Endmember Extraction Using the Physics-Based Multi-Mixture Pixel Model

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ABSTRACT

A method of incorporating the multi-mixture pixel model into hyperspectral endmember extraction is presented and discussed. A vast majority of hyperspectral endmember extraction methods rely on the linear mixture model to describe pixel spectra resulting from mixtures of endmembers. Methods exist to unmix hyperspectral pixels using nonlinear models, but rely on severely limiting assumptions or estimations of the nonlinearity. This paper will present a hyperspectral pixel endmember extraction method that utilizes the bidirectional reflectance distribution function to model microscopic mixtures. Using this model, along with the linear mixture model to incorporate macroscopic mixtures, this method is able to accurately unmix hyperspectral images composed of both macroscopic and microscopic mixtures. The mixtures are estimated directly from the hyperspectral data without the need for *a priori* knowledge of the mixture types. Results are presented using synthetic datasets, of multi-mixture pixels, to demonstrate the increased accuracy in unmixing using this new physics-based method over linear methods. In addition, results are presented using a well-known laboratory dataset.

Keywords: Hyperspectral image analysis, physics-based mixture models, reflectance spectroscopy, nonlinear unmixing, microscopic mixture, macroscopic mixture, multi-mixture pixel

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1. INTRODUCTION

A common research problem in hyperspectral image (HSI) analysis is that of estimating endmembers from a given set of pixels, often referred to as endmember extraction.[1-16] Often endmembers are extracted simultaneously with estimating of their respective proportions, this is known as pixel unmixing.[1-17] A vast majority of approaches to this problem rely on a linear model to describe the mixing relationships between endmembers.[17] An example is the linear mixture model (LMM) shown in Equation (1), with the corresponding constraints in Equation (2), where M is the number of endmembers in the scene, ϵ_i is an error term, and e_k and p_{ik} are the endmembers and proportions, respectively, of a given pixel x_i.[1, 6] Reliance on the linear model is a result of the mathematical amenability of linear models and the prevalence of macroscopic mixtures, also known as areal or checkerboard mixtures. Macroscopic mixtures occur when two or more endmembers are discretely present within the instantaneous field of view of a given pixel. [17] This mixing is caused by the coarse spatial resolution of the hyperspectral sensor and does not represent a physical mixing of endmembers.

$$x_i = \sum_{k=1}^{M} e_k p_{ik} + \epsilon_i \tag{1}$$

$$\forall_{ik}\ p_{ik} \geq 0 \quad \forall_i \sum_{k=1}^{M} p_{ik} = 1 \tag{2}$$

Research, however, has shown that nonlinear mixtures are present in hyperspectral images and have a substantial effect on measured spectral reflectance signatures over a given image. [17-19] Recently the impact of nonlinear mixtures in HSIs has garnered much attention. [17-52] Keshava and Mustard describe the effects of nonlinear mixing by stating[17]:

In tests of linear versus nonlinear mixing on laboratory data, the fractions calculated may be in error by as much as 30% absolute. In addition, the linear model can cause considerable ambiguity and false fractions when used on nonlinear mixtures. Absorption bands and continua in nonlinear mixtures cannot be adequately fit with a linear model.

Microscopic mixtures, also called intimate mixtures, are known to be present in many hyperspectral images. [17, 40, 53-62] Unlike the macroscopic mixture, microscopic mixtures form non-linear mixtures of endmember spectra. [54-57, 61, 62] Consequently, the LMM has been shown inadequate for modeling this type of mixing in hyperspectral data. [17, 40, 53-62] While microscopic mixing does represent physical mixtures of endmembers, it is important to note that it is not a chemical reaction (i.e., the constituent endmember substances still exist).

Attempts to incorporate the nonlinearity of microscopic mixtures into the hyperspectral pixel unmixing problem have been largely black-box approaches and often assume a known set of endmembers, thereby ignoring the endmember extraction problem. Traditional methods of reproducing an unknown nonlinear function such as neural networks [33, 37-39] and kernel methods [41, 49, 59, 60, 63-65] have been used to estimate the latent nonlinear function in the system. Recent research has introduced manifolds to model the nonlinearity in hyperspectral data.[20, 22-28, 46-48, 51, 52, 66-81] Typically used in hyperspectral classification applications, endmember and proportion estimation has also been pursued with manifold based algorithms. [35, 36, 82] These methods all attempt to account for the nonlinearity with a generic machine learning model to approximate the mixture; however they do not explicitly model the underlying physics of the mixture.

