Quasi-Gray Labelling for Grassmannian Constellations

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***Abstract*—This paper presents two polynomial-complexity techniques for assigning Gray-like binary labels to arbitrary Grassmannian constellations. In the first technique, the constellation of interest, $\mathcal{C}$, is matched directly to an auxiliary constellation that can be readily Gray labelled. The optimal matching in this technique can be obtained efficiently, but its application is limited to cases in which an auxiliary constellation with a geometric structure that resembles that of $\mathcal{C}$ can be identified. In the second technique no auxiliary constellation is required and the labels are generated by matching the distance spectrum of $\mathcal{C}$ with that of a hypothetical constellation that is assumed to be perfectly Gray labelled. Optimal matching in this case is computationally prohibitive. Instead, an efficient suboptimal matching algorithm is proposed. When compared with several existing schemes, the proposed labellings provide better performance in both uncoded and BICM-based non-coherent MIMO systems with iterative demapping and decoding (IDD). Furthermore, with the proposed labels, the Grassmannian-based BICM-IDD scheme performs better than a training-based counterpart that employs the Golden code and optimal demapping.**

***Index Terms*—Non-coherent MIMO communication, Grassmannian constellations, Gray labelling, combinatorial assignment problem, quadratic assignment problem.**

I. Introduction

THE compact complex Grassmann manifold, $\mathbb{G}_M(\mathbb{C}^T)$, is the set of equivalence classes of tall $T \times M$ unitary matrices, where $T \geq 2M$, in which two unitary matrices are said to be equivalent if they are related by right multiplication with a square $M \times M$ unitary matrix [1]. A Grassmannian constellation, $\mathcal{C}$, is a set of discrete points on the complex Grassmann manifold, and if the distribution of these points is invariant under rotation, the constellation is said to be isotropically distributed. Isotropically distributed Grassmannian constellations play a key role in signalling schemes for non-coherent multiple-input multiple-output (MIMO) communication systems [2], and in limited feedback schemes for coherent MIMO systems [3]–[5]. Using geometrical techniques, Grassmannian constellations with an approximately isotropic distribution can be efficiently generated; see for example [6], [7].

The application considered in this paper will be that of non-coherent MIMO communication. For a richly-scattered MIMO channel, isotropically distributed Grassmannian constellations can achieve the non-coherent capacity at high SNRs [2]. Two important aspects of the design of practical communication systems that provide good performance at rates close to this limit are the design of the constellation and the labelling of the points of that constellation with binary vectors. Although there are constellations that can be readily labelled [8], [9], those constellations are not necessarily close to being isotropically distributed. There are several techniques for the direct design of Grassmannian constellations that are close to being isotropically distributed [6], [7], but these constellations are not necessarily easy to label. In most communication systems, it appears that an exhaustive search will be required in order to find an optimal labelling, but of the structured labelling schemes, Gray labelling is known to have some desirable properties in both scalar [10]–[13] and MIMO systems [9], [14]. The goal of this paper is to develop Gray-like labelling techniques for arbitrary Grassmannian constellations.

The basic principle that underlies Gray labelling is that points that are close in a Euclidean sense are assigned labels that are close in a Hamming distance sense; true Gray labelling schemes assign neighbouring constellation points labels that differ by only one bit. While it is possible to assign Gray labels to elementary two and three-dimensional constellations, assigning such labels to constellations of high dimensions is typically difficult [15]. This is especially true for non-uniform constellations and for constellations in which the number of neighbouring points is not known and possibly not identical for every point in the constellation. In such cases, even finding a quasi-Gray labelling scheme becomes a formidable task involving an exhaustive search over $|\mathcal{C}|!$ candidate labellings, where $|\mathcal{C}|$ denotes the cardinality of $\mathcal{C}$.

In this paper two techniques are provided for generating quasi-Gray labels for arbitrary Grassmannian constellations that have favourable geometric properties, but that otherwise do not possess a particular structure that facilitates their labelling. The labels assigned by the proposed techniques follow the general Gray labelling principle of mapping labels

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that are close in a Hamming distance sense to points that are close in the signalling space.

In the first technique, which will be referred to as the match-and-label algorithm, the Grassmannian constellation of interest is matched directly to an auxiliary constellation, which can be readily Gray labelled, but may not have the same favourable geometric properties. The matching of the original and the auxiliary constellations is identified with the combinatorial assignment problem [16], wherein the cost of assigning N tasks to N workers is to be minimized. Identifying tasks with points in the original constellation and workers with points in the auxiliary constellation, the assignment cost becomes the sum of the distances between points in the original constellation and the corresponding points in the auxiliary constellation. The optimal solution of this problem can be obtained with polynomial complexity using the Hungarian technique [17]. With the constellations matched, the labels of the points of the auxiliary constellations are assigned to the corresponding points of the original constellation.

Labels generated by the match-and-label algorithm will follow a Gray-like pattern if the auxiliary and the constellation of interest, $\mathcal{C}$, have a similar geometric structure. However, when the auxiliary constellation and $\mathcal{C}$ possess fundamentally different geometric structures, e.g., number of nearest neighbours, the labels obtained by their matching can deviate significantly from the Gray principle. Another drawback is that the auxiliary constellations used in this technique are only available for certain cardinalities and dimensions of the underlying manifold.

To resolve these issues, we propose a second technique, which will be referred to as the successive matching algorithm. This algorithm employs a hypothetical constellation that is assumed to be perfectly Gray labelled and can be generated for any dimension and cardinality. A labelling for the actual constellation can be obtained by matching its distance spectrum with the Hamming distance spectrum of the hypothetical constellation. To do this, the matching of the distance spectra is identified with the quadratic assignment problem (QAP), wherein two weighted graphs are to be matched such that the difference between corresponding edge weights is minimized. In a similar observation, but in the context of coherent MIMO systems, optimal labelling of QAM and PSK symbols has been identified with the QAP in [18]. Cast as the minimization of a quadratic expression in a permutation matrix, the QAP can be shown to be NP-hard [19], and to become intractable for graphs with more than 30 nodes [20]. To find good solutions to this problem for constellations with cardinalities of practical importance, we propose an efficient greedy algorithm in which the permutation matrix is constructed on a block-by-block basis. This matching technique falls under the category of constructive methods described in [21] and allows us to match large constellations efficiently. For example, herein we match constellations of size 4096, a computationally prohibitive task for most of the techniques described in [21], including those that use semidefinite relaxation [22]. Similar to the first technique, once the constellations are matched, the points in the constellation of interest are assigned the labels of the corresponding points in the hypothetical constellation.

We assess the performance of the proposed labelling schemes in both an uncoded non-coherent MIMO system and a BICM-IDD system. It is shown that the labels assigned with the proposed techniques yield Grassmannian-based non-coherent communication systems that perform better than some existing systems, with the successive technique providing the better performance of the two. Furthermore, the proposed labelling schemes enable the Grassmannian-based BICM-IDD system to perform better than its training-based counterpart with Gray-labelled Golden-encoded symbols and optimal demapping [23], even at moderate SNRs.

Standard notation is adopted throughout the paper: $\|\cdot\|_F$ denotes the Frobenius norm, $(\cdot)^T$ and $(\cdot)^\dagger$ denote the transpose and the Hermitian transpose, respectively, $\mathrm{Tr}(\cdot)$ denotes the trace operator, $\odot$ denotes the Hadamard product and $\mathrm{diag}(\cdot)$ denotes the operator that turns a vector into a diagonal matrix with the corresponding dimension.

