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# Automated Endmember Selection for Nonlinear Unmixing of Lunar Spectra

M. P. Felder[I], A. Grumpe[I], C. Wöhler[I] and U. Mall[II]

[I] Image Analysis Group, Technische Universität Dortmund, Otto-Hahn-Str. 4, 44227 Dortmund, Germany
{Marian.Felder | Arne.Grumpe | Christian.Woehler}@tu-dortmund.de
[II] Max Planck Institute for Solar System Research, Max Planck Straße 2, 37199 Katlenburg-Lindau, Germany
mall@mps.mpg.de

## 1. Introduction

An important aspect of the analysis of remotely sensed lunar reflectance spectra is their decomposition into intimately mixed constituents. While some methods rely on unmixing of the observed reflectance spectra [1] or on the identification of minerals by extracting the depths and positions of mineral-specific absorption troughs [2, 3], these approaches do not allow for an automated selection of the (a priori unknown) endmembers from a large set of possible constituents. In this study, a non-linear spectral unmixing approach combined with an automated endmember selection scheme is proposed. This method is applied to reflectance spectra of the SIR-2 point spectrometer [4] carried by the Chandrayaan-1 spacecraft.

## 2. Spectral unmixing method

The basis of our approach is a genetic algorithm [5] in which the genomes with binary genes represent the occurrence or non-occurrence of mineral endmembers in the mixture. The fitness function evaluating the generated endmember mixture combines a normalized spectral parameter error and an unconstrained linear unmixing in terms of the single-scattering albedo ($w$) spectra [6] based on the Hapke AMSA model [7]. The physically reasonable constraint of non-negative mineral fractions is considered by a penalty fitness value. The linear unmixing model is a simple least squares inversion using the pseudoinverse on the $w$ spectra obtained by inverting the Hapke model [7]. We add to the mineral spectra an "agglutinate endmember" spectrum modeled by a 2$^{nd}$ order polynomial in $w$ in order to account for the effects of spaceweathering [8].

In this context, a novel error measure defined in the space of spectral parameters has been devised. The extraction of spectral parameters is based on [9] and relies on the continuum-removed reflectance spectrum, where the Hapke AMSA reflectance model [7] is used to compute the reflectance of the mixture under study. Gaussian functions are fitted to the characteristic absorptions at 1300 nm and 2000 nm [10] (the prominent ferrous absorption trough near 1000 nm is neglected as it is not fully contained in the SIR-2 wavelength range). The extracted spectral parameters are the minimum wavelength (LMIN), band depth (BD), full width at half maximum (FWHM), and continuum slope (CSL) (Fig. 1).

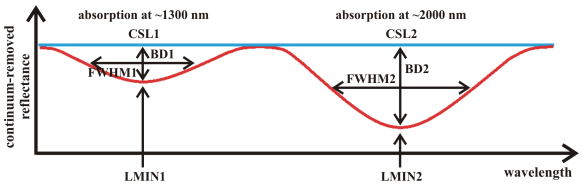


Figure 1: Extracted spectral parameters

The potential spectral endmembers are laboratory spectra from the RELAB database of minerals with particulate surfaces obtained during the Apollo 15 and 17 missions ([11], e.g. LR-CMP-{168-182,208-222}). Our endmember catalog contains 29 different RELAB spectra of the minerals pyroxene, olivine and plagioclase.

## 3. First Results

In our experiments, we analyzed SIR-2 reflectance spectra which were coregistered to simultaneously acquired image data of the M$^3$ instrument [12] according to [13, 14], thermally and topographically corrected [14], and normalized to a standard illumination and viewing geometry (30° incidence angle, 0° emission angle, 30° phase angle [13]) based on the Hapke AMSA model [7].

The results of our method for a SIR-2 spectrum located on the floor of the lunar crater Copernicus (Fig. 2) are shown in Fig. 3. The algorithm indicates a mixture containing approximately $3.5\%$ LR-CMP-213 [light-brown-pyroxene-D], $34.9\%$ LR-CMP-217 [plagioclase-D] and $8.4\%$ LR-CMP-220 [light-brown-pyroxene-D]. The endmember fractions sum up to a total of $k = 46.8\%$ such that the relative amount of agglutinates corresponds to $1 - k = 53.2\%$.

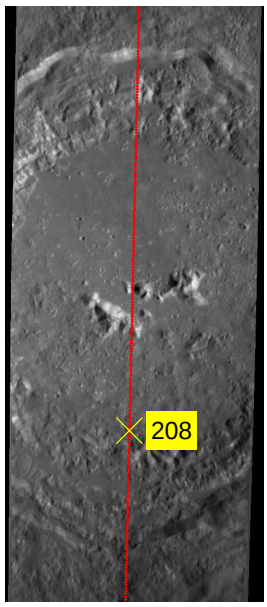


Figure 2: Sample location in Copernicus crater coregistered to $M^3$ image

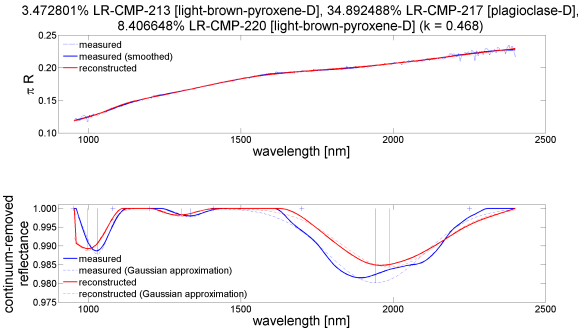


Figure 3: Unmixing results for the examined SIR-2 spectrum.

# 4. Summary and Conclusion

We have presented a nonlinear unmixing method for lunar reflectance spectra involving an automated selection of endmember spectra from a comprehensive catalog of laboratory spectra based on a genetic algorithm. Spaceweathering effects are taken into account by including an agglutinate endmember. The fitness function of the genetic algorithm relies on a similarity measure defined in terms of spectral parameters extracted from the continuum-removed reflectance spectrum.

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