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SPECTRAL VARIABILITY IN A MULTILINEAR MIXING MODEL

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ABSTRACT

We present a new method for spectral unmixing which takes both nonlinear mixing and spectral variability into account. This is accomplished by combining the multiple endmember spectral mixture analysis (MESMA) approach with the recently developed multilinear mixing model (MLM). As the traditional approach of nonlinear unmixing of all combinations is very time consuming, we investigate a second approach, where endmember model selection is linearly performed by a fast alternative for MESMA, followed by nonlinear unmixing. We show that this approach yields similar reconstruction errors (REs) as the full combinatorial approach, and hence results in a relatively fast method for nonlinear unmixing with variability.

Index Terms— Spectral unmixing, hyperspectral image processing

1. INTRODUCTION

Hyperspectral unmixing in realistic scenarios is often hampered by strong variability in the endmember spectra, and nonlinear mixing effects such as higher-order optical interactions between macroscopic objects such as buildings or vegetation canopies, or intimate mixing between microscopic mineral grains. Several approaches for dealing with variability have been proposed (see e.g. [1, 2] for overviews), and these can be roughly divided into two classes: One either tries to model the variability in the endmember spectra with probability distributions, or one employs a discrete approach, where representative spectra for each endmember are collected in a library or bundle. These approaches are often very time consuming, and faster iterative optimization schemes have been recently proposed [3]. Many models and techniques have also been proposed to deal with nonlinear mixing effects in hyperspectral imagery [4]. Models that take higher orders of interactions into account, such as bilinear models, have become very popular in the remote sensing literature, and some higher-order models have been recently proposed. We will focus on the MLM in this work [5], where all orders of interactions are considered. While many papers exist on both variability and nonlinear unmixing, not many techniques consider both at the same time. This is perhaps with good reason: Variability techniques are very time consuming even in a lin-

ear mixing setting, and introducing nonlinearities will further exacerbate this. In this work, we will combine the MLM with the MESMA algorithm [6], and demonstrate that the resulting algorithm performs better than MESMA or MLM alone on real data sets. Furthermore, because simply combining both algorithms is inherently very slow, we propose a two-step solution, where MESMA is employed to identify which endmembers to use from the spectral libraries, and MLM is used to obtain the abundances. It is shown that this approach yields similar REs to the combined algorithm, but has runtimes that can be used in practical situations. Finally, by employing the alternating angle minimization (AAM) algorithm as an alternative for MESMA, we show that very similar results can be obtained, but with improved runtimes.

2. THE ALGORITHMS

2.1. MESMA

Consider a library-based approach for spectral variability, where p libraries $\{L_i\}_{i=1}^p$ exist, each containing N_i representative spectra for an endmember respectively in a d -dimensional spectral space. The MESMA algorithm will unmix a spectrum \mathbf{x} with respect to all models, where a model is a set of endmembers drawn from their respective endmember libraries. The model which yields the smallest RE and obeys the abundance nonnegativity constraint (ANC) and abundance sum-to-one constraint (ASC) is retained, and the unmixing results with respect to this model are returned. By considering all possible subsets of libraries as well, one can avoid having to perform a constrained optimization (either fully or non-negatively), typically resulting in an overall faster algorithm. See Algorithm 1 for the algorithm, and [6, 3] for more information on MESMA.

2.2. AAM

The AAM algorithm is an alternative for MESMA based on alternating optimization, where a local minimum is obtained by optimizing with respect to each spectral library in turn. The optimization with respect to a single library itself can be rewritten as an angle minimization problem by considering the geometrical implications of sum-to-one constrained unmixing. We have shown [3] that the AAM algorithm obtains identical results as MESMA in the majority of pixels

Algorithm 1: MESMA algorithm

```
1 for Every subset of libraries do
2   for Every model drawn from these libraries do
3     Determine the abundances with sum-to-one
       constrained unmixing;
4     if all abundances are non-negative then
5       Determine the RE;
6     else
7       Set RE to  $\infty$ ;
8 Return the solution with smallest reconstruction
   error;
```

in a real-world application, but can be orders of magnitude faster, especially when the libraries are large.

