H-COMP: A Tool for Quantitative and Comparative Analysis of Endmember Identification Algorithms

Javier Plaza, Antonio Plaza, Pablo Martínez and Rosa Pérez

Neural Networks and Signal Processing Group (GRNPS) Computer Science Department, University of Extremadura Avda. de la Universidad s/n, 10071 Caceres, Spain e-mail: inlaga@unex.es

e-mail: jplaza@unex.es

Abstract— Over the past years, several endmember extraction algorithms have been developed for spectral mixture analysis of hyperspectral data. Due to a lack of quantitative approaches to substantiate new algorithms, available methods have not been rigorously compared using a unified scheme. In this paper, we describe H-COMP, an IDL (Interactive Data Language)-based software toolkit for visualization and interactive analysis of results provided by endmember selection methods. The suitability of using H-COMP for assessment and comparison of endmember extraction algorithms is demonstrated in this work by a comparative analysis of three standard algorithms: Pixel Purity Index (PPI), N-FINDR, and Automated Morphological Endmember Extraction (AMEE). Simulated and real hyperspectral datasets, collected by the NASA/JPL Airborne Visible-Infrared Imaging Spectrometer (AVIRIS), are used to carry out a comparative effort, focused on the definition of reliable endmember quality metrics.

Keywords-Spectral mixture analysis, Comparative framework, Endmember extraction, Endmember quality metrics.

I. INTRODUCTION

The interpretation of mixed pixels is a key factor in the analysis of hyperspectral imagery. Spectral mixture analysis techniques usually involve two steps: to find spectrally unique signatures of pure ground components (usually referred to as endmembers) and to express individual image pixels in terms of linear/nonlinear combinations of endmembers [1]. Nonlinear mixing constitutes an area of active research in particular applications such as vegetation and canopy studies, which mostly rely on rigorous, complex and highly-parameterized models for plant canopies. Contrary to nonlinear models, the inherent simplicity of the linear model has made it a standard choice in general-purpose applications. As a result, most available endmember selection methods rely on the assumption that spectral mixtures can be modelled by linear combinations of ground constituents.

A number of algorithms have been developed over the past decade to accomplish the task of finding appropriate image endmembers for spectral mixture analysis, including Pixel Purity Index (PPI) [2], NFINDR [3] and Automated Morphological Endmember Extraction (AMEE) [4]. With an increasing number of methods readily available, the need for standardized strategies to evaluate the quality of selected endmembers has been identified as a desired goal by the scientific community dedicated to hyperspectral data analysis. Several approaches are currently available in the literature. However, these approaches are only possible when highquality ground-truth information concerning the original scene is available. The generation of reliable ground-truth in real scenarios is difficult and expensive, a fact that has traditionally prevented the existence of comparative surveys using large databases of real images. In order to avoid this shortcoming, simulation of hyperspectral imagery has been suggested as a simple and intuitive way to perform a preliminary evaluation of analysis techniques. In this paper, we describe H-COMP, a novel software toolkit for evaluation of endmember extraction and spectral unmixing techniques. This tool represents a first step in the standarization of quantitative and comparative strategies in hyperspectral data analysis. The tool incorporates a module for generation of synthetic hyperspectral imagery with high-quality ground-truth that can be used as standardized benchmark data for endmember extraction accuracy assessment. In the following section we provide a description of the comparative strategies implemented in H-COMP. Section 3 describes the simulated imagery-generation module. The paper ends by describing a comparison of three standard endmember extraction algorithms, carried out using H-COMP.

II. TOOL DESCRIPTION

H-COMP is an IDL (Interactive Data Language)-based software toolkit for visualization and interactive analysis of results provided by hyperspectral remote sensing data analysis algorithms. It provides an "easy to use" tool which can be used to evaluate new and existing techniques for endmember extraction and spectral unmixing in standardized fashion. H-COMP has been developed taking into account several major design criteria [5], which are briefly summarized next.

- Multi-platform (Supported OS: Microsoft Windows 98/2000/ME/XP, Unix, Linux).
- Scalable (object-oriented implementation, easy incorporation of new comparative strategies).
- Fully compatible with many standard file output formats, including Excel, Postscript, ASCII.
- Supports many different standard remote sensing data formats, including BSQ, BIL, raw data.
- Easy to be implemented online (we are currently working toward an online version of the tool).

