AUTOMATIC BLIND SPECTRAL UNMIXING USING LINEAR UNMIXING UNDER SPATIAL AUTOCORRELATION CONSTRAINTS

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1. INTRODUCTION

Spectral unmixing or analysis seeks to estimate the number of endmembers, their spectral signatures and abundance patterns, using only the mixed data and physical models (Boardman, 1993). Spectral unmixing usually includes two main procedures, (1) extracting endmembers and (2) inversing mixed pixels. The most popular algorithms for autonomous endmember extraction include Pixel Purity Index (Boardman, 1993), N-FINDR (Winter, 1999) and Vertex Component Analysis (Nascimento and Bioucas-Dias, 2005). The often-used algorithms for image inversion include Linear Spectral Mixture analysis (Keshava and Mustard, 2002), Probabilistic Model (Ju et.al., 2003), artificial intelligence (Penn, 2002), and so on.

As Dobigeon (2009) mentioned, the above methods avoid the difficult problem of direct parameter estimation, by assuming the presence of pure pixels for each endmember in the observed scene. However, the pure pixels usually do not exist in scenes, for example, the coarse spatial resolution images like MODIS or the scenes acquired when the plant at early growing stage does not cover land completely yet. If the number of endmembers, their spectra and abundances are not known at all, the spectral unmixing falls into the class of blind source separation (BSS) problem. There are several approaches, such as ICA (Chiang, 2000), NMF (Sajda, 2004) and Joint Bayesian Algorithm (Dobigeon et.al., 2009), which have been used to solve this kinds of problem. ICA is based on the assumption of mutually independent sources (abundance fractions), which is not the case of hyperspectral data, since the sum of abundance fractions is constant. The NMF was used successfully to solve the BSS problem under non-negative constraints, but it has not taken into account the additivity constraint. The recent progress made by Dobigeon, 2009 is Joint Bayesian estimator that estimates the endmember spectra and their respective abundances using linear unmixing with non-negativity constraints for endmember spectra and non-negativity and additivity constraints for abundances.

This work proposes a new approach to automate blind spectral unmixing using linear unmixing with spatial autocorrelation constraints. The linear spectral mixture model assumes that a mixed pixel is a linear combination of

endmembers spectra weighted by the correspondent abundance fractions. The endmember spectra are constrained by non-negativity, while their abundances are constrained by non-negativity and additivity (sum-to-one), as reported by Dobigeon (2009). Based on the geospatial autocorrelation, we assume the number of endmembers and their spectra and abundances are similar (close each other) among the mixed pixels which are labeled as the same land cover class, but quite different among those pixels belonging to different land cover classes. The Global and Local Moran's I are used to describe such spatial autocorrelation of particular endmember among pixels falling into the same class, at class level and local pixel level, respectively. Those two Moran's I indices constrain the distribution of the endmember fractions within one class or among neighbor pixels. By minimizing mean square error of mixed spectral values under all the above constraints, the genetic algorithm is applied to solve the number of endmembers and their spectra and abundances.

2. METHODS

2.1. Linear Spectral Mixture Model

Linear model for a mixed pixel:

$$R_j = \sum_{i=1}^{I} a_i r_{i,j} + \varepsilon_j, i = 1, 2, ..., I, j = 1, 2, ..., J \quad (1)$$

Where, I is the number of endmembers, J is the number of spectra bands, R_j is the jth spectra value of the mixed pixel, ε_j is the additive noise, $r_{i,j}$ is the spectra of the ith endmember, a_i is the fraction of the ith endmember at current mixed pixel.

