

PREDICTION OF BIODIVERSITY - CORRELATION OF REMOTE SENSING DATA WITH LICHEN FIELD SAMPLES

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ABSTRACT:

The objective of the present study was to develop a model to predict lichen species richness for six test sites in the Swiss Pre-Alps following a gradient of land use intensity combining airborne remote sensing data and regression models. This study ties in with the European Union Project *BioAssess* which aimed at quantifying patterns in biodiversity and developing “Biodiversity Assessment Tools” that can be used to rapidly assess biodiversity. For this study lichen surveys were performed on a circular area of 1ha on 96 sampling plots in the six test sites. Lichen relevés were carried out on three different substrates: trees, rocks and soil.

In a first step, ecological meaningful variables derived from CIR orthoimages were calculated using both spatial and spectral information and additional lichen expert knowledge. In a second step, all variables were calculated for each sampling plot and correlated with the different lichen relevés. Multiple linear regression models were built containing all extracted variables and a stepwise variable selection was applied to optimize the final models. The predictive power of the models (r ranging from 0.79 for lichens on trees to 0.48 for lichens) can be regarded as good to satisfactory, respectively. Species richness for each pixel within the six test sites was then calculated. The present ecological modelling approach also reveals two main restrictions 1) this method only indicates the potential presence or absence of species and 2) the models may only be useful for calculating species richness in neighboring regions with similar landscape structures.

KURZFASSUNG:

Die vorliegende Studie hatte zum Ziel, flugzeuggestützte Fernerkundungsdaten mit Feldaufnahmen von Flechten zu korrelieren, um die Anzahl Flechtenarten in sechs Untersuchungsgebieten in den schweizer Voralpen zu modellieren. Diese Studie knüpft an das EU-Projekt *BioAsses* an, welches zum Ziel hatte Biodiversitäts-Indikatoren zu entwickeln, mittels welcher rasch die Biodiversität eines Gebietes abgeschätzt werden kann. Basis für diese Studie bilden Feldaufnahmen von Flechten, welche in den sechs Untersuchungsgebieten an insgesamt 96 Aufnahmeorten durchgeführt wurden – jedes der Grösse von 1 Hektare, was einem Kreis mit 56 m Radius entspricht. Flechten wurden auf den drei Substraten Baum, Stein und Boden aufgenommen. In einem ersten Schritt wurden ökologisch-relevante Variablen aus CIR Orthobildern, hauptsächlich basierend auf räumlicher und spektraler Information abgeleitet und mittels zusätzlichem Expertenwissen berechnet. In einem zweiten Schritt wurden für alle 96 Aufnahmeorte die entsprechenden Variablen berechnet und anschliessend mit den Feldaufnahmen korreliert. Um optimale Modelle zu erhalten wurden multiple lineare Regressionsmodelle mit einer schrittweisen Variablen Selektion verwendet. Für das Baumflechten-Modell wurde ein r von 0.79, für Bodenflechten ein r von 0.48 erreicht, was als gut bis genügend eingestuft werden kann. Schliesslich wurde mit Hilfe dieser Modelle die potentielle Anzahl Arten für jedes Pixel in den sechs Untersuchungsgebieten berechnet. Die Studie zeigt ferner, dass der ökologische Modellierungsansatz auch seine Grenzen hat: 1) mittels dieser Methode kann nämlich nur die potentielle Anzahl Flechten berechnet werden und 2) das Anwendungspotential der Modelle beschränkt sich wahrscheinlich auf benachbarte Regionen mit einer ähnlichen Landschaftsstruktur.

1. INTRODUCTION

The need for conserving biodiversity has become increasingly imperative during the last decade as rates of habitat and species destruction continue to rise (Noss and Cooperrider, 1994, Nagendra 2001). At the same time inventorying biodiversity and monitoring efficacy of measures for its conservation have emerged as important scientific challenges of recent years (Jørgensen 1997, Nagendra and Gadgil 1999). For monitoring biodiversity on a general level, homogenous consistent land cover information is primarily required as it is obtained using remote sensing data (Townshend et al. 1991, Chuviebo 1999). According to Palmer (1995) and Wohlgemuth (1998) it is

almost impossible to have a complete biodiversity survey at regional scale of 1-100 square kilometers. Therefore methods for extrapolations are needed that provide information that is remotely similar to field samples and which would allow to considerably reduce extensive field surveys. New techniques and data sets now enable remote sensing, in conjunction with ecological models, to shed more light on some of the fundamental questions regarding biodiversity (Cousins and Ihse 1998). Furthermore, remote sensing also may help calculating biodiversity hotspots to facilitate biodiversity field surveys, e.g. to focus the sampling of biological data on these hotspots (Kerr and Ostrovsky 2003).

