Library-Based Linear Unmixing for Hyperspectral Imagery via Reversible Jump MCMC Sampling

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Abstract— This paper studies a semi-supervised algorithm for linear hyperspectral unmixing. The proposed unmixing method assumes that the pure material spectra denoted as endmembers belong to a library that is *a priori* available. However, the number and the nature of endmembers appearing in the pixel are not known *a priori*, resulting in a model selection problem. This paper proposes to handle this model selection problem within a fully Bayesian framework. First, appropriate distributions are elected as prior distributions for the unknown parameters. Particularly, a distribution defined on a simplex is chosen as prior for an appropriate partial abundance vector to ensure the positivity and the sum-to-one constraints of the mixing coefficients. Due to the complexity of the posterior distribution, a reversible jump Markov chain Monte Carlo algorithm is proposed to estimate the number and the nature of the macroscopic materials, as well as their respective proportions in the pixel. The accuracy of the proposed method is illustrated by simulations on synthetic hyperspectral data.

1. INTRODUCTION

For few decades, hyperspectral imagery has been receiving increasing interest in the geoscience and image processing literatures [1]. Indeed, current spectro-imagers, such as AVIRIS, CASI or Hyperion, are able to acquire a same scene in several hundreds of contiguous bands, providing spectrally resolved images. Hyperspectral imagery has demonstrated its interest for numerous applications. These applications include geologic cartography [2], environmental [3] or military monitoring [4]. However, to benefit from the amount of information contained in these images, innovative strategies have to be developed to improve the accuracy of standard estimation, detection and classification algorithms [5]. One of the main steps in the analysis of such images consists of identifying the pure materials, or *endmembers* that are present in the observed scene. Then, an inversion step estimates their respective proportions in each pixel. This paper introduces a semi-supervised algorithm that can be used to perform this so-called *spectral unmixing*. In the literature, two models have been investigated to describe how endmember mixing is achieved. According to the first model, the observed pixel spectrum is assumed to be related to the unobserved material spectra via a linear mixture whose coefficients are the concentrations, or *abundances*, of the macroscopic components in the pixel [6]. The second model introduced in [7] refers to an intimate model that assumes a non-linear combination of the endmembers. However, as noted in [8], this intimate model can be easily linearized. Consequently, this paper concentrates on the Linear Mixing Model (LMM) that has received considerable attention in the literature [9], [10].

The proposed unmixing method assumes that the pure material spectra belong to a library that is *a priori* available. In our work, the number and the nature of endmembers appearing in the pixel are not known *a priori*. Estimating the number and the nature of the endmembers involved in the mixture is a classical model selection task. In this paper, this challenging problem will be handled within a fully Bayesian framework. Due to obvious physical reasons, the abundance vectors have to satisfy positivity and sum-to-one constraints. The Bayesian estimation procedure proposed here allows one to incorporate these constraints easily into the model. First, appropriate distributions are elected as prior distributions for the unknown parameters. Particularly, a distribution defined on a simplex is chosen as prior for an appropriate partial abundance vector to ensure the positivity and the additivity of the mixing coefficients, as in [11]. Because of the complexity of the posterior distribution, deriving standard Bayesian estimators remains difficult. In such cases, stochastic simulation methods can be used to overcome the difficulty. In this paper, a Markov chain Monte Carlo (MCMC) algorithm is proposed to generate samples asymptotically distributed according to the posterior distribution of the abundances and endmembers. Then, the generated samples will be used to approximate the Bayesian estimators. More precisely, as the number of endmembers is not *a priori* known, the unknown full parameter vector belongs to a space with unknown dimension. A reversible jump MCMC algorithm will allow ones to explore spaces with different dimensions [12].

This paper is organized as follows. The linear unmixing problem for hyperspectral images is formulated in Section 2. The hierarchical Bayesian model associated to this problem is described in Section 3. Section 4 details the reversible jump MCMC algorithm that generates samples distributed according to the abundance and endmember distribution. Simulation results obtained from synthetic hyperspectral data are presented in Section 5. Conclusions are reported in Section 6.

