

Piece-wise Convex Spatial-Spectral Unmixing of Hyperspectral Imagery using Possibilistic and Fuzzy Clustering

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Abstract—Imaging spectroscopy refers to methods for identifying materials in a scene using cameras that digitize light into hundreds of spectral bands. Each pixel in these images consists of vectors representing the amount of light reflected in the different spectral bands from the physical location corresponding to the pixel. Images of this type are called hyperspectral images. Hyperspectral image analysis differs from traditional image analysis in that, in addition to the spatial information inherent in an image, there is abundant spectral information at the pixel or sub-pixel level that can be used to identify materials in the scene. Spectral unmixing techniques attempt to identify the material spectra in a scene down to the sub-pixel level. In this paper, a piece-wise convex hyperspectral unmixing algorithm using both spatial and spectral image information is presented. The proposed method incorporates possibilistic and fuzzy clustering methods. The typicality and membership estimates from those methods can be combined with traditional material proportion estimates to produce more meaningful proportion estimates than obtained with previous spectral unmixing algorithms. An analysis of the utility of using all three estimates produce a better estimate is given using real hyperspectral imagery.

Index Terms—hyperspectral, endmember, spectral unmixing, possibilistic, fuzzy, piece-wise convex, linear mixing, convex geometry model.

I. INTRODUCTION

Hyperspectral images are three-dimensional data cubes that have two spatial and one spectral dimension. Hyperspectral imagers collect data about an image scene across many narrow, contiguous spectral wavelengths. As opposed to image processing, spectral information (rather than spatial information) is generally the focus in hyperspectral image analysis. *Endmember detection* and *spectral unmixing* are two major goals in hyperspectral image analysis. Endmembers are spectra that are defined by analogy to standard spectroscopy.

In standard spectroscopy, the basic elements (oxygen, nitrogen, etc.) making up a substance are identified. Each element has a unique spectral signature and the spectral properties of the substance are defined by combinations of the pure elements in the substance. Endmembers are thought of as representing the “pure” spectral signatures of the materials found in the scene. However, the analogy is not strict for several reasons. It is generally not possible to get enough resolution to identify

pure elements. In addition, it may not even be useful to identify them. For example, when an intelligent system is analyzing a scene, it may only need to know where the grass, trees, concrete, water, etc. are located in a scene. Therefore, in hyperspectral image analysis applications, the endmembers represent spectra of the basic scene elements such as these. We refer to these endmembers as “pure materials” in the scene with the understanding that they may really represent the types of materials discussed above.

Spectral unmixing determines the *proportion* (or *abundance*) of each endmember found in every hyperspectral pixel. The standard model applied during hyperspectral unmixing is the linear mixing model [?]. In the linear mixing model, the spectral signatures in a hyperspectral scene are modeled as convex combinations of the endmember signatures. This model can be written as follows.

$$\mathbf{x}_i = \sum_{k=1}^M p_{ik} \mathbf{e}_k + \epsilon_i, \quad 1 \leq i \leq N \quad (1)$$

where N is the number of pixels, M is the number of endmembers, ϵ_i is an error term, p_{ik} is the abundance of endmember k in pixel i , and $\mathbf{e}_k$ is the k^{th} endmember. The abundances of this model satisfy the following constraints.

$$p_{ik} \geq 0 \quad \forall k = 1, \dots, M \quad (2)$$

$$\sum_{k=1}^M p_{ik} = 1 \quad (3)$$

Given the input hyperspectral data, $\mathbf{X}$, endmember detection estimates the spectral signatures of the endmembers, $\mathbf{E}$, and spectral unmixing determines the values of the proportions (or abundances) $\mathbf{P}$ of each endmember in every hyperspectral data point. By following this model, finding endmembers amounts to estimating the spectral signatures whose convex hull enclose the hyperspectral data.