II. Grassmannian Constellations

As discussed in the Introduction, isotropically distributed Grassmannian constellations play an important role in moderate-to-high SNR non-coherent MIMO communications systems [2] and in coherent MIMO communication systems with limited feedback [3]–[5]. A key component in the design of such constellations is the choice of the design metric. In the case of the projection Frobenius norm, several optimal constructions for small constellations on the real Grassmann manifold were provided in [24]. However, in general the optimality of these constructions does not extend to the complex Grassmann manifold, to large constellations, nor to other metrics that may be more appropriate for the applications of interest. In this section we review methods for obtaining two families of Grassmannian constellations that will be used to test the labelling techniques presented later. Although the constellations generated with these methods perform well in practice, they do not necessarily correspond to optimal packings.

A. Systematic Constellations

A sequential technique for designing a Grassmannian constellation, $\mathcal{C}$, with cardinality N is proposed in [6]. In this method, the first subspace, $\mathbf{Q}_{X_1}$, is obtained by taking M columns of the $T \times T$ discrete Fourier transform matrix. The other subspaces in the constellation, $\mathbf{Q}_{X_i}$, $i = 2, \ldots, N$, are then generated using:

$$\mathbf{Q}_{X_i} = \mathbf{\Phi}^i \mathbf{Q}_{X_1} \tag{1}$$

where $\mathbf{\Phi} = \mathrm{diag}(e^{\jmath 2\pi u_1/N}, e^{\jmath 2\pi u_2/N}, \cdots, e^{\jmath 2\pi u_T/N})$, and u_i, $i = 1, \ldots, T$, are integers that maximize the minimum chordal distance between subspaces [24]:

$$\min_{i,j} \; d_F(\mathbf{Q}_{X_i}, \mathbf{Q}_{X_j}) = \min_{i,j} \; \frac{1}{\sqrt{2}} \|\mathbf{Q}_{X_i}\mathbf{Q}_{X_i}^\dagger - \mathbf{Q}_{X_j}\mathbf{Q}_{X_j}^\dagger\|_F. \tag{2}$$

The generation of Grassmannian constellations with this technique is computationally efficient because the constellation is generated by rotating an initial subspace and the rotation matrix is optimized over a relatively small set of integers. However, the stringent constellation structure imposed by this technique can result in a significant performance degradation.

Such a degradation can be avoided by designing the Grassmannian constellations directly using geometric techniques that enable all the design degrees of freedom to be exploited. One of these techniques will be described in the next section.

B. Geometrically designed constellations

Operating a non-coherent MIMO communication system close to the high SNR ergodic capacity is equivalent to sphere packing on the Grassmann manifold [2]. Using this observation, the problem of designing rate-efficient Grassmannian constellations can be cast as an optimization problem in which the minimum distance between any pair of constellation points is maximized:

$$\begin{aligned} &\max_{\{\mathbf{Q}_{X_i}\}_{i=1}^{N}} \quad \min_{i\neq j} \quad d(\mathbf{Q}_{X_i}, \mathbf{Q}_{X_j}), \\ &\text{subject to} \quad \mathbf{Q}_{X_i} \in \mathbb{G}_M(\mathbb{C}^T), \quad \forall i \in \{1,\ldots,N\}, \end{aligned}$$

where $d(\mathbf{Q}_{X_i}, \mathbf{Q}_{X_j})$ is the distance between the points $\mathbf{Q}_{X_i}$ and $\mathbf{Q}_{X_j}$. In [7] it was argued that the chordal Frobenius norm given by [25]

$$d(\mathbf{Q}_{X_i}, \mathbf{Q}_{X_j}) = \sqrt{M - \mathrm{Tr}(\mathbf{\Sigma}_{ij})} \tag{3}$$

is an appropriate metric for the design of these constellations, where $\mathbf{\Sigma}_{ij}$ is the diagonal matrix of singular values of $\mathbf{Q}_{X_i}^{\dagger}\mathbf{Q}_{X_j}$. Using this metric, several approaches for designing Grassmannian constellations were developed in [7]. These approaches rely on using derivative-based optimization techniques that exploit the smooth geometry of the Grassmann manifold. Geometric techniques have also been used to design Grassmannian constellations that meet alternate objectives; for example, see [26], [27].

In spite of their favourable geometric properties, the constellations generated by the aforementioned techniques do not have a known structure that facilitates their Gray labelling in a systematic manner. Addressing this drawback is the focus of the paper.

III. Two Techniques for Quasi-Gray Labelling

In this section we present two methods for assigning quasi-Gray labels to arbitrary Grassmannian constellations. In the first technique, labelling is identified with the combinatorial assignment problem [16] which can be optimally solved with polynomial complexity, and in the second technique, labelling is identified with the quadratic assignment problem (QAP). The latter problem is significantly harder, and approximate solutions are available only for relatively small problems.

A. The match-and-label algorithm with the Hungarian method

The match-and-label idea was first presented in [28] as a method for providing quasi-Gray labels to a Grassmannian constellation of interest, $\mathcal{C}$. The principle that underlies this algorithm is to match $\mathcal{C}$ to an auxiliary constellation, $\mathcal{C}_A$, that has the same cardinality and can be readily Gray labelled, but may have a distance spectrum that is less favourable than that of $\mathcal{C}$. Such auxiliary constellations can be generated using the method in [8] and labelled using the method in [9]. In particular, in the design technique in [8] tall unitary matrices, $\{\mathbf{Q}_{Z_i}\}$, representing the points of the auxiliary constellation are constructed in the following way:

$$\mathbf{Q}_{Z_i} = \begin{bmatrix}\mathbf{G}^T & \mathbf{D}_i^T\end{bmatrix}^T, \tag{4}$$

where the constant matrix $\mathbf{G}$ is common for all constellation points and the matrix $\mathbf{D}_i$ is distinct for each constellation point. The sizes of $\mathbf{G}$ and $\mathbf{D}_i$ are chosen to satisfy the orthogonality condition. For example, for $M = 2$ and $T = 4$, the matrix $\mathbf{D}_i$ can be chosen to have the structure of a Q-ary phase-shift keying (PSK) Alamouti scheme [8], [9]

$$\mathbf{G} = \frac{1}{2}\begin{bmatrix}1 & 1\\ -1 & 1\end{bmatrix} \text{ and } \quad \mathbf{D}_i = \frac{1}{2}\begin{bmatrix}e^{\jmath\frac{2\pi}{Q}k(i)} & e^{\jmath\frac{2\pi}{Q}\ell(i)}\\ e^{-\jmath\frac{2\pi}{Q}\ell(i)} & -e^{-\jmath\frac{2\pi}{Q}k(i)}\end{bmatrix},$$

where the pair of integers $(k(i), \ell(i))$ is distinct for each point $i \in \{1,\ldots,|\mathcal{C}_A|\}$, where $\mathcal{C}_A$ is the auxiliary constellation generated by (4), $k(i), \ell(i) \in \{0,\ldots,Q-1\}$ and $Q = \sqrt{|\mathcal{C}_A|}$.

Let (k,ℓ) and (k',ℓ') be two pairs of integers corresponding to the distinct points i and i' in $\mathcal{C}_A$, respectively. In this case, the two singular values of $Q_{Z_i}^{\dagger}Q_{Z_{i'}}$ are equal and are given by

$$\frac{1}{2}\sqrt{2 + \cos\left(\tfrac{2\pi}{Q}(k-k')\right) + \cos\left(\tfrac{2\pi}{Q}(\ell-\ell')\right)}. \tag{5}$$

From (5) and (3) it can be shown that for each constellation point with indices (k,ℓ) there exist exactly four nearest neighbours with indices $(k, (\ell \pm 1) \mod Q)$ and $((k \pm 1) \mod Q, \ell)$ [9]. Each of the integers k, ℓ, k', ℓ' corresponds to a point in a PSK constellation. It was concluded in [9, Theorem 1] that if the PSK constellations indexed by the integers k, ℓ, k', ℓ' are identically Gray labelled, $\mathcal{C}_A$ will also be Gray labelled.