H-COMP incorporates a diverse array of comparative and quantitative approaches that have been used in the literature

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for evaluation of endmember extraction and spectral unmixing techniques. In addition, it utilizes innovative, custom-designed frameworks that takes into account both the spectral and spatial information. Evaluation strategies implemented in H-COMP rely on two major criteria. Firstly, we assume that ground-truth information for a certain hyperspectral scene is available, either as a spectral library of endmember signatures measured on the ground, or as a series of fractional maps representing the abundance of constituent materials at each pixel. A novel reconstruction-based approach is used to assess algorithms when no ground-truth information is available.

A. Evaluation strategies in case of ground-truth availability

1) Scenario 1. Ground-truth available as a spectral library of ground constituents.

Let $\{\lambda_1\}_{i=1}^{L}$ be a set containing L wavelengths present in original hyperspectral scene. Similarly, let the $e_i = [(e_i(\lambda_1), e_i(\lambda_2), ..., e_i(\lambda_L))]^T$ be a spectral signature selected from the simulated scene by an endmember extraction algorithm, and $\mathbf{r}_{i} = [(r_{i}(\lambda_{1}), r_{i}(\lambda_{2}), ..., r_{i}(\lambda_{L}))]^{T}$ be a ground-truth spectral signature available in a spectral library of ground measures or image-derived spectra. H-COMP allows direct comparison of (e_i, r_i) pairs by means of several point-wise vector distance metrics. In the current version, the tool supports a variety of distance metrics, including the spectral angle distance, euclidean distance, city-block distance, Tschebychev distance, correlation coefficient, spectral similarity and spectral information divergence. Once a measure is selected for the comparison, a matrix of distance values is generated, containing the scores between all possible pairs from the two (endmembers and reference signatures) spectral libraries. A spectral similarity matching algorithm (SSMA) is then used to produce matchings between extracted endmembers and available reference signatures. Two output vectors with E dimensions (where E is the number of extracted endmembers) are generated. The first one contains the labels of the most appropriate matches in the library of reference signatures for each extracted endmember. The second vector contains the distance values between each endmember and its matching signature.

2) Scenario 2. Ground-truth available as a collection of fractional abundance maps.

In this particular scenario, we assume that each extracted endmember e_i has been matched by SSMA to a reference spectra r_j . With the above assumption in mind, we use the abundance map associated to r_j as ground-truth for the estimated fractional abundance map for e_i . In this context, the comparative methodology adopted by H-COMP is based on the following definitions. Let $I = \{p_k\}_{k=1}^{P}$ be the original hyperspectral image, where each pixel is defined as $p_k = [p_k(\lambda_1), p_k(\lambda_2), ..., p_k(\lambda_L)]^T$. We denote by $\theta_k(e_i)$ the estimated fractional abundance of e_i at pixel p_k . Similarly, we denote by $\theta_k(r_j)$ the ground-truth fractional abundance of r_j at pixel p_k . If we denote by $A(e_i) = \{\theta_k(e_i)\}_{k=1}^{P}$ the abundance map for endmember e_i and by $A(r_i) = \{\theta_k(r_i)\}_{k=1}^{P}$ the abundance map associated to reference spectral signature r_j , then the similarity between $A(e_i)$ and $A(r_i)$ can be quantitatively assessed by the root mean square error (RMSE).

$$\text{RMSE}[A(\boldsymbol{e}_{i}), A(\boldsymbol{r}_{j})] = \left(\frac{1}{P}\sum_{k=1}^{P} \left[\theta_{k}(\boldsymbol{e}_{i}) - \theta_{k}(\boldsymbol{r}_{i})\right]^{2}\right)^{1/2}.$$
 (1)

For illustrative purposes, Fig. 1 shows a screenshot of the available option in H-COMP to perform endmember quality assessment using derived fractional abundance maps. In this run of H-COMP, a 1997 AVIRIS hyperspectral image over Cuprite mining district, NV (hereinafter, AVCUP97), is used to illustrate the performance of the PPI algorithm. This scene covers a well understood mineralogically area, and has reliable ground-truth in several forms, i.e. a library of a spectral library of ground constituents, collected by USGS, and a series of ground-truth fractional abundance maps [6]. The matrix of RMSE errors between each pair of abundance maps is shown at the top of the screen, along with compared fractional abundance maps at the bottom. In order to provide a visually intuitive comparison, H-COMP also visualizes the scatterplot of true versus estimated abundance fractions. The example shown in Fig. 2 reveals high correlation between true and estimated values, which results in optimum (almost linear) scatterplot diagrams.



