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Matched shrunken subspace detectors for hyperspectral target detection

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ABSTRACT

In this paper, we propose a new approach, called the matched shrunken subspace detector (MSSD), to target detection from hyperspectral images. The MSSD is developed by shrinking the abundance vectors of the target and background subspaces in the hypothesis models of the matched subspace detector (MSD), a popular subspace-based approach to target detection. The shrinkage is achieved by introducing simple l_2-norm regularisation (also known as ridge regression or Tikhonov regularisation). We develop two types of MSSD, one with isotropic shrinkage and termed MSSD-i and the other with anisotropic shrinkage and termed MSSD-a. For these two new methods, we provide both the frequentist and Bayesian derivations. Experiments on a real hyperspectral imaging dataset called Hymap demonstrate that the proposed MSSD methods can outperform the original MSD for hyperspectral target detection.

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1. Introduction

Target detection or anomaly detection is an important task of hyperspectral image (HSI) analysis [1–6]. To target detection, the matched subspace detector (MSD) [7,8] is one of the most widely-used subspace-based approaches, underlying which is the idea of the linear mixing model (LMM) [9].

The LMM [9] is a typical approach to unmixing a mixed pixel. Suppose there are p spectral bands and thus a mixed pixel $\mathbf{x}$ is represented by a p-dimensional vector/spectrum. Let us assume there are K types of materials potentially constituting a pixel; these component materials are often referred to as endmembers, the spectra of which can be represented by $\mathbf{m}_1, \ldots, \mathbf{m}_K$, where each $\mathbf{m}_k$ is a p-dimensional vector. Then the LMM of pixel $\mathbf{x}$ models the spectral signature of $\mathbf{x}$ as a linear combination of endmembers $\mathbf{m}_1, \ldots, \mathbf{m}_K$ with corresponding abundance fractions $a_1, \ldots, a_K$. More specifically, $\mathbf{x} = [x_1, \ldots, x_p]^{\mathrm{T}}$ can be expressed as an additive mixture of K endmembers $\mathbf{m}_k$ plus noise:

$$\mathbf{x} = \Sigma_{k=1}^{K} a_k \mathbf{m}_k + \mathbf{n} = \mathbf{M}\mathbf{a} + \mathbf{n}, \quad (1)$$

where $\mathbf{M}$ is a $p \times K$ matrix whose columns are the K endmember spectra $\mathbf{m}_k = [m_{k,1}, \ldots, m_{k,p}]^{\mathrm{T}}$ for $k = 1, \ldots, K$, respectively; $\mathbf{a} = [a_1, \ldots, a_K]^{\mathrm{T}}$ denotes the abundance vector; and $\mathbf{n} = [n_1, \ldots, n_p]^{\mathrm{T}}$ represents the additive Gaussian white noise, i.e. $\mathbf{n} \sim \mathcal{N}(\mathbf{0}, \sigma^2\mathbf{I})$, where $\mathbf{I}$ is a $p \times p$ identity matrix. In classical unmixing problems, the abundances $a_1, \ldots, a_K$ need to satisfy two conditions, which are the non-negative constraint and the sum-to one constraint, i.e. $a_k \geq 0$ and $\Sigma_{k=1}^{K} a_k = 1$, respectively. However, in target detection problems, as explained in [9], both constraints will complicate the solution; as usually is the case, we can relax both constraints in target detection.

To achieve an HSI target detection, the MSD determines whether a test pixel can be represented by a linear combination of target spectral signatures and background spectral signatures. To this end, two subspaces are constructed: the target subspace and the background subspace. In each subspace, the MSD assumes that each basis vector represents an endmember, which is in line with the assumption of the LMM for HSI analysis.

To construct the two subspaces, the MSD usually acquires their basis vectors from the eigendecomposition of covariance matrices of the training samples [1,10]. The eigenvectors with dominant eigenvalues, termed leading eigenvectors, are selected as bases to span the subspaces, while those with small eigenvalues are discarded. This is essentially a scheme of basis selection, or say 0/1 weighting, which extracts a subspace out of the full eigenspace.

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In fact, the 0/1 weighting scheme of the MSD implicitly imposes a sparseness constraint or say an l_0-norm regularisation while building its LMM. However, it is well known that such a "hard" selection may exhibit high variance on the selected leading eigenvectors. Alternatively, explicit sparse representation (SR)-based techniques have also been developed in hyperspectral target detection [11–13], with selection of a small number of atoms from a large dictionary. That is, these SR methods model a test HSI pixel as a linear combination of only few atoms from an over-complete dictionary; atoms in the dictionary are usually also samples, hence, these SR methods can be viewed as being developed in the original sample space. Regarding the construction of the dictionary, [11] propose to construct a background spectra dictionary and a target spectra dictionary separately; on the other hand, [12,13] propose to construct an over-complete dictionary including both background spectra and target spectra.