Having generated and labelled the auxiliary constellation, $\mathcal{C}_A$, each point in $\mathcal{C}$ is matched to a point in $\mathcal{C}_A$ and is assigned the label associated with that point. To match the two constellations, the cost of matching point i in $\mathcal{C}$ with point i' in $\mathcal{C}_A$ is set to be the chordal Frobenius norm, $d_{ii'}$, cf. (3). The overall cost of matching the two constellations is then the total sum of the distances between the corresponding points. A suboptimal method for minimizing this cost was proposed in [28]. However, by representing the pairwise distance between the points of each constellation in the form of a matrix, the matching problem can be shown to be equivalent to the combinatorial assignment problem [16] wherein N tasks are to be assigned to N workers such that the overall cost is minimized. This problem can be solved optimally using the so-called Hungarian method [17] with complexity $\mathcal{O}(N^3)$. In particular, given an $N \times N$ cost matrix, $\mathbf{A}$, with non-negative entries representing the costs associated with assigning task i to worker i', the Hungarian method seeks a permutation matrix, $\mathbf{P}$, that minimizes $\mathrm{Tr}(\mathbf{PA})$. The method proceeds by eliminating the points in $\mathcal{C}_A$ (workers) that can be readily matched to corresponding points in $\mathcal{C}$ (tasks): these are the points for which the minimum value of each row in $\mathbf{A}$ is unique and happens to be in a column other than that in which the minima of other rows lie. The method then considers the unmatched points to determine the best match by iterating between the best match from the perspective of the auxiliary constellation and the perspective of

the constellation of interest. Using this algorithm, our match-and-label technique for the constellation of interest, $\mathcal{C}$, can be formally stated as follows:

Algorithm 1 (The match-and-label algorithm):

- Construct and Gray label an auxiliary constellation, $\mathcal{C}_A$, with the same cardinality as $\mathcal{C}$. (Herein, $\mathcal{C}_A$ is generated as in [8] and is Gray labelled as in [9].)
- Match $\mathcal{C}$ and $\mathcal{C}_A$ using the Hungarian method described above [17].
- To every point in $\mathcal{C}$ assign the label of the corresponding point in $\mathcal{C}_A$.

As will be shown in Sec. V-C, this algorithm efficiently generates labels that result in significantly better performance than quasi-set-partitioning labellings when used in a BICM-based non-coherent MIMO system. However, even though the Hungarian method yields optimal matching, this labelling technique has two drawbacks. First, it requires the generation of an auxiliary constellation that can be readily Gray labelled and has the same dimensions and cardinality as the constellation of interest. Such constellations are only available for specific dimensions. Second, when $\mathcal{C}$ and $\mathcal{C}_A$ possess fundamentally different geometric structures, e.g., number of nearest neighbours, the labels generated by the matching do not necessarily follow the Gray principle. That is, for the match-and-label algorithm to yield Gray-like labels, the two constellations to be matched must have a similar geometric structure. In the next section we will present another labelling technique that circumvents these difficulties.

B. The successive matching algorithm

In this section we provide a method for assigning quasi-Gray labels to an arbitrary Grassmannian constellation, $\mathcal{C}$, of cardinality $N = 2^{N_B}$, where N_B is the number of bits of the binary labels. In this method the distance spectrum of $\mathcal{C}$ is matched to the distance spectrum of a hypothetical constellation that is assumed to be perfectly Gray labelled. We first note that the labels of the points of $\mathcal{C}$ are the binary form of the integers between 0 and $N-1$. Assuming a perfectly Gray-labelled constellation were available, its distance spectrum would be the same as that of the Hamming distances among the labels. That is, the ideal distance spectrum is embedded in the inherent Hamming distance relationship among the labels. Therefore, one way to obtain quasi-Gray labels is to seek a permutation of the constellation points so that the distance spectrum of the permuted points resembles the distance spectrum of the labels. After matching, each point in the constellation is assigned the corresponding label.

To begin this procedure, we construct an $N \times N$ matrix, $\mathbf{H}$, that represents the Hamming distance spectrum of the perfectly labelled hypothetical constellation. We then construct the ranking matrix, $\mathbf{R}$, that represents the chordal Frobenius norm spectrum of $\mathcal{C}$.

1) The Hamming distance spectrum matrix $\mathbf{H}$*:* Let $\boldsymbol{\ell}_r$ be the binary vector of length $N_B = \log_2(N)$ containing the binary expansion of the integer $r \in \{0, \ldots, N-1\}$. For ease of exposition, these labels are ordered numerically here; in practice, it may be useful to consider other label orders. We define the (r,s)-th entry of $\mathbf{H}$ to be the Hamming distance between the vectors $\boldsymbol{\ell}_r$ and $\boldsymbol{\ell}_s$, i.e., the sum of $\boldsymbol{\ell}_r \oplus \boldsymbol{\ell}_s$, where $\oplus$ denotes the modulo-2 addition. For example, for $N = 4$ the matrix $\mathbf{H}$ is given by

$$\mathbf{H} = \begin{bmatrix} 0 & 1 & 1 & 2 \\ 1 & 0 & 2 & 1 \\ 1 & 2 & 0 & 1 \\ 2 & 1 & 1 & 0 \end{bmatrix}. \tag{6}$$

2) The ranking matrix $\mathbf{R}$*:* The distance spectrum of the constellation $\mathcal{C}$ can be characterized by a matrix, $\mathbf{E}$, in which the (i,j)-th entry is the chordal Frobenius norm between the i-th and j-th constellation points. However, since many constellations of interest are generated using numerical techniques, such as the one presented in Sec. II-B, the constellation has an irregular structure, resulting in pairs of points having similar, but not identical distances in the signalling space. When sufficiently small, these perturbations have a negligible effect on the performance of the resulting constellation. They can, however, complicate the matching of the Euclidean distance spectrum with the Hamming one.

To overcome this difficulty, we introduce a ranking matrix, $\mathbf{R}$, that captures the relative proximity of points in the constellation and has a similar distribution of entries to the Hamming matrix. To construct this matrix, we note that, for a constellation of size $N = 2^{N_B}$, each label has $\binom{N_B}{k}$ neighbours with Hamming distance k. Now, for each row of $\mathbf{E}$ the corresponding row of $\mathbf{R}$ is formed as follows: the minimum $\binom{N_B}{1}$ distances are represented by the ranking 1, the next nearest $\binom{N_B}{2}$ distances are represented by the ranking 2, and so on.

This method of tailoring $\mathbf{E}$ can be modified to stress different aspects of the labelling problem, such as incorporating information known about the structure of the constellation to be labelled or its eventual application. In particular, by manipulating $\mathbf{R}$, it is possible to obtain labelling patterns that may suit other applications, such as set-partitioning. However, an in-depth treatment of tailoring schemes for $\mathbf{E}$ is beyond the scope of this paper.