Two commonly referenced physics-based techniques for microscopic mixture pixel unmixing are Mustard and Pieters's least squared error (LSE) unmixing of single-scattering albedo data[53] and Guilfoyle, et al. use of a radial basis function neural network (RBFNN)[33]. However, these methods of microscopic mixture pixel unmixing require the assumption that a data set contains only macroscopically mixed data or microscopically mixed data and assume an known set of endmembers. [33, 40, 53, 54, 83-85]

Recently, two methods for pixel unmixing were developed that allow for proportion estimation in the presence of both macroscopic and microscopic mixtures. The first is a physics-based kernel approach that approximates Hapke's reflectance model. [59, 60, 63] The second is the microscopic mixture iterated constrained endmembers (MICE) algorithm.[86] These two approaches, however, assume that a given HSI pixel is composed exclusively of a single mixture type (i.e. either macroscopically or microscopically mixed). This assumption is valid for some HSIs. However, the assumption is violated in HSIs that contain overlapping heterogeneous regions of different mixture types. In these scenes a pixel may be composed of a macroscopic mixture, a microscopic mixture, or a combination of the two mixture types. A second violation to this assumption occurs when one or more endmembers of a microscopic mixture clump together. These particles cause macroscopic mixing with the surrounding microscopic mixture. These observations led to a new HSI pixel model, the multi-mixture pixel (MMP).[87] The MMP characterizes a pixel as a macroscopic mixture of endmembers and a microscopic mixture, i.e., a mixture of mixtures. The MMP model's introducing publication, however, assumed that the endmembers where known *a priori*. Often this assumption is not valid. This paper will build upon the MMP model and the introduced method of estimating proportions by adding the ability to extract endmembers simultaneously.

The remainder of this paper is organized as follows. Section 2 gives a review of microscopic mixtures and the bidirectional reflectance distribution function (BRDF). Next, in Section 3 the MMP model and the associated MMP proportion estimation (MPE) algorithm is discussed. Section 4 will introduce the MMP endmember extraction (MEE) algorithm. Section 5 presents experimental results on both synthetic data sets and well-known sets of laboratory mineral mixtures, the RELAB data sets. Finally, in Section 6 conclusions and future research is discussed.

2. REVIEW OF MICROSCOPIC MIXTURES

Microscopic mixing occurs when particles of different endmembers are homogenously distributed within the instantaneous field of view of a given pixel. Light incident on this mixed surface is scattered.[56, 61] The close proximity of endmembers particles, occurring in a microscopic mixture, causes multi-scattering between particles with differing spectral properties. [17, 54] This multi-scattering between particles causes a nonlinear mixture in reflectance spectra. To accurately estimate endmembers and proportions within the context of microscopic mixture reflectance spectra, a model for reflectance is needed.

Reflectance is characterized by the collimation of the light source and the detector (or sensor). Because perfect collimation and perfect diffuseness do not exist, in reality all reflectances are biconical. [56, 61] However, on a clear, sunny

day, the sun can be reasonably approximated as a collimated source (i.e., directional). [56] An air or space borne sensor looking at the ground approximates a directional detector. [56] Therefore, under these basic remote sensing assumptions (including assuming minimal cloud cover), the BRDF is the appropriate model for hyperspectral image applications.

Hapke's BRDF has been validated through experimentation and is widely accepted as an accurate model. [33, 38, 40, 41, 53-63, 83-85] Hapke's reflectance coefficient BRDF is given by Equation (3), where c_i and c_e are the cosine of the angles of incidence and emergence, respectively, g is the phase angle, $P(g)$ is the phase function for particles, $B(g)$ is the backscatter function given by Equation (4), $H(\mu)$ is Hapke's approximation to Chandrasekhar's function for isotropic multi-scattering given by Equation (5), and w is the average single-scattering albedo given by Equation (6) with P_S and P_A being the power of the incident irradiance scattered and absorbed by the particle, respectively. [33, 53-56, 59-61, 63] To clarify terms, c_i and c_e are used for the cosine of the angles of incidence and emergence instead of the traditional μ_0 and μ. The phase angle and the angles of incidence and emergence describe the geometries of the light source and detector. Scattering properties of the surface are described by the $P(g)$ function. The backscatter function $B(g)$ models the opposition effect, as given by Equation (4) where B_0 describes the magnitude of the opposition effect and h depends on the interparticle spacing.

$$R = \frac{w}{4(c_i + c_e)}\{[1 + B(g)]P(g) + H(c_i)H(c_e) - 1\} \tag{3}$$

$$B(g) = \frac{B_0}{1 + \left(\frac{1}{h}\right)\tan\left(\frac{g}{2}\right)} \tag{4}$$

$$H(c_{[i,e]}) = \frac{1 + 2c_{[i,e]}}{\left(1 + 2c_{[i,e]}(1 - w_\lambda)^{1/2}\right)} \tag{5}$$

