MAPPING OF PIONEER VEGETATION IN POST MINING AREAS BY MEANS OF HYPERSPECTRAL FIELD MEASUREMENTS

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ABSTRACT:

The very high spectral diversity and spatial in-homogeneity of surfaces is a well known phenomenon in remote sensing especially for vegetation studies. This paper describes an investigation carried out for a first succession stage composed of three typical pioneer plants (*Trifolium arvense, Hieracium pilosella, Rumex acetosella*) at the post mining site Goitzsche, Germany. One of the aims of this research was to find the most representative spectra for these plants during the growing season. To define representative spectra is very complex and requires a novel approach constituting a modular and flexible concept to enable multiple taxonomic and -temporal elements to be treated and compared, while retaining simplicity. Before adding them to an optimized multi-temporal and -taxonomic spectral library, they have been controlled by a statistics table called Nearest Spectrum Matrix (NSM). The processing logic manages the outputs of the statistics and at the end the best matched spectra will be separated. In this concept, reflectance spectra originating from different time loops are integrated into a spectro-temporal database.

1. INTRODUCTION

1.1 Motivation

Plant colonization of man-made habitats is promoted by the disturbed condition of the surface, and these open conditions can favor only those species that establish themselves very quickly. If succession is allowed to continue, the early pioneer vegetation including many annuals are soon crowded out by perennials because they can spread vegetatively (Smith 1984).

Pioneer plants are good targets because they are cosmopolitan, have excellent adaptation potential, and are easy to plant. Hyperspectral field measurements were taken of these three species in phenologically relevant sampling intervals in 2008. The following three questions were formed before starting the experiment.

Which approach could be applicable to describe a multi-taxonomic and multi–temporal phenomenon?

How can well known spectral analytical methods be assimilated into an innovative approach for evaluating and comparing of spectra?

What is the use of a multi-taxonomic and -temporal spectral library?

1.2 Aims

An important part of this work was to develop a modular and flexible concept that can meet two objectives. The first is to enable modularity by treating and comparing multiple taxonomic and -temporal elements without methodological limitations; in other words, without limiting neither the elements of analysis nor the number of statistical methods for comparing. The second objective was to keep it all as simple as possible.

If the multi-taxonomic and -temporal approach proves effective and the questions listed above are addressed, the following statements and results could be formed.

Most suitable time to separate species spectrally from each other (best-time-to-identify).

The minimum number of spectral samples required for a given species or community at a vegetation period (minimal sampling-maximal matching).

Phenologically optimized spectral library for pioneer plant communities (Pioneer Spectral Library).

The requirement for a general reference spectrum is still present in practice. This expectation cannot be kept for long time, especially for measurements with high spatial, temporal, and spectral resolution. Spectral sampling of plant species and communities must be optimized and treated flexibly by time-, species- and environment dependent spectral properties (Kumar et al., 2001; Segl et al, 2003; Jung et al. 2004; 2007). For phenological research, time is one of the most important influencing factors.

2. METHODS

Measurements were carried out during the 2008 growing season. Every species had its own growing pot filled with unmanipulated soil. Watering and air conditioning were set and controlled by a computer aided remote system. Measurements were taken in the laboratory in order to keep the proper temporal resolution.

The field spectrometer (ASD FieldSpec FR Pro) was used with tripods to guarantee stability and constant viewing geometry. White reference was taken with Spectralon® (Labsphere, 2009). Methods for comparing spectra used in this work are widely employed in hyperspectral image classification (Leone & Sommer, 2000) but less common in analyses of time series for one-point measurements. In this paper, three different kinds of methods were applied to compare spectral features within a hyperspectral data set (Aspinall et al., 2002).

Binary Encoding (BE): It is a classification method that encodes the data and reference spectra into 0-s and 1-s based on whether a band falls below or above the spectrum mean. An exclusive ´OR´ function is then used to compare each encoded reference spectrum with the encoded data spectra and classify the dataset (Mazer et al. 1988). Each pixel is classified to the material with the greatest number of bands that match above a minimum match threshold. Another important algorithm, the Continuum Removal, normalizes reflectance spectra to allow comparison of individual absorption features from a common baseline (Clark et al. 1987, Kruse et al. 1993a). A convex hull that is fitted to the spectrum describes the continuum. Lastly, straight-line segments connect local spectra maxima to define the convex hull, the first and last spectral data values being on the hull by definition.