Non-negativity and additivity constraints (reported by Dobigeon, 2009):

$$r_{i,j} \geq 0, j = 1, 2, ..., J \quad\quad\quad (2)$$

$$a_i \geq 0, i = 1, 2, ..., I \quad\quad\quad (3)$$

$$\sum_{i=1}^{I} a_i = 1 \quad\quad\quad (4)$$

Spatial autocorrelation constraints (proposed in this work):

Supposing there are I endmembers and K land cover classes in the image, each class may correspond to a particular subset of I endmembers, L_k (called dominating endmembers). Assuming that the fraction of the ith endmember falling into L_k, has a significant spatial autocorrelation among those mixed pixels belonging to the kth class, we can apply the *Moran's I* to describe the spatial autocorrelation of the ith endmember fraction for the kth class.

$$II_{k,i} = \frac{\sum_{m=1}^{M}\sum_{n=1}^{N} w_{mn}\left(x_{m,i} - \bar{x}\right)\left(x_{n,i} - \bar{x}\right)}{\sum_{p=1}^{M+N}\left(x_{p,i} - \bar{x}\right)^2 \sum_{m=1}^{M}\sum_{n=1}^{N} w_{mn}} \quad\quad\quad (5)$$

Where, $w_{m,n}$ is the weight represented by $1/d_{m,n}$, $d_{m,n}$ is the distance between the mth and nth pixel, $x_{m,i}$ is the fraction of the ith endmember at the mth pixel, $x_{n,i}$ is the fraction of the ith endmember at the nth pixel, N is the number of the neighbor pixels surrounding the mth pixel, M is number of pixels falling into the current kth land cover class.

If the *Moran's I* for the ith endmember is great than $E(II_i)$, an expectation of I in spatial randomness case, it means that the fraction of this endmember has a strong spatial relationship. So it can be determined as the dominating endmembers for the kth class during the evolution process of genetic algorithm.

Assuming there are not big verities that exist on the endmember fraction among those pixels falling into the same class. So, we can use *Local Moran's I* , local indicators of spatial association, to describe the spatial autocorrelation at local pixel level.

$$II_{m,i} = \frac{M\left(x_{m,i} - \overline{x}\right)^2 \sum\limits_{n=1}^{N} w_{mn}\left(x_{m,i} - \overline{x}\right)\left(x_{n,i} - \overline{x}\right)}{\sum\limits_{m=1}^{M}\left(x_{m,i} - \overline{x}\right)^2} \qquad (6)$$

If $I_{m,i}$ is positive and has a big number, meaning the mth pixel has the fraction of the ith endmember similar as its neighbors'. If $II_{m,i}$ is negative and has a big number, meaning the mth pixel has a big difference on the fraction of the ith endmember from its neighbors, that does not follow our assumption so the endmember fraction should be adjusted during the evolution process of genetic algorithm (GA).

2.2. Solution using global optimization with genetic algorithm

The estimation of $r_{i,j}$ and a_i coefficients of Eq (1) under the constraints of Eq (2) – (6) is a NP-hard problem. We choose genetic algorithm (GA) to solve it. The spatial autocorrelations described by Eq (5)-(6) are normalized and integrated into the fitness function of GA, in term of exterior penalty functions. So, the objective function (*f*) of GA including three partial items – the average of the mean square errors, global *Moran's I*, and local *Moran's I*, is defined as follows.

$$f = \frac{1}{T \times I \times J}\sum_{m=1}^{T}\sum_{i=1}^{I}\sum_{j=1}^{J}(R_j - \sum_{i=1}^{I}a_i r_{i,j})^2 + \frac{\alpha}{K \times I}\sum_{k=1}^{K}\sum_{i=1}^{I}norm(II_{k,i}) + \frac{\beta}{M \times I}\sum_{m=1}^{T}\sum_{i=1}^{I}norm(II_{m,i}) \qquad (7)$$

Where, T is the image pixel number, α and β are the scale factors for global and local spatial correlation, respectively.

To estimate the $r_{i,j}$ and a_i, we need to minimize the Eq(7) iteratively using the GA algorithm. The evolution process is controlled by two genetic operators: crossover and mutation. The crossover operation exchanges genes between two individuals, while the mutation operation randomly introduces a new gene into a high-fitness individual to prevent convergence from local optima. The evolution operations at each iterative step will lead to vast candidates

or offsprings, and those high quality offsprings (namely having a small objective value) will be selected. The evolution is stopped when the objective value becomes stable or the iteration reaches a certain number.

3. DEMONSTRATIONS

The Chinese HJ-Satellite images are applied for spectral unmixing experiments.

4. REFERENCES

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