$$w = \frac{P_S}{P_S + P_A} \tag{6}$$

Under remote sensing assumptions, the angle of incidence is commonly 15^0 to 40^0 and the angle of emergence 0^0, under these conditions the phase angle is between 15^0 and 40^0. [53] Additionally, under remote sensing assumptions, these angles are assumed constant over a given collection. Mustard and Pieters demonstrated that at phase angles greater than 15^0 the $B(g)$ was negligible. [53] Additionally, under the assumption of isotropic scattering (all light is scattered equally in all directions) the phase function is defined to be $P(g) = 1$. [56, 61] Using these remote sensing assumptions and the consequential results for $B(g)$ and $P(g)$, a simplified reflectance coefficient function can be derived as shown in Equation (7) where the λ subscript is used to signify the wavelength dependence of the reflectance function. Also, w_λ was added as a parameter to Chandrasekhar's function to represent the single-scattering albedo as an input parameter to the function. As the reflectance coefficient function, under the described assumptions, is the only model for reflectance used in this research it will simply be referred to as the reflectance function. The resulting reflectance function can be seen plotted against single-scattering albedo in Figure 1.

$$R_\lambda = \frac{w_\lambda}{4(c_i + c_e)}H(c_i, w_\lambda)H(c_e, w_\lambda) \tag{7}$$

The reflectance of a microscopic mixture is described by the reflectance function (Equation (7)) and the average single-scattering albedo of the mixture, shown in Equation (8). [53, 54, 56] The average single-scattering albedo is a linear combination of endmember's single-scattering albedos where Ψ_k, q_k, and d_k are the mass fraction, single particle density, and average effective particle size for a given mixture component (i.e., endmember). [56]

$$w_\lambda = \frac{\sum_{k=1}^{M}(\Psi_k/q_k d_k)\,w_{k\lambda}}{\sum_{k=1}^{M}(\Psi_k/q_k d_k)} \tag{8}$$

The average single-scattering albedo can also be represented as a relative geometric cross-section (F_k) or endmember proportion (f_k), shown in Equation (9) for the kth component. [56] This representation is important, because often in remote sensing the particle density and particle size of endmembers is not known. Therefore, the particle density and particle size are assumed roughly equal for all endmembers. Under this assumption, the proportion of an endmember composing a mixed pixel's spectra (i.e., the relative geometric cross-section of the pixel composed of the endmember) is equal to its mass fraction.

$$F_k = f_k = \frac{(\Psi_k / q_k d_k)}{\sum_{k=1}^{M}(\Psi_k / q_k d_k)} \qquad (9)$$
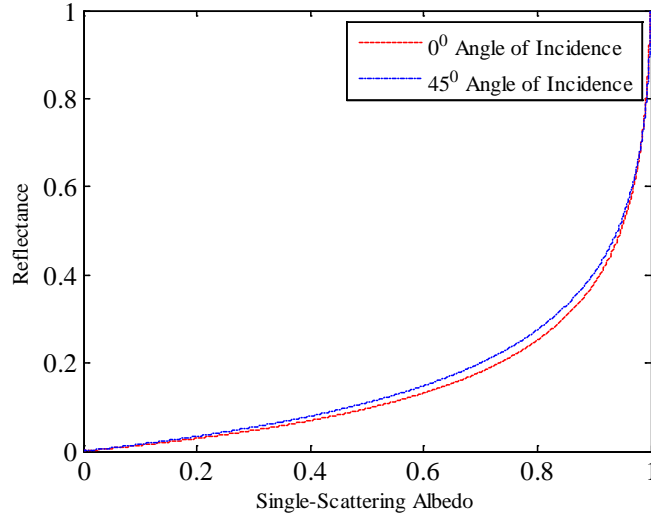

Figure 1: Reflectance function curve versus single-scattering albedo (angle of emergence is $\mathbf{0^0}$).

Using the relative geometric cross-section representation for each endmember, the equation for the average single-scattering albedo can be written as Equation (10). This formulation leads to constraints similar to those of the LMM: $f_k \geq 0$ and $\sum_{k=1}^{M} f_k = 1$. Additionally, the albedo-domain formulation given in Equation (10) can be represented in the reflectance-domain as shown by Equation (11), with the same constraints.

$$w_\lambda = \sum_{k=1}^{M} f_k w_{k\lambda} \qquad (10)$$

$$x_i = R\left(\sum_{k=1}^{M} f_{ik} w_k\right) \qquad (11)$$

3. MULTI-MIXTURE PIXELS

3.1 Multi-Mixture Pixel Model

The MMP model, shown in Equation (12), characterizes a pixel as a macroscopic mixture of endmembers and a microscopic mixture, i.e., a mixture of mixtures.

$$x_i = \sum_{k=1}^{M} p_{ik} e_k + p_{iM+1} R\left(\sum_{k=1}^{M} f_{ik} w_k\right) + \varepsilon_i \qquad (12)$$