Spectral Angle Mapper (SAM): It matches pixel spectra to reference spectra using a measure of spectral similarity based on the angle between the spectra treated as vectors in an n-dimensional space with dimensionality (n) equal to the number of image bands. Smaller angles represent closer matches. The angle between each pixel and all reference spectra can be mapped, and pixels assigned to the material for which the spectral angle is smallest and within a defined limiting angle (Kruse et al. 1993b). When used on calibrated reflectance data, the SAM is relatively insensitive to effects of illumination because the angle between vectors is measured rather than the length of the vector. Because it uses only the ´direction´ of the spectra, and not their ´length´, the method is insensitive to the unknown gain factor. All possible illuminations are treated equally. The SAM algorithm generalizes this geometric interpretation. Spectral Feature Fitting (SFF):

It uses least squares methods to compare the fit of image spectra to selected reference spectra (Crowley & Clark, 1992). Reference spectra are scaled to match the image spectra after continuum removal from both data sets. The method measures absorption feature depth which is related to material abundance. The pixel spectra are then compared to the target spectrum using two measurements: the depth of the feature is compared to the depth of the feature in the target; and, the shape of the feature is compared to the shape of the feature in the target (using a least-squares technique).

Every phenological stage of vegetation has its own reflectance spectrum that could be representative spectrally for a longer or shorter period (Zagajewski et al. 2006; Shaokui et al. 2006, Lawrence et al. 2006; Darvishzadeh et al. 2008). One of the aims was to find the most representative spectra for plants during the growing season. When plant communities have been detected, the result is unique in time and spectral interactions caused by actual phenological stages are overwhelming. Spectral identification of communities might succeed when single spectra of single plants with representative spectra are collected from the very beginning. After having completed a timely shifted and phenologically relevant set of spectra it might have a higher spectral coincidence within phenologically realistic plant communities which could be used for further identification.

To meet the above mentioned objectives, methodological developments were undertaken which belong to the results of the work. In the following a brief description of the investigated pioneer plans will be given.

Hieracium pilosella (Hp): It is a hispid (hairy) perennial plant, with a basal rosette of leaves. The whole plant, with the exception of the flower parts, is covered in glandular hairs, usually whitish, but sometimes reddish on the stem. The rosette leaves are entire, acute to blunt, and range from 10-120 mm long and 5-20 mm broad.

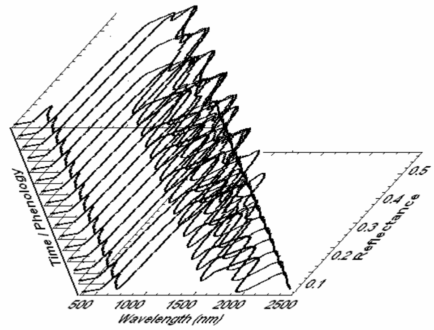
Trifolium arvense (Ta): The leaves have a pair of stipules at the base, often tipped in red. The flowers are grouped in a dense inflorescence 20-30 mm long and 10-15 mm broad; each flower is 4-5 mm long, rosy white in color, and especially characterized by the many silky white hairs which tip the five calyces, which are much larger than the corollas.

Rumex acetosella (Ra): It has green arrowhead-shaped leaves and red-tinted deeply ridged stems, and it sprouts from an aggressive rhizome. The flowers emerge from a tall, upright stem. Female flowers are maroon in color. The plant is native to Eurasia but has been introduced to most of the northern hemisphere. It favors moist soil; hence, it thrives in floodplains and near marshes.