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2. PROBLEM FORMULATION

In this section, we describe the observation model which is classically assumed to perform spectral unmixing of hyperspectral pixels. As noticed in the previous section, this paper focuses on the LMM that constitutes a good approximation in the reflective domain ranging from 0.4μm to 2.5μm (see [5] and [9]). The LMM assumes that the spectrum $\boldsymbol{y} = [y_1, \ldots, y_L]^T$ of a mixed pixel is a linear combination of R endmember spectra $\boldsymbol{m}_r$ corrupted by additive noise:

$$\boldsymbol{y} = \sum_{r=1}^{R} \boldsymbol{m}_r \alpha_r + \boldsymbol{n}, \tag{1}$$

where L is the number of available spectral bands of the pixel, $\boldsymbol{m}_r = [m_{r,1}, \ldots, m_{r,L}]^T$ is the spectrum of the rth material, α_r is the fraction of the rth material in the pixel and R is the number of pure materials (or *endmembers*) present in the observed pixel. Here we consider $\boldsymbol{n} = [n_1, \ldots, n_L]^T$ as an additive white noise sequence which is classically assumed to be an independent and identically distributed (i.i.d.) Gaussian sequence with variance σ^2, denoted as $\boldsymbol{n} \sim \mathcal{N}\left(\mathbf{0}_L, \sigma^2 \mathbf{I}_L\right)$, where $\mathbf{I}_L$ and $\mathbf{0}_L$ are the identity matrix of dimension $L \times L$ and the $L \times 1$ vector made of 0's, respectively. Note that more complicated noise models that take into account some correlations might be studied (see for instance [13]).

Due to physical reasons, the abundance vector $\boldsymbol{\alpha}(R) = [\alpha_r, \ldots, \alpha_R]^T$ has to ensure the following non-negativity and sum-to-one constraints:

$$\begin{cases} \alpha_r \geq 0, \ \forall r = 1, \ldots, R, \\ \sum_{r=1}^{R} \alpha_r = 1. \end{cases} \tag{2}$$

It is important to mention here that the number R of endmembers involved in the mixture is not known *a priori*. However, the endmember spectra $\boldsymbol{m}_r$ ($r = 1, \ldots, R$) belong to a spectral library

$$\mathcal{S} = \left\{\boldsymbol{s}_1, \ldots, \boldsymbol{s}_{R_{\max}}\right\}, \tag{3}$$

composed of $R_{\max}$ materials. These endmember spectra $\boldsymbol{s}_r$ ($r = 1, \ldots, R_{\max}$) have been for instance identified by one of the numerous endmember extraction algorithms such as N-FINDR [14], MVT [15] or ICE [16].

The problem addressed in this paper consists of estimating the number of endmembers R, the spectra $\boldsymbol{m}_r$ ($r = 1, \ldots, R$), the fraction coefficient α_r ($r = 1, \ldots, R$) and the noise variance σ^2 under the constraints in (2) given the observed pixel $\boldsymbol{y}$ and the spectral library $\mathcal{S}$.

3. HIERARCHICAL BAYESIAN MODEL

Likelihood

The LMM (1) and the statistical properties of the noise vector yield $\boldsymbol{y}|R, \mathbf{M}, \boldsymbol{\alpha}, \sigma^2 \sim \mathcal{N}(\mathbf{M}\boldsymbol{\alpha}, \sigma^2 \mathbf{I}_L)$, where $\mathbf{M} = [\boldsymbol{m}_1, \ldots, \boldsymbol{m}_R]$. Consequently, the likelihood function of $\boldsymbol{y}$ can be expressed as:

$$f(\boldsymbol{y}|R, \boldsymbol{\alpha}, \mathbf{M}, \sigma^2) = \left(\frac{1}{2\pi\sigma^2}\right)^{\frac{L}{2}} \exp\left[-\frac{\|\boldsymbol{y} - \mathbf{M}\boldsymbol{\alpha}\|^2}{2\sigma^2}\right], \tag{4}$$

where $\|\boldsymbol{x}\| = \sqrt{\boldsymbol{x}^T\boldsymbol{x}}$ is the standard ℓ_2 norm.

Parameter priors

Prior for the number of endmembers — A discrete uniform distribution on $[1, \ldots, R_{\max}]$ is chosen for the prior associated to the number of mixture components R:

$$f(R) = \frac{1}{R_{\max}}, \quad R = 1, \ldots, R_{\max}. \tag{5}$$

Endmember matrix prior — Conditionally upon the number R of materials involved in the mixture, all combinations of R spectra belonging to the library $\mathcal{S}$ are assumed to be equiprobable:

$$\begin{aligned} f(\mathbf{M} \mid R) &= \binom{R_{\max}}{R}^{-1} \\ &= \frac{\Gamma(R+1)\,\Gamma(R_{\max} - R + 1)}{\Gamma(R_{\max} + 1)}, \end{aligned} \tag{6}$$

where $\Gamma(\cdot)$ denotes the Gamma function.