The macroscopic proportions (p_{ik}) in the MMP model are dependent on the reflectance of the component microscopic mixture. Therefore, the macroscopic proportions are dependent on the microscopic proportions (f_{ik}). Estimation of the microscopic proportions is an ill-posed inversion problem. Ignoring noise, consider the following case, as illustrated in Figure 2. An MMP x is composed of two endmembers, e_1 and e_2. The MMP mixture point is constrained by the set of possible macroscopic mixtures between the endmembers, illustrated as a dashed blue line, and the set of possible microscopic mixtures between the endmembers, illustrated as a solid red curve. Recall that the MMP model treats the microscopic mixture as an endmember. Therefore, the MMP model can represent x with 0 residual error using e_1, e_2, and $r = R(\sum_{k=1}^{M} f_{ik} w_k)$ for any point r on the arc A. More precisely, $\forall r \in A \,\exists\, p_1, p_2, p_3 : x = p_1 e_1 + p_2 e_2 + p_3 r$.

As a pixel's microscopic mixture proportion (p_{iM+1}) increases, the MMP mixture point moves closer to the microscopic mixture line, as shown in Figure 3. Therefore, the plausible proportions of the microscopic mixture become increasingly constrained and even unique in the case of a 100% microscopic mixture, i.e., the arc A of plausible points r shrinks. As an MMP mixture point's microscopic mixture proportion lessens, the MMP mixture point moves closer to the

macroscopic mixture, as shown in Figure 4. This causes the plausible microscopic proportions to be less constrained, i.e., the arc A of plausible points r increases. However, as the microscopic mixture proportion decreases (i.e., the MMP is dominated by a macroscopic mixture) the microscopic mixture becomes less of a factor in the overall pixel's mixture proportions. Therefore, the error caused by the ill-posed inversion of estimating the microscopic proportions is a small factor in accurately estimating the mixture proportions.

3.2 MMP Proportion Estimation

Estimating proportions of the MMP model, termed MMP proportion estimation (MPE), is composed of two steps. First, the reflectance signature of the microscopic mixture component of the MMP must be estimated. To determine this reflectance signature, the microscopic mixture proportions are estimated using an albedo-domain microscopic mixture, given by Equation (13). This albedo-domain microscopic mixture term is derived from Equation (11), where $\boldsymbol{\beta_i}$ is an assumed zero-mean Gaussian additive noise term. . [1, 17, 53, 54, 59, 60, 63, 88] Estimation of the microscopic mixture proportions is accomplished by using quadratic programing to minimize the residual sum of squares (RSS) of Equation (13), as shown in Equation (14), with its associated constraints. Secondly, the macroscopic proportions are estimated by minimizing the RSS objective function shown in Equation (15), derived from the MMP model (Equation (12)). When estimating the macroscopic mixture proportions, the microscopic mixture proportions are held fixed.

$$R^{-1}(x_i) = \sum_{k=1}^{M} f_{ik} w_k + \beta_i \tag{13}$$

$$RSS = \sum_{i=1}^{N} \left(\left(R^{-1}(x_i) - \sum_{k=1}^{M} f_{ik} w_k \right)^T \left(R^{-1}(x_i) - \sum_{k=1}^{M} f_{ik} w_k \right) \right) \tag{14}$$

$$RSS = \sum_{i=1}^{N} \left(\left(x_i - \sum_{k=1}^{M} p_{ik} e_k - p_{iM+1} R\left(\sum_{k=1}^{M} f_{ik} w_k \right) \right)^T \left(x_i - \sum_{k=1}^{M} p_{ik} e_k - p_{iM+1} R\left(\sum_{k=1}^{M} f_{ik} w_k \right) \right) \right) \tag{15}$$

The final MPE algorithm is as follows:

1. Take as input a set of pixels from an HSI and a set of endmembers

2. Use quadratic programming to estimate the microscopic mixture proportions (f_{ik}'s) by minimizing the RSS in Equation (14)

3. Use quadratic programming to estimate the macroscopic mixture proportions (p_{ik}'s) by minimizing the RSS in Equation (15)

The resulting proportions are interpreted as follows. The macroscopic proportions *1* through *M* ($p_{i1} \cdots p_{iM}$) represent the proportions of endmembers macroscopically mixed. The *M+1* macroscopic proportion (p_{iM+1}) is the estimated proportion of the pixel composed of a microscopic mixture. Therefore, $p_{iM+1} f_{ik}$ is the proportion of the pixel described by a microscopic mixture of the kth endmember.

