BLIND IDENTIFICATION OF PAM-MIMO SYSTEMS BASED ON THE DISTRIBUTION OF OUTPUT DIFFERENCES

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ABSTRACT

In this paper, we present, a new method for the Blind Identification and Source Separation of a convolutive Multi-Input Multi-Output (MIMO) system driven by multi-level inputs. The method takes advantage of the special properties of the observation differences distribution. We show that a specific set of differences can be used to reconstruct the mixing operator. Exhaustive search of the observation symbols yields sources separation. The method can be coupled with a simple clustering technique in order to treat noisy cases. Results on both noiseless and noisy scenarios show the efficiency of our approach.

Index Terms— Blind Idendification, Blind Source Separation, MIMO system, PAM modulation

1. INTRODUCTION

Blind Source Separation (BSS) is the task of recovering the n unobserved sources from the m observation signals without any quantitative information of the mixing procedure. The BSS methods can be divided according to the model mixing operator into linear mixture BSS ones (also known as instantaneous BSS) and convolutive mixture BSS ones (also referred to as multichannel blind deconvolution/equalization). Higher-Order Statistics (HOS) based methods and especially FastICA [1] has solved the problem of linear BSS in its general case ($n = m$ independent sources), by maximizing the inter-signal mutual independence. Current research on the field is interested in ill-posed cases of the same scenario, involving under-determined systems [2], time-varying filters [3], sparse [4] or statistically dependent [5] sources. The Blind Deconvolution scenario is more complex to treat and the papers attacking the problem are fewer than the ones treating the linear model. The first attempts were aiming at creating overdeterming systems by transforming the multichannel system into a set of simpler Single-Input Multi-Output systems [6]. Chen in [7] investigated the special case of i.i.d. sources using HOS. The treatment of colored sources have been explored using both Second-Order Statistics (SOS) [8] and HOS [9].

Alternatively, the linear or convolutional BSS problem has been studied from a geometric point of view. Typically these methods exploit the geometric properties of the observations distribution. The problem was investigated by Puntonet in et al. [10] for the separation of two sources, by finding the angle between the slopes of the observations scatter plot. A clustering based approach was introduced by Babaie-Zadeh et al. [11]. Diamantaras et al. in [12] introduced a novel method for linear MISO systems driven by binary antipodal sources. The model filter is recursively deflated, yielding in the final step: the filter and the source signals. The method was extended to the convolutive case in [13].

In this paper, we extend the basic concepts introduced in [14] to the MIMO case. We explore the special characteristics of the probability distribution of the observation differences. The most probable differences relate to the columns of the system transfer matrix and from those we can estimate the unknown mixing filters.

The paper is organized as follows: Section 2 gives the problem formulation. In Section 3 we explore the indeterminacies of the problem. The proposed solution is presented in Section 4 for the noiseless case and in Section 5 for the noisy case. Results on various simulations can be found in Section 6. We finally conclude in Section 7.

2. PROBLEM FORMULATION

The MIMO convolutional system with m observation signals and n input signals passing through an $m \times n$, L-tap filter $h_{p,q}(l)$ is defined as:

$$x_p(k) = \sum_{q=1}^{n} \sum_{l=0}^{L-1} h_{p,q}(l) s_q(k-l), \qquad p = 1, \cdots, m. \tag{1}$$

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If the sources are Pulse Amplitude Modulated (PAM) with M levels, then each sample $s_q(k)$, takes values from a discrete set $V = \{0, \cdots, M-1\}$.

By stacking column vectors $\mathbf{x}_p(k)$ containing time windows of length W of the output signals x_p

$$\mathbf{x}_p(k) = [x_p(k), \cdots, x_p(k-W+1)]^T,$$

into a "tall" vector $\mathbf{x}(k)$

$$\mathbf{x}(k) = [\mathbf{x}_1(k)^T, \cdots, \mathbf{x}_m(k)^T]^T \ , \tag{2}$$

we transform the system model equation Eq. (1) into the following equivalent matrix form:

