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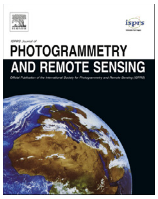

Leveraging in-scene spectra for vegetation species discrimination with MESMA-MDA

Brian D. Bue [a,*], David R. Thompson [a], R. Glenn Sellar [a], Erika V. Podest [a], Michael L. Eastwood [a], Mark C. Helmlinger [a], Ian B. McCubbin [a], John D. Morgan [b]

[a] Jet Propulsion Laboratory, California Institute of Technology, 4800 Oak Grove Drive, Pasadena, CA 91109, United States
[b] Citrus Research Board, 1201 Research Park Drive, Riverside, CA 92057, United States

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ABSTRACT

We describe an approach to improve Multiple Endmember Spectral Mixture Analysis (MESMA) results for applications involving discrimination among spectrally-similar species, and commonly occur in multi-spectral and hyperspectral vegetation remote sensing studies. Such applications are inherently difficult, due to the high degree of similarity between distinct species, coupled with potentially high intra-species variability caused by factors such as growing conditions, canopy structure, ambient illumination, or substrate characteristics. We describe a method to map spectra to a feature space where distinctions between plant species are emphasized using a transformation based on Multiclass Discriminant Analysis. We compute this transformation using groups of pixels that represent individual plant canopies similar to the endmembers in MESMA's spectral library, and describe a technique to automatically select such spectra from a given image. Compared to conventional MESMA, and also to several alternative MESMA formulations, we observe up to twofold increases in accuracy, along with a factor of ten reduction in computation time using our MESMA approach in several species discrimination applications. We demonstrate the effectiveness of our approach for agricultural species discrimination applications using spectra captured by two different imaging spectrometers.

1. Introduction

Airborne and satellite imaging spectrometers are often used for remote identification of species of vegetation and their functional types (Clark et al., 2005; Ustin and Gamon, 2010; Kokaly et al., 2007; Chen et al., 1998; Elvidge et al., 1993; Thenkabail et al., 2002; Galvão et al., 2005). Consequently, researchers have identified a wide range of distinctive, species-specific spectral cues from 400 to 2500 nm (Clark et al., 2005; Lee et al., 2007) that can be exploited in vegetation mapping applications. Absorption features from 400 to 700 nm indicate concentrations of leaf chemicals, such as chlorophyll a and b as well as carotenoid pigments (Asner et al., 2008; Cochrane, 2000). Absorptions from 700 to 1300 nm reveal species-specific leaf structure and water abundance, and leaf nitrogen and lignin content are observable in absorptions at wavelengths longer than 1500 nm (Ustin and Gamon, 2010). Modern imaging spectrometers can capture these distinctive spectral characteristics with unprecedented fidelity, providing a range of useful new vegetation mapping applications for ecosystem studies (Schaepman et al., 2009; Naidoo et al., 2012), forest management (Féret and Asner, 2012) and agriculture (Ben-Dor et al., 2009).

Nevertheless, precision vegetation mapping efforts using imaging spectroscopy face several challenges. Due to their common chemical composition, distinct plant species are often distinguished by subtle differences in their spectral signatures (Cochrane, 2000). Conversely, spectra representing the same species may vary substantially due to factors such as differences in growing conditions, varying canopy structure, stress factors such as air pollution, seasonal effects, ambient illumination, or substrate characteristics (Li et al., 2005; Clark et al., 2005; Youngentob et al., 2011). Combined, these factors demand advanced techniques capable of disambiguating potentially subtle vegetation species signals from spectral variability induced by varying spatial, temporal and instrument conditions.

A variety of techniques have been proposed for automated vegetation mapping applications using spectroscopic imagery (Clark and Swayze, 1995; Clark et al., 2005; Garcia and Ustin, 2001;

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[*] Corresponding author. Tel.: +1 (818) 354 2234.
E-mail address: Brian.D.Bue@jpl.nasa.gov (B.D. Bue).

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Thenkabail et al., 2002). Of these, spectral Mixture Analysis (SMA, Adams et al., 1993) techniques have a long history in vegetation mapping applications (Ustin et al., 1993; Roberts et al., 1998; Asner and Heidebrecht, 2002) and have become a *de facto* benchmark for evaluating species discrimination approaches (Somers et al., 2014; Tits et al., 2012; Fernández-Manso et al., 2012). SMA-based techniques model a given spectrum as a (typically linear) mixture of two or more "endmember" spectra, where each endmember typically represents a "pure" spectrum composed of a single material. Historically, SMA has been used for sensors with relatively low spatial resolution, where each pixel represents a mixture of multiple materials. More recently, modern sensors have been enabling SMA applications involving fine-grained discrimination at both high spatial (e.g., individual tree canopies) and spectral (e.g., vegetation versus substrate, subspecies discrimination) resolution. However, the performance of SMA-based techniques largely depends on how accurately the endmembers capture characteristic spectral variations of relevant species (Roth et al., 2012; Somers et al., 2011; Tompkins et al., 1997). However, accurately incorporating species-specific spectral variability in SMA is a difficult problem, and has been recognized as a principal source of error with SMA-based techniques (Bateson et al., 2000; Somers et al., 2011; Dennison and Roberts, 2003).