C. Successive matching

With the Hamming distance matrix and the ranking matrix constructed as above, our goal is to find a permutation matrix $\mathbf{P}$ that minimizes

$$\|\mathbf{H} - \mathbf{P}\mathbf{R}\mathbf{P}^T\|_F^2 = \mathrm{Tr}(\mathbf{H}\mathbf{H}^T + \mathbf{R}\mathbf{R}^T) - 2\,\mathrm{Tr}(\mathbf{H}^T\mathbf{P}\mathbf{R}\mathbf{P}^T). \tag{7}$$

In contrast to the minimization required to match the constellations directly in Sec. III-A, in which the objective is a linear function of $\mathbf{P}$, the minimization required to match the distance spectra is a quadratic function of $\mathbf{P}$. The minimization is an instance of the QAP problem, which is known to be NP-hard [19]. Although many algorithms have been developed to provide suboptimal solutions for this problem, these algorithms are only effective for relatively small problems [19], [22], in which the dimension of $\mathbf{P}$ is typically less than 100. However, to operate a non-coherent MIMO system close to the high SNR ergodic capacity, the size of the underlying matching problem can be well above 1000. To mitigate this difficulty, in this section we develop an efficient suboptimal

method for determining a 'good' permutation matrix, $\mathbf{P}$. In the following sections we present single branch and multiple branch versions of this algorithm, and in Sec. V-C we will show that this algorithm can yield labels that result in significantly better performance than those obtained using the match-and-label algorithm.

1) Single branch successive matching: In the proposed algorithm, the first row of the permutation matrix is arbitrarily selected to be the first row of the identity matrix $\mathbf{I}_N$, denoted $\mathbf{i}_1$. The permutation matrix is then successively augmented by D rows from $\mathbf{I}_N$, where D is a parameter of the algorithm which will be referred to as the search depth. At each iteration of the algorithm, the D rows are chosen to minimize the Frobenius norm of the difference between the permuted ranking matrix and the corresponding portion of $\mathbf{H}$. When $D = N-1$, the matching algorithm amounts to finding the global minimizer of (7). We now describe this algorithm in more detail.

Let $\mathbf{i}_j$ denote the j-th row of $\mathbf{I}_N$, $\mathbf{H}_{kk}$ denote the upper left square $(kD+1)$ submatrix of $\mathbf{H}$, and $\mathbf{P}_k$ denote the portion of the permutation matrix that is available after k iterations, where $k = 1, \ldots, \frac{N-1}{D}$, and, for simplicity, we assume that $\frac{N-1}{D}$ is an integer. The matrix $\mathbf{P}_k$ is generated by appending a $D \times N$ block to the matrix $\mathbf{P}_{k-1}$. The algorithm can be formally described as follows.

Algorithm 2 (The successive matching algorithm):

- Initialize: $\mathcal{L} = \{2, \ldots, N\}$, $\mathbf{P}_0 = \mathbf{i}_1$.
- For every $k = 1, \ldots, \frac{N-1}{D}$,
  - Find distinct $r_1, \ldots, r_D \in \mathcal{L}$ such that $\mathbf{A}_{r_1,\cdots,r_D} = \begin{bmatrix}\mathbf{i}_{r_1}^T & \cdots & \mathbf{i}_{r_D}^T\end{bmatrix}^T$ satisfies
$$\mathbf{A}_{r_1,\cdots,r_D} = \arg \min_{q_1,\ldots,q_D \in \mathcal{L}} \Big\| \mathbf{H}_{kk} - \begin{bmatrix}\mathbf{P}_{k-1}^T & \mathbf{A}_{q_1,\cdots,q_D}^T\end{bmatrix}^T \mathbf{R} \begin{bmatrix}\mathbf{P}_{k-1}^T & \mathbf{A}_{q_1,\cdots,q_D}^T\end{bmatrix} \Big\|_F^2. \quad (8)$$
  - Set $\mathbf{P}_k \leftarrow \begin{bmatrix}\mathbf{P}_{k-1}^T & \mathbf{A}_{r_1,\cdots,r_D}^T\end{bmatrix}^T$.
  - $\mathcal{L} \leftarrow \mathcal{L} \setminus \{r_1, r_2, \ldots, r_D\}$.
- Set $\mathbf{P} \leftarrow \mathbf{P}_{\frac{N-1}{D}}$.

If $\frac{N-1}{D}$ is non-integer, the minimization in the final iteration will be over fewer than D rows.

2) Multiple branch successive matching: At the k-th step of the single branch sequential technique above, $\mathbf{P}_k$ is constructed by appending a block of D rows to $\mathbf{P}_{k-1}$, the minimizer of the objective at the $(k-1)$-th step. This technique can be identified with a tree search in which only the branch of the minimizer of the objective at the $(k-1)$-th step is considered in subsequent steps and branches in the tree corresponding to other candidate truncated permutations are eliminated. The greedy nature of this elimination can result in a significant degradation in the quality of the approximation provided by the final permutation matrix.

To reduce the potential of premature elimination of 'good' branches, we modify the algorithm presented in the previous section so that, at the k-th step, not only the minimizer of the $(k-1)$-th objective is considered, but also all those truncated permutations that yield the next smallest $L-1$ values of the objective. This algorithm can be identified with a tree search in which L branches are considered at each step.

As in the single branch algorithm, in the L-branch algorithm the initial truncated permutation matrix $\mathbf{P}_{0,1}$ is chosen to be $\mathbf{i}_1$. (In the multiple branch algorithm we use a double index for the successively generated matrices to distinguish the different branches in each iteration.) Again, each iteration of the algorithm augments the candidate truncated permutation matrices by D rows and retains the candidates that yield the smallest $L < N$ values of the objective. At iteration $k = 1$, we construct all $\frac{(N-1)!}{(N-D-1)!}$ candidate matrices of size $(D+1) \times N$ of the form $\mathbf{P} = \begin{bmatrix}\mathbf{P}_{0,1}^T & \mathbf{A}_{q_1,\cdots,q_D}^T\end{bmatrix}^T$, where $q_1, \ldots, q_D \in \{2, \ldots, N\}$. The corresponding metric $\|\mathbf{H}_{11} - \mathbf{P}\mathbf{R}\mathbf{P}^T\|_F$ is then calculated for all candidates and those yielding the smallest L metrics are retained. These candidates are denoted $\mathbf{P}_{1,1}$ to $\mathbf{P}_{1,L}$, where $\mathbf{P}_{1,1}$ is the candidate yielding the smallest metric. Similarly, at the k-th iteration, all possible $\frac{(N-kD-1)!}{(N-(k+1)D-1)!}$ candidate matrices of size $(kD+1) \times N$ of the given structure are formed, and the corresponding metric is calculated for each. Again, L candidates are retained and are denoted $\mathbf{P}_{k,1}$ to $\mathbf{P}_{k,L}$. At the last iteration, $k = \frac{N-1}{D}$ and the final permutation matrix $\mathbf{P}$ is chosen to be $\mathbf{P}_{\frac{N-1}{D},1}$.

As an illustrative example, in Fig. 1 we consider using the L-branch method with $L = 2$ and $D = 1$ for matching an 8-point constellation generated using the systematic technique of Sec. II-A. The grid is set up with the indices of the constellation points down the left side and the iteration number along the top. In the figure, the notation in parentheses at the grid points corresponds to the candidate matrices retained at the end of an iteration, e.g., (1278) corresponds to $\mathbf{P}_{3,1} = \begin{bmatrix}\mathbf{i}_1^T & \mathbf{i}_2^T & \mathbf{i}_7^T & \mathbf{i}_8^T\end{bmatrix}^T$. For $k = 0$, the first constellation point is assigned the first label. This is represented by the upper left grid point. For the $k = 1$ iteration, the 7 possible two-row candidate matrices are formed and the corresponding metrics are calculated. It is found that the two best candidates are $\mathbf{P}_{1,1} = \begin{bmatrix}\mathbf{i}_1^T & \mathbf{i}_2^T\end{bmatrix}^T$ and $\mathbf{P}_{1,2} = \begin{bmatrix}\mathbf{i}_1^T & \mathbf{i}_6^T\end{bmatrix}^T$. These two branches remain in the tree diagram and are labelled (12) and (16). The other 5 candidates are discarded and their corresponding branches are pruned. At the $k = 2$ iteration, the metrics corresponding to all possible three-row candidates with either $\mathbf{P}_{1,1}$ or $\mathbf{P}_{1,2}$ as the first two rows are calculated and the two candidates that yield the smallest metrics are retained. The retained branches can originate from a single node as in the $k = 2$ iteration or can come from a combination of the nodes in the previous iteration, as for $k = 3$. The process of forming, testing and retaining candidate matrices continues until the last iteration. The resulting permutation matrix is used to permute the constellation points. This complete branch is shown in bold in the figure.

