A Gaussian Mixture Model for Image Segmentation and Enhancing Spectral Unmixing using Cross Entropy

Saranya devi .S
PG Scholar, Department of ECE,
Sri Krishna College Of Technology, India

Thiyagupriyadharsan.M.R
2nd Asst. Professor, Department of ECE,
Sri Krishna College Of Technology, India

ABSTRACT
The main problem of segmentation in spectral images that containing mixed pixels is addressed. Linear spectral unmixing is a procedure by which mixed pixels are decomposed into a collection of pure spectra, or endmembers, with their corresponding proportions, or abundances. Markov random field (MRF) is used to model the spatial correlation between pixels and segment the image into multiple classes. Pixels in each class have the same spectral values. A new numerical method was introduced to estimate the abundance and its parameters by using EM-algorithm and Gaussian mixture model which is termed as EM-MAP algorithm. A new solver, namely cross entropy (CE) was proposed for hyperspectral image unmixing. CE achieves higher performance of finding more global optima because of its stochastic property. The experiments show that CE can give more accurate segmentation results.

Keywords
Hyperspectral images, Markov random field(MRF), Gaussian Mixture Model(GMM), spectral unmixing, Cross entropy(CE).

1. INTRODUCTION
Hyperspectral image analysis is a fast growing technology in the field of remote sensing. Analysis of these images involves many technical issues such as image classification, image segmentation, target detection and the crucial step of spectral unmixing. The particular attention has been devoted to the spectral unmixing. Hyperspectral unmixing consists of decomposing the measured pixels into mixtures of pure spectra (*or endmembers)* whose fractions are referred to as *abundances* [1]. The linear relationship between the fractional abundance of the substance and the spectra are referred to as linear mixing model (LMM). For an observed pixel *p* in L bands, it is expressed as

$$y_p = Ma_p + n_p \qquad (1)$$

Where $\boldsymbol{M} = [\boldsymbol{m}_1, \ldots, \boldsymbol{m}_R]$ is the $\boldsymbol{L} \times \boldsymbol{R}$ spectral signature matrix, $\boldsymbol{a}_p$ is the $\boldsymbol{R} \times \boldsymbol{1}$ abundance vector and $\boldsymbol{n}_p$ is the $\boldsymbol{L} \times \boldsymbol{1}$ additive noise vector. For a hyperspectral image with *P* pixels are considered, block notation is utilized, such that

$$Y = MA + N \qquad (2)$$

The LMM requires to have known endmember signatures. These signatures can be obtained from a spectral library or by using an endmember extraction algorithm (EEA). Once the endmembers that appear in a given image have been identified, the corresponding abundances have to be estimated in an *inversion* step. Due to physical considerations, the abundances have to satisfy positivity and sum-to-one constrains. All the inversion strategies have been developed in a pixel-by-pixel context and, consequently, do not exploit the possible spatial correlation between the different pixels of the hyperspectral image. In this paper, we taking these spatial correlations into account allow one to improve the unmixing procedure. More precisely, the Bayesian algorithm initially developed [2], [3] is modified to introduce spatial constraints between the pixels of an image.

Within Bayesian estimation, a very popular strategy for modeling spatial information in an image is based on Markov random fields (MRFs). MRFs have been widely used in the image processing for modeling spatial correlations. MRFs describe neighbourhood dependence between image pixels. MRFs and their pseudo-likelihood approximations have been introduced by Besag in [4]. A likelihood term which is based on the data captures the pixel intensity information, while MRF captures the spatial location information. The major drawback or MRFs is their computational cost, which is proportional to the image size.

This paper introduces spatial correlation between adjacent pixels of a hyperspectral image allowing computational cost of MRFs to be reduced significantly. The neighbourhood relations are usually defined between spatially close pixels or *sites.* This contribution proposes to define a new neighbourhood relation between sites regrouping spectrally consistent pixels. After pre-processing step defining the similarity regions, a classification is carried out by assigning hidden discrete variables or class *labels* to regions. A potts-Markov field [5] is chosen as prior for the labels. This distribution enforces the neighbouring pixels to belong to the same class. A pixel belonging to a given similarity region must belong to the class that shares not only the same abundance mean vector and covariance matrix but also the same spectral characteristics. In addition to the label prior, the abundance vectors are assigned appropriate prior distributions with unknown means and variances that depend on the pixel class. This prior distribution is subjected to the positivity and sum-to-one constraints.