To avoid the problem of high variance from such a "hard" selection, shrinkage methods [14] have been developed in statistical learning, mainly due to such a problem in regression analysis. Among the shrinkage methods, the most popular one is called ridge regression, also known as Tikhonov regularisation [15] in other disciplines; it shrinks the regression coefficients through imposing an l_2-norm constraint. In this way, the estimates of the coefficients become more stable and therefore can improve the performance of regression.

The l_2-norm regularisation has been investigated for analysing hyperspectral imagery [4,16–20]. For the HSI classification, [16] and [17] assume that a test pixel can be collaboratively represented by raw spectral signatures. It is shown that l_2-norm constraints can actually improve the classification, instead of the "competitive" nature imposed by sparseness constraints (as l_1-norm or l_0-norm regularisation). For the HSI target detection, [4,18–20] add a scaled identity matrix to the background clutter covariance matrix before inverting it, in order to avoid an ill-conditioned problem. It is worth noting that these l_2-norm regularisation methods are developed in the original sample space, rather than in the eigenspace as this work.

In this paper, focusing on the popular MSD, we propose a new approach, called the matched shrunken subspace detector (MSSD), to target detection from hyperspectral images. Our MSSD is developed by shrinking the abundance vectors of the target and background subspaces in the hypothesis models of the MSD. The shrinkage is simply achieved by introducing l_2-norm regularisation into the MSD. We develop two types of the MSSD, one with isotropic shrinkage (and termed MSSD-i) and the other with anisotropic shrinkage (and termed MSSD-a). For these two new methods, we provide both the frequentist and Bayesian derivations. Experiments on a real hyperspectral imaging dataset called Hymap demonstrate that the proposed MSSD-i and MSSD-a can outperform the original MSD for hyperspectral target detection.

The main contributions of this paper are two-fold. (1) Through introducing the l_2-norm regularisation terms into the MSD, we shrink the abundance vectors so that the variance in each basis direction of the subspaces is also reduced, leading to a more stable estimation. (2) We derive the proposed MSSD-i and MSSD-a from both the frequentist and Bayesian perspectives, with the latter showing how the proposed methods preserve Gaussian prior distributions of the abundance vectors, instead of the uniform prior distribution that is implicitly imposed by the original MSD.

The rest of this paper is organised as follows. Section 2 reviews the original MSD. In Sections 3.1 and 3.2, detailed formulation of the two proposed methods, MSSD-i and MSSD-a, are introduced. Then the two proposed methods are derived from the Bayesian perspective and shown in Section 4. The links of MSD, MSSD-i and MSSD-a are discussed in Section 5. Section 6 presents the experimental results, with the whole work concluded in Section 7.

2. Matched subspace detector (MSD)

2.1. Overview of the binary hypothesis testing model

From a statistical perspective, target detection is typically derived from a binary hypothesis testing problem [3]. It is based on the likelihood ratio of the conditional probability density functions (pdfs) of two competing hypotheses, given that the spectral signature of an HSI pixel $\mathbf{x}$ is treated as a continuous random vector:

$$\begin{aligned} &H_0 : \mathbf{x} \text{ is a background pixel,}\\ &H_1 : \mathbf{x} \text{ is a target pixel,}\\ &\Rightarrow D(\mathbf{x}) = \frac{f_{\mathbf{x}|H_1}(\mathbf{x})}{f_{\mathbf{x}|H_0}(\mathbf{x})} \underset{H_0}{\overset{H_1}{\gtrless}} \nu, \end{aligned} \tag{2}$$

where $f_{\mathbf{x}|H_0}(\mathbf{x})$ and $f_{\mathbf{x}|H_1}(\mathbf{x})$ are two conditional pdfs of $\mathbf{x}$ under the null hypothesis H_0 and the alternative hypothesis H_1, respectively; ν is the detection threshold; and $D(\mathbf{x})$ is an output detector. In reality, the conditional pdfs are usually not available and are expressed parametrically. Hence, the generalised likelihood ratio test (GLRT) [21] is commonly used to replace the unknown parameters by their maximum likelihood estimates (MLEs):

