detector in Stage-1.

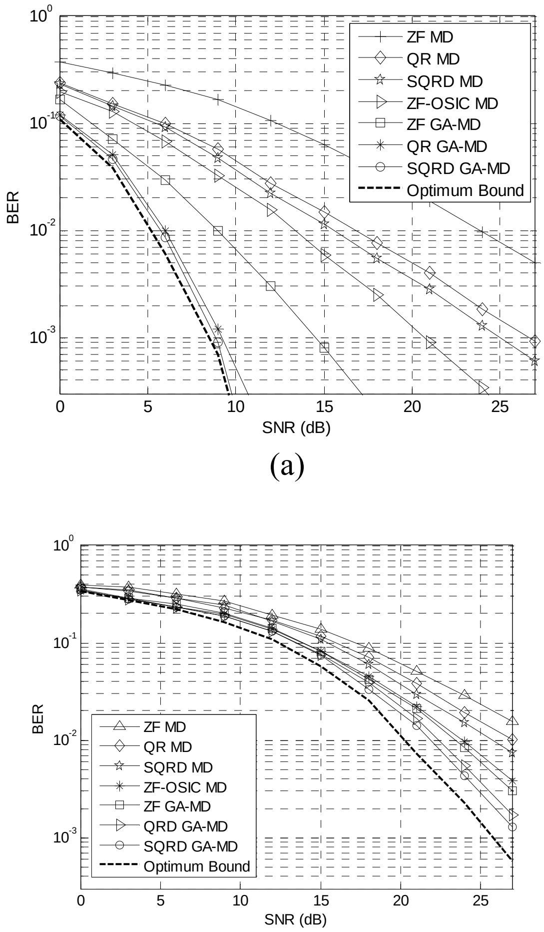
Particularly, with $N > M$, ZF-SQRD GA-MD has a better performance than others due to invoking the OSIC scheme.



(a)

(b)

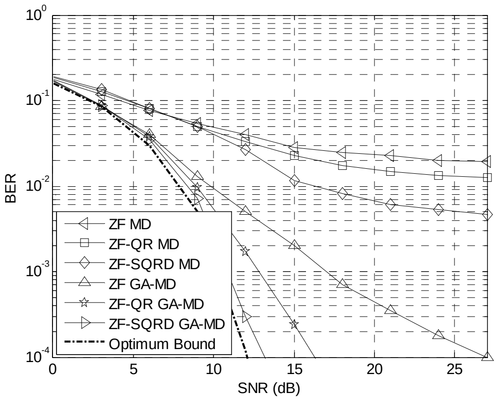
Fig. 5. BER versus SNR performance comparison of the various creation strategy employing in (a) $N = 9$, $M = 10$ for BPSK modulation and $N = 2$, $M = 3$ for 16QAM modulation and the GA-related configuration is $N_P = 10$ and $N_G = 15$. (b) $N = 10$, $M = 9$ for BPSK modulation and $N = 3$, $M = 2$ for 16QAM modulation and the GA-related configuration is $N_P = 25$ and $N_G = 5$ (The UM rate is 0.1).



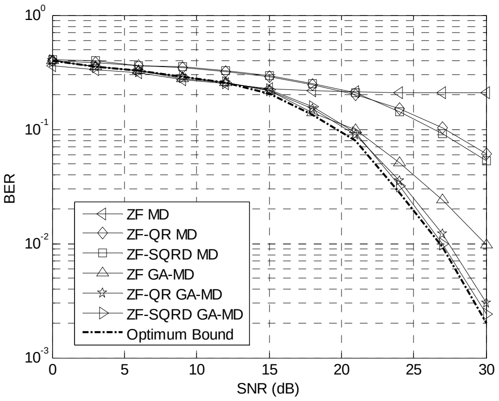
(a)

(b)

Fig. 6. BER versus SNR performance for different initial setting methods employing in (a) $N = 10$, $M = 10$, BPSK modulation and the GA-related configuration is $N_P = 21$ and $N_G = 10$. (b) $N = 4$, $M = 4$, 16QAM modulation and the GA-related configuration is $N_G = 50$ and $N_P = 33$ (BF is used in the initial setting and UM = 0.1).