According to Turner et al. (2003) the direct remote sensing of individual organisms, species assemblages, or ecological communities from airborne or space borne becomes more and more important. Remote sensing data provide increased opportunities to develop quantitative models on the relationship between species diversity and the diversity of land cover elements (Noss 1990, Nagendra and Gadgil 1999). Providing consistent and reproducible information on land cover at different scales proves to be the main advantage of remote sensing as a tool for both ecological analyses and biodiversity assessment studies. Particularly regression analyses have been broadly applied for the modelling of the spatial distribution of species and communities up to date (Guisan et al. 2002). Thus, in combination with regression analyses high resolution remote sensing data may considerably help to assess biodiversity of a region. Estimates of species richness of a region can then be used to focus on targets in inventories so that appropriate levels of sampling can be reached in these areas. Calculation of potential biodiversity hotspots might be helpful for conservation efforts in a region, e.g. for an assessment of the landscape itself and for future protection planning.

The present study is focused on an assessment of lichen species richness for six test sites in the Swiss Pre-Alps following a gradient of land use intensity combining remote sensing techniques and regression analyses. This study ties in with the European Union Project *BioAssess* which aimed at quantifying patterns in biodiversity and developing "Biodiversity Assessment Tools" that can be used to rapidly assess biodiversity. For the *BioAssess* project seven biological indicators (soil macrofauna, collembola, ground beetles, plants, butterflies, birds and lichens) as well as remote sensing based indicators (non-biological) for a biodiversity assessment were collected in the test sites for eight participating countries. Lichens are mutualistic symbiotic organisms. Many species have evolved a requirement for substrates that are themselves by-products of advanced succession in more dominant ecosystems. Lichens are affected by various forms of anthropogenetic disturbance such as agricultural and forest management (Scheidegger and Goward 2002), atmospheric pollution and climate change (Nimis et al. 2002). These disturbances can be detected using remote sensing data and ecological modeling. Some studies show the combination of lichens with remote sensing methods: e.g. in Nordberg and Allard (2002) lichens have particularly been used as an indicator of ecosystem disturbance or serve as indicators of forest age (Nilsson 2004).

The objective of the present study is to correlate ecological meaningful variables derived from airborne remote sensing data with field sampled lichen species richness and to develop regression models to predict lichen diversity on the investigated test sites.

2. MATERIAL AND METHODS

2.1 Study area

The study area is located in the northern Pre-Alps of the central part of Switzerland in the region of Entlebuch which has been accredited as an UNESCO Biosphere Reserve since September 2001. The region is characterized by a complex topography with impenetrable gorges, rocky slopes, karst areas and fluvial deposits. The region covers an area of 395 square kilometres and ranges from the montane (700 m) to alpine zone (2300 m). It is mainly dominated by fragments of forest, rich and poor pastures and natural grassland, mires as well as rocks and small settlements. The study area consists of six landscape

types also called land use units (LUU) with an extent of 1 km x 1 km along the *BioAssess* gradient of land use intensity (see fig. 1). LUU1 contains more than 50 % old-grown forest and represents extensive land use. LUU6 on the other end of the gradient contains more than 50 % grassland and represents intensive land use. The other LUUs are distributed according to management intensity, which is defined after the percentage of different land use classes inside the test areas.

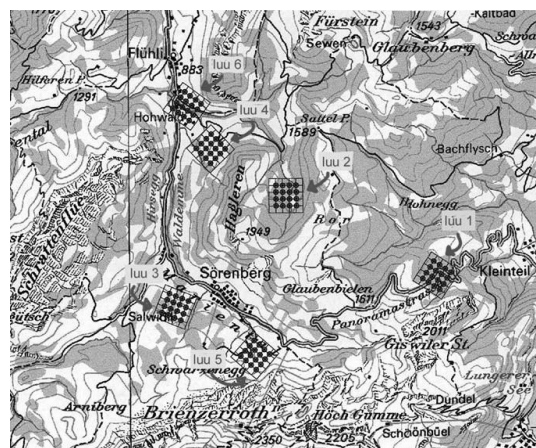


Figure 1. Locations of LUU1-6 with 6x16 sampling plots

2.2 Training and reference data sets

2.2.1 Field data – lichen relevés: A training data set is required to calibrate the models whereas reference data are required to validate the quality of the calibrated models. In our case we used training data of the lichen surveys. A total of 96 sampling plots (6 x 16) were collected that form a grid of 200 m mesh size (fig. 2). All 96 lichen sampling plots were set up by differential GPS measurements with an accuracy of +/- 0.5 m. Lichen surveys were carried out in the years 2001-02 on the 96 sampling plots (16 per LUU) on a circular area of 1 ha (56.41 m radius). Within each sampling plot 12 collecting sites were selected randomly (fig. 3).