Abundance prior — The abundance vector can be written as $\boldsymbol{\alpha} = \left[\boldsymbol{c}^T, \alpha_R\right]^T$ with $\boldsymbol{c} = [\alpha_1, \ldots, \alpha_{R-1}]^T$ and $\alpha_R = 1 - \sum_{r=1}^{R-1} \alpha_r$. The constraints (2) inherent to the LMM impose that $\boldsymbol{c}$ belongs to the simplex $\mathbb{S}$ defined by:

$$\mathbb{S}_R = \left\{ \boldsymbol{c} \,\middle|\, c_r \geq 0, \ \forall r = 1, \ldots, R-1, \ \sum_{r=1}^{R-1} c_r \leq 1 \right\}. \tag{7}$$

To reflect the absence of prior knowledge regarding the abundance vector, a uniform distribution on $\mathbb{S}$ is chosen as prior distribution for $\boldsymbol{c}$:

$$f(\boldsymbol{c}|R) = \frac{1}{\mathrm{vol}\left(\mathbb{S}_R\right)} \mathbf{1}_{\mathbb{S}_R}(\boldsymbol{c}), \tag{8}$$

where $\mathbf{1}_{\mathbb{S}_R}(\cdot)$ stands for the indicator function defined on $\mathbb{S}_R$:

$$\mathbf{1}_{\mathbb{S}_R}(\boldsymbol{c}) = \begin{cases} 1, & \text{if } \boldsymbol{c} \in \mathbb{S}_R; \\ 0, & \text{otherwise.} \end{cases} \tag{9}$$

Noise variance prior — A conjugate inverse Gamma distribution is chosen as prior distribution for σ^2:

$$\sigma^2 \mid \nu, \gamma \sim \mathcal{IG}\left(\frac{\nu}{2}, \frac{\gamma}{2}\right), \tag{10}$$

where ν will be fixed to $\nu = 2$ (as in [17]) and γ is an adjustable hyperparameter.

Hyperparameter prior distribution

The accuracy of the unmixing procedure may depend on the value of the unknown hyperparameter γ. As in [11], the hierarchical model proposed here uses a non-informative Jeffreys' prior for γ:

$$f(\gamma) \propto \frac{1}{\gamma}\mathbf{1}_{\mathbb{R}^+}(\gamma). \tag{11}$$

Posterior distribution

The posterior distribution of the unknown parameter vector $\boldsymbol{\theta} = \left\{R, \mathbf{M}, \boldsymbol{\alpha}, \sigma^2\right\}$ can be computed from the following hierarchical structure:

$$f(\boldsymbol{\theta}|\boldsymbol{y}) \propto \int f(\boldsymbol{y}|\boldsymbol{\theta}) f(\boldsymbol{\theta}|\gamma) f(\gamma) d\gamma, \tag{12}$$

where $\propto$ means "proportional to", $f(\boldsymbol{y}|\boldsymbol{\theta})$ and $f(\gamma)$ have been defined in (4) and (11). Conditionally upon R, by assuming the prior independence between σ^2, $\boldsymbol{c}$ and $\mathbf{M}$ i.e. $f(\boldsymbol{\theta}|\gamma) = f(R) f(\boldsymbol{c}|R) f(\mathbf{M}|R) f(\sigma^2|\nu,\gamma)$, the hyperparameter γ can be integrated out from the joint distribution $f(\boldsymbol{\theta}, \gamma|\boldsymbol{y})$, yielding:

$$f\left(R, \boldsymbol{c}, \mathbf{M}, \sigma^2|\boldsymbol{y}\right) \propto \frac{1}{\sigma^{L+2}} \exp\left[-\frac{\|\boldsymbol{y} - \mathbf{M}\boldsymbol{\alpha}\|^2}{2\sigma^2}\right] \times \frac{1}{\mathrm{vol}\left(\mathbb{S}_{\mathrm{R}}\right)} f(R) f(\mathbf{M}|R) \mathbf{1}_{\mathbb{S}_R}(\boldsymbol{c}), \tag{13}$$

where the dimensions of $\mathbf{M}$ and $\boldsymbol{\alpha}$ depend on the unknown parameter R. The next section shows that an appropriate hybrid Gibbs sampling strategy allows one to generate samples distributed according to the joint distribution $f(R, \boldsymbol{c}, \mathbf{M}, \sigma^2|\boldsymbol{y})$.