3) Obtaining the labels corresponding to $\mathbf{P}$*:* Both the single and L-branch successive matching techniques yield a permutation matrix $\mathbf{P}$. Obtaining the labels corresponding to this permutation is straightforward: the label assigned to the i-th constellation point is simply the N_B-bit binary expansion of the i-th entry of the vector $\mathbf{P}\mathbf{e}$, where $\mathbf{e} = [0 \quad 1 \quad \cdots \quad N-1]^T$.

4) Computational complexity reduction methods: Although the successive matching algorithm is efficient (see Sec. IV), further computational gains can be obtained as outlined below.

Some of the constellations that are geometrically designed

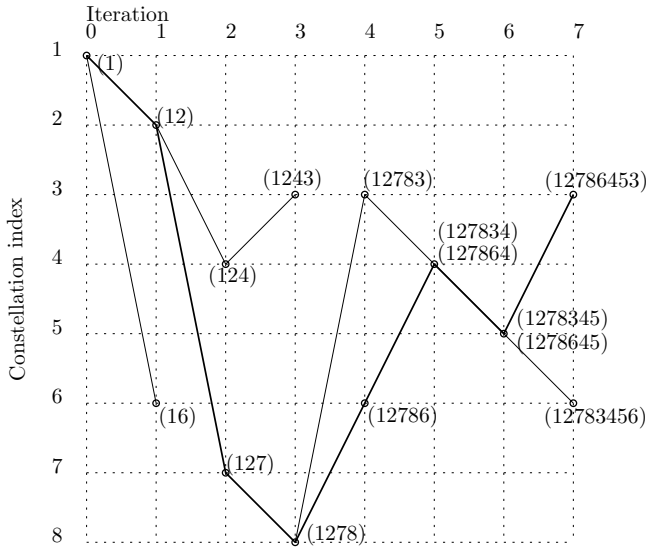

Fig. 1. Example: L-branch successive matching of an 8-point constellation with $L = 2$ and $D = 1$. The surviving branch is shown in bold. Surviving branches correspond to candidate truncated permutation matrices, e.g., the branch denoted (1278).

using the technique presented in Sec. II-B possess an antipodal symmetry whereby every point in the constellation has an opposing point with maximal chordal distance [7]. For these constellations, the number of iterations in the successive matching algorithm can be halved by considering these opposing points together and assigning them to complementary labels. This technique can be also used to generate labels that mimic the special structure of binary reflected Gray labels, cf. [12].

Another computational saving can be obtained by noting that the cost of calculating the Frobenius norm at the k-th step can be reduced to computing the norm components corresponding to the bottom D-rows of the updated permutation matrix. This is because the norm components corresponding to the first $(k-1)D+1$ rows have already been calculated in the previous iteration. The computational complexity of this technique will be discussed in the following section.

IV. Complexity of the Successive Matching Algorithm

In this section we analyze the number of multiplications invoked by the different versions of the successive matching algorithm. We notice that in (8), the multiplication by truncated permutation matrices of the form $[\mathbf{P}_{k-1}^T \quad \mathbf{A}_{q_1,\cdots,q_D}^T]^T$ amounts to selecting certain $(kD+1)\times(kD+1)$ blocks from the matrix $\mathbf{R}$, a process that incurs negligible computational complexity. The objective in (8) can be then expressed as

$$\begin{aligned}&\operatorname{Tr}(\mathbf{H}_{kk}\mathbf{H}_{kk}^T) - 2\operatorname{Tr}(\mathbf{H}_{kk}^T\mathbf{R}_{k-1,q_1,\cdots,q_D})\\ &\quad + \operatorname{Tr}(\mathbf{R}_{k-1,q_1,\cdots,q_D}\mathbf{R}_{k-1,q_1,\cdots,q_D}^T),\end{aligned} \tag{9}$$

where $\mathbf{R}_{k-1,q_1,\cdots,q_D} = [\mathbf{P}_{k-1}^T \quad \mathbf{A}_{q_1,\cdots,q_D}^T]^T\mathbf{R}[\mathbf{P}_{k-1}^T \quad \mathbf{A}_{q_1,\cdots,q_D}^T]$. The first term in (9) is not necessary to compute because it is independent of the permutations to be optimized. To compute the last term efficiently, we evaluate the matrix $\mathbf{R}\odot\mathbf{R}$ at the beginning of the algorithm and at each iteration compute the last term by adding the entries of $\mathbf{R}\odot\mathbf{R}$ that are selected by $[\mathbf{P}_{k-1}^T \quad \mathbf{A}_{q_1,\cdots,q_D}^T]^T$. Evaluating $\mathbf{R}\odot\mathbf{R}$ involves (N^2-N) multiplications. The remaining complexity of the algorithm can be computed by calculating the number of multiplications required for successive evaluations of the middle term in (9).

A. Complexity of the single branch successive matching algorithm with $D = 1$

In this case, because $D = 1$, the matrix $\mathbf{A}_{q_1,\ldots,q_D}$ contains one row of $\mathbf{I}_N$, i.e., $\mathbf{A}_{q_1,\ldots,q_D} = \mathbf{i}_s$. At the k-th step of the single branch approach, the middle term in (9) is computed $(N-k+1)$ times for $k\times k$ matrices. Since each evaluation of this term requires k^2 multiplications, the total computational complexity of this search is given by

$$N^2-N+\sum_{k=2}^{N-1}(N-k+1)k^2 = \frac{1}{3}N^4+\frac{1}{6}N^3+\frac{5}{12}N^2-\frac{11}{6}N. \tag{10}$$

Therefore, it is seen that the computational complexity of the direct implementation of the single branch approach is $\mathcal{O}(N^4)$, which is one order higher than the complexity of the Hungarian technique used in the technique outlined in Sec. III-A and can be computationally prohibitive for large QAPs.

In Sec. III-C4 it was observed that at each step the computational complexity of computing the objective can be reduced by exploiting the computation at the preceding step. To quantify this reduction, we write

$$\mathbf{H}_{(k+1)(k+1)} = \begin{bmatrix}\mathbf{H}_{kk} & \mathbf{t}\\ \mathbf{t}^T & c\end{bmatrix}, \tag{11}$$

where $\mathbf{t}$ is the $k\times 1$ vector containing the first k entries of the $(k+1)$-th column of $\mathbf{H}$ and c is its $(k+1)$-th diagonal entry. Using this notation, the objective in (8) can be expressed as (12) on the next page. Notice that, even though the Euclidean distance matrix $\mathbf{E}$ described in Sec. III-B2 is symmetric, the ranking matrix $\mathbf{R}$ derived from it is generally not symmetric and hence the second and third terms in this expansion are generally not identical. From (12) it is seen that the first term is computed at the k-th iteration and is independent of $\mathbf{i}_s$, which is the optimization variable at the $(k+1)$-th iteration. Now the computational complexity for evaluating the norms in the second and third terms on the right hand side is $2k+1$. Using ideas similar to the ones above, it can be shown that the number of multiplications in the efficient implementation of the single branch version of Algorithm 2 is

$$N^2-N+\sum_{k=2}^{N-1}(2k+1)(N-k+1) = \frac{1}{3}N^3+\frac{5}{2}N^2-\frac{29}{6}N-1. \tag{13}$$