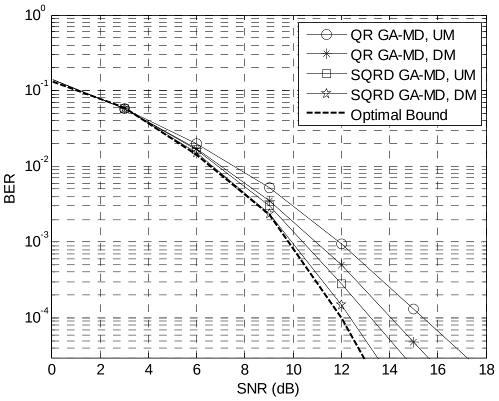


(a)

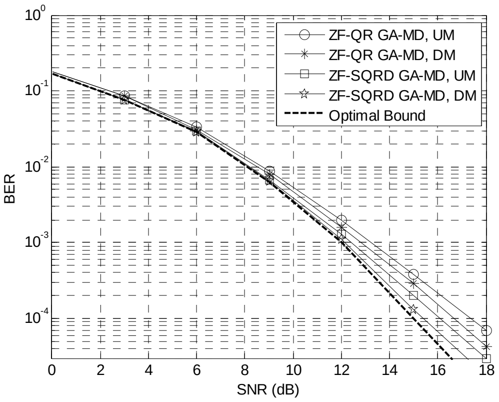


(b)

Fig. 7. BER versus SNR performance for different initial setting methods employing in (a) $N = 8$, $M = 6$, BPSK modulation and the GA-related configuration is $N_P = 17$ and $N_G = 10$. (b) $N = 3$, $M = 2$, 16QAM modulation and the GA-related configuration is $N_P = 25$ and $N_G = 15$ (BF and UM = 0.1).



(a)



(b)

Fig. 8. BER versus SNR performance comparison for various mutation schemes employing in (a) $N = 5$, $M = 5$, BPSK modulation and the GA-related configuration is $N_P = 6$ and $N_G = 3$. (b) $N = 5$, $M = 4$, BPSK modulation and the GA-related configuration is $N_P = 6$ and $N_G = 3$ (BF and UM = 0.2).

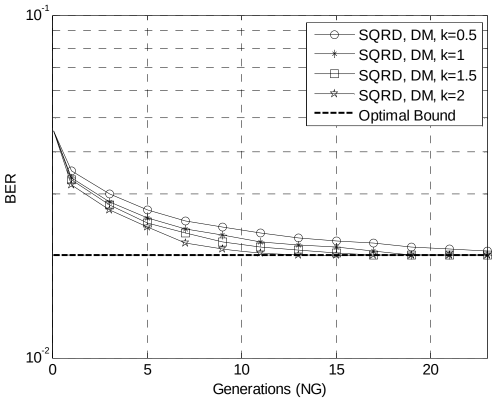


Fig. 9. Generations versus SNR performance comparison for various mutation schemes employing in $N = 2$, $M = 2$, 16QAM modulation, and the GA-related configuration is $N_P = 10$ when BF is used.

B. Effect of Mutation Schemes

The proposed DM scheme is developed from (40) as depicted in [32]. In Fig. 8, various mutation schemes include DM and uniform mutation (UM) [21], [38]. These mutation schemes are employed in both SQRD GA-MD and unsorted QR GA-MD. With $N = M$, Fig. 8(a) shows the proposed DM scheme is better than the UM scheme by about 1 dB for both SQRD GA-MD and unsorted QR GA-MD, respectively. The DM rate from layer 1 to layer 5 is given as $P_{m,1} = 0.25$, $P_{m,2} = 0.2$, $P_{m,3} = 0.15$, $P_{m,4} = 0.1$, and $P_{m,5} = 0.05$. With $N > M$, Fig. 8(b) shows the proposed DM scheme is better than the UM scheme by about 1 dB for both ZF-SQRD GA-MD and unsorted ZF-QR GA-MD, respectively. The DM rate from layer 1 to layer 5 is given as $P_{m,1} = 0.3$, $P_{m,2} = 0.2\ 5$, $P_{m,3} = 0.2$, $P_{m,4} = 0.15$, and $P_{m,5} = 0.1$. This is better because the DM scheme invoking the SIC operation of (7) and (43) considers the diversity order, modulation order and SNR issue. Specifically, using the DM scheme, the mutation rate of upper layers decay more steeply due to higher diversity levels than the layer detected first (see Fig. 1). That is, substreams in high diversity levels will be less mutated and therefore obtain reliable offspring to enter the population of GA.