4. REVERSIBLE JUMP MCMC ALGORITHM

This section studies an hybrid Metropolis-within-Gibbs algorithm that samples according to $f\left(R, \boldsymbol{c}, \mathbf{M}, \sigma^2|\boldsymbol{y}\right)$. The vectors to be sampled belong to a space whose dimension depends on R, requiring to use a dimension matching strategy as in [12], [18], [19]. More precisely, the proposed algorithm consists of three different moves:

1. updating the endmember spectrum matrix $\mathbf{M}$,
2. updating the endmember abundance vector $\boldsymbol{c}$,
3. updating the noise variance σ^2.

These three moves are scanned systematically as in [12]. They are detailed below.

Updating the endmember spectrum matrix $\mathbf{M}$

The endmember spectra involved in the mixture (1) are updated by using three kinds of move. These moves are called *birth*, *death* and *switch* moves, as in [20, p. 53]. The first two moves consist of increasing or decreasing the number of pure components by 1. These moves allow the sampler to explore sets with different dimensions. Thus, they require the use of the reversible jump MCMC algorithm [12]. The third move does not affect the model dimension and requires a standard Metropolis-Hastings algorithm.
Assume that at iteration t of the sampler, the current model is defined by the vector $\boldsymbol{\theta}^{(t)} = \left\{R^{(t)}, \mathbf{M}^{(t)}, \boldsymbol{c}^{(t)}, \sigma^{2(t)}\right\}$. The three moves are defined as follows.

Birth — A birth move is proposed with the probability $b_{R^{(t)}}$. The current number of endmember $R^{(t)}$ is increased by 1

$$R^\star = R^{(t)} + 1.$$

A new spectrum $\boldsymbol{m}^\star$ is randomly chosen with equal probability[1] among the available materials of the spectral library $\mathcal{S}$. The new endmember matrix $\mathbf{M}^\star$ is:

$$\mathbf{M}^\star = \left[\mathbf{M}^{(t)}, \boldsymbol{m}^\star\right].$$

A new corresponding abundance has to be drawn ensuring the constraints in (2). This coefficient $\alpha^{(t)}$ is proposed according a rule inspired by [18]:

- draw a new abundance coefficient $w^\star$ from the Beta distribution $\mathcal{B}e\left(1, R^{(t)}\right)$,
- re-scale the existing fractions so that all of them sum to 1:

$$\alpha_r{}^\star = \alpha_r^{(t)}\left(1 - w^\star\right),\ r = 1, \ldots, R^{(t)}, \tag{14}$$

- set $\boldsymbol{\alpha}^\star = \left[\alpha_1{}^\star, \ldots, \alpha_R{}^\star, w^\star\right]^T$.

Death — A death move is proposed with the probability $d_{R^{(t)}}$. The current number of endmember $R^{(t)}$ is decreased by 1:

$$R^\star = R^{(t)} - 1.$$

One of the spectra chosen with equal probability in the endmember matrix $\mathbf{M}^{(t)}$ is removed, as well as the corresponding abundance coefficient. The remaining abundances coefficients are re-scaled to sum to 1.

Switch — A switch move is proposed with the probability $u_{R^{(t)}}$. A spectrum randomly chosen in $\mathbf{M}^{(t)}$ is replaced by another spectrum randomly chosen in the library $\mathcal{S}$.

At iteration t of the sampler, one of the moves *birth*, *death* and *switch* is randomly chosen with the probabilities $b_{R^{(t)}}$, $d_{R^{(t)}}$ and $u_{R^{(t)}}$, with $b_{R^{(t)}} + d_{R^{(t)}} + u_{R^{(t)}} = 1$. Of course, the death move is not allowed for $R^{(t)} = 1$ and the birth move is impossible for $R^{(t)} = R_{\max}$, i.e. $d_1 = b_{R_{\max}} = 0$. The different moves are assumed to be equiprobable such that $b_{R^{(t)}} = d_{R^{(t)}} = u_{R^{(t)}} = \frac{1}{3}$ for $R^{(t)} \in \{1, \ldots, R_{\max} - 1\}$ and $b_1 = u_1 = d_{R_{\max}} = u_{R_{\max}} = \frac{1}{2}$. The acceptance rates of the *birth* and *death* moves are $\rho = \min\{1, A_{\mathrm{b}}\}$ and $\rho =$

[1] Of course, when prior knowledge regarding the probability of each spectrum to be in the image is available, this information can be used to randomly select a spectrum of the library.