Within the past decade, several techniques have been proposed to account for spectral variability in SMA applications (for an in-depth review of such techniques, see Somers et al., 2011). Of the proposed techniques, Multiple Endmember Spectral Mixture Analysis (MESMA, Roberts et al., 1998, 2003) is one the most accurate and widely-used. MESMA models each pixel as the mixture of endmembers selected from a predefined spectral library that reconstruct the pixel with the least Root Mean Squared Error (RMSE). The algorithm accounts for spectral variability by allowing the endmembers to vary on a per pixel basis. MESMA was first applied to map vegetation in scenes containing a few canonical canopy types at dekameter spatial resolution (Roberts et al., 1998), but has since been successfully demonstrated for a diverse range of vegetation mapping (e.g., Roth et al., 2012; Li et al., 2005; Van Beek et al., 2015; Fernández-Manso et al., 2012; Somers et al., 2009a; Youngentob et al., 2011) and related terrestrial and planetary applications (e.g., Franke et al., 2009; Roberts and Herold, 2004; Wendt et al., 2009; Combe et al., 2008; Li, 2003).

Extending MESMA to precision vegetation mapping applications requires that it generalizes well, assigning diverse species variants to appropriate classes. MESMA can account for spectral diversity by including representative endmembers in its spectral library that characterize species of interest. Unfortunately, MESMA scales exponentially in computation time with the number of endmembers in the library, so increasing the number of endmembers in the library quickly becomes intractable. Researchers have developed heuristics, such as Count Based (COB) endmember selection approach of Roberts et al. (2003) and the RMSE-based methods of Dennison and Roberts (2003), to reduce the number of endmembers in the library to a representative subset. However, such techniques only consider intra-class spectral variability and not for spectral variability between different classes (Roth et al., 2012), and can have a negative impact in scenarios demanding subtle delineation of spectrally-similar species. An alternative method to increase MESMA's resilience to intra-/inter-class spectral variability is to replace its RMSE-based objective with a spectral similarity measure such as the Spectral Angle Mapper (SAM) distance, which promotes invariance to geometric albedo (Tits et al., 2012). A similar approach is to apply MESMA to continuum-removed spectra, which emphasizes characteristic absorption features (Youngentob et al., 2011). These approaches are attractive as they can be deployed with only minor changes to the conventional MESMA algorithm, and do not require a substantial increase in computational resources. However, such techniques can be confused by spectral artifacts or features unrelated to the species of interest, as they assume all spectral channels are equally discriminative (Bue and Merényi, 2012; Bue, 2014).

Dimensionality reduction and feature extraction algorithms present an attractive alternative to the aforementioned techniques. By emphasizing discriminative species-specific spectral features while attenuating irrelevant or noisy channels, such techniques have demonstrated substantially improved accuracy in vegetation species discrimination (Sankaran and Ehsani, 2011) and other related applications (Harsanyi and Chang, 1994; Bue, 2014; Dopido et al., 2012). In particular, Multiclass Discriminant Analysis (MDA, otherwise known as "Fisher Discriminant Analysis" or "Canonical Discriminant Analysis", Fisher, 1936) is a well-established dimensionality reduction technique that has been applied successfully in vegetation species discrimination (Alonzo et al., 2013; Pu and Liu, 2011; Yu et al., 1999) and monitoring (Roggo et al., 2003; Backhaus and Seiffert, 2013) applications. MDA computes a linear transformation matrix that maximizes separation between different classes while minimizing intra-class variance based on a set of labeled training spectra. In SMA applications, applying a MDA prior to unmixing has been shown to improve abundance estimates (Chang and Ji, 2006a,b), and similar techniques were shown to improve species discrimination using MESMA (Somers et al., 2009b, 2010). Supervised techniques such as MDA require a representative set of labeled spectra to train the algorithm. However, the available labeled data in typical SMA applications is limited to the endmembers in the spectral library, containing only a handful of endmembers for each species. Consequently, it is often necessary to collect additional spectra to effectively apply techniques like MDA.

In this work, we describe an approach to improve both the accuracy and computational efficiency of MESMA. Our goal is effective discrimination of spectrally similar materials. We focus on the problem of distinguishing spectra associated with distinct species – domesticated citrus plants in particular – to assist disease monitoring and mitigation. Our motivation to pay specific attention to citrus species is Huanglongbing (HLB), or citrus greening: a vector-borne disease that has already caused significant damage to orchards in Florida and Texas. It is caused by a bacterium transmitted by an invasive species known as the Asian Citrus Psyllid; the bacterium infects citrus plants and relatives within the Ruticae genus, ruins their fruit, and eventually kills the host. HLB also threatens orchards worldwide from Mexico to South America and the Mediterranean. In 2012 the disease was discovered for the first time at an urban residence in Southern California (Wang and Polek, 2013) and further spread is considered a major threat to the California citrus industry. Slowing HLB's progress requires close monitoring of susceptible orchards as well as the large population of residential trees that could serve as entry points or pathogen reservoirs. Imaging spectroscopy has been used to track the progress of invasive species (Underwood et al., 2003) and combinations of high-resolution spectral data with LiDAR have also been combined to detect invasive tree species in the Hawaiian rain forest (Asner et al., 2008). Using imaging spectroscopy to discriminate citrus species from other types of vegetation would be useful for allocating ground monitoring teams to high risk areas, and could direct the deployment of new in situ instruments, such as Volatile Organic Compound (VOC) sensors, that might detect diseases like HLB at an early stage (Dandekar et al., 2010). Moreover, spectroscopic observations of sufficient spectral resolution have been used to discriminate between healthy versus HLB-infected plants in the laboratory (Sankaran et al., 2013; Mishra et al., 2012), and recent results have demonstrated the potential for remote HLB detection with imaging spectroscopy (Kumar et al., 2012).