Numerous hyperspectral unmixing methods based on the linear mixing model have been developed in the literature. Generally, these methods search for a single set of endmembers and, therefore, assume that pixels are a combination of all endmembers in the scene. However, in real hyperspectral

data, pixels are often combinations of only a subset of the endmembers.

In this paper, an endmember extraction and spectral unmixing algorithm using fuzzy and possibilistic clustering methods is presented. The proposed method represents an input hyperspectral scene using multiple sets of endmembers with a piece-wise convex representation. By estimating fuzzy membership and typicality values for each set of endmembers (i.e. a convex region) meaningful proportion values are estimated where the majority of pixels are combinations of a subset of the endmembers in the scene, some pixels may be identified as highly-mixed and combinations of most or all of the endmembers in the scene, and some pixels are identified as outliers. We refer to pixels in categories as single-region pixels,

The piece-wise convex representation for hyperspectral imagery was first developed in [?] and [?]. Endmember detection methods that incorporate spatial information include [?], [?], [?]. However, these methods do not employ a piece-wise convex model.

An exciting contribution of this approach is that the initial estimates of the proportions, memberships, and typicality all play important roles in defining more meaningful and realistic final proportion estimates. There are three categories of pixels: single-region pixels, overlap-region pixels, and outlier pixels.

A single-region pixel is composed of only those endmembers that are associated with one convex region. In this case, the typicality value for the convex region containing the pixel should be 1, the membership value for the corresponding region should also be 1, and the proportion values should be the proportions of the endmembers associated with that convex region for the data point. Therefore, in the single convex region case, the final proportion vector will be the proportion values found for the endmembers in the convex region containing the data point.

Overlap-region pixels are convex combination of endmembers associated with two or more convex regions in the data. The typicality values for the pixel in all of the associated convex regions should be 1, the product of the membership values and the proportion vectors for each convex region will sum-to-one. This product will result in a final proportion vector for the data point with appropriate weights for all of the endmembers that compose the pixel.

In the outlier pixel case, the pixels are not convex combinations of the endmembers found in the scene. In this case, the typicality values for all convex regions should be small and tend towards zero. By using the product of the typicality, membership and proportion values, the final proportions for the outlier pixels should sum to less than one. This indicates that the pixel is not fully described by the endmembers found in the scene. This lack of information is represented directly in the final proportions rather than indirectly by large error. If only membership is used, then the proportions will still sum to one but they will certainly not be correct. Thus, the final proportion values calculated using the initial proportions, the memberships, and the typicality will represent the true level of information available in the scene.

In the following, Section 2 outlines the algorithm, Section 3 presents experimental results and Section 4 provides a discussion and conclusions.

II. METHOD

A. P-COMMEND

The P-COMMEND (Piece-wise Convex Multiple Model Endmember Detection) algorithm [?] performs alternating optimization to autonomously estimate the endmembers, $\mathbf{E}$, abundances, $\mathbf{P}$, and membership values, $\mathbf{U}$, for a given hyperspectral image. P-COMMEND iteratively minimizes the objective function in Equation ?? subject to the constraints in Equation ??, $\sum_{i=1}^C u_{ij} = 1$ and $u_{ij} \geq 0$.

$$J = \sum_{i=1}^C \sum_{j=1}^N u_{ij}^m (\mathbf{x}_j - \mathbf{p}_{ij} \mathbf{E}_i) (\mathbf{x}_j - \mathbf{p}_{ij} \mathbf{E}_i)^T + \alpha \sum_{i=1}^C (M \cdot \text{trace}(\mathbf{E}_i \mathbf{E}_i^T) - \mathbf{1}_{1 \times M} \mathbf{E}_i \mathbf{E}_i^T \mathbf{1}_{M \times 1}) \quad (4)$$