3. RESULTS

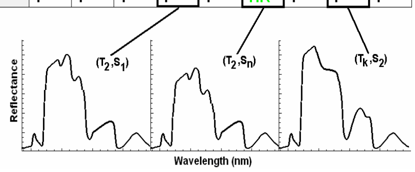
To ensure a transparent working concept, the three-step work flow scheme was employed in this research depicted in Fig. 2. It can be seen that reflectance spectra originating from different time loops (Step 1) and different vegetations are integrated into one database. Before they were added to the optimized multi-temporal and multi-taxonomic spectral library, they had been selected out by a modular processing logic (Step 2). Statistical methods applied in spectral pre-processing tools in remote sensing are well known (BE, SAM, SFF) and are changeable due to modularity. The novel processing logic manages the outputs of the statistics. At the end, the best matched spectra will be separated and saved in a spectral library dataset (Step 3). Best matched means that between the pheno-spectral signatures must be at least one spectrum which matches with almost all remaining spectra at the highest coincidence level (see Figure 2). After having calculated BE, SAM and SFF, one score value was created from the simple arithmetic sum of BE, SAM and SFF. List of scores were then evaluated to see ranking between matches to determine first and second highest matches. The Nearest Spectrum Matrix (NSM) is a statistics table that demonstrates which spectrum matches with which spectrum at the highest level. All spectra are compared to all spectra in order to preserve separability.

Step 1. (Input) All measurements taken during the phenology are saved into an unselected database that serves as input into Step 2.



Step 2. (Logic): Modular Processing Logic.

	Time	T_1			T_2			T_k		
Time	Species	S_1	S_2	S_n	S_1	S_2	S_n	S_1	S_2	S_n
T_1	S_1	HR	F	F	HR	F	F	F	F	F
	S_2	F	HR	F	F	HR	F	HF	HR	F
	S_n	F	F	HR	F	F	HR	F	F	HR
T_2	S_1	F	HF	HF	HR	HF	F	HR	F	F
	S_2	F	F	F	F	F	F	F	HR	F
	S_n	HF	F	F	F	F	HR	F	F	HR
T_k	S_1	HR	F	HF	HR	F	F	HR	F	F
	S_2	F	HR	F	F	HR	F	F	HR	HF
	S_n	F	F	F	F	F	HR	F	F	F



Step 3. (Output): By Step 2 selected spectra will be integrated into an optimised spectral library.

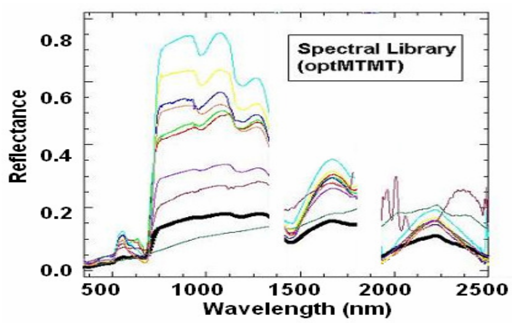


Figure 2. Illustration of workflow for evaluating spectra and collecting them in spectral libraries. Abbreviations: S=Species, T=Time, HR=Highest Right, HF=Highest False, F=False.

If this is not the case, it might be found that one species with a given sampling time could best match with a non-identical population from other sampling time; however this is not allowed due to coherency.

From the NSM you can derive diverse information on spectra and time. Fig. 2 demonstrates how this matrix works and how to draw conclusions. For instance, the species S_1 should match (theoretical) every S_1 during phenology (T_1, T_2, T_k) but it is normally not the case and controversies are not untypical in nature. It can be seen that S_1 in Fig. 2 matches S_n in T_2 better then S_1 in T_2 which is not rare to find. It is very often because of phenotypical changes of vegetation.

False matches (marked as black) are clearly presented. Good matches (decision made on cumulative score values composed of BE, SAM and SFF and marked as green) can be summed in the \`Distribution\` part of the table in relative or percent values.

The NSM is able to analyze separability and similarity between different plants (taxon-dependent) and their different phenological (time-dependent) phases. The main results of this work could be summarized and divided into three parts.

•Elaboration of research concept and workflow for analyzing taxon- and time dependent spectral properties for vegetation.

•Determination of best matched spectra to keep the number of reference spectra low.

•Development of an optimized multi-temporal and multi-taxonomic spectral library.

Fig. 3 clearly demonstrates which plants, between the three analyzed were spectrally representative for a longer period. It also portrays that *Trifolium arvense* (Ta) in the middle of the growing period (circa 60 days after first sampling) shows, compared to others, very good matching with other phenological stages within its own population, and shows high separability from other species. *Rumex acetosella* (Ra) (circa 90 days after first sampling) was relatively ahead for matching with its own population compared to every other plant and *Hieracium pilosella* (Ta) shows (within the first 60 days after first sampling) relatively good matches compared to all participating members of the investigation. However, this catalogue proved too large and complex to systemize.