Returning to the diagram in Figure 2, the estimated microscopic mixture proportions result in a point r on the arc A that is the closest to the MMP mixture point. The estimated macroscopic mixture proportions find a minimal RSS solution within the simplex formed by the endmembers and the previously estimated point r. Typically, a unique estimation of the microscopic mixture proportions is not possible with the information contained within a given HSI pixel. Therefore, it is probable that some amount of estimation error will be introduced into the microscopic proportion estimation. This introduced error is due to the ill-posed inversion and is unavoidable in estimating proportions in the MMP model using only HSI spectral information.
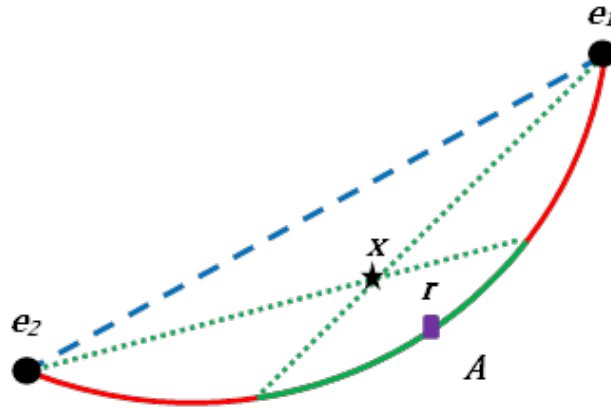
Figure 2: Diagram of multi-mixture pixel (black star) contained within the region bounded by the possible macroscopic mixtures (dashed blue line) and the possible microscopic mixtures (solid red curve) with plausible constituent microscopic mixture point (purple square).
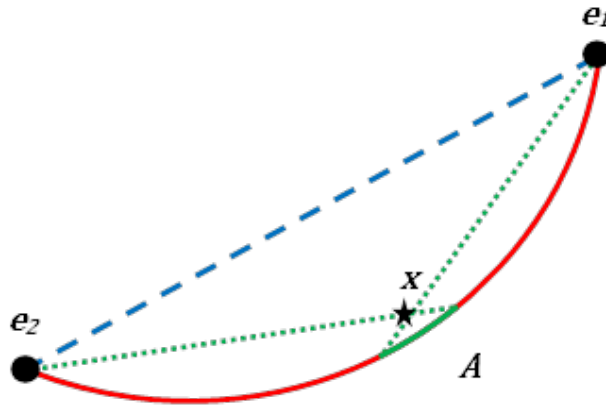

Figure 3: Diagram of multi-mixture pixel x contained within the region bounded by the possible macroscopic mixtures (dashed blue line) and the possible microscopic mixtures (solid red curve) with plausible constituent microscopic mixtures (green arc).
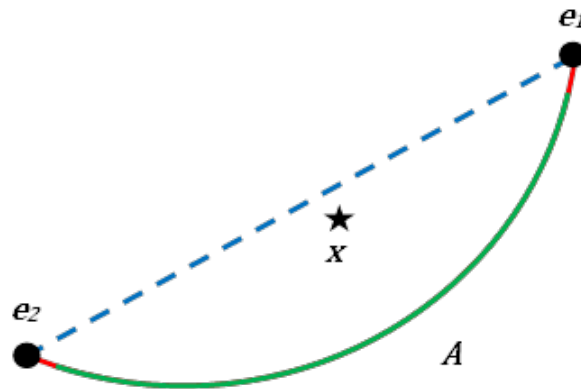

Figure 4: Diagram of multi-mixture pixel x contained within the region bounded by the possible macroscopic mixtures (dashed blue line) and the possible microscopic mixtures (solid red curve) with plausible constituent microscopic mixtures (green arc).

4. MMP ENDMEMBER EXTRACTION

The MMP model, shown in Equation (12), is composed of K endmembers, represented as e_k, and their respective albedo-domain signatures, represented by w_k where $w_k = R^{-1}(e_k)$. The MMP endmember extraction (MEE) algorithm uses an alternating optimization technique to minimize the regularized RSS shown in Equation (16), where the RSS term is given by Equation (15). The sum of squared differences (SSD) term, shown in Equation (17), keeps the endmembers

close to the data and the μ controls the tradeoff between error and regularization. This approach is derived from the Iterative Constrained Endmembers (ICE) algorithm.[1]

$$RSS_{reg} = (1 - \mu)\frac{RSS}{N} + \mu\frac{SSD}{M(M-1)} \tag{16}$$

$$SSD = \sum_{k=1}^{M-1} \sum_{l=k+1}^{M} (e_k - e_l)^t(e_k - e_l) \tag{17}$$

The algorithm alternates between estimating the proportions, using MPE, and the endmembers using Newton's method (Equation (18)). The derivative of RSS_{reg} for the jth endmember is shown in Equation (19), where $E = [e_1 | \cdots | e_M]$ and $= [w_1 | \cdots | w_M] = [R^{-1}(e_1) | \cdots | R^{-1}(e_M)]$. In this formulation u_i is the derivative of the reflectance function (Equation (7)) at the albedo-domain microscopic mixture (i.e., $u_i = \frac{\partial R}{\partial w_\lambda}(Wf_i)$) and v_j is the slope of the inverse reflectance function of the jth endmember. The second derivative of RSS_{reg} is given by Equation (20).