where $\mathbf{x}_j$ is a $1 \times d$ vector representing the j^{th} pixel of the image, N is the number of pixels in the image, M is the number of endmembers in each convex region (or model), P_i is a $N \times M$ matrix such that $\mathbf{p}_{ij}$, is the vector of abundances associated with pixel j with respect to model i , p_{ijk} is the proportion of endmember k in pixel j with respect to model i , and $\mathbf{E}_i$ is a $M \times d$ matrix such that each row of $\mathbf{E}_i$, $\mathbf{e}_{ik}$, is a $1 \times d$ vector representing the k^{th} endmember with respect to model i . The notation $\mathbf{1}_{S \times T}$ denotes an $S \times T$ matrix with all entries equal to 1. The multiple models compete for data $\mathbf{X}$ through a set of weights u_{ij} which represent the memberships of the data points $\mathbf{X}$ in the i^{th} model where m is the ‘‘fuzzifier’’ parameter controlling the degree to which the data points are shared among the models.

The first term of this objective function represents the residual error incurred by representing each spectra using the estimated endmembers, abundances and fuzzy membership values. The use of the fuzzy membership values is related to the fuzzy c-means and the Multiple Model General Linear Regression algorithms [?], [?]. The second term is related to the volume enclosed by the endmembers by representing the sum of squared distances (SSD) between the endmembers and encourages the endmembers to have a tight fit around the data. The SSD term is the same volume-related term used by ICE (Iterated Constrained Endmembers) and SPICE (Sparsity Promoting Iterated Constrained Endmembers) for endmember detection [?], [?].

When updating membership values, the objective function is minimized subject to the constraint that all the membership values for a data point must sum to one. This results in the following update equation given abundances and endmembers,

$$u_{ij} = \frac{1}{\sum_{q=1}^C \left(\frac{(\mathbf{x}_j - \mathbf{p}_{ij} \mathbf{E}_i)(\mathbf{x}_j - \mathbf{p}_{ij} \mathbf{E}_i)^T}{(\mathbf{x}_j - \mathbf{p}_{qj} \mathbf{E}_q)(\mathbf{x}_j - \mathbf{p}_{qj} \mathbf{E}_q)^T} \right)^{\frac{1}{m-1}}}. \quad (5)$$

The endmembers are updated given the following equation,

$$\mathbf{E}_i = \left(\sum_j u_{ij}^m \mathbf{p}_{ij}^T \mathbf{p}_{ij} + 2\alpha D \right)^{-1} \left(\sum_j u_{ij}^m \mathbf{p}_{ij}^T \mathbf{x}_j \right) \quad (6)$$

where $D = MI_{M \times M} - 1_{M \times M}$. Finally, abundance values are updated by minimizing Equation ?? subject to the constraints in Equation ?? by using a Lagrange multiplier term and evaluating and applying the required KKT conditions to enforce Equation ?. The resulting update equations are

$$\mathbf{p}_{ij}^T = (\mathbf{E}_i \mathbf{E}_i^T)^{-1} \left(\mathbf{E}_i \mathbf{x}_j^T - \frac{\lambda_{ij}}{2} 1_{M \times 1} \right) \quad (7)$$

and

$$\mathbf{p}_{ij}^{KKT} = \max(\mathbf{p}_{ij}^T, 0) \quad (8)$$

$$\text{where } \lambda_{ij} = 2 \frac{1_{1 \times M} (\mathbf{E}_i \mathbf{E}_i^T)^{-1} \mathbf{E}_i \mathbf{x}_j^T - 1}{1_{1 \times M} (\mathbf{E}_i \mathbf{E}_i^T)^{-1} 1_{M \times 1}}.$$

B. FLICM

Spatial information is incorporated by encouraging neighboring pixels in the image to have similar membership values to the different convex regions. This is accomplished by adopting the spatially-smooth fuzzy c-means method, FLICM (Fuzzy Local Information C-Means), developed in [?]. The FLICM algorithm adds a term, G , to the objective function that influences the updates of the membership values by incorporating spatial information. The G term, adapted for use in the proposed algorithm, is shown in Equation ?.