Figure 1. Evaluation of endmember quality in H-COMP by comparing estimated and ground-truth fractional abundance maps.

B. Evaluation strategies when no ground-truth is available

Our comparative framework in this situation is based on the reconstruction of the original image by using a simple linear mixture model, i.e. the reconstruction is generated using both extracted endmembers and estimated fractional abundance maps. The process relies on the asumption that each pixel p_k of the original dataset can be approximated by \hat{p}_k as follows.

$$\boldsymbol{p}_{k} \approx \hat{\boldsymbol{p}}_{k} = \sum_{i=1}^{E} \boldsymbol{\theta}_{k} (\boldsymbol{e}_{i}) \cdot \boldsymbol{e}_{i} , \qquad (2)$$

where E is the number of extracted endmembers. Let $I = (\mathbf{p}_k)_{k=1}^{P}$ be the original image and $R = (\hat{\mathbf{p}}_k)_{k=1}^{P}$ be the linear

mixture model-based reconstructed image. Reconstruction accuracy can be quantified by the RMSE between I and R, using the following expression.

$$\operatorname{RMSE}(I, R) = \left(\frac{1}{P} \sum_{k=1}^{P} [\boldsymbol{p}_{k} - \hat{\boldsymbol{p}}_{k}]^{2}\right)^{1/2}.$$
 (3)

Fig. 2 shows a screenshot of the H-COMP option that performs the quantitative assessment of endmembers using linear mixture model-based reconstruction of AVCUP97. As Fig. 3 shows, the tool allows visualization of both the original and reconstructed spectral signatures at each pixel, along with the reconstruction error at the pixel, displayed at the bottom. Error images are shown at the top of the screen, revealing features in the scene that have not been accurately reconstructed, an indicator of poorly selected endmembers in that particular areas.



Figure 2. Evaluation of endmember quality in H-COMP by comparing linear mixture-based reconstructed scene to the original hyperspectral dataset.

III. GENERATION OF SYNTHETIC IMAGES

In this section, we briefly describe the procedure used by H-COMP to generate simulated hyperspectral imagery. Fig. 3 shows a screenshot of the correspondent H-COMP option, where the dimensions of the simulated image are previously specified .The user can interactively draw regions on the generated image, and associate spectral signatures from available libraries to each region. A spectral mixture tool is also available in H-COMP to generate linear combinations of spectra. In addition, standard designs for automated generation of simulated imagery are implemented. Currently available designs include both abrupt and progressive mixtures, from simple binary mixtures to more complex mixtures with many endmember materials involved. Spatial distributions for automated generation include horizontal/vertical stripes, as well as elliptic and square-shaped organizations. Random noise can be added to scenes to simulate contributions from ambient (clutter) and instrumental sources. The user interactively selects the desired signal-to-noise ratio (SNR). Noise is created by using numbers with a standard normal distribution, obtained from a pseudorandom number generator and added to each pixel. Following a standard definition [1], we consider the SNR for each band as the ratio of the 50% signal level to the standard deviation of the noise.



Figure 3. Generation of simulated hyperspectral scenes using H-COMP.

IV. QUANTITATIVE COMPARISON OF STANDARD ALGORITHMS

Three standard endmember extraction algoritms: PPI, NFINDR and AMEE are compared in this final section using available metrics in H-COMP. The three above methods have been applied to AVCUP97, which has become a test image for endmember extraction assessment due to available groundtruth. Table I reports quantitative results obtained by the three methods on four minerals that can be found prominently and in pure form in the test site. In the table, SAD denotes the spectral angle distance between the SSMA-matched endmember and the correspondent USGS spectral reference; A is the RMSE error between the estimated fractional abundance and groundtruth; and R denotes the total RMSE error in the reconstruction of the original image using extracted endmembers.

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Method	SAD	А	SAD	А	SAD	А	SAD	А	n
PPI	0.119	0.071	0.188	0.170	0.084	0.011	0.093	0.048	0.032
NFINDR	0.119	0.072	0.167	0.150	0.085	0.023	0.127	0.089	0.049
AMEE	0.119	0.070	0.125	0.157	0.084	0.020	0.100	0.009	0.042

TABLE I. COMPARISON OF STANDARD ALGORITHMS (PPI, NFINDR, AMEE) USING METRICS IMPLEMENTED IN H-COMP.

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