This paper proposes to estimate hyperparameters by introducing a second level of hierarchy in the Bayesian interface. Non-informative prior distributions are assigned to the hyperparameters. The unknown parameters (labels and abundance vectors) and hyperparameters (prior abundance mean and variance for each class) are then obtained from their joint posterior distribution. The Bayesian estimators such as the minimum mean square error (MMSE) and maximum posterior (MAP) estimators are too difficult to derive from this posterior distribution. Markov chain Monte Carlo (MCMC) techniques are studied to alleviate the numerical problems related to the LMM with spatial constraints. MCMC allow one to generate samples asymptotically distributed

according to the joint posterior. The samples generated by the MCMC method are used to compute the Bayesian estimators and class parameters. These methods have worked well in last decades. In this paper, a new expectation maximization (EM) algorithm and Gaussian mixture model (GMM) has constructed. In this algorithm, we have made a sequence of the priors, posteriors and they then convergent to a posterior probability that is called the reference posterior probability. So, maximum a posterior estimation can be determined by this reference posterior probability which will make labeled image. Note that the underlying classification and abundance estimation problems are jointly solved within this Bayesian framework.

A new stochastic solver was introduced for MRF modeling, which is termed as cross entropy (CE). CE makes no assumption on the form of the objective function so it is able to solve more complicated MRF models. CE shows higher segmentation accuracy than any other models.

The paper is organised as follows. The unmixing problem associated to the LMM with spatial correlations is formulated in section 2. Section 3 introduces a Gaussian mixture model and EM-MAP algorithm to approximate the Bayesian estimators. Section 4 describes the Cross entropy technique used for unmixing of hyperspectral images. Simulation results conducted on hyperspectral data are provided in section 5. Finally, conclusions related to this work are reported in section 6.

2. TECHNICAL BACKGROUND AND PROBLEM FORMULATION

2.1 Spatial Dependencies between Abundances

In this paper, we propose to exploit some spatial correlations between the pixels of the hyperspectral image to be analyzed. It is interesting to consider that the abundances of a given pixel are similar to the abundances of its neighboring pixels. The hyperspectral image is assumed to be partitioned into K regions or *classes*. If we denote as $C_1, \ldots, C_k$ the image classes, a label vector of size $S \times 1$ (with $S \geq K$) denoted as $z = [z_1, \ldots, z_S]^T$ with $z_S \in \{1, \ldots, K\}$ is introduced to identify the class of each region $\mathbf{\Omega}_s$, i.e., $z_s = k$ if and only if all pixels of $\mathbf{\Omega}_s$ belong to C_k. In each class, the abundance vectors to be estimated are assumed to share the first and second order statistical moments, i.e., $\forall k \in \{1, \ldots, K\}$, $\forall \mathbf{\Omega}_s \in C_k$, $\forall p \in \mathbf{\Omega}_s$

$$E[a_p] = \mu_k \quad (3)$$

$$E[(a_p - \mu_k)(a_p - \mu_p)^T] = \Lambda_k \quad (4)$$

Therefore, the kth class of the hyperspectral image to be unmixed is fully characterized by its abundance mean vector and the abundance covariance matrix.

2.2 Markov random field

The MRFs have been used for hyperspectral image analysis in [6] and for spectral unmixing in [7]. To describe spatial correlations between pixels, it is important to define a neighborhood structure. Considering two image pixels *i* and *j*, the neighborhood relation between these pixels must be symmetric: if *i* is a neighbor of *j* then *j* is a neighbor of *i*. This neighborhood relation is applied to the nearest neighbors of the considered pixel, for example the fourth, eighth twelfth nearest pixels.

Once the neighborhood structure has been established, the MRF can be defined. Let z_p denote a random variable associated to the pth pixel of an image of P pixels. The variables $z_1, \ldots, z_p$ indicate the pixel classes and take their values in a finite set {1, . . . , K} where K is the number of possible classes. The whole set of random variables $\{z_1, \ldots, z_p\}$ forms a random field. An MRF is then defined when the conditional distribution of z_i given the other pixels z_{-i} only depend on its neighbors $z\nu(i)$, i.e.,

$$f(z_i \mid z_{-i}) = f(z_i \mid z\nu(i)) \quad (5)$$

Where $\nu(i)$ is the neighborhood structure considered and $z_{-i} = \{z_j ; j \neq i\}$.

Two specific MRFs are appropriate for image analysis: the Ising model and the Potts-Markov model. This paper focuses on the Potts-Markov model since it is very appropriate to hyperspectral image segmentation. Given a discrete random field z attached to an image with P pixels, the Hammersley-Clifford theorem yields,

$$f(z) = \frac{1}{G(\beta)} \exp[\sum_{p=1}^{p} \sum_{p'=\gamma(p)} \beta\delta(z_p - z_{p'})] \quad (6)$$

Where β is a *granularity* coefficient, G(β) is the normalizing constant or *partition function* and $\delta(x)$ is a Kronecker function

$$\delta(x) = 1, \text{ if } x = 0,$$
$$0, \text{ otherwise}$$

Note that drawing a label vector $z = [z_1, \ldots, z_p]$ from the distribution can be easily achieved without knowing G(β) by using a Gibbs sampler. A major difficulty with the distribution comes from partition function that has no closed-form expression and depends on the hyperparameter β.