$$G_{ij} = \sum_{\substack{k \in N_j \\ j \neq k}} \frac{1}{d_{jk} + 1} (1 - u_{ik})^m \|\mathbf{x}_k - \mathbf{p}_{ik} \mathbf{E}_i\|_2^2 \quad (9)$$

where the $\mathbf{x}_j$ is the center pixel in the local window under consideration, N_j is the neighborhood around the center pixel (such as a 3x3 window), d_{ij} is the Euclidean distance in pixel space of the image indices between pixels $\mathbf{x}_j$ and $\mathbf{x}_k$. Therefore, the G term scales the influence of neighboring pixels based on their distance in the index space. Also, when a neighboring pixel has high membership in a convex region, the point under consideration is encouraged to also have a high membership in that region. G_{ij} term is updated each iteration and treated as a constant during updates to the endmembers, abundances and membership values. With the addition of G , the objective function for is shown in Equation ?.

$$\begin{aligned} J = & \sum_{i=1}^C \sum_{j=1}^N u_{ij}^m \left((\mathbf{x}_j - \mathbf{p}_{ij} \mathbf{E}_i) (\mathbf{x}_j - \mathbf{p}_{ij} \mathbf{E}_i)^T + G_{ij} \right) \\ & + \alpha \sum_{i=1}^C (M \cdot \text{trace}(\mathbf{E}_i \mathbf{E}_i^T) - 1_{1 \times M} \mathbf{E}_i \mathbf{E}_i^T 1_{M \times 1}) \end{aligned} \quad (10)$$

When incorporating FLICM into the P-COMMEND algorithm, the update equations for the endmembers and abun-

dances remain the same as in Equations ?? and ?. Membership updates change as shown below.

$$u_{ij} = \frac{1}{\sum_{q=1}^C \left(\frac{(\mathbf{x}_j - \mathbf{p}_{ij} \mathbf{E}_i) (\mathbf{x}_j - \mathbf{p}_{ij} \mathbf{E}_i)^T + G_{ij}}{(\mathbf{x}_j - \mathbf{p}_{qj} \mathbf{E}_q) (\mathbf{x}_j - \mathbf{p}_{qj} \mathbf{E}_q)^T + G_{qj}} \right)^{\frac{1}{m-1}}}. \quad (11)$$

C. PFCM Clustering

The proposed method adopts the approach presented in the PFCM (Possibilistic Fuzzy Clustering Method) [?]. PFCM determines both typicality and membership values for each data and every cluster.

D. Proposed Method

Incorporating FLICM and PFCM into the P-COMMEND objective function results in the objective function shown in Equation ?.

$$\begin{aligned} J = & (1 - \alpha) \sum_{i=1}^C \sum_{j=1}^N a u_{ij}^m \left((\mathbf{x}_j - \mathbf{p}_{ij} \mathbf{E}_i) (\mathbf{x}_j - \mathbf{p}_{ij} \mathbf{E}_i)^T + G_{ij} \right) \\ & + b t_{ij}^n (\mathbf{x}_j - \mathbf{p}_{ij} \mathbf{E}_i) (\mathbf{x}_j - \mathbf{p}_{ij} \mathbf{E}_i)^T \\ & + \alpha \sum_{i=1}^C (M \cdot \text{trace}(\mathbf{E}_i \mathbf{E}_i^T) - 1_{1 \times M} \mathbf{E}_i \mathbf{E}_i^T 1_{M \times 1}) \\ & + \sum_{i=1}^C \gamma_i \sum_{j=1}^N (1 - t_{ij})^n \end{aligned} \quad (12)$$

As shown in the equation above, spatial information is used in the membership terms only. In future work, incorporating this information when updating typicality will be investigated and implemented as well. The update equations for the proportions remain the same as for the P-COMMEND algorithm described in Section II A. The membership update equations remain the same shown in Equation ?. The endmember update equation becomes as shown below.