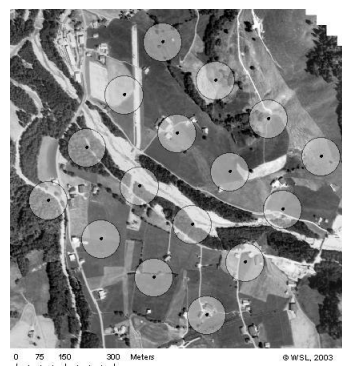


Figure 2. *BioAssess* sampling design for LUU6 with the 16 corresponding sampling plots (circles of 56 m radius)

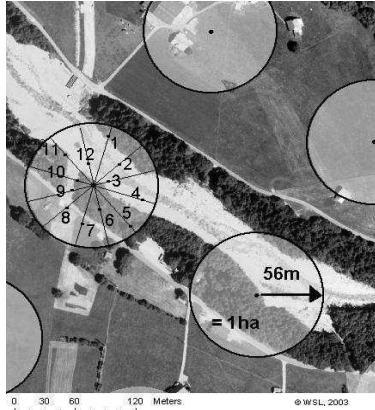


Figure 3. Lichen relevés were carried out at 1-12 randomly selected collecting sites

At each of the 12 collecting sites, lichen relevés were carried out on three different substrates, i.e. trees, rocks and soil - representing all major lichen substrates which could be affected by changes of the agricultural and forestry management. For relevés on trees the nearest tree within the border of the sampling plot was selected and for relevés on rocks, the nearest saxicolous object within the border of the sampling plot was selected (for both starting from the center of a collecting site). For relevés on soil in the center of each collecting site a frequency grid of 50 x 40 cm mesh size 10 cm) was placed on the ground. For each lichen species the number of unit areas (10 x 10 cm) where the species occurred was counted (a value ranging from 1 to 20). Since delimitation of individuals is often difficult or even not possible in lichens, we used the number of occupied unit areas as abundance measure. As the calibration data set every second sampling plot was chosen. The remaining 48 sampling plots served as reference data set.

2.2.2 Calibration data: In order to calibrate our model of prediction of species richness we tried to find biological / ecological meaningful features as explanatory variables. For this purpose we used original and derived spectral and spatial information of airborne remote sensing data. Six digital CIR orthoimages of the years 1999 and 2001 served as the basis for this study. Each orthoimage covers an area of approx. 2 square kilometers. The scale of 1:10'000 provides a ground resolution of 0.3 m. Each image offers three color bands of numerical information with 256 intensity levels: visible green (500-600 nm), visible red (600-700 nm) and near infrared (750-1000 nm). Additionally to the original spectral and spatial information several derivatives of the CIR orthoimages were calculated. For our approach we decided to extract derivatives both using standard methods and additional expert knowledge. Furthermore we used a digital terrain model with a spatial resolution of 25 m (DHM25 © 2003 Bundesamt für Landestopographie, DV 455.2) and digital surface models (DSM). A spatial resolution of 0.5 m was chosen for all data sets used in this study. To assess and categorize the contribution of ecological meaningful variables to the model we decided to distinguish between two levels of detail. 1st level variables provide information of spatial heterogeneity, spectral reflection, absorption and transmission, chlorophyll content and above-ground phytomass of vegetation cover. This implies simple image processing methods (standard methods) of the CIR orthoimages, and was performed without additional expert

knowledge, e.g. of biologists. In addition to the three original channels (red, green, NIR) several new variables were generated using both spatial and spectral information within a moving window of different sizes. The wider the window, the more these new variables tend to reflect features of the landscape. The window size of 6x6 pixels turned out to be the most adequate. Table 1 lists all variables applied in this study.

ID	Name	Comments
1st level variables		
1-3	Mean, majority, minority, sum of: Red, green, NIR	original channels of CIR orthoimage
4	Ratio1	Channel green / Channel (red + NIR)
5	Ratio2	Channel red / Channel (green + NIR)
6	Ratio3	Channel NIR / Channel (red + green)
7-9	Variance red, green, NIR	returns variance in a moving window
10-12	Skewness	returns skewness in a moving window
13-15	Contrast red, green, NIR	returns contrast in a moving window
16	Vegetation Index	NIR - red
17	NDVI	NIR - red / NIR + red
2nd level variables		
18-20	Fraction of land cover (3 classes)	forest, non-forest, non-vegetation
21-29	Fraction of land cover (9 classes)	forest, grassland light, grassland dark, rock&gravel&soil, sealed surface, single trees & hedges, shadows, wetlands, water bodies