$$e_j^{new} = e_j^{old} - \eta \left(\frac{\frac{\partial RSS_{reg}}{\partial e_j}}{\frac{\partial^2 RSS_{reg}}{\partial e_j^2}} \right) \tag{18}$$

$$
\frac{\partial RSS_{reg}}{\partial e_j} = -2\frac{1-\mu}{N}\sum_{i=1}^{N} \left((p_{ij} + p_{iM+1}f_{ij}\odot v_j\odot u_i)\left(x_i - E^{old}p_i - p_{iM+1}R(Wf) \right) \right) \\
+ \frac{2\mu}{M(M-1)}\sum_{k=1;k\neq j}^{M} \left(e_j^{old} - e_k \right) \tag{19}
$$

$$\frac{\partial^2 RSS_{reg}}{\partial e_j^2} = 2\frac{1-\mu}{N}\sum_{i=1}^{N}\left(p_{ij} + p_{iM+1}f_{ij}\odot v_j\odot u_i \right)^2 + \frac{2\mu}{M} \tag{20}$$

The complete MEE algorithm is as follows:
1. Initialize by selecting a starting set of HSI pixels as the endmembers
2. Use the MPE algorithm to estimate the proportions of each pixel with the current endmembers
3. Use Newton's method to update the endmembers
4. Repeat steps 1 – 3 until a stopping criteria is met

5. EXPERIMENTAL RESULTS

A quantitative evaluation of the MEE algorithm was conducted using synthetic data and RELAB measurements of well-known mineral mixtures. Mean absolute band error (MABE), given by Equation (21), was used to quantify error between true (e_{dk}) and estimated ($\hat{e}_{dk}$) endmembers.

$$MABE = \frac{1}{N \cdot D}\sum_{d=1}^{D}\sum_{k=1}^{M}|e_{dk} - \hat{e}_{dk}| \tag{21}$$

5.1 Synthetic Data Sets Results

Synthetic data sets were created using the MMP model and three 38-dimensional endmembers obtained from the ASTER spectral library with proportions sampled from a Dirichlet distribution with additive zero-mean Gaussian noise.[89] Each data set consisted of 1,000 data points. A sample synthetic data set is shown in Figure 5 and Figure 6.
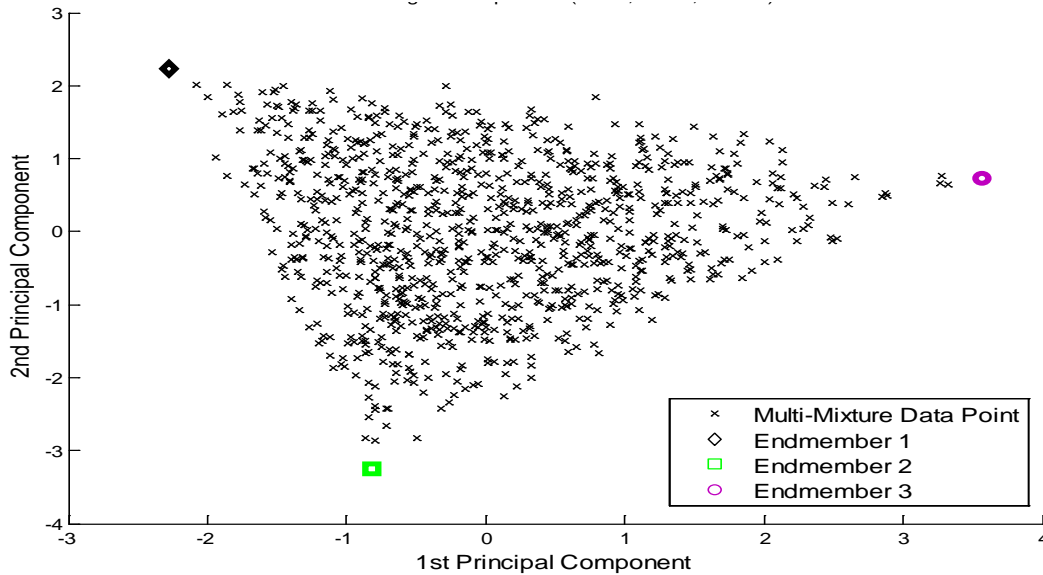
Figure 5: First and second principal components of a synthetic MMP data set created using three endmembers and proportions drawn from a Dirichlet distribution.
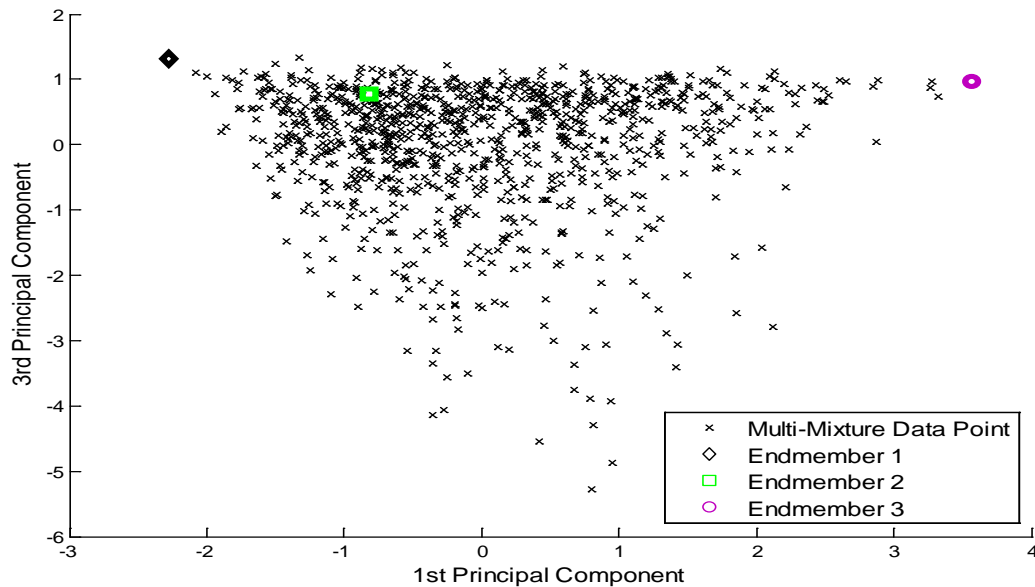