2.3. MLM MODEL

The MLM model is based upon some simple probabilistic assumptions about the propagation of light rays in a scene: The probability of interacting with any given endmember e_i , for $i \in [1, \dots, p]$, has to be proportional to its abundance a_i . After each interaction, we have a probability P of undergoing further interactions and probability $(1 - P)$ of reaching the observer. This leads to mixing equation (1), where P indicates the size of the nonlinearity in each pixel. Constrained minimization of the reconstruction error versus the model can be employed to solve for P and the abundances $\{a_i\}_{i=1}^p$. See [5] for more details.

$$\mathbf{x} = \frac{(1 - P) \sum_{i=1}^p a_i \mathbf{e}_i}{1 - P \sum_{i=1}^p a_i} \quad (1)$$

2.4. COMBINING MESMA AND MLM

We can combine the MESMA algorithm and the MLM model by unmixing with the MLM model instead of performing linear unmixing for every endmember model. This leads to algorithm 2.

Algorithm 2: MESMA+MLM algorithm

```
1 for Every model drawn from the libraries do
2   Unmix using the MLM model;
3   Determine the RE;
4 Return the solution with smallest reconstruction
   error;
```

2.5. MESMA FOR SELECTION, MLM FOR UNMIXING

A proposed faster alternative for the previous algorithm is employing MESMA for model selection, followed by nonlinear unmixing with the MLM using these EMs. Note that the bottleneck will still be the MESMA algorithm in this sequence. Furthermore, the AAM algorithm can be employed as a faster alternative for MESMA [3], as this algorithm largely replicates the results from MESMA.

3. EXPERIMENTS

To assess the performance of these algorithms, we have unmixed a selection of the Gulfport data set from the University of Florida [7]. This data set is a 13×19 pixel reflectance image in 53 bands spanning the visible and NIR regions (see Fig. 1), contains 4 classes, and has a spectral library obtained in the field available for each of these classes. The classes (# of samples) are “asphalt” (10), “curb” (10), “trees” (10), and “grass” (50). Classification ground truth is available as well.

We consider the following unmixing algorithms and methods:

1. LMM: The linear mixing model (LMM), with the library averages as endmembers.
2. MLM: The MLM, with the library averages as endmembers.
3. MESMA: MESMA with the LMM
4. AAM: the AAM algorithm
5. MESMA_MLM: MESMA with the MLM
6. MESMA+MLM: MESMA for endmember extraction, MLM for unmixing
7. AAM+MLM: AAM for endmember extraction, MLM for unmixing

To assess the performance, we consider the RE between the reconstructed image \mathbf{Y} and the original image \mathbf{X} :

$$\text{RE} = \|\mathbf{Y} - \mathbf{X}\|_F^2 \quad (2)$$

We consider also the average correlation between the abundance vectors: Let \mathbf{a}_i^1 and \mathbf{a}_i^2 be the abundance vectors belonging to pixel \mathbf{x}_i , obtained by method 1 and 2 respectively. Then the average correlation \bar{C} is given by

$$\bar{C} = \frac{1}{N} \sum_{i=1}^N \text{corr}(\mathbf{a}_i^1, \mathbf{a}_i^2) \quad (3)$$

The abundance maps obtained by the different techniques are plotted in Fig. 2, along with the classification maps. One



Fig. 1: Part of the Gulfport data set, with the region under consideration indicated by the red square.

can see that all abundance maps are correlated with their classification maps. The methods that include variability via linear techniques (MESMA and AAM) both obtain very similar abundance maps. Linear model selection, followed by nonlinear unmixing via MLM, is qualitatively similar to linear unmixing. MESMA with the MLM shows larger deviations in some abundance maps compared to the other variability techniques. Using the LMM or the MLM with library averages yields significantly different abundance maps.

These results can be made more quantitative by considering the correlations between the abundance maps. To do so, we calculate the pixel-wise correlation between abundance vectors, and average these for all pixels. These results are shown in table 1 for all combinations of techniques. It can be seen that these results confirm the qualitative description given above.

The RE, calculated as the frobenius norm between the image and the reconstruction, and the runtimes for the Gulfport data set, are given in table 2. The reconstruction error is the smallest for the MESMA method combined with the MLM. The reconstruction errors for linear model determination, followed by MLM unmixing, are of similar size. Linear unmixing with variability (MESMA and AAM) yield the same reconstruction errors, slightly higher than employing the MLM with variability. The MLM on the library average performs better than the LMM, but both have worse REs than the variability approaches.