$\min\left\{1, A_{\mathrm{b}}^{-1}\right\}$, respectively, with (see [11] for more details):

$$A_{\mathrm{b}} = \exp\left[-\frac{\|\boldsymbol{y}-\mathbf{M}^{\star}\boldsymbol{\alpha}^{\star}\|^2 - \left\|\boldsymbol{y}-\mathbf{M}^{(t)}\boldsymbol{\alpha}^{(t)}\right\|^2}{2}\right] \times \frac{d_{R^{(t)}+1}}{b_{R^{(t)}}} \frac{1}{g_{1,R^{(t)}}\left(w^{\star}\right)} \left(1-w^{\star}\right)^{R^{(t)}-1} \times \frac{\Gamma\left(\delta R^{(t)}+\delta\right)}{\Gamma\left(\delta R^{(t)}\right)\Gamma\left(\delta\right)} w^{\star\delta-1}\left(1-w^{\star}\right)^{(\delta-1)R^{(t)}}, \quad (15)$$

with $\delta = 1$.

The acceptance probability for the *switch* move is the standard Metropolis Hastings ratio $\rho = \min\{1, A_{\mathrm{s}}\}$ with

$$A_{\mathrm{s}} = \exp\left[-\frac{\|\boldsymbol{y}-\mathbf{M}^{\star}\boldsymbol{\alpha}^{\star}\|^2 - \left\|\boldsymbol{y}-\mathbf{M}^{(t)}\boldsymbol{\alpha}^{(t)}\right\|^2}{2}\right]. \quad (16)$$

Updating the endmember abundance vector $\boldsymbol{c}$

Updating the endmember abundance vector $\boldsymbol{c}$ is classically conducted by generating samples $\boldsymbol{c}^{(t)}$ according to the posterior conditional distribution $f\left(\boldsymbol{c}|R, \mathbf{M}, \sigma^2, \boldsymbol{y}\right)$. By denoting $\mathbf{M}_{-R}$ the matrix $\mathbf{M}$ whose Rth column has been removed, i.e. $\mathbf{M}_{-R} = [\boldsymbol{m}_1, \ldots \boldsymbol{m}_{R-1}]$, this conditional distribution is

$$f\left(\boldsymbol{c}|R, \mathbf{M}, \sigma^2, \boldsymbol{y}\right) \propto \exp\left[-\frac{\left(\boldsymbol{c}-\boldsymbol{\mu}\right)^T \boldsymbol{\Lambda}^{-1}\left(\boldsymbol{c}-\boldsymbol{\mu}\right)}{2}\right] \mathbf{1}_{\mathbb{S}}(\boldsymbol{\alpha}), \quad (17)$$

where

$$\begin{cases} \boldsymbol{\Lambda} &= \left[\frac{1}{\sigma^2}\left(\mathbf{M}_{-R} - \boldsymbol{m}_R\mathbf{u}^T\right)^T\left(\mathbf{M}_{-R} - \boldsymbol{m}_R\mathbf{u}^T\right)\right]^{-1}, \\ \boldsymbol{\mu} &= \boldsymbol{\Lambda}\left[\frac{1}{\sigma^2}\left(\mathbf{M}_{-R} - \boldsymbol{m}_R\mathbf{u}^T\right)^T\left(\boldsymbol{y} - \boldsymbol{m}_R\right)\right], \end{cases} \quad (18)$$

with $\mathbf{u} = [1, \ldots, 1]^T \in \mathbb{R}^{R-1}$. This distribution indicates that $\boldsymbol{c}|R, \mathbf{M}, \sigma^2, \boldsymbol{y}$ is distributed according to a truncated Gaussian distribution:

$$\boldsymbol{c}|R, \mathbf{M}, \sigma^2, \boldsymbol{y} \sim \mathcal{N}_{\mathbb{S}}\left(\boldsymbol{\mu}, \boldsymbol{\Lambda}\right). \quad (19)$$

As in [11], sampling according to a truncated Gaussian distribution can be achieved using a standard accept-reject procedure, when the number of endmembers is relatively small (as in the examples studied in this paper). More efficient simulation techniques based on Gibbs moves can be used for high dimension problems (see [21] or [22] for more details).