Figure 6: First and third principal components of a synthetic MMP data set created using three endmembers and proportions drawn from a Dirichlet distribution.

In these experiments 50 data sets were generated. For each of the 50 synthetic data sets six algorithms were run and the MABE calculated. The paired difference between MEE algorithm's MABE and the resulting MABE for the remaining algorithms was calculated. These results are shown in the histogram in Figure 7. The algorithms were MEE (shown in the figure's key as MMP), vertex component analysis (VCA)[12], ICE[1], regularized linear mixture model – gradient descent (RLMM-GD), albedo-domain RLMM-GD (AD-RLMM-GD), and macroscopic microscopic iterated constrained endmembers (MICE)[86]. RLMM-GD is a gradient descent solution to estimating the regularized RSS using the LMM. The RLMM-GD algorithm was used to make an algorithm as close to possible as MEE with the only exception being the linear only objective. The AD-RLMM-GD is similar to RLMM-GD except that the data points are converted to albedo-domain first and then solved with the LMM. The AD-RLMM-GD algorithm was used to ensure that the MEE algorithm is not solely benefiting from access to the albedo-domain form of the HSI pixels.
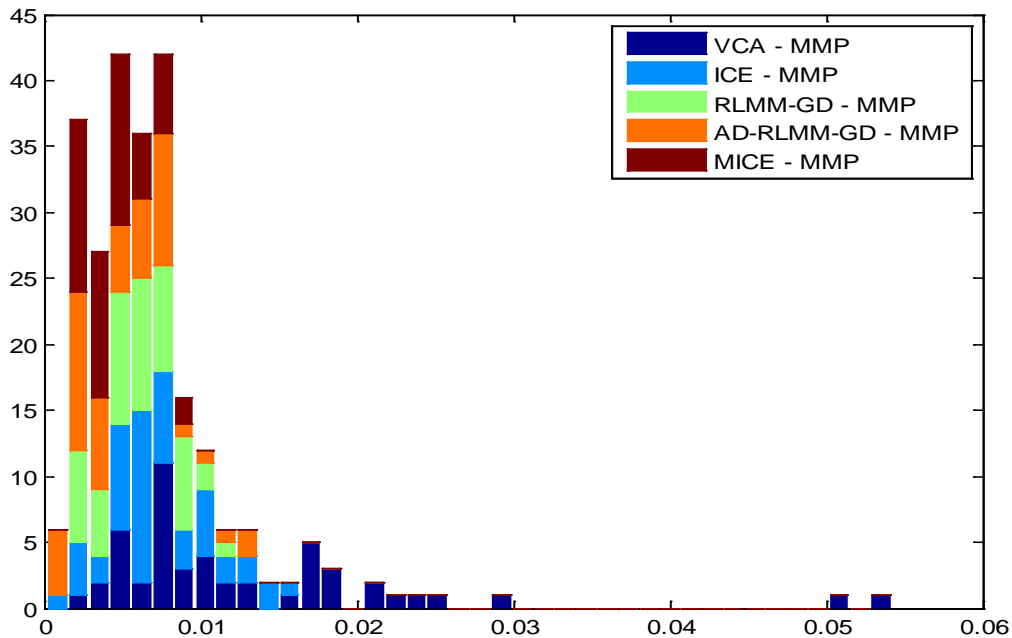
Figure 7: Histogram of paired MABE differences.

