IDENTIFICATION AND CHARACTERIZATION OF MARTIAN SERPENTINE USING TARGET TRANSFORMATION AND CRISM DATA. N. H. Thomas¹, J. L. Bandfield², and E. S. Amador¹ ¹Earth and Space Sciences, University of Washington, Seattle (nancyth@u.washington.edu), ²Space Science Institute.

Introduction: The mineralogical signatures of serpentinization, including serpentine, carbonates, talc, and saponite, indicate geochemical environments and processes on Mars that could have been hospitable to microbial life. On Earth, these processes have been shown to sustain dense microbial communities [e.g., 1]. The identification of serpentine in particular uniquely indicates that serpentinization reactions occurred, which has significant astrobiological implications. Ehlmann et al. [2] identified serpentine in three geologic settings on Mars. Here, factor analysis techniques are applied to CRISM data to confirm these detections and search for new identifications in regions with olivine-rich basalts investigated by Amador et al. [3].

Factor analysis and target transformation are a set of methodologies that allow for rapid and automated analysis of large spectral datasets. These methods can be used globally to both identify the number of individual components and test for the presence of and isolate individual endmembers from mixed spectral data. These methodologies have been previously applied to laboratory and spacecraft thermal infrared (TIR) spectral data [4-7] and recently adapted and applied [8] to near-infrared (NIR) spectral data collected by the Compact Reconnaissance Imaging Spectrometer for Mars (CRISM) on board the Mars Reconnaissance Orbiter [9].

Methods: Factor Analysis. Factor analysis can be used to gain insight about the number of independent components present in a mixed system. This method uses a set of mixed spectra to derive a set of orthogonal eigenvectors and associated eigenvalues. This allows for the dimensionality of the system to be reduced to the number of independent variables present in the set of mixed spectra. In an ideal system, if there are n independent components present in the system, the first n orthogonal eigenvectors should fully describe the system's variation while higher order eigenvectors will contain only noise. Interpretation of the output of factor analysis relies on two basic assumptions: (1) the spectral data contains independently varying components and (2) the components add linearly. Previous work by Bandfield et al. [4] indicates that factor analysis can still be applied to spectral datasets despite the presence of systematic errors and non-linear systems.

For this work, we applied the factor analysis techniques of Thomas and Bandfield [8] to a spectral range of 133 CRISM bands from 1.7 – 2.6 μm. This spectral region contains diagnostic spectral features present in a variety of phases and is sufficient to accurately determine their presence.

Target Transformation. The significant eigenvectors (those containing information besides random noise) can reconstruct not only the original data, but also the spectral endmembers present in a system of mixed spectra. This is the case even if the spectral endmembers themselves are not present in the original data. As a result, we can test for the presence of a spectral endmember in the original mixed data using linear fits to the laboratory endmembers with the significant eigenvectors. If the test spectrum can be closely matched, then it is confirmed as a possible endmember present in the system. By using only the significant eigenvectors (typically overestimated as 10 in this case), the dimensionality of the set of mixed data is reduced from 133 to 10.

Automation. The factor analysis and target transformation techniques can be automated to test CRISM data for the presence of a specific set of spectral endmembers. Factor analysis is applied to one in every five pixels in every 5th row of the CRISM image to reduce computation time. Target transformation is then performed on a standard set of 12 laboratory spectral endmembers chosen to represent a diverse set of spectral features. This set of endmembers includes products of serpentinization such as serpentine, talc, and carbonates. The results are saved as a series of plots in a single image that can be visually inspected for spectral matches. In this manner, the spectral endmember content of an image can be quickly assessed.

Noise Removal. Using the assumption that the first 10 eigenvectors contain all the variation present in the system, the eigenvectors with order greater than 10 will only contain noise. We have found that reconstructing every spectrum in the entire CRISM image using the first 10 eigenvectors significantly reduces noise and limits the variation present in the image to significant sources. This reconstructed data can then be used with traditional analysis techniques such as index maps and spectral ratios. We are currently developing an index map for characteristic serpentine absorption features. Using factor analysis noise removal methods, these indices could give a clearer indication of the relative locations of geologic units associated with serpentinization.
**Target Locations:** Amador et al. [3] identified olivine-rich basalts using TIR multispectral decorrelation stretch (DCS) images from the Thermal Emission Imaging System (THEMIS) [10]. Serpentine may be associated with these olivine-rich basalts globally [3] and CRISM data in these regions will be analyzed using the automated target transformation routine to search for its presence. We have selected three regions for initial testing: (1) Isidis Basin (southern rim), (2) Argyre Basin, and (3) Valles Marineris. The CRISM FRT images associated with olivine-rich basalts along the southern rim are identified in Figure 1.

**Preliminary Results:** Our initial application in Nili Fossae shows that the factor analysis and target transformation methods are effective at detecting weak spectral signatures. Even when the signal is low, spectral variability is still present. Factor analysis is sensitive to small variations in spectra such the characteristic spectral feature for serpentine, a broad, shallow absorption near 2.12 µm. This small absorption feature of serpentine at ~2.12 µm is generally difficult to detect using standard processing methods, but spectral ratios. However, we have been able to consistently identify this feature along with other diagnostic serpentine spectral features where they are present in CRISM data. Target transformation of eigenvectors derived from CRISM data acquired over Nili Fossae (Figure 2) confirmed the presence of serpentine in the image originally identified by Ehlmann et al. [2].

Automated factor analysis and target transformation techniques have been applied to the CRISM FRTs in the southern Isidis target region (Figure 1). To date, 5 FRTs in the region show matches to laboratory serpentine. For example, FRT00008CA3 is a potential candidate for serpentine (Figure 2).

To definitively test for the presence of serpentine in these images, factor analysis will be applied with better spatial coverage to individual CRISM images of interest. This will allow us to map the spatial distribution of serpentine across the region, especially with the creation of a noise-removed serpentine index. We will also apply this index and the automated routine to map the spatial distribution of serpentine and associated minerals in other regions associated with olivine-rich basalts identified by Amador et al. [3]. Ultimately, target transformation provides the rapid ability to identify faint spectral signatures, from endmembers like serpentine, from large datasets across large regions.


Figure 1: CRISM images targeted for automated factor analysis technique in Southern Isidis Basin target region.

Figure 2: CRISM spectrum of serpentine in Nili Fossae (red) and candidate serpentine spectrum in Isidis Basin (green) recovered using a laboratory spectrum of serpentine (blue) as the test vector.