$$\mathbf{x}(k) = \mathbf{H}\mathbf{s}(k), \qquad k = 1, \cdots, K \tag{3}$$

where

$$\mathbf{H} = \begin{bmatrix} \bar{\mathbf{H}}_{1,1} & \cdots & \bar{\mathbf{H}}_{1,n} \\ \vdots & & \vdots \\ \bar{\mathbf{H}}_{m,1} & \cdots & \bar{\mathbf{H}}_{m,n} \end{bmatrix}, \tag{4}$$

with $\bar{\mathbf{H}}_{p,q} \in \mathbf{R}^{W \times N}$, $N = W + L - 1$,

$$\bar{\mathbf{H}}_{p,q} = \begin{bmatrix} h_{p,q}(0) & \cdots & h_{p,q}(L-1) & & 0 \\ & \ddots & & \ddots & \\ 0 & h_{p,q}(0) & \cdots & & h_{p,q}(L-1) \end{bmatrix},$$

$$\mathbf{s}(k) = [\mathbf{s}_1(k)^T, \cdots, \mathbf{s}_n(k)^T]^T,$$
$$\mathbf{s}_q(k) = [s_q(k), \cdots, s_q(k-N+1)]^T.$$

The identification task for system (1) is equivalent to identifying $\mathbf{H}$ in (3).

The above MIMO model appears in various applications. For instance, in digital communications, the transmission of $n/2$ rectangular QAM sources propagating towards $m/2$ sensors through a multipath environment modelled by the complex filters is described by Eq. (1).

3. ASSUMPTIONS AND INDETERMINACIES

In the blind deconvolution scenario we assume that the filter matrix $\mathbf{H}$, as well as the vector source sequence $\mathbf{s}(k)$, are unknown. However, we make the following assumptions which are suitable to the communications problem described above:

1 *The signals s_q are independent to each other*

2 *The samples $s_q(k)$ are i.i.d.*

3 *For all sources, s_q, the symbol transmission probabilities are uniform:*

$$p_s = Prob(s_q(k) = r) = \frac{1}{M}, \ \forall k, q, r. \tag{5}$$

It is well known that the blind identification has certain indeterminacies pertaining to the sign and order of the sources. Any permutation and sign change of the sources does not change the observed signal $\mathbf{x}$ as long as the submatrices $\tilde{\mathbf{H}}_q = [\bar{\mathbf{H}}_{1,q}^T \cdots \bar{\mathbf{H}}_{m,q}^T]^T$ are also permuted and signed appropriately. It follows that a successful Blind Identification algorithm is able to estimate the submatrices $\tilde{\mathbf{H}}_q$ only up to sign and in no order.

4. BLIND IDENTIFICATION

In analogy to the treatment of the convolutive Multi-Input Single-Ouput (MISO) case in [15] our approach will be based in the distribution of the output signal differences. Let's call $\mathbf{d_s} = \mathbf{s}(k) - \mathbf{s}(k')$ and $\mathbf{d_x} = \mathbf{x}(k) - \mathbf{x}(k')$ the input and output differences between the samples at time instances k and k'. Then, clearly,

$$\mathbf{d_x}(k, k') = \mathbf{H}\mathbf{d_s}(k, k'). \tag{6}$$

with

$$\mathbf{d_s}(k, k') = [\mathbf{d}_{\mathbf{s}_1}(k, k')^T, \cdots, \mathbf{d}_{\mathbf{s}_n}(k, k')^T]^T, \tag{7}$$

$\mathbf{d}_{\mathbf{s}_q}(k, k') = [\delta_q(k, k'), \cdots, \delta_q(k-N+1, k'-N+1)]^T$, $\delta_q(k, k') = s_q(k) - s_q(k')$. In the subsequent analysis, due to input stationarity, we can drop the indices k and k' without affecting our results. The vector $\mathbf{d_s}$ contains totally $C = n \times N$ elements. The distribution of $\mathbf{d_x}$ depends directly on the distribution of $\mathbf{d_s}$, which in turn depends on the distribution of the input differences $\mathbf{d}_{\mathbf{s}_q}$.