$$\begin{aligned} D_{GLRT}(\mathbf{x}) &= \frac{f_{\mathbf{x}|H_1}(\mathbf{x};\hat{\omega}_1)}{f_{\mathbf{x}|H_0}(\mathbf{x};\hat{\omega}_0)} \underset{H_0}{\overset{H_1}{\gtrless}} \nu\\ &= \frac{\max_{\omega_1}\{f_{\mathbf{x}|H_1}(\mathbf{x};\omega_1)\}}{\max_{\omega_0}\{f_{\mathbf{x}|H_0}(\mathbf{x};\omega_0)\}} \underset{H_0}{\overset{H_1}{\gtrless}} \nu, \end{aligned} \tag{3}$$

where ω_0 and ω_1 are unknown parameters of pdf $f_{\mathbf{x}|H_0}(\mathbf{x};\omega_0)$ and pdf $f_{\mathbf{x}|H_1}(\mathbf{x};\omega_1)$, respectively; and $\hat{\omega}_0$ and $\hat{\omega}_1$ are their MLEs. In this paper, "$\hat{}$" denotes the estimates of unknown parameters.

2.2. Formulation of the matched subspace detector (MSD)

Following the idea of LMM (1) [9], the MSD models a test pixel by a linear combination of target spectral endmembers and background spectral endmembers, and these endmembers are represented by the basis vectors of the target subspace and the background subspace, respectively.

That is, derived from the binary hypothesis model (2), the MSD model [7] is constructed as

$$\begin{aligned} &H_0 : \mathbf{x} = \mathbf{B}\boldsymbol{\beta} + \mathbf{n}_0, \ \mathbf{x} \text{ is a background pixel,}\\ &H_1 : \mathbf{x} = \mathbf{T}\boldsymbol{\gamma} + \mathbf{B}\boldsymbol{\beta} + \mathbf{n}_1, \ \mathbf{x} \text{ is a target pixel,} \end{aligned} \tag{4}$$

where $\mathbf{T} = [\mathbf{t}_1, \ldots, \mathbf{t}_{r_t}]$ is a $p \times r_t$ matrix representing the target subspace, and $\mathbf{B} = [\mathbf{b}_1, \ldots, \mathbf{b}_{r_b}]$ is a $p \times r_b$ matrix representing the background subspace; $\mathbf{T}$ is derived from a training target matrix $\mathbf{M}_T \in \mathbb{R}^{p \times N_t}$ whose columns are the N_t target spectra, and $\mathbf{B}$ is derived from a training background matrix $\mathbf{M}_B \in \mathbb{R}^{p \times N_b}$ whose columns are the N_b background spectra; $\boldsymbol{\gamma}$ and $\boldsymbol{\beta}$ are the corresponding abundance vectors of the subspaces $\mathbf{T}$ and $\mathbf{B}$, respectively; and $\mathbf{n}_0$ and $\mathbf{n}_1$ are p-dimensional vectors of Gaussian white noise: $\mathbf{n}_0 \sim \mathcal{N}(\mathbf{0}, \sigma_0^2\mathbf{I})$ and $\mathbf{n}_1 \sim \mathcal{N}(\mathbf{0}, \sigma_1^2\mathbf{I})$.

In general, a set of orthogonal basis vectors that spans the corresponding subspace are used as the column vectors of $\mathbf{T}$ or $\mathbf{B}$. In common practice, the leading eigenvectors of the target covariance matrix $\mathbf{C}_T$ and those of the background covariance matrix $\mathbf{C}_B$ are used as the columns of $\mathbf{T}$ and $\mathbf{B}$, respectively, as with [1,10]. In other words, when the test pixel $\mathbf{x}$ is a target pixel, it is decomposed into two components by linear combinations of the bases of $\mathbf{B}$ and $\mathbf{T}$, denoted by model H_1. When $\mathbf{x}$ is a background pixel, it is adequately described by model H_0, which is a reduced order model.

Let $\mathbf{V}$ be the concatenated matrix of $\mathbf{T}$ and $\mathbf{B}$, i.e. $\mathbf{V} = [\mathbf{T}\ \mathbf{B}] = [\mathbf{t}_1, \ldots, \mathbf{t}_{r_t}, \mathbf{b}_1, \ldots, \mathbf{b}_{r_b}]$, then the abundance vectors $\boldsymbol{\gamma}$ and $\boldsymbol{\beta}$ of model H_1 can be concatenated into a single vector,

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