3. GAUSSIAN MIXTURE MODEL

Image is a matrix within which each element is a pixel. The value of the pixel is a number that shows intensity or color of the image. Let X be a random variable that takes these values. For a probability model determination, we can suppose to have mixture of Gaussian distribution as the following form:

$$f(x) = \sum_{i=1}^{k} p_i N(x \parallel \mu_i, \sigma_i^2) \quad (7)$$

Where K is the number of components or regions and $p_i > 0$ are weights such that

$$\sum_{i=1}^{k} p_i = 1$$

$$N(\mu_i, \sigma_i^2 = \frac{1}{\sigma\sqrt{2\pi}} \exp(\frac{-(x-\mu_i)^2}{2\sigma_i^2}) \quad (8)$$

Where μ_i ,σ_i^2 are mean and standard deviation of class i. For a given image X, the lattice data are the values of pixels and GMM is our pixel base model. μ_i, σ_i^2

EM-MAP algorithm

There are several published articles about EM algorithm for GMM [8], [9]. The process of E-MAP algorithm can be defined:

0. Input: observed image in a vector x_j , $j = 1,2,\ldots, n$ and $I \in \{1,2,\ldots,k\}$ labels set

1. Initialize:

$$\theta^{(0)} = (p_1^{(0)},\ldots, p_k^{(0)}, \mu_1^{(0)},\ldots, \mu_k^{(0)}, \sigma_1^{2(0)},\ldots, \sigma_k^{2(0)})$$

2. (E-step)

$$p_{ij}^{(r+1)} = p^{(r+1)}(i \mid x_j) = \frac{p_i^{(r)} N(x_j \parallel \mu_i^{(r)}, \sigma_i^{2(r)})}{f(x_j)}$$

3. (M-step)

$$p_i^{(r+1)} = \frac{1}{n}\sum_{j=1}^{n} p_{ij}^{(r)}$$

$$\mu_i^{(r+1)} = \frac{\sum_{j=1}^{n} p_{ij}^{(r+1)} x_j}{n p_i^{(r+1)}}$$

$$\sigma_i^{2(r+1)} = \frac{\sum_{j=1}^{n} p_{ij}^{(r+1)} (x_j - \mu_i^{(r+1)})^2}{n p_i^{(r+1)}}$$

4. Iterate steps 2 and 3 until an arbitrary error i.e.,

$$\sum_i e_i^2 < e$$

5. Compute $p_{lj} = Arg\max_i \; p_{ij}^{(final)}$

J = 1, 2 ,…,n

6. Construct labeled image corresponding of each image.

In this algorithm, a sequence of priors and then posteriors were made until to get convergence. The labeled images choose with MAP of the final posterior.

4. CROSS ENTROPY

Cross entropy has few successful applications in operations research and machine learning [10]. CE method is a simple accurate solver for MRF modelling.

Consider the general energy minimization problem of MRFs. Let *F* be the configuration space of MRF, and f is one configuration of *F*. the energy minimization of MRF is formulated by

$$f^* = \arg\min_{f \in F} E(f) \qquad (9)$$

Where E(.) is the energy function to be minimized and f^* is the wanted F configuration. CE method associates an estimation problem with the optimization problem (Eq.9). An indicator function $I_{\{event\}}$, which is equal to 1. When the event is true otherwise 0. Then *p(.; v)* is a family of discrete probability density functions on *F* and *v* is its parameter. Let us estimate the following probability

$$p_v(E(F) \le e) = \sum_x I_{\{E(f) \le e\}} p(f; v) \qquad (10)$$

Where P_v is the probability measure and F is a vector of configurations that has pdf *p(.;v).*

CE Algorithm for MRF

1. Set level $t = 1$ and the initial parameter vector $v_0 = \{v_{0,1},\ldots,v_{0,n}\}$. Each $v_{t,i} = \{v^1_{t,i},\ldots,v^m_{t,i}\}$ is a vector with *m* elements for site *i*.

2. Generate a collection of samples $F_1,\ldots,F_N$ ($F = \{f_1,\ldots,f_n\}$ is one MRF configuration) from the density *p(.;v)* and compute the energy $E_i(F_i)$ for every $i \in \{1,\ldots,N\}$.

3. Sort all the $E_i(F_i)$ in a non-increasing order to $\{E_1,\ldots,E_N\}$. Then pick $e_t = E_{[(1-\rho)^N]}$.

4. Use the samples $F_1,\ldots,F_N$ to update *vt* by

$$v^j_{t,i} = \frac{\sum_{k=1}^{N} I_{\{E_k(F_k) \le e_t\}} I_{\{F_{kt=j}\}}}{\sum_{k=1}^{N} I_{\{E_k(F_k) \le e_t\}}}$$

5. If e_t remains unchanged for several iterations, go to step 6; else, set $t = t + 1$ and go to step 2.

6. The final $E_N(F_N)$ of *T* -th iteration is the estimated minimal MRF energy. The corresponding configuration is embodied by the parameter vector v_T, where each element $v^j_{T,i}$ assigns most probability mass to a preferable label among *m* labels for site *i*.

