SUMMARIZING THE SPECTRAL VARIABILITY OF CRISM IMAGES WITH ENDMEMBER EXTRACTION

Mario Parente[1], John F. Mustard[1], Scott Murchie[2] and Frank P. Seelos[2], [1]Brown University, Providence, RI, USA (mario_parente@brown.edu), [2]Applied Physics Lab, Johns Hopkins University, Laurel, MD.

Introduction: Planetary missions such as the Compact Reconnaissance Imaging Spectrometer for Mars (CRISM) [1, 2] can benefit from the use of automatic approaches and statistical learning techniques due to the amount of data involved. Thanks to its high sensor resolution, CRISM data volumes overwhelm scientists capacity for exhaustive manual analysis. Automated summary analysis could benefit investigations by identifying the unique spectral signatures present in a CRISM scene and store them automatically for further examination or interpretation. If installed aboard an orbital system, such a tool could relieve transmission constraints for high-bandwidth hyperspectral datasets by giving priority to the most informative data products.

This paper introduces an algorithm that extracts image endmembers of a CRISM scene, which can be used as the scene concise mineralogical representation for cataloging purposes, in addition to existing browse products and parameter maps [3].

Automatic endmember extraction algorithms applied to CRISM datasets face particular challenges due to the fact that CRISM is a dataset with peculiar noise characteristics [4, 5]. The proposed algorithm uses robust techniques, resilient to CRISM noise. This work benefits from the results of previous efforts [6].

Method: CRISM images are first reduced by standard techniques to allow scientific analysis [1, 2].

The endmember extraction procedure [7] has several stages. In the first stage, the algorithm focuses on smaller areas of interest based where available spectral parameter maps show higher spectral variability and higher concentrations of minerals of interest. Otherwise, the algorithm divides the image in smaller sub-images and operates separately on each one.

The steps that follow leverage the representation of the hyperspectral image as a cloud of pixel vectors in a space of dimension equal to the number of spectral channels. A nonlinear dimensionality reduction technique enhances the geometric distances between natural clusters in the cloud, facilitating the identification of endmembers. The technique aims at capturing nonlinear structures in the data while preserving local differences in the spectral shapes of the image pixels. The technique tends to produce a lower dimensional representation of the data with well separated components that are successively identified as natural clusters by a spectral clustering technique. Each cluster or family is further analyzed by an unmixing algorithm that describe the roughly convex shapes of the regions with convex polyhedra whose vertices are local endmembers. The list of candidate endmembers has to be screened since the endmembers locally to a cluster might not be global endmembers for the whole data cloud. This happens, for example when a corner of a cluster lies in the interior of the data cloud. The procedure screens the candidate spectra based on a spectral similarity score. Two spectra are considered similar if their score is smaller than a threshold.

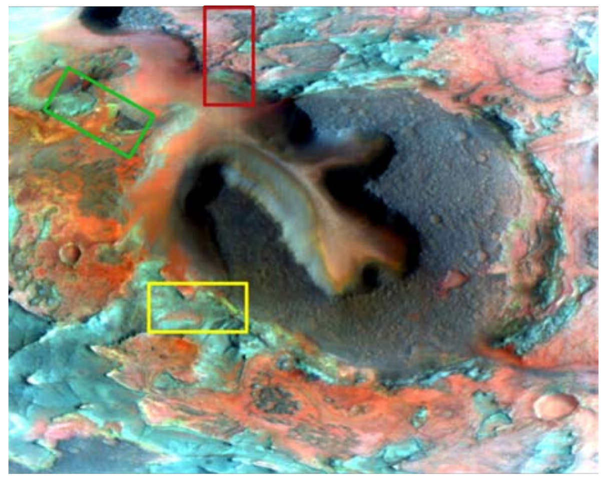
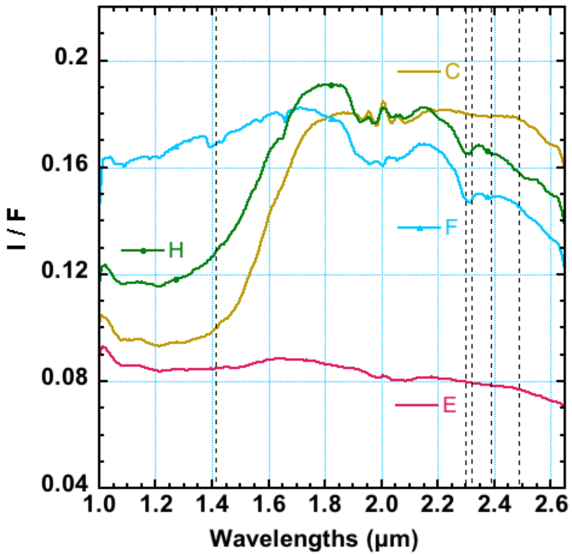


Figure 1: The algorithm focuses on areas of interest in CRISM FRT00003E12 marked by colored boxes