$$\mathbf{E}_i = \left(\sum_j (a u_{ij}^m + b t_{ij}^n) \mathbf{p}_{ij}^T \mathbf{p}_{ij} + 2\alpha D \right)^{-1} \left(\sum_j (a u_{ij}^m + b t_{ij}^n) \mathbf{p}_{ij}^T \mathbf{x}_j \right) \quad (13)$$

The update equation for the typicality results the following.

$$t_{ij} = \frac{1}{1 + \left(\frac{b}{\gamma_i} \|\mathbf{x}_j - \mathbf{p}_{ij} \mathbf{E}_i\|_2^2 \right)^{\left(\frac{1}{n-1} \right)}} \quad (14)$$

The γ_i value in the above equation is set to be the mean of the $\|\mathbf{x}_j - \mathbf{p}_{ij} \mathbf{E}_i\|_2^2$ value for all of the pixels in the associated convex region. Therefore, each iteration, the γ_i value gets updated.

The final proportion values are computed by taking the production of the initial proportion values, membership and typicality for data point and convex region.

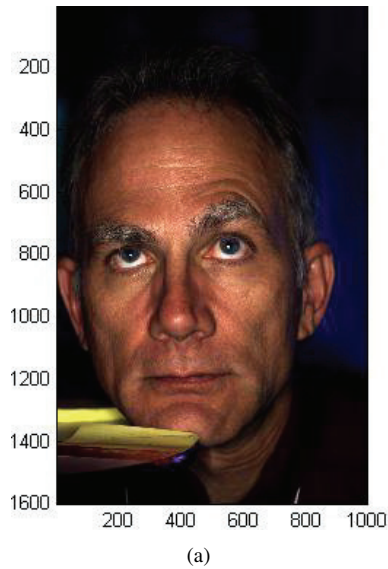


Fig. 1. Color image of hyperspectral face data used for testing.

III. EXPERIMENTAL RESULTS

The proposed algorithm was tested on VIS/NIR hyperspectral face imagery. This data was collected by Norsk Elektro Optikk using their HySpex hyperspectral sensor on participants at the 2010 IEEE Workshop on Hyperspectral Image and Signal Processing: Evolution in Remote Sensing (WHISPERS10). The data contain 160 spectral bands ranging in wavelength from 410 to 990nm. An image was selected from this data set and spatially sub-sampled by selecting every 4th row and column in the image. A color image created using the hyperspectral data is shown in Figure ???. The size of this image is 400×250 pixels.

Using the PCA algorithm, the dimensionality of the hyperspectral data was reduced from 160 dimensions to 5 dimensions. The algorithm was run on the dimensionality-reduced imagery using the following parameters: $\alpha = 0.001$, $a = 20$, $b = 0.1$, $m = 2$ and $n = 1.1$. Results are shown in the following figures.

By examining the final proportion maps shown in Figure ??, it can be seen that an effective segmentation of the imagery is found by the method. The first convex region corresponds to skin, both shadowed and bright skin. The second convex region corresponds to the table and eyes. The third convex region corresponds to background. The fourth convex region corresponds to the shirt. The fifth convex region corresponds to hair and eyebrows.

The membership and typicality maps associated with each convex region is shown in Figure ??.