Function *p(.;v)* can be any kind of pdf but the simple m-point Bernoulli distribution is usually enough. This means each label *j* is randomly chosen for site *i* according to the probability of $v^j_{t,i}$. Two parameters need to be pre-defined, ρ and *N*. Usually, ρ is a small value between 1% and 10%. When the site number *n* is large, we tend to choose a large value of ρ. Regarding the sample size *N*, we set $N = cn$, where *c* is a constant and often between 1 and 10. Notice that there are other alternative stopping criteria, such as when the parameter ***vt*** converges to a binary (0 or 1) vector.

5. SIMULATION RESULTS

The In this section, the simulation results obtained are presented. The experiments evaluate the performance of the proposed algorithm for segmentation and unmixing of image with K = 2 different classes. A principal component analysis has been conducted as a preprocessing step to determine the number of endmembers present in the scene. The image contains R = 2 mixed components (buildings and trees). The algorithm proposed in section III has been applied on this image with N = 30 iterations. The proposed Markov random field with EM-MAP algorithm has segment the observed image into two classes. For each iteration, the GMM parameters μ and σ are calculated. Then energy is estimated by using these parameters. The observed and segmented images were presented in fig. 1 and fig. 2.

Fig 1. The observed image

Fig 2. The segmented image

The calculated μ and σ values for each iteration have been reported in the Table I.

Table I. GMM Parameters

ITERATIONS	MEAN (μ)	VARIANCE (σ)
Iteration 1	130.5689	1.1932e+03
Iteration 2	131.5899	1.2051e+03
Iteration 3	132.3873	1.2097e+03
Iteration 4	133.0986	1.2124e+03
Iteration 5	133.8416	1.2164e+03
Iteration 6	134.5653	1.2206e+03
Iteration 7	135.1368	1.2234e+03
Iteration 8	135.7413	1.2293e+03
Iteration 9	136.2725	1.2325e+03
Iteration 10	136.8344	1.2387e+03
Iteration 11	137.4437	1.2454e+03
Iteration 12	138.0039	1.2522e+03
Iteration 13	138.4873	1.2596e+03
Iteration 14	138.9156	1.2658e+03
Iteration 15	139.3062	1.2728e+03
Iteration 16	139.6764	1.2787e+03
Iteration 17	140.0511	1.2845e+03
Iteration 18	140.4344	1.2905e+03
Iteration 19	140.7515	1.2955e+03
Iteration 20	141.0159	1.3004e+03
Iteration 21	141.3462	1.3081e+03
Iteration 22	141.5786	1.3122e+03
Iteration 23	141.8058	1.3168e+03
Iteration 24	141.9748	1.3199e+03
Iteration 25	142.1582	1.3244e+03
Iteration 26	142.3023	1.3269e+03
Iteration 27	142.4248	1.3304e+03
Iteration 28	142.6041	1.3342e+03
Iteration 29	142.8654	1.3367e+03
Iteration 30	142.8654	1.3404e+03

After thirty iterations, the mean and variance value remains constant. From the segmented image, the mixed pixels are addressed. The Cross entropy technique is employed to unmixing the mixed pixels.

Fig 3. The image after Cross entropy

In this method, choose one energy value as threshold value. It is an iterative procedure and for each iteration, decreases the energy of an image and compared it with the threshold. It provides more accurate segmentation results. The image after unmixing is shown in fig. 3.

6. DISCUSSION AND CONCLUSION

A segmentation and unmixing algorithm based on a new Markov random field has been introduced. A hidden discrete label was introduced for each pixel of the image to identify several classes defined by homogeneous abundances. We derived the joint posterior distribution of the unknown parameters and hyperparameters associated to the proposed Gaussian Mixture Model. We have used known EM-algorithm and we added numerically MAP estimation. Also

the initial values by histogram of image have suggested which is caused to convergence of EM-MAP method. After convergence of our algorithm, we had stability in entropy.

In this paper, a new MRF solver namely cross entropy (CE), has been introduced for image unmixing. CE algorithm is a general solver that can be applied to any type of MRF models. It is an iterative procedure and in each iteration, a sequence of samples is generated according to a certain probability distribution. The method chooses one threshold of objective function value (i.e., energy) and just focuses on those samples whose performance (e.g., lower energy) is better than this threshold. CE is obviously more efficient because it concentrates on a few high performance samples among a large collection of random samples and quickly converges to states which have good performance.

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