4. DISCUSSION UND CONCLUSIONS

Hyperspectral remote sensing with high spatial resolution has been a very successful study until the dynamic complexity and changing variables of vegetation have been analyzed. Reflectance spectra of living objects are not universal. Hyperspectral remote sensing is a very promising technology and in many other non-vegetative scientific applications has succeeded in practical applications. Methods and results of this investigation show that detecting, identifying and classifying of vegetation spectra is still a challenging problem and will remain also in the future because of the temporal and phenotypical changes of plants. The generic spectral analytical approach described in this paper might provide an original starting point for detecting vegetation, especially pioneer vegetation in different environments effected by spatial, taxonomic, temporal, and biological conditions.

Many solutions and methods have been found in the scientific literature to address this complex problem, but there is always room for additional improvement, such as a finer separation of reflectance spectra of different pioneers. From a practical point of view, the complexity of spectral properties of vegetation should be kept simple since users need straightforward solutions. To test the validity of the investigation's concept, further measurements will be needed to be taken in order to control the stability of the results and improve on weaknesses. Results provided by the latest data base of the period 2008 were promising and encouraging. It is supposed that an optimized, multi-temporal, and multi-taxonomic reference library can supply valuable information on optimizing hyperspectral field-, airborne and spaceborne campaigns. If an optimized spectral library contained all the best matched spectra of the whole phenology for every species the results could be integrated into a sophisticated spatial decision-making system.

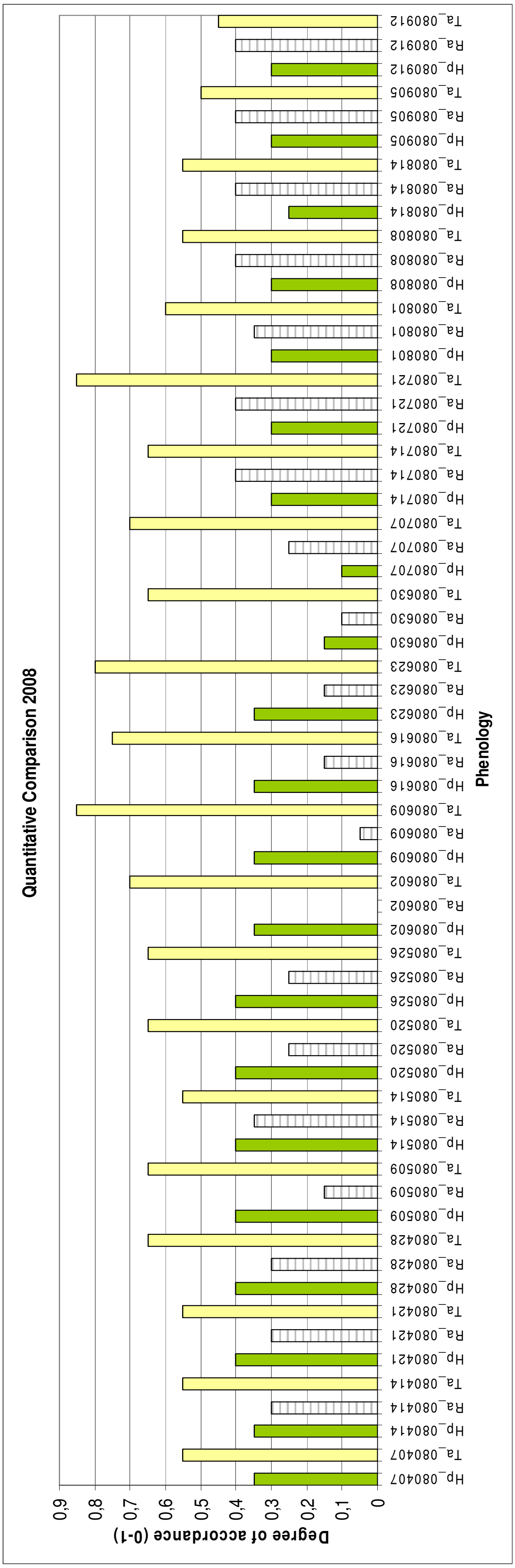


Figure 3. Results of matches as function of time.

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