Updating the noise variance σ^2

Integrating out the hyperparameter γ from the joint posterior distribution $f\left(\boldsymbol{\theta}, \gamma|\boldsymbol{y}\right)$ leads to:

$$\sigma^2|R, \boldsymbol{\alpha}, \mathbf{M}, \boldsymbol{y} \sim \mathcal{IG}\left(\frac{L}{2}, \frac{\|\boldsymbol{y}-\mathbf{M}\boldsymbol{\alpha}\|^2}{2}\right), \quad (20)$$

from which it is straightforward to sample.

5. Simulation results

This section presents simulation results conducted on a synthetic mixed pixel. This pixel results from the combination of three endmembers (green grass, bare red brick, galvanized steel metal) with the abundance vector $[0.4, 0.2, 0.4]^T$. The observation is corrupted by an additive Gaussian noise with signal to noise ratio SNR = 20dB. A typical resulting mixed pixel is depicted in Fig. 1 (below).

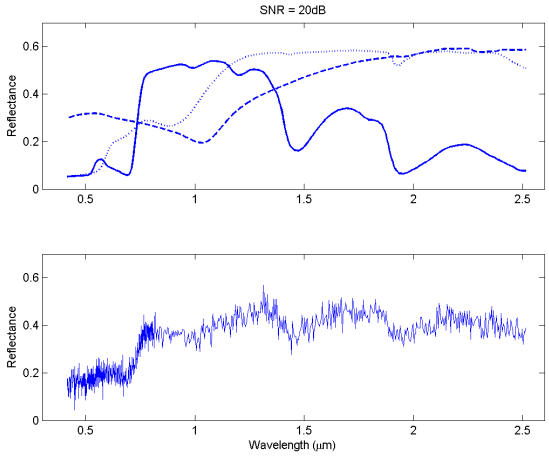

Figure 1. Top: endmember spectra: green grass (solid line), bare red brick (dotted line), galvanized steel metal (dashed line). Bottom: resulting spectrum of the mixed pixel (SNR = 20dB).

This simulation considers a spectrum library composed of 6 endmembers that are provided by the ENVI software [23, p. 1035]. These spectra, representative of a urban or suburban environment, are depicted in Fig. 2.

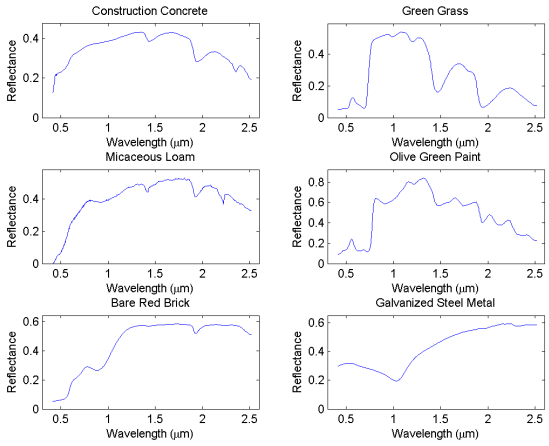

Figure 2. Endmember spectra of the library.

The results presented here are obtained for $N_{\mathrm{MC}} = 20000$ iterations, including $N_{\mathrm{bi}} = 200$ burn-in iterations. The first step of the analysis consists of identifying the different combinations of endmembers in the matrices $\mathbf{M}^{(t)}$ generated by

the sampler. Among the $N_r = N_{\mathrm{MC}} - N_{\mathrm{bi}}$ matrices $\mathbf{M}^{(t)}$ drawn by the sampler, 7 different combinations of spectra from the library $\mathcal{S}$ have been generated. The probabilities of each of these combination occurrence, depicted in Fig. 3, are clearly in favor of the endmember matrix $\mathbf{M} = [\boldsymbol{s}_2 \boldsymbol{s}_5 \boldsymbol{s}_6]$, which is in good agreement with the mixing scenario. Indeed, the maximum probability $\mathrm{P}\left[\mathbf{M} = [\boldsymbol{s}_2, \boldsymbol{s}_5, \boldsymbol{s}_6] \mid \boldsymbol{y}\right] = 0.98$ corresponds to the actual spectra involved in the mixture.