B. Complexity of the multiple branch successive matching algorithm with $D = 1$

The difference in complexity in the multiple branch approach is that at every iteration the links emerging from L branches, instead of one branch, are examined. Hence, the computational complexity associated with this modification is bounded by L times the expression in (13); that is, the number of multiplications required in this approach is $\mathcal{O}(LN^3)$.

$$\left\| \begin{matrix} \mathbf{H}_{kk} - \mathbf{P}_k \mathbf{R} \mathbf{P}_k^T & \mathbf{t} - \mathbf{P}_k \mathbf{R} \mathbf{i}_s^T \\ \mathbf{t}^T - \mathbf{i}_s \mathbf{R} \mathbf{P}_k^T & c - \mathbf{i}_s \mathbf{R} \mathbf{i}_s^T \end{matrix} \right\|^2 = \|\mathbf{H}_{kk} - \mathbf{P}_k \mathbf{R} \mathbf{P}_k^T\|^2 + \|\mathbf{t} - \mathbf{P}_k \mathbf{R} \mathbf{i}_s^T\|^2 + \|\mathbf{t}^T - \mathbf{i}_s \mathbf{R} \mathbf{P}_k^T\|^2 + |c - \mathbf{i}_s \mathbf{R} \mathbf{i}_s^T|^2. \tag{12}$$

Therefore, as the size of the constellation grows, successive matching becomes as efficient as the Hungarian technique used to solve the assignment problem in the method in Sec. III-A. We will show in Sec. V-C that it yields significantly better labels for the constellations considered.

C. Complexity of successive matching algorithm with $D > 1$

In the first step of this approach, when $D > 1$, there are $\frac{(N-1)!}{(N-D-1)!}$ $D \times N$ permutation blocks over which the objective in (8) is minimized. Hence, this minimization involves $(2D + D^2)\frac{(N-1)!}{(N-D-1)!}$ multiplications. The total number of branches after this step is $\prod_{k=1}^{D}(N-k)$, from which we choose L branches to initiate the next step in the minimization. For each of the L branches, the number of $D \times N$ permutation blocks over which the objective in (8) is minimized in the next step is $\frac{(N-D-1)!}{(N-2D-1)!}$. Hence, the number of multiplications involved in this step is $L(6D + D^2)\frac{(N-D-1)!}{(N-2D-1)!}$. Assuming that $\frac{N-1}{D}$ is an integer, it can be seen that the total number of multiplications involved in using the permutation search with L branches and depth D is

$$N^2 - N + (2D + D^2)\frac{(N-1)!}{(N-D-1)!} + L \sum_{k=3}^{(N-1)/D} \big(2kD + D^2\big)\frac{\big(N-(k-2)D-1\big)!}{\big(N-(k-1)D-1\big)!}. \tag{14}$$

Observe that when $L = 1$ and $D = 1$, this expression yields (13). For $D = N - 1$, the expression in (14) yields $(N^2 - 4N - 1)\big((N-1)!\big)$, which is the number of multiplications required to perform an exhaustive search to find the optimal labelling.

V. Application of Quasi-Gray Labelled Constellations

In this section we assess the performance of the labelling techniques presented in Sec. III in two applications: uncoded non-coherent MIMO transmission using a 256-point Grassmannian constellation and a BICM-based non-coherent MIMO system using a 4096-point constellation.

A. A non-coherent MIMO communication system

In a non-coherent MIMO communication system neither the transmitter nor the receiver has access to channel state information (CSI). We consider the case in which the transmitter has M antennas, the receiver has K antennas, and the system is operated over a frequency-flat richly-scattered block-fading channel of coherence time T[1]. We will denote the signal vector transmitted at each channel use by the rows of a $T \times M$ matrix $\mathbf{Q}_X$. Hence, the $T \times K$ received signal matrix $\mathbf{Y}$ is

$$\mathbf{Y} = \mathbf{Q}_X \mathbf{H}_c + \mathbf{V},$$

[1]In this model, the channel remains constant for a block of T channel uses, and in each block the channel coefficients are statistically independent of those in other blocks, e.g., [2].

where $\mathbf{H}_c$ is the $M \times K$ channel matrix whose entries are drawn independently from the standard complex Gaussian distribution $\mathcal{CN}(0,1)$, and $\mathbf{V}$ is the $T \times K$ additive noise matrix whose entries are drawn independently from $\mathcal{CN}(0, M/\rho T)$, where ρ is the SNR. The conditional likelihood of the received signal is [29]

$$p(\mathbf{Y}|\mathbf{Q}_X) \propto \exp\Big(-\tfrac{\rho T}{M}\mathrm{Tr}\Big(\mathbf{Y}^\dagger\Big(\mathbf{I}_T - \tfrac{\rho T}{\rho T + M}\mathbf{Q}_X\mathbf{Q}_X^\dagger\Big)\mathbf{Y}\Big)\Big). \tag{15}$$

When $K = M$, $T \geq 2M$ and the SNR is high, the capacity-achieving input signals, $\{\mathbf{Q}_{X_i}\}$, are $T \times M$ unitary matrices that are isotropically distributed on $\mathbb{G}_M(\mathbb{C}^T)$ [2].

B. A BICM-IDD scheme

Even in scalar coherent BICM systems, the labelling of the channel symbols is a key component of the design [10], [11], [13]. It has been suggested that the optimal labelling is dependent on the SNR [11], [13], [30], with the binary reflected Gray labelling [12] providing superior performance at moderate-to-high SNRs [30]. When BICM is combined with iterative demapping and decoding (IDD), labelling selection is further complicated by the influence of the labelling on the convergence properties of the receiver. In that context, it is known that there are labellings that have better extrinsic information transfer (EXIT) characteristics than the Gray labelling, e.g., [31], and that there are labelling schemes that have the potential to out-perform Gray labelling at high SNR [32]. The BICM-IDD framework extends naturally to coherent MIMO systems, and although Gray labelling is not necessarily optimal in that setting either, e.g., [15], it does have some desirable attributes [9], [14]. In fact, when used in a BICM-IDD system, Gray labelling can provide effective communication at rates close to the ergodic capacity [33].

In [34], a BICM-IDD system was developed for Grassmannian-based non-coherent MIMO systems, cf. Fig. 2. That system used a labelling scheme that mimicked the principles of set-partitioning labelling. Since it is not known whether insights into effective labelling schemes made for coherent BICM-IDD systems can be applied effectively to non-coherent systems, in Sec. V-C we will compare the performance of the BICM-IDD system in Fig. 2 with the proposed quasi-Gray labelling schemes against that of the system with the original quasi-set-partitioning labelling.