Beside, the choice of mutation probability has also effects on the residual BER and the convergence rate. This is illustrated in Fig. 9 employing different κ values, where $P_{m,1} = 0.3$, $P_{m,2} = 0.1$. It is seen that higher values of mutation rate can improve the

SQRD GA-MD performance. It indicates the higher mutation rate in order to produce new individuals.

C. Evaluation of Computational Complexity

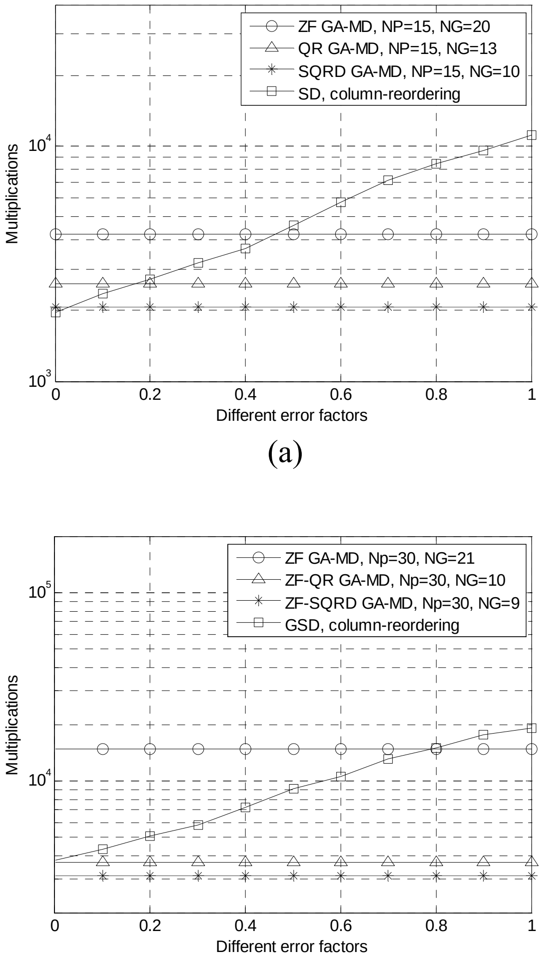
To compare the computational complexity (multiplications) for SD, we derive the inaccurate radius from (18) when the error of the noise estimation is considered as

$$\tilde{d} = \alpha M \breve{\sigma}_v^2 = \alpha M(\sigma_v^2 + \varepsilon\sigma_v^2) = \alpha M\sigma_v^2(1+\varepsilon)\,, \qquad (53)$$

where $\breve{\sigma}_v^2$ is an estimated noise power and ε is an error factor. With $N = M$ in Fig. 10(a), because of an increase of the error factor of the noise estimation, the computational complexity of SD increases when the radius is enlarged [14]-[16]. Obviously, the proposed SQRD GA-MD has fewer multiplications than SD when $\varepsilon > 0.01$ in (53). With $N > M$, we derive the inaccurate radius from (30) and (53) when the error of the noise estimation is considered as

$$d^2 = \alpha(\phi(N-M)|a|^2 + M\sigma_v^2(1+\varepsilon))\,, \qquad (54)$$

where ϕ = 1.8 employing at normalized 16QAM signals in this simulation. In Fig. 10(b), the proposed QR-based GA-MD has fewer multiplications than GSD when a = 0.1 + 0.1i in (25) and $\varepsilon \geq 0$ in (54) at the underdetermined MIMO systems. This is better because the choice of the parameter a of (24) is more sensitive to approximating the pseudo received vector of (25) in affecting the computational complexity of GSD [19]. Therefore, consider a robust detector in RVC, GA-based detectors can achieve optimal performance without utilizing the noise information, and therefore the complexity of the GA-based detectors is unchanged when ε is increasing. Also, proposed QR-based GA-MD has fewer multiplications than ZF GA-MD due to good initial setting and reducing matrix multiplication, as depicted in (50) and (51).



(a)

(b)

Fig. 10. (a) Average multiplications of the four algorithms versus different error factors of the noise estimation for 16QAM modulation employing in (a) SNR = 12 dB, BER = 0.13, α = 7, N = 3 and M = 3. (b) SNR = 24 dB, BER = 0.032, α = 100, N = 3 and M = 2 (BF and UM = 0.1).