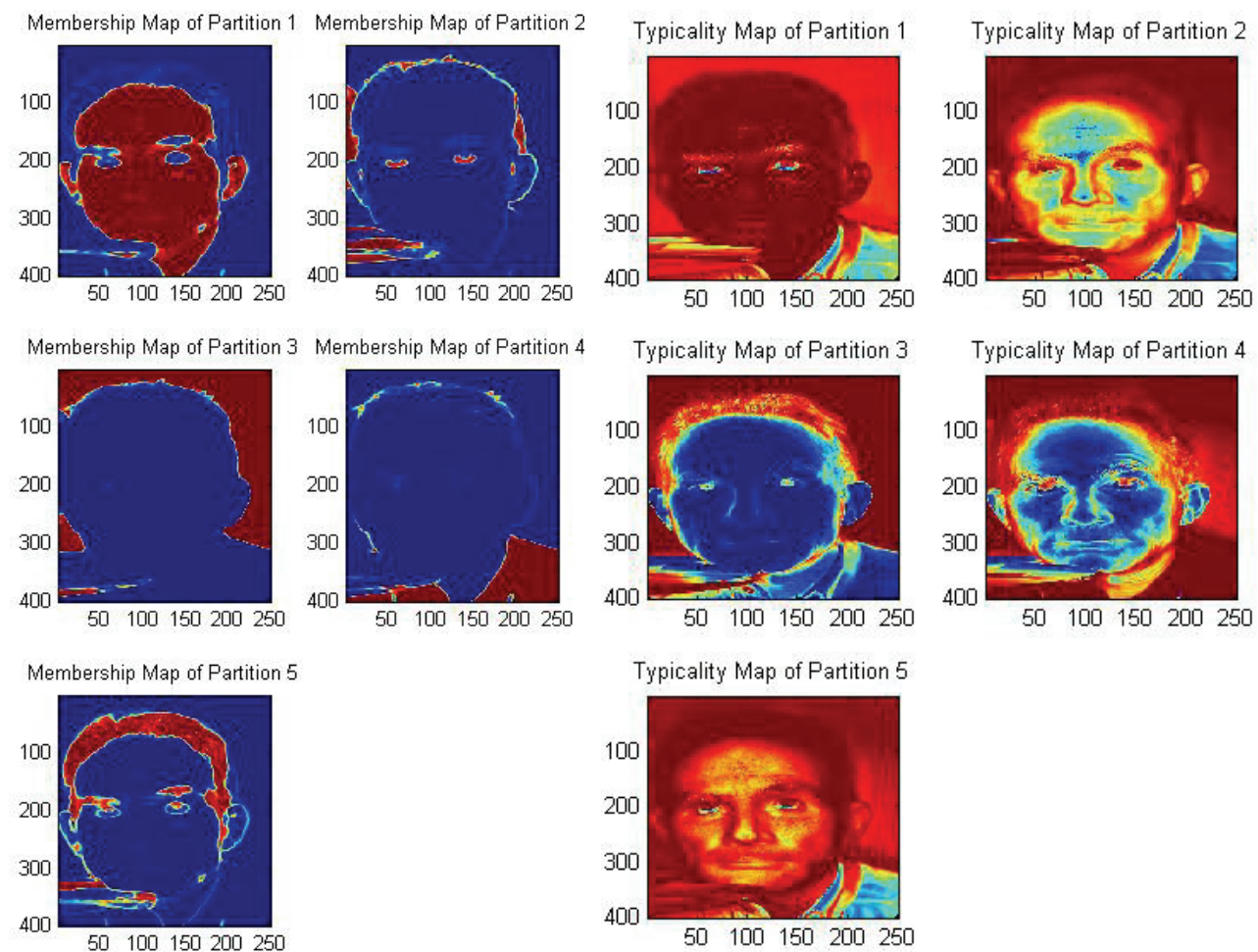
There were several pixels of glare with a high specular reflection in the imagery. These pixels were a result of reflection from the lighting in the room on pixels in the eyes of the photographed individual. As desired, the typicality for these outliers were found by the method to be zero for all convex regions.

IV. CONCLUSION

By using a combination of initial proportions, typicality, fuzzy membership and fuzzy spatial information, excellent segmentation and identification of endmembers in the scene is achieved. Future work will involve applying this algorithm to a large set of data. Also, parameter sensitivity and a reduction in the number of parameters will be investigated.

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(a) Membership maps found for each convex region using the proposed method. (b) Typicality maps found for each convex region using the proposed method.

Fig. 2.