In Fig. 2, $\mathbf{x}$ denotes a vector of length n of encoded interleaved bits. Let x_k be the entry of this vector corresponding to the k-th bit of the label of the transmitted signal matrix, $\mathbf{Q}_{X_i}$, and let $\mathbf{Y}$ be the corresponding received signal matrix. The conditioned log likelihood ratio of x_k is given by $L_{D_1}(x_k|\mathbf{Y})$ [33], where

$$L_{D_1}(x_k|\mathbf{Y}) = \log\frac{P(x_k = +1|\mathbf{Y})}{P(x_k = -1|\mathbf{Y})} = \log\frac{\sum_{\mathbf{Q}_{X_i} \in \mathcal{X}_{k,+1}} p(\mathbf{Y}|\mathbf{Q}_{X_i})P(\mathbf{Q}_{X_i})}{\sum_{\mathbf{Q}_{X_i} \in \mathcal{X}_{k,-1}} p(\mathbf{Y}|\mathbf{Q}_{X_i})P(\mathbf{Q}_{X_i})}, \tag{16}$$

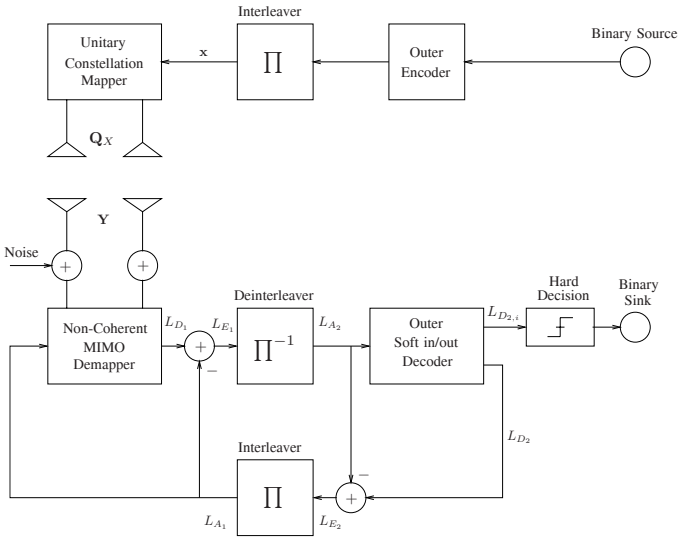

Fig. 2. A BICM-IDD scheme for non-coherent MIMO communication [34].

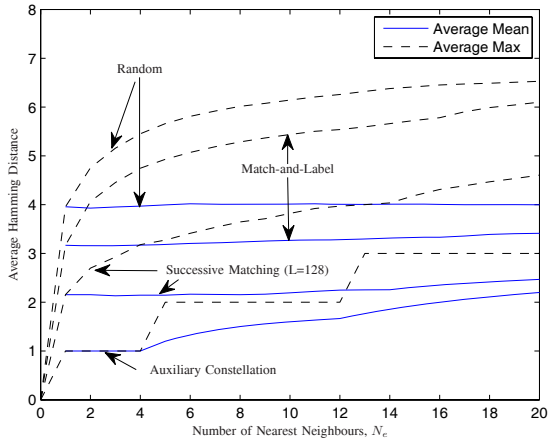

Fig. 3. Average mean and average maximum Hamming distance obtained for a 256-point constellation designed with the systematic technique in Sec. II-A and labelled with various labelling techniques.

where $p(\mathbf{Y}|\mathbf{Q}_{X_i})$ is given in (15), and an approximation to $P(\mathbf{Q}_{X_i})$ can be obtained from the decoder outputs at the previous iteration using the standard assumption of local independence of the interleaved encoded bits, i.e., [33], $P(\mathbf{Q}_{X_i}) \approx \prod_{k=1}^{n} P(x_k = [\mathcal{G}(i)]_k)$, where $[\mathcal{G}(i)]_k$ denotes the k-th element of the label $\mathcal{G}(i)$. The set $\mathcal{X}_{k,+1}$ contains all the matrices $\{\mathbf{Q}_{X_i}\}$ in the constellation whose indices have $x_k = +1$; i.e., $\mathcal{X}_{k,\pm 1} = \{\mathbf{Q}_{X_i} \in \mathcal{C} | x_k = [\mathcal{G}(i)]_k = \pm 1\}$.

C. Numerical examples

In both examples presented in this section Grassmannian constellations are employed for signalling in a non-coherent MIMO communication system with $M = K = 2$ transmit and receive antennas and coherence time $T = 4$. Since the constellations used in these examples are relatively large, the successive matching algorithm was implemented with a depth $D = 1$, in order to limit the computational complexity; a search depth $D > 1$ can yield better permutations, but is computationally prohibitive for constellations with the considered cardinalities.

1) Uncoded 256-point constellation: In this example we show the Hamming properties when various labelling techniques are applied to a representative constellation with $N = 256$ points generated using the method described in Sec. II-A [6]. In particular, in Fig. 3 we show the average over all constellation points of the mean and maximum Hamming distances of the N_e nearest neighbours for a range of values of N_e. These measures have a direct impact on the bit error rate (BER) performance of uncoded and coded communication systems, respectively. As a comparison of the effectiveness of the labelling methods, these measures have also been shown for the 256-point constellation presented in [8] which can be readily Gray labelled [9] and is used as the auxiliary constellation for the match-and-label algorithm of Sec. III-A. From this figure it is seen that for the randomly chosen labelling the average mean Hamming distance is, as expected, approximately equal to $\frac{N_B}{2} = 4$, regardless of the number of nearest neighbours. Using the match-and-label algorithm of

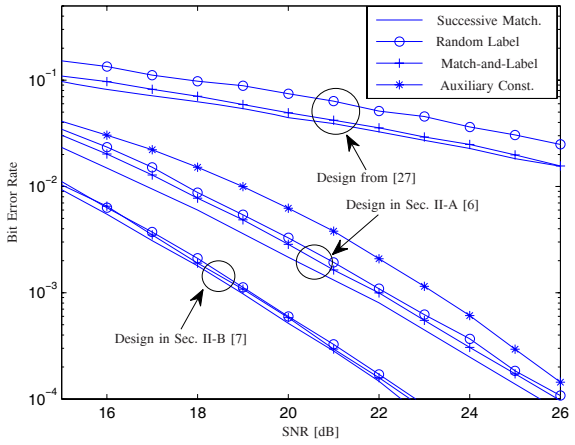

Fig. 4. A comparison between the performance of 256-point constellations labelled with various techniques. The performance of a Gray-labelled auxiliary constellation is also shown.

Sec. III-A results in an improvement of the average mean Hamming distance of slightly less than one bit. A further reduction of 1.2 bits in this distance was obtained by using the successive matching algorithm of Sec. III-C with $L = 128$ branches. The resulting mean Hamming distances of the nearest neighbours are about half of those obtained with the randomly chosen labelling.

The impact of the proposed labellings on the performance of an uncoded Grassmannian-based non-coherent MIMO system is demonstrated in Fig. 4 for 256-point constellations generated using the techniques in Sec. II-A and II-B and the technique in [27]. When the constellation in [8] is used as an auxiliary constellation, the labels generated by the match-and-label algorithm provide a performance gain over the randomly generated labels of approximately 0.2 dB and 0.1 dB for the constellations generated using the techniques outlined in Sec. II-A and II-B, respectively, and 2 dB for constellations generated using the technique in [27]. This gain could be increased if an auxiliary constellation with a geometric structure that resembles that of the constellation

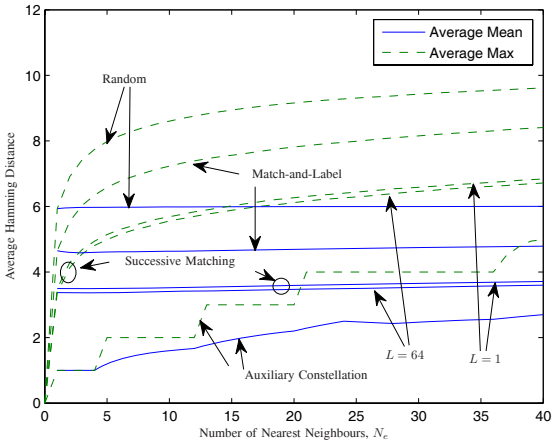

Fig. 5. Average mean and average maximum Hamming distance obtained for a 4096-point constellation designed with the geometry-based technique in Sec. II-B and labelled with various labelling techniques.