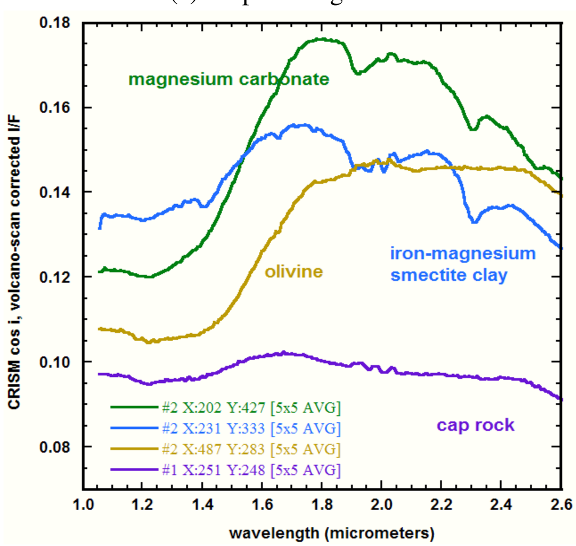
Results and evaluation: We performed the procedure described above for the CRISM image FRT00003E12. The algorithm selected 3 areas of interest based on the parameter maps for band depths at 1 , 2.3 and 2.5 μm and extracted endmembers from each of them.

In order to evaluate the endmember detection method we first note that a good automated system should detect the same features that would be found from an exhaustive manual search. For the image under study FRT00003E12 we collect the endmembers found by the algorithm over the interesting areas and compare them with expert manual selections in Figure 2. The ratioed version of the spectra in Figure 2 (b) have been posted on the Mars Reconnaissance Orbiter (MRO) press release [8] and individual spectra are published in several sources (e.g. [9]).

The spectra labeled H, C and F and E in Figure 2 (a) present similar features with respect to the spectra labeled 'magnesium carbonate', 'olivine', 'iron-magnesium smectite clay' and 'cap-rock' in Figure 2 (b). The spectrum labeled H is identified as magnesium carbonate by virtue of the 2 absorptions around 2.3 and 2.5 μm. The spectrum labeled C is identified as olivine due to the broad absorption around 1 μ. The smectite clay label for spectrum F comes from the absorption around 2.29 μm (and a smaller absorption around 2.4 μm). As an additional test of performance, we want to visually compare the endmembers retrieved by the proposed ap-



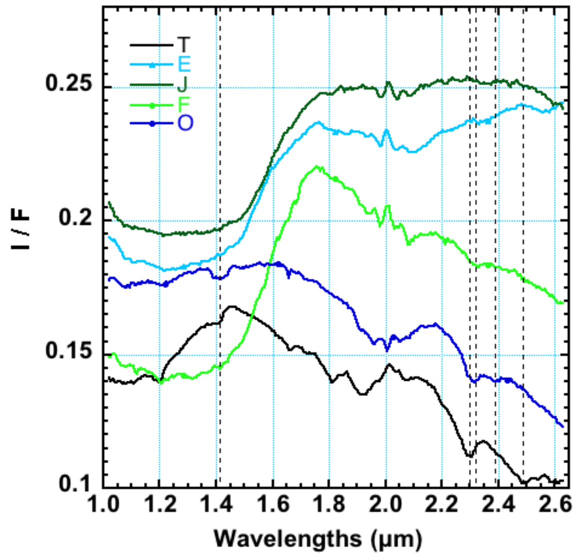
(a) Proposed algorithm



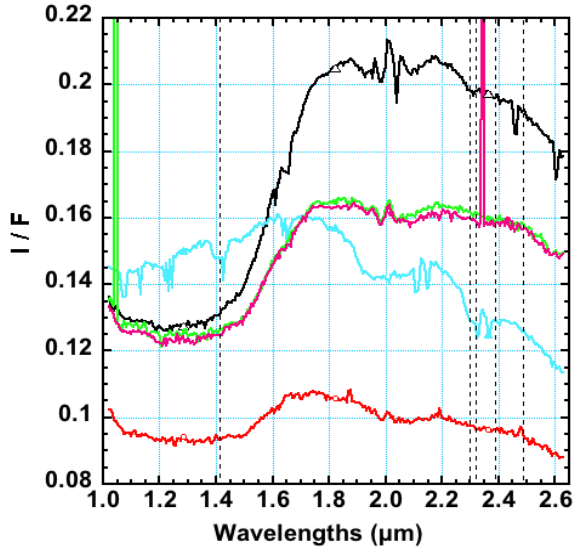
(b) Manual selection from an expert

Figure 2: Comparison of selected endmembers with expert assessment from the whole image

proach with the output of an automated state-of-the-art spectral unmixing algorithm on a case study, i.e. the area under the red box in Figure 1. The algorithm we will use as an antagonist is the sequential maximum angle convex cone (SMACC) [10], an endmember extraction method that constructs a convex cone around the data cloud. The results of the comparison are shown in Figure 3. The proposed approach highlights the spectral variability in the area with detections that share much of the same spectral features of results in Figure 2 with, possibly, some additional mafic species. SMACC however is sensitive to CRISM spiking noise. SMACC identifies spectra with a large spike as endmembers as reflected by the green and magenta endmembers in Figure 3 (b). This sensitivity to noise limits the ability of SMACC to fully appreciate the spectral variability in the study area.



(a) Proposed algorithm



(b) SMACC

Figure 3: Comparison of endmembers extracted by the proposed approach and SMACC in the study area

Summary: We presented an endmember extraction technique that performed well on CRISM data when compared to manual selection of endmembers and a currently available endmember selection competitor. We will propose this technique as a possible data summarization tool for the CRISM team.

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