6 Conclusion

In this paper, without the needs of noise information, a robust two-stage procedure is proposed to achieve ML performance with low computational complexity for MIMO communications. Moreover, this novel two-stage can realize OSIC when an overdetermined and/or underdetermined is employed. Consider low-complexity, we propose a novel, near-optimal and robust two-stage which has three main contributions as follows. First, the QR-based schemes can be applied to GA-MD to obtain better performance due to reliable initial knowledge concerning the setting. Second, the proposed QR-based GA-MDs are made computationally cost-effective due to applying a triangular form of the MIMO channel matrix. Third, the effect of the mutation scheme on the various diversity gains was also explored in this study; it is called the DM scheme. However, this sample DM scheme is not easy to obtain a suitable κ value. Our future work will develop an adaptive probability of mutation in SQRD GA-MD for mobile broadband wireless access applications.

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Appendix

To show that if (27) is a convex optimization problem via (5) and (6) and hence we have

$$\begin{aligned}\underset{\mathbf{x}(k)\in\Omega}{\arg\min}\|\mathbf{y}(k)-\mathbf{H}\mathbf{x}(k)\|^2 &= \underset{\mathbf{x}(k)\in\Omega}{\arg\min}(\mathbf{x}(k)-\tilde{\mathbf{x}}(k))^H H^H H(\mathbf{x}(k)-\tilde{\mathbf{x}}(k)) \\ &= \underset{\mathbf{x}(k)\in\Omega}{\arg\min}(\mathbf{x}(k)-\tilde{\mathbf{x}}(k))^H \mathbf{R}^H \mathbf{R}(\mathbf{x}(k)-\tilde{\mathbf{x}}(k)) \\ &= \underset{\mathbf{x}(k)\in\Omega}{\arg\min}\|\mathbf{z}(k)-\mathbf{R}\mathbf{x}(k)\|^2, \qquad \text{(A.1)}\end{aligned}$$

where $\tilde{\mathbf{x}}(k)=(\mathbf{H}^H\mathbf{H})^{-1}\mathbf{H}^H\mathbf{y}(k)$. In addition, the error distance vector is denoted as $\mathbf{e}(k) = (\mathbf{x}(k) - \tilde{\mathbf{x}}(k))$ between transmit signal vector and estimated signal vector and $\mathbf{L} = \mathbf{R}^H\mathbf{R}$. Therefore, (5) can be rewrite as

$$\begin{aligned}\mathbf{x}^*_{\mathrm{GA}}(k) = \underset{\mathbf{x}(k)\in\Omega}{\arg\min}\|\mathbf{z}(k)-\mathbf{R}\mathbf{x}(k)\|^2 &= \underset{\mathbf{e}(k)\in C^N}{\arg\min}\, \mathbf{e}(k)^H\mathbf{L}\mathbf{e}(k) \\ &= \underset{\mathbf{E}(k)\geq 0}{\arg\min}\, tr(\mathbf{L}\mathbf{E}(k)), \qquad \text{(A.2)}\end{aligned}$$

where $tr(\cdot)$ is the trace of matrix and error matrix is given as

$$\mathbf{E}(k) = \mathbf{e}(k)\mathbf{e}(k)^H. \qquad \text{(A.3)}$$

Then, we begin with the Definition 1 and Definition 2 to introduce the prototypes that the objective function is the convex function and the feasible set is also the convex set, respectively, as follows [39].

Definition 1: Let a function f $: \Omega \rightarrow$ is given by a convex set $\Omega \subset {}^{n}$ is convex if and only if for all **u**, **v** $\in \Omega$ and all$\alpha \in (0,1)$, we have

$$f(\alpha\mathbf{u} + (1-\alpha)\,\mathbf{v}) \leq \alpha f(\mathbf{u}) + (1-\alpha)\,f(\mathbf{v}). \qquad \text{(A.4)}$$

Definition 2: A set Ω is convex if the line segment between any two points in Ω lies in Ω, i.e. if for any **u**, **v** $\in \Omega$ and any α with $0 \leq \alpha \leq 1$, we have

$$\alpha\mathbf{u} + (1-\alpha)\,\mathbf{v} \in \Omega. \qquad \text{(A.5)}$$

First, we prove the objective function of (A.2) is the convex function as follow.