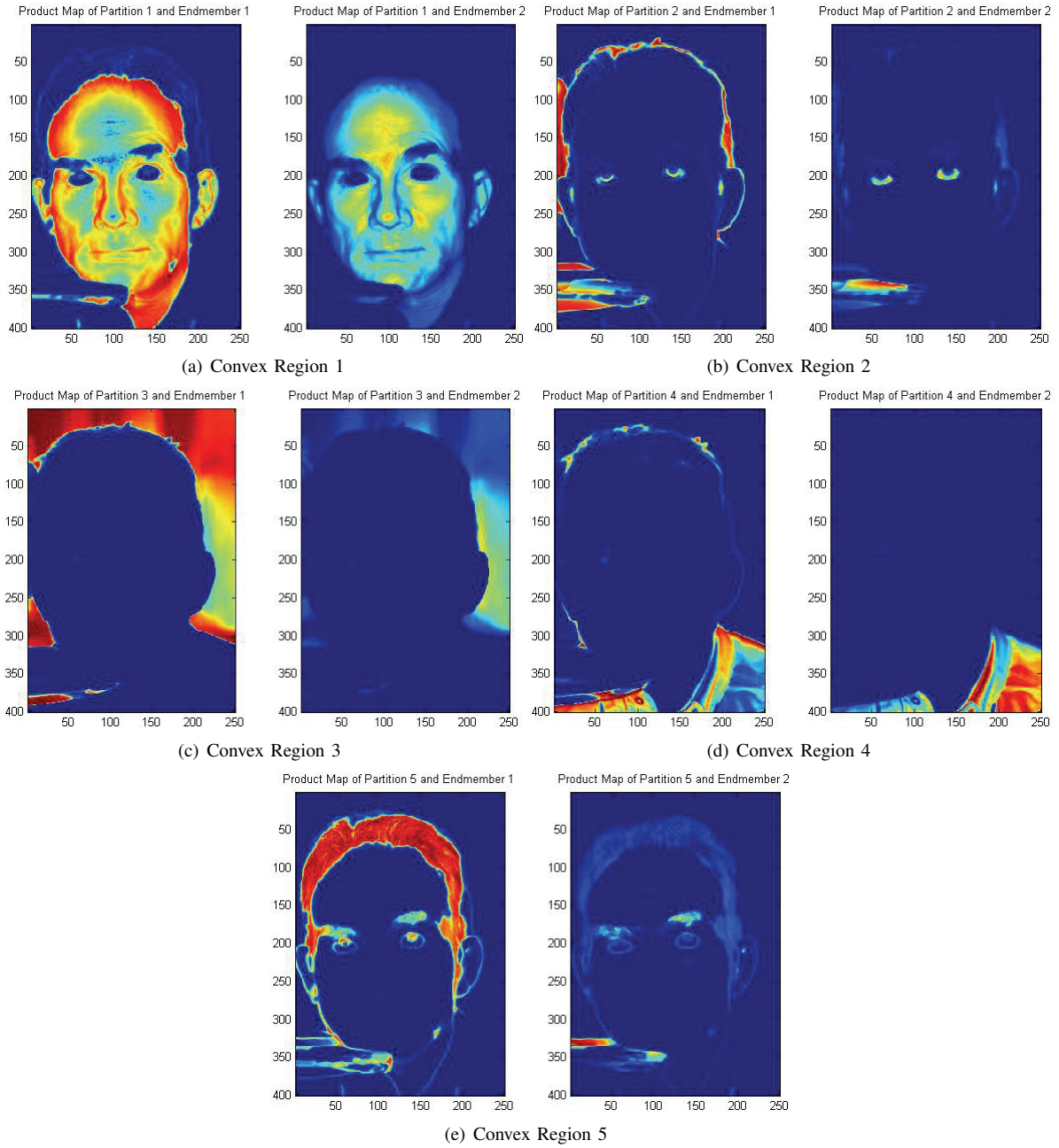


Fig. 3. Final proportion maps found using the proposed method. Final proportion maps are computed using the product of the typicality, membership and initial proportion values for each convex region. Each pair of images corresponds to one convex region. Each convex region consists of two endmembers.