Due to the PAM nature of the sources, the difference signal δ_q is discrete, taking values from the set

$$\Delta_V = \{-(M-1), -(M-2), \cdots, (M-2), (M-1)\}.$$

There are M equiprobable input symbols in V (with probabilities $p_s = \frac{1}{M}$), and M^2 equiprobable input symbol couples in $V \times V$. It is not difficult to compute the probabilities of the input symbol differences δ_q and see that they are independent of q:

$$p_\delta(\mu) \stackrel{\triangle}{=} Prob(\delta_q = \mu) = (M - |\mu|)/M^2, \tag{8}$$

$\mu = 0, \pm 1, \pm 2, \cdots, \pm(M-1)$. According to the assumption 1, the elements of the input vector difference $\mathbf{d_s}$ are independent, so the vector probability can be written as

$$p_{\mathbf{d_s}}([\mu_1, \cdots, \mu_C]^T) = \prod_{i=1}^{C} p_\delta(\mu_i) \tag{9}$$

As in [15] we make the assumption that the columns $\mathbf{h}_i$ of $\mathbf{H}$ are *Delta-independent*, i.e.

4 In (6) if $\mathbf{d_s}, \mathbf{d}'_\mathbf{s} \in \Delta_V$ and $\mathbf{d_s} \neq \mathbf{d}'_\mathbf{s}$ then $\mathbf{H}\mathbf{d_s} \neq \mathbf{H}\mathbf{d}'_\mathbf{s}$.

We now observe the following facts:

- The most likely input difference vector $\mathbf{d_s}$, is the zero vector with probability

$$P_0 = p_{\mathbf{d_s}}(\mathbf{0}) = \prod_{i=1}^{C} p_\delta(0) = \frac{1}{M^C}. \qquad (10)$$

- The next most likely input difference vectors are those of the form $[\pm 1, 0, \cdots, 0]^T$, $[0, \pm 1, \cdots, 0]^T$, ..., $[0, 0, \cdots, \pm 1]^T$, containing $C-1$ zeros and one element 1 or -1. There are $2C$ such vectors (call them $\mathbf{b}_q$, $q = 1, \cdots, 2C$) with equal probabilities of appearance:

$$P_1 = p_{\mathbf{d_s}}(\mathbf{b}_q) = p_\delta(\pm 1) \prod_{i=1}^{C-1} p_\delta(0) = \frac{M-1}{M^{C+1}} \qquad (11)$$

  According to the definition in (7) and Assumption 4 the corresponding output vectors are:

$$\mathbf{d}_\mathbf{x}^{(q)} = \mathbf{H}\mathbf{b}_q = \pm \mathbf{h}_q, \qquad q = 1, \cdots, 2C \qquad (12)$$

  where $\mathbf{h}_q$ is the q-th column of the matrix filter $\mathbf{H}$.

- All other input difference vectors have lower probabilities than P_1 because they include two or more non-zero elements.

Based on Eq. (12), it is therefore possible to extract the columns of $\mathbf{H}$ (up to the sign and in arbitrary order) by arranging the output difference vectors $\mathbf{d_x}$ in decreasing probability order and collecting the vectors with rank $2, \cdots, 2C+1$.

4.1. Ordering the columns

The matrix $\mathbf{H}$ is composed of multiple Toeplitz blocks as described in (4.1). This imposes constraints in the order of the columns. In particular, for all integers $\alpha > 0$, if the indexes (p, q), and $(p', q') = (p - \alpha, q - \alpha)$, belong to the same Toeplitz block then we must have $h_{p,q} = h_{p',q'}$. However, these constraints are not enough to uniquely identify $\mathbf{H}$ since any matrix

$$\hat{\mathbf{H}} = \begin{bmatrix} \bar{\mathbf{H}}_{1,\pi(1)} & \cdots & \bar{\mathbf{H}}_{1,\pi(n)} \\ \vdots & & \vdots \\ \bar{\mathbf{H}}_{m,\pi(1)} & \cdots & \bar{\mathbf{H}}_{m,\pi(n)} \end{bmatrix},$$

will satisfy them for any permutation function π.