Proof: The result follows from **Definition 1**. Indeed, the objective function $f(\mathbf{E}(k)) = tr(\mathbf{L}\mathbf{E}(k))$ of (A.2) is the convex function if and only if for every $\alpha \in (0,1)$, and every **u**, **v** $\in \Omega$ we can obtain the equivalent equation from (A.4) as

$$f(\alpha\mathbf{u} + (1-\alpha)\,\mathbf{v}) - \alpha f(\mathbf{u}) - (1-\alpha)\,f(\mathbf{v}) \qquad 0. \quad \text{(A.6)}$$

Substituting for f into the left-hand side of the above equation yields as

$$\begin{aligned}&tr(\mathbf{L}(\alpha\mathbf{u} + (1-\alpha)\mathbf{v}) - \alpha(tr(\mathbf{L}\mathbf{u})) - (1-\alpha)(tr(\mathbf{L}\mathbf{v})) \\ &= tr(\mathbf{L}(\alpha\mathbf{u}) + \mathbf{L}((1-\alpha)\mathbf{v})) - \alpha(tr(\mathbf{L}\mathbf{u})) - (1-\alpha)(tr(\mathbf{L}\mathbf{v})) \\ &= tr(\alpha(\mathbf{L}\mathbf{u}) + (1-\alpha)(\mathbf{L}\mathbf{v})) - \alpha(tr(\mathbf{L}\mathbf{u})) - (1-\alpha)(tr(\mathbf{L}\mathbf{v})) \\ &= tr(\alpha(\mathbf{L}\mathbf{u}) + (1-\alpha)(\mathbf{L}\mathbf{v})) - \alpha(tr(\mathbf{L}\mathbf{u})) - (1-\alpha)(tr(\mathbf{L}\mathbf{v})) \\ &= \alpha(tr(\mathbf{L}\mathbf{u})) + (1-\alpha)(tr(\mathbf{L}\mathbf{v})) - \alpha(tr(\mathbf{L}\mathbf{u})) - (1-\alpha)(tr(\mathbf{L}\mathbf{v}))=0 \\ &0. \qquad \text{(A.7)}\end{aligned}$$

Thus, the proof is completed.

Second, we prove the feasible set of (A.2) is the convex set as follows.

Proof: The result follows from **Definition 2**. Indeed, with (A.2), the feasible set $\mathbf{E}(k) \geq 0$ is the convex set if and only if for every $\alpha \in (0,1)$, and every **u**, **v**

$\in \Omega$. Then, we let $\alpha\mathbf{u} + (1-\alpha)\ \mathbf{v} = \mathbf{w}$ and $\mathbf{w} \in \Omega$. Note that $\mathbf{E}(k)$ is the positive semidefinite and symmetric; the quadratic form $\mathbf{w}^T\mathbf{E}(k)\mathbf{w}$ with (A.2) can be expressed as

$$\begin{aligned}\mathbf{w}^H\mathbf{E}(k)\mathbf{w} &= (\alpha\mathbf{u} + (1-\alpha)\ \mathbf{v})^H\mathbf{E}(k)\ (\alpha\mathbf{u} + (1-\alpha)\ \mathbf{v}) \\ &= \alpha^2\mathbf{u}^H\mathbf{E}(k)\mathbf{u} + 2\alpha(1-\alpha)\mathbf{v}^H\mathbf{E}(k)\mathbf{u} + (1-\alpha)^2\mathbf{v}^H\mathbf{E}(k)\mathbf{v} \\ &= \alpha^2\mathbf{u}^H\mathbf{e}(k)\mathbf{e}^H(k)\mathbf{u} + 2\alpha(1-\alpha)\mathbf{v}^H\mathbf{e}(k)\mathbf{e}^H(k)\mathbf{u} + (1-\alpha)^2\mathbf{v}^H\mathbf{e}(k)\mathbf{e}^H(k)\mathbf{v} \\ &= \|\alpha\mathbf{u}^H\mathbf{e}(k) + (1-\alpha)\mathbf{v}^H\mathbf{e}(k)\|^2 \geq 0.\end{aligned} \tag{A.8}$$

Thus, the proof is completed.

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