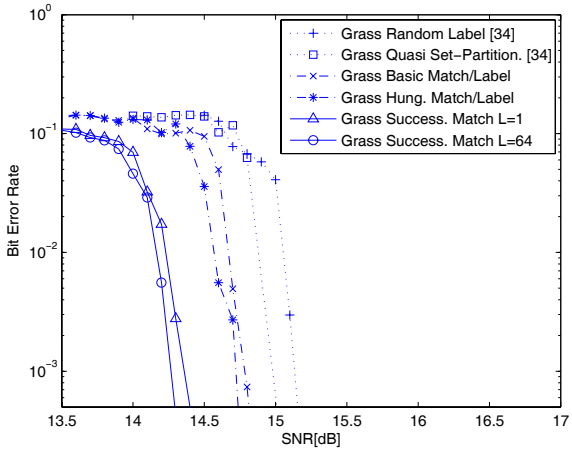

Fig. 6. Bit error rate performance of the proposed Grassmannian BICM-IDD scheme with a randomly chosen labelling, quasi-set-partitioning labelling, and the proposed quasi-Gray labellings. The approximate SNR threshold for a rate of 2.4 bpcu is 11.7 dB.

of interest were available. At a bit error rate of 10^{-3}, the multiple branch successive matching algorithm results in an approximate gain over the random labelling of 1 dB and 0.2 dB for the constellations generated using the techniques outlined in Sec. II-A and II-B, respectively, and 2.2 dB for the constellations generated using the technique in [27]. With the multiple branch successive matching algorithm, constellations designed systematically as in Sec. II-A provide an approximate performance gain of 2 dB over the Gray-labelled constellation from [8]. Even though the constellation in [8] is perfectly Gray labelled, its distance properties result in a relatively poor BER performance [28]. Below, we will show that the application of quasi-Gray labelled constellations to turbo-coded systems can have an even greater impact on error performance, since, in addition to decreasing the average Hamming distance, the maximum Hamming distance of the nearest neighbours has been substantially reduced, cf. Fig. 3.

2) A BICM-encoded 4096-point constellation: For this example we use a Grassmannian constellation with $N = 4096$ points that was designed using a rotation-based version of the technique in Sec. II-B [7] and labelled using different techniques. In Fig. 5 we show the average mean and maximum Hamming distances generated by different labelling strategies. For the match-and-label algorithm, the auxiliary constellation is generated using the method in [8] and for the successive matching technique the numbers of branches are $L = 1$ and $L = 64$. Similar to the case of the 256-point constellation, Fig. 5 shows that the multiple branch successive matching technique with $L = 64$ yields labels that are slightly better than those generated with its single branch counterpart, i.e., with $L = 1$. However, both techniques yield labels that perform significantly better than those generated randomly or via the match-and-label technique.

The impact of labelling on a practical communication system is investigated using the 4096-point Grassmannian constellation with different labels in the BICM-IDD system depicted in Fig. 2. The outer encoder in Fig. 2 is chosen to be a systematic parallel concatenated turbo code with identical recursive convolutional constituent codes. Using the notation in [35], the partition of each constituent convolutional code was $(2, 1, 1, 1)$, and its octal generators were $z^{\{i1\}} = (6, 0, 2, 3)$, $h^{\{1i\}} = (0, 6, 0, 5)$, $h^{\{2i\}} = (0, 3, 0, 1)$, $h^{\{3i\}} = (1, 2, 0, 3)$, and $h^{\{4i\}} = (2, 3, 3, 2)$. The conditioned log-likelihood ratios of the encoded bits at the output of the demapper are computed using (16) and the BICM and turbo interleavers were selected from a set of pseudo-randomly generated candidates. At the receiver, four demapping-decoding iterations were performed for each block, with eight BCJR-based turbo iterations being performed within the outer decoder for each demapping-decoding iteration. The input block length is 32016 bits and the outer code is a rate-4/5 punctured turbo code which yields an overall data rate of 2.4 bits per channel use (bpcu).

In Fig. 6 we provide a comparison between the performance of the quasi-Gray labelling schemes proposed herein with a randomly chosen labelling and the quasi-set-partitioning scheme proposed in [34]. At a BER of 10^{-3}, quasi-set-partitioning provides an SNR gain of 0.15 dB over the random labelling. The basic match-and-label algorithm presented in [28] yields a further gain of 0.35 dB, which improves slightly when the optimal Hungarian matching presented in Sec. III-A is used. A significant SNR gain over these labelling techniques is obtained when the successive matching technique of Sec. III-C is employed. For this technique we used the search depth $D = 1$ and the number of branches $L = 1$ and $L = 64$. For comparison, the SNR threshold for the high-SNR approximation of the non-coherent ergodic capacity [2] corresponding to the 2.4 bpcu rate considered in this example is 11.7 dB. Hence, the successive matching technique with $L = 64$ branches enables the proposed Grassmannian-based BICM-IDD scheme to perform within 2.8 dB of the approximate non-coherent ergodic capacity. We are not aware of any scheme that has been shown to approach the non-coherent capacity this closely.

Training-based techniques offer an alternative signalling method that achieves the communication degrees of freedom of the non-coherent MIMO channel [2], [36]. In Fig. 7,

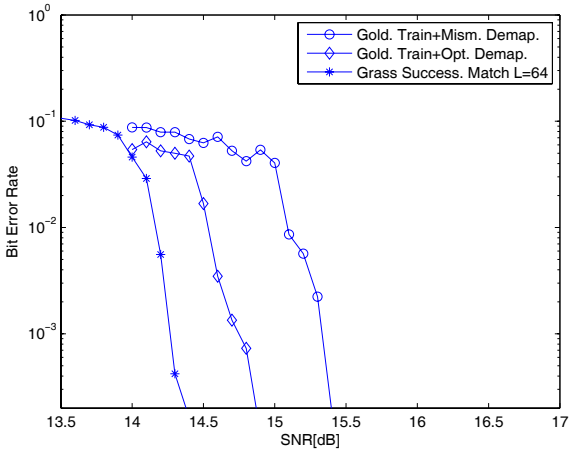

Fig. 7. Bit error rate performance of the proposed Grassmannian BICM-IDD scheme with quasi-Gray labelling. Performance is compared with that of a training-based system operating at the same data rate with an underlying Golden code with Gray-labelled 8-QAM symbols and optimal or mismatched demapping.

we consider using this technique in the same BICM-IDD framework. The training-based system operates at the same data rate as the 4096-point Grassmannian constellation using an underlying Golden code with Gray-labelled 8-QAM symbols. For this system the optimal training interval, $T_p = M = 2$, yields a coherent communication interval of length $T_d = T - T_p = 2$ [36]. The optimal training symbol in this case is proportional to $\mathbf{I}_M$, with power equally split between the training and data symbols [36]. For this system, both the mismatched and optimal detectors developed in [23] are considered. From Fig. 7 it is seen that the successive matching labelling technique enables Grassmannian-based non-coherent MIMO communication systems to outperform Gray-labelled Golden-encoded training-based systems with optimal demapping.

VI. Conclusion

This paper presented two techniques for assigning quasi-Gray labels to arbitrary Grassmannian constellations. In the first technique, the constellation of interest is directly matched to an auxiliary constellation that can be readily Gray labelled. The performance of this technique depends primarily on the similarity between the geometric structures of the matched constellations. For cases in which an auxiliary constellation with a similar structure is not available, a second technique is proposed wherein the matching is based on the distance spectra of the constellation of interest and a perfectly Gray-labelled hypothetical constellation. This technique is versatile as it does not require an auxiliary constellation and can be applied for generic constellations, including Grassmannian ones, with any dimension and cardinality. The efficacy of the labels generated by the proposed techniques have been illustrated for both coded and uncoded non-coherent MIMO communication systems. It was shown that, with these labels, non-coherent Grassmannian-based signalling can have a significant performance advantage over Golden-encoded Gray-labelled training-based systems with optimal demapping.

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