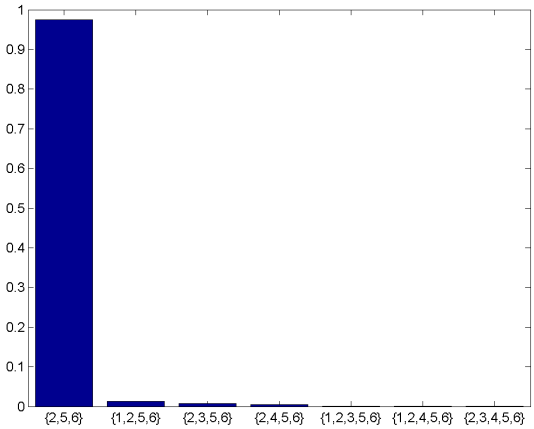

Figure 3. Posterior probabilities of occurrence of the endmember combinations.

The posterior distributions of the corresponding abundances are finally estimated following the MMSE principle:

$$\hat{\boldsymbol{c}}_{\mathrm{MMSE}} = \frac{1}{N_r} \sum_{t=1}^{N_r} \boldsymbol{c}^{(N_{\mathrm{bi}}+t)}. \tag{21}$$

Conditionally upon the *maximum a posteriori* estimate of the endmember matrix $\hat{\mathbf{M}}_{\mathrm{MAP}} = [\boldsymbol{s}_2, \boldsymbol{s}_5, \boldsymbol{s}_6]$, the posterior distributions of the corresponding abundance coefficients are depicted in Fig. 4. These posteriors are clearly in good agreement with the actual values of the abundances $\boldsymbol{\alpha} = [0.4, 0.2, 0.4]^T$.

The performance of the proposed algorithm is compared with a fully supervised Bayesian approach similar to [11]. First, 100 synthetic signals have been generated as described above: $\boldsymbol{\alpha} = [0.4, 0.2, 0.4]^T$, $\mathbf{M} = [\boldsymbol{s}_2, \boldsymbol{s}_5, \boldsymbol{s}_6]$, SNR = 20dB. The supervised algorithm assumes that the 6 endmember spectra of the library (depicted in Fig. 2) are involved in the mixture. Hence, with this approach, the vector to be estimated is $[0.0, 0.4, 0.0, 0.0, 0.2, 0.4]^T$. The mean squared errors (MSE) for the supervised algorithm and our library-based algorithm are reported in Table 1. These results show that the proposed semi-supervised approach outperforms the supervised algorithm.

6. CONCLUSIONS

This paper presented a hierarchical Bayesian model for hyperspectral linear unmixing. This model relied on appropriate prior distributions chosen for the unknown parameters.

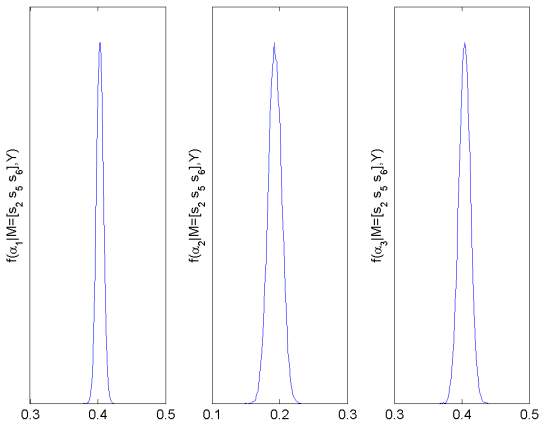

Figure 4. Posterior distribution of the estimated abundances $\boldsymbol{\alpha} = [\alpha_1, \alpha_2, \alpha_3]^T$ conditioned upon $\mathbf{M} = [\boldsymbol{s}_2, \boldsymbol{s}_5, \boldsymbol{s}_6]$.

Table 1. MSE for supervised and semi-supervised algorithms

	Supervised	Semi-supervised
MSE	5.4×10^{-2}	4.7×10^{-2}

It provided the posterior distribution of the abundance coefficients that can be used for their estimation. Assuming that the endmembers belong to a known spectral library, a reversible-jump MCMC method allowed one to identify the macroscopic materials actually involved in the mixture. In that sense, it constituted an original semi-supervised algorithm for linear unmixing of hyperspectral images.

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