4.2. Blind Identification and Source Separation

The preceding analysis leads to the following algorithm for identifying the MIMO filter $\mathbf{H}$ (up to the aforementioned indeterminacies):

Algorithm 1 ***Noiseless Blind Identification***

- *Compute the output differences $\mathbf{d_x}(k, k')$ for all pairs of indexes k, k'*
- *Estimate the distribution $p_{\mathbf{d_x}}$ of $\mathbf{d_x}$*
- *Sort the probabilities $\hat{p}_{\mathbf{d_x}}$. Let $\hat{\mathbf{h}}_q$, $q = 1, \cdots, 2C$, be the values of $\mathbf{d_x}$ with probabilities ranging from the 2nd highest to the (2C+1)-th highest probability.*
- *Arrange the vectors $\hat{\mathbf{h}}_q$ by forcing the satisfaction of the Toeplitz-based structure. From the elements of the submatrices we obtain our estimates of the mixing filters.*

From the estimated MIMO filter matrix $\hat{\mathbf{H}}$ the reconstruction of the sources can be achieved by minimizing

$$\hat{\mathbf{s}} = \arg \min_{\mathbf{s} \in V_s} \|\mathbf{x} - \hat{\mathbf{H}}\mathbf{s}\|^2 \qquad (13)$$

where $V_s = V^C$ is the input alphabet for the vector $\mathbf{s}$. Since the input alphabet is discrete, we can perform an exhaustive search in the grid of the input space and keep the minimum input vector.

5. NOISY CASE

The presence of noise in the observations can be introduced by modifying Eq. (3) as:

$$\mathbf{x}(k) = \mathbf{H}\mathbf{s}(k) + \mathbf{e}(k). \qquad (14)$$

with $\mathbf{e}(k) \in \mathbf{R}^{mW}$ being the additive Gaussian noise; $\mathbf{e}(k)$ is assumed statistically independent to $\mathbf{s}(k)$. Our method uses the observation difference as it is described in (6). The equivalent equation for the noisy scenario is

$$\mathbf{d_x}(k, k') = \mathbf{H}\mathbf{d_s}(k, k') + \mathbf{d_e}(k, k'), \qquad (15)$$

where the noise difference $\mathbf{d_e}$ is also Gaussian. Algorithm 1 cannot be used as it is, because we need first to identify the noiseless values $\mathbf{H}\mathbf{d_s}(k, k')$. These values should be the centers of Gaussian clusters as described in (15) therefore, we apply a clustering scheme in (mW)-dimensional space. We employ the Basic Sequential Clustering Algorithm (BSAS) [16][chapter 12] since the algorithm is suitable for detecting compact groups of data, as long as they are well separated in space. In this algorithm, each pattern creates a new cluster unless its distance from one of the existing cluster centers is smaller than some threshold θ.

The most challenging problem of the BSAS algorithm is the proper choice of θ. Luckily, we know in advance that the most probable cluster is centered around zero and its probability is P_0 as given in Eq. (10). Therefore, we choose θ as follows: we arrange the norms $\nu(k, k') = \|\mathbf{d_x}(k, k')\|^2$ in increasing order $\nu^{(1)}, \nu^{(2)}, \cdots, \nu^{(K^2)}$, and we set θ such that

(a) $\theta \geq \nu^{(\lfloor \alpha P_0 K^2 \rfloor)}$, where α less than, but close to 1, eg. $\alpha = 0.9$; in other words, at least $\alpha P_0 K^2$ many differences $\mathbf{d_x}$ have norm less than θ (out of the total K^2 differences)

(b) the difference $\nu^{(p+1)} - \nu^{(p)}$ is a local peak in the range $\lfloor \alpha P_0 K^2 \rfloor \leq p \leq \lfloor \beta P_0 K^2 \rfloor$, with $\beta > 1$, but close to 1, for instance $\beta = 1.2$.

The overall identification algorithm is summarized below:

Algorithm 2 *Noisy MIMO Identification*

- *Collect the noisy differences* $\mathbf{d_x}(k, k')$, $k, k' = 1, \cdots, K$, *and initialize the set of cluster centers to* $Y = \{\mathbf{d_x}(1, 1) = \mathbf{0}\}$*; Set* θ *as described above*
- *For each* $\mathbf{d_x}(k, k')$ *find the distance* $D(k, k')$ *to the closest center* $\mathbf{c}_i$ *in* Y
  - *If* $D(k, k') > \theta$*, then update* $\mathbf{c}_i$ *to be the average of the vectors that belong to its corresponding cluster*
  - *otherwise, add this difference vector to the set of centers,* $Y = Y \cup \{\mathbf{d_x}(k, k')\}$
- *Use the cluster centers as the noiseless difference vectors* $\mathbf{d_x}$ *and proceed with the identification as in Algorithm 1.*