As expected, the runtime for the MESMA method that incorporates MLM unmixing is quite large, in the order of 30 hours for an image of only 247 pixels. Employing lin-

	MLM	MESMA	AAM	MESMA_MLM	MESMA+MLM	AAM+MLM
LMM	0.72	0.85	0.85	0.64	0.79	0.78
MLM		0.73	0.73	0.87	0.74	0.75
MESMA			0.98	0.80	0.96	0.93
AAM				0.78	0.95	0.95
MESMA_MLM					0.81	0.81
MESMA+MLM						0.96

Table 1: The average correlation between the abundance vectors, for the different methods

Method	RE	Runtime (s)
LMM	2.51	0.144
MLM	2.17	1.98
MESMA	1.81	16.4
AAM	1.81	12.7
MESMA_MLM	1.56	1.39e5
MESMA+MLM	1.57	18.9
AAM+MLM	1.58	15.2

Table 2: The reconstruction error and the runtime in seconds of the different methods.

ear variability techniques for determining the model, followed by MLM unmixing, is orders of magnitude faster, and only slightly slower than linear MESMA or AAM, while yielding very similar REs. The abundance maps will be similar to the MESMA or AAM ones, and show larger differences with MESMA_MLM. Note that the AAM alternative is faster than MESMA, but not overly so for this data set as the spectral libraries are relatively small. The AAM algorithm scales linearly in the library sizes however, where the MESMA algorithm scales combinatorially.

4. CONCLUSIONS

We have proposed a combination of MESMA with the MLM model for nonlinear unmixing, which yields improved REs and slightly different abundance maps from linear methods for variability. As a straightforward combination of MESMA with MLM unmixing is very slow, we proposed an alternative where the right endmember model is selected with linear methods (MESMA or AAM), followed by nonlinear unmixing with MLM. We show that this approach yields very comparable REs to the combined method, but that the abundance maps better resemble those obtained with MESMA and AAM.

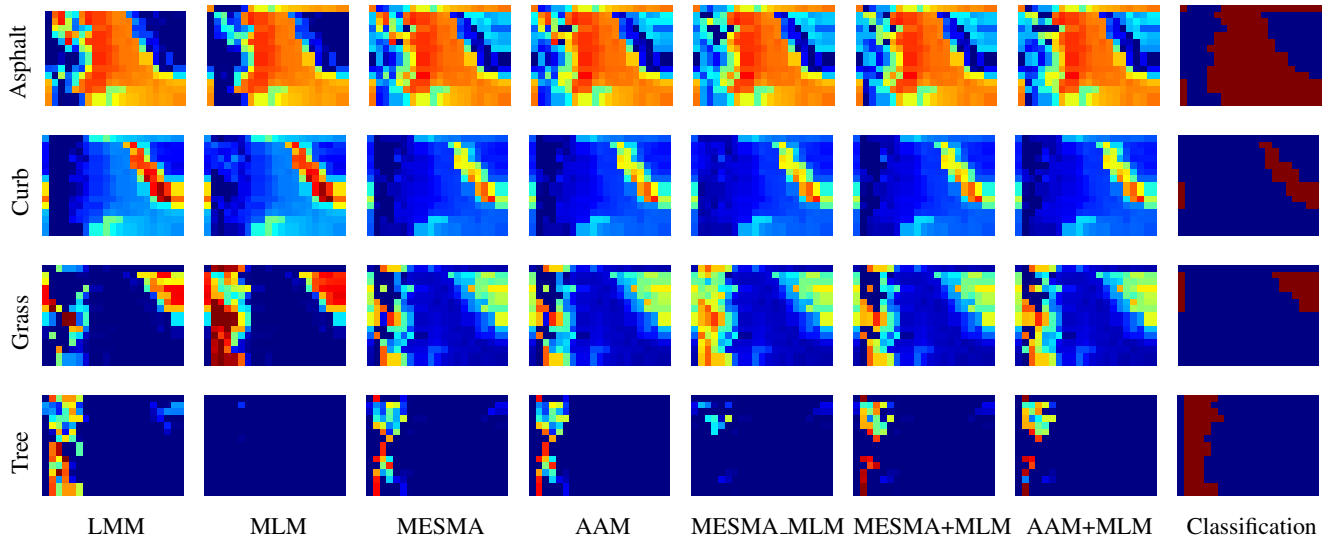


Fig. 2: Gulfport abundance maps

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