As can be seen from the histogram in Figure 7, in all cases the MEE algorithm created less error when estimating the endmembers of the synthetic data sets. VCA scored the worst, which is not surprising given its need for a pure-pixel assumption.[12] MICE scored best of the remaining algorithms, even though MEE still outperformed it. This result is also not surprising as MICE incorporates both macroscopic and microscopic mixtures but without the ability to model a multi-mixture pixel.[86]

5.2 RELAB Data Sets Results

The RELAB data sets used consist of mixtures of Enstatite with Olivine and Magnetite with Olivine. These mixtures where prepared and measured by Professors John Mustard and Carle Pieters of Brown University, as specified in their paper.[53] The spectra were collected with RELAB, a high-resolution bidirectional reflectance spectrometer with a specified angle of emergence of 0^0 and angle of incidence of 30^0.[53] Each mixture data set is composed of spectra from five mixed samples and two endmembers. The spectra have 211 dimensions with wavelengths ranging from 400 nm to 2,500 nm. These data sets have become a *de facto* standard for evaluating microscopic unmixing algorithms.[33, 38, 53, 59, 60]

The MABE resulting from the endmembers estimated with both MEE and ICE is shown in Figure 8. This histogram demonstrates that MEE is able to estimate the RELAB endmembers with less error than ICE. It should be noted that the RELAB data sets only contain five samples each.
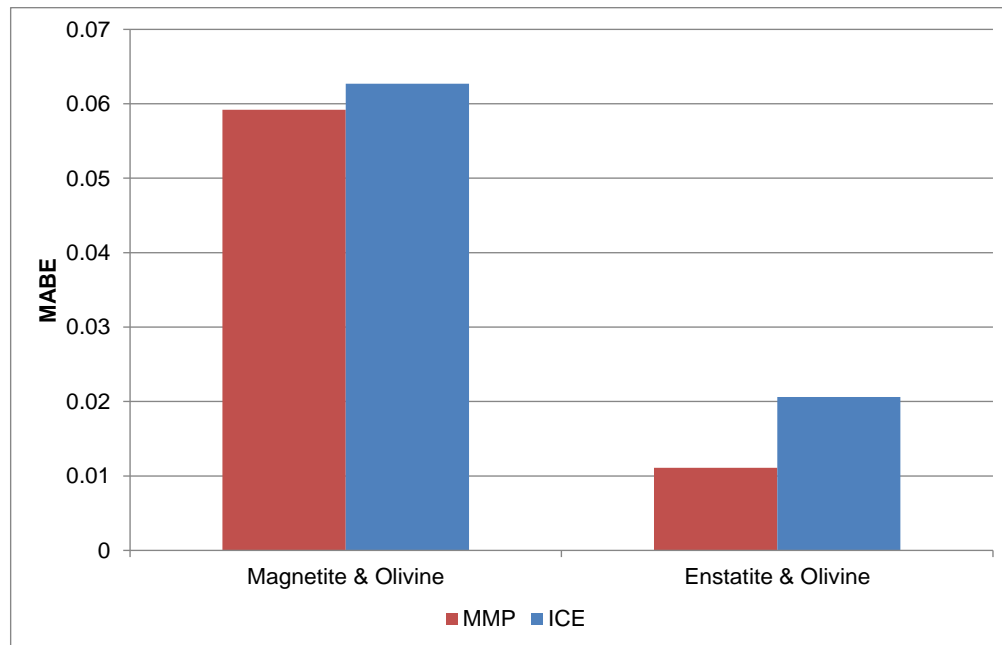
Figure 8: MABE histogram for RELAB data sets.

6. CONCLUSIONS AND FUTURE WORK

In this paper an algorithm, MEE, was presented to estimate endmembers of HSI pixels using the MMP model. Using synthetic data sets, it was demonstrated that pixels composed of multiple mixture types create increased error in estimating endmembers when using a linear model, or even the MICE algorithm. Through experimentation it was shown that MEE is able to accurately estimate the endmembers of data sets composed of multi-mixture pixels. Further analysis was done using the RELAB laboratory data sets of known microscopic mixtures. Using these data sets MEE was compared against a popular LMM endmember extraction algorithm, ICE.[1] Analysis revealed that MEE was able to accurately estimate the endmembers of the given RELAB data sets. Future research could investigate alternate ways of estimating the endmembers during the alternating optimization of the objective function. Also, future work could utilize LIDAR sensor data to increase the accuracy in estimating the angles of incidence and emergence used in the BRDF.

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