6. SIMULATIONS

We have tested the identification algorithm on various artificial data sets generated by random MIMO systems. Due to lack of space we show here two experiments. In the first experiment we simulated a noiseless system with $n = 2$ sources with $M = 2$ PAM levels, $m = 8$ outputs, filter length $L = 2$, and window size $W = 2$ (so $C = 6$). The mixing filters were

$$h_{1,1} = [-0.3005, -1.0025] \qquad h_{1,2} = [0.4238, -0.3287]$$
$$h_{2,1} = [-0.0658, 0.0313] \qquad h_{2,2} = [0.6463, -0.6827]$$
$$h_{3,1} = [0.2226, -1.1322] \qquad h_{3,2} = [1.0467, -0.5247]$$
$$h_{4,1} = [1.0593, -0.7430] \qquad h_{4,2} = [1.2548, 0.4496]$$
$$h_{5,1} = [0.4933, 0.5957] \qquad h_{5,2} = [0.3018, -0.2308]$$
$$h_{6,1} = [-0.5215, -1.9079] \qquad h_{6,2} = [0.8483, 0.1546]$$
$$h_{7,1} = [0.9549, -1.4300] \qquad h_{7,2} = [-0.7538, -0.3955]$$
$$h_{8,1} = [0.2790, 1.4017] \qquad h_{8,2} = [-0.2967, 0.0629]$$

The data set size was $K = 300$ samples, thus generating $K^2 = 90,000$ pairwise differences. Figure 1 shows the probability of the most likely clusters produced by BSAS with θ automatically set to 0.1289. Algorithm 2 yields the matrix $\hat{\mathbf{H}}$ whose columns $\hat{\mathbf{h}}_i$ are *perfect reconstructions* of the original comlumns of $\mathbf{H}$ although with mixed order and for both signs. In particular: $\hat{\mathbf{h}}_1 = -\mathbf{h}_2$, $\hat{\mathbf{h}}_2 = \mathbf{h}_2$, $\hat{\mathbf{h}}_3 = \mathbf{h}_1$, $\hat{\mathbf{h}}_4 = \mathbf{h}_6$, $\hat{\mathbf{h}}_5 = -\mathbf{h}_1$, $\hat{\mathbf{h}}_6 = -\mathbf{h}_6$, $\hat{\mathbf{h}}_7 = \mathbf{h}_5$, $\hat{\mathbf{h}}_8 = -\mathbf{h}_5$, $\hat{\mathbf{h}}_9 = -\mathbf{h}_3$, $\hat{\mathbf{h}}_{10} = \mathbf{h}_3$, $\hat{\mathbf{h}}_{11} = \mathbf{h}_4$, $\hat{\mathbf{h}}_{12} = -\mathbf{h}_4$.

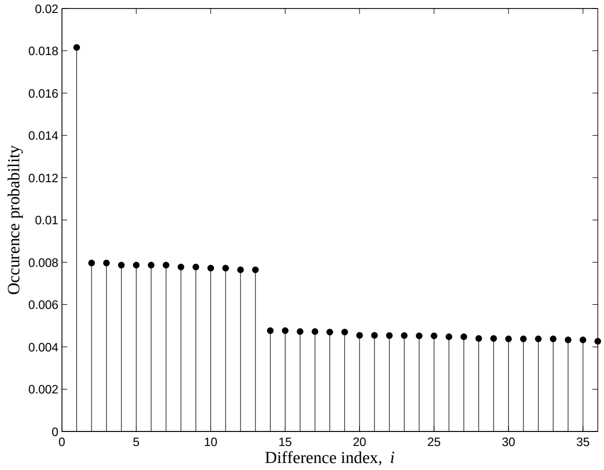

Fig. 1. Sorted probabilities of the most likely differences in a noiseless MIMO system ($C = 6$). Notice that the probabilities from $i = 2$ to $i = 13$ are almost equal and there is a clear jump for $i = 1$ and $i = 14$.

In the second experiment, the same MIMO system incorporates additive Gaussian white noise with SNR = $25dB$. In this case, we use $\theta = 0.7213$ and obtain almost perfect reconstruction of the original columns,

$$\hat{\mathbf{h}}_1^T \mathbf{h}_1 = 0.9997 \|\hat{\mathbf{h}}_1\| \|\mathbf{h}_1\|, \ \hat{\mathbf{h}}_2^T \mathbf{h}_1 = -0.9992 \|\hat{\mathbf{h}}_2\| \|\mathbf{h}_1\|,$$
$$\hat{\mathbf{h}}_3^T \mathbf{h}_3 = -0.9998 \|\hat{\mathbf{h}}_3\| \|\mathbf{h}_3\|, \ \hat{\mathbf{h}}_4^T \mathbf{h}_3 = 0.9997 \|\hat{\mathbf{h}}_4\| \|\mathbf{h}_3\|,$$
$$\hat{\mathbf{h}}_5^T \mathbf{h}_5 = 0.9997 \|\hat{\mathbf{h}}_5\| \|\mathbf{h}_5\|, \ \hat{\mathbf{h}}_6^T \mathbf{h}_2 = 0.9997 \|\hat{\mathbf{h}}_6\| \|\mathbf{h}_2\|,$$
$$\hat{\mathbf{h}}_7^T \mathbf{h}_5 = -0.9999 \|\hat{\mathbf{h}}_7\| \|\mathbf{h}_5\|, \ \hat{\mathbf{h}}_8^T \mathbf{h}_6 = -0.9971 \|\hat{\mathbf{h}}_8\| \|\mathbf{h}_6\|,$$
$$\hat{\mathbf{h}}_9^T \mathbf{h}_2 = -0.9993 \|\hat{\mathbf{h}}_9\| \|\mathbf{h}_2\|, \ \hat{\mathbf{h}}_{10}^T \mathbf{h}_4 = 0.9987 \|\hat{\mathbf{h}}_{10}\| \|\mathbf{h}_4\|,$$
$$\hat{\mathbf{h}}_{11}^T \mathbf{h}_4 = -0.9986 \|\hat{\mathbf{h}}_{11}\| \|\mathbf{h}_4\|.$$

except that $\mathbf{h}_6$ is not extracted (only $-\mathbf{h}_6$ matches $\hat{\mathbf{h}}_8$). This is due to the fact that the difference vectors ranking 2nd to 13th are not so clearly separated from the 14th vector, as shown in Fig. 2, and therefore a mixup happened in the last vector. More simulations results and theoretical analysis on the effect of noise will be presented in a future full paper.

7. CONCLUSIONS

We have presented a novel method for the blind identification and separation of MIMO convolutive systems excited by PAM modulated inputs. The method is similar to the MISO approach proposed in [15] except that we use a new clustering method based on the BSAS scheme which gives better results even in the presence of noise. The proposed method exploits the properties of the data difference distribution. It turns out that the most probable differences reveal the columns of the mixing filter matrix, upto a permutation and sign. The block

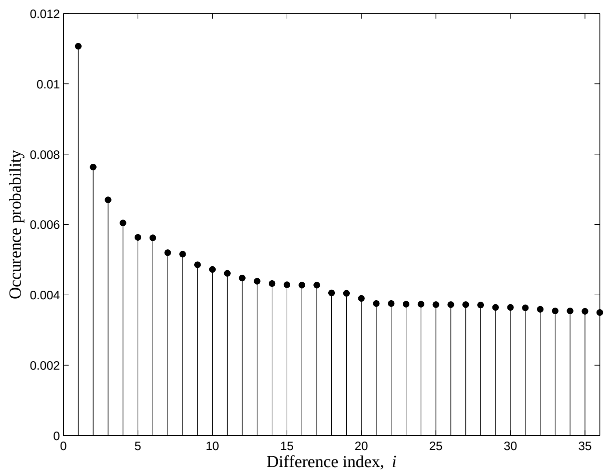

Fig. 2. Probabilities of the most likely differences in a noisy MIMO system with SNR at $25dB$.

Toeplitz structure of the matrix can be used to recover the order of the columns within a block although it cannot recover the order of the blocks which is linked with the indeterminacy of the input order. An important feature of the method is the fact that the size of the differences population depends quadratically on the number of observed samples, meaning that even with relatively few samples (e.g. less than 500) we can perform reliable clustering and solve the blind MIMO problem.

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