Table 1. A total of 29 explanatory variables were derived

On the 2nd level, new variables based on 1st level variables were built using expert knowledge and field experiences. To meet these requirements, new image processing techniques were applied to produce homogenous objects and well defined object edges. Two land cover classifications were performed: 1) a simple classification only distinguishing between forest, non-forest and non-vegetation and 2) a more detailed classification distinguishing nine land cover classes, representing the three lichen substrates of the field survey: 1. forest, 2. grassland light (mown and intensively used), 3. grassland dark (unmown and not intensively used), 4. rock & gravel & bare soil, 5. sealed surface, 6. single trees & hedges, 7. shadows, 8. wetlands and 9. water bodies. For this classification an object-oriented approach was applied. The method is based on hierarchical segmentation not only of the CIR orthoimages but also of their derivatives (Batz and Schäpe 1999). To summarize, we produced a total of 29 explanatory variables for the model. 17 of them were allocated to 1st level variables, mainly based on simple reflection values of the three channels of the CIR orthoimages as well as on spatial information. The remaining 12 were allocated to the 2nd level variables. Finally, in accordance with the lichen relevés that are representative for a 56 m circle, for each variable the sum of values was calculated within a 56 m radius circle for each of the 96 sampling plots. This was performed using a moving window approach - in our case a moving circle (see fig. 4).

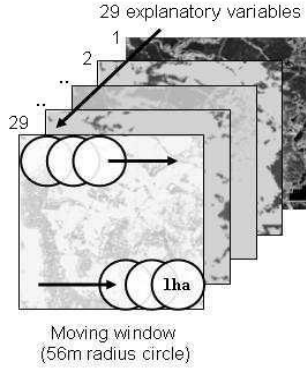


Figure 4. Moving window approach within the 56 m radius circle as applied for all 1- 29 explanatory variables

2.3 Model development

The choice of the “right” model should be carefully made considering possible advantages and disadvantages. According to Austin and Gaywood (1994) a model used for biodiversity assessment should not only be precise but also ecologically sensible, meaningful and interpretable. An important statistical development of the last 30 years has been the advance in regression analysis provided by various linear models (Yee and Mackenzie 2002). Linear least-square regression can be generalized by transforming the dependent variable (McCullagh and Nelder 1989). Generalized linear models (GLM) comprise a number of model families e.g. binomial, Poisson, etc. (Guisan and Zimmermann 2000). However, assuming a specific theoretical distribution for the data used in this study seems to be difficult. Differing collecting procedures (i.e. different ways to the next tree and rock patch) rules out the model of the data as a Poisson process. Therefore we used the simplest “first aid” transformation (square root transformation) that allows coping with count data. For each of the four field data sets (total species richness, species richness for lichens on trees, on rocks and on soil) we performed a stepwise dropping of our 29 explanatory variables – allowing both backward and forward selection to build the models. We assumed that the relatively high number of explanatory variables, often intercorrelated, would be handled adequately by this stepwise methodology. Among the variables remaining in the final models, 1st level variables are used as single and as quadratic terms, whereas 2nd level variables were square-root transformed. The complete final models and their explanatory variables are listed below:

- Richness_total ~ variance_nir + variance_nir² + ratio2 + ratio2² + sqrt(forest) + sqrt(grass_light)
 - Richness_trees ~ variance_nir + variance_nir²
 - Richness_rocks ~ variance_nir + variance_nir² + skewness + skewness² + sqrt(grass_light)
 - Richness_soil ~ ratio1 + ratio1² + skewness + skewness² + sqrt(rock&gravel&soil)
- [1]

The 96 sampling plots are divided into a calibration data set of 48 randomly sampled relevés and a reference data set consisting of the remaining 48. With this calibration data set the model was built and prediction values were calculated for the 48 sampling plots of the reference data. This was carried out 100 times. The means of the 100 runs are shown in table 2.

2.4 Validation

Several statistic measures were applied to evaluate the predicted species richness against the measured species richness of the sampling plots. Correlation of the fitted values with the calibration data values was chosen as a measure for the model quality (r model in table 2). The predictive power of the model is estimated by the correlation of predicted data values with the reference data values (r reference in table 2).

In the present study, the 95% quantile of the absolute errors, the bias (difference between the mean values and the mean fitted values), mean of absolute errors MAE (predicted species richness compared to reference species richness) and the G-value are applied as accuracy measures. The G-value (G) is a measure of accuracy in the case of a quantitative response and gives an indication of how effective a prediction might be, relative to that which could have been derived from using the sample mean alone. G is given by the equation 2:

$$G = 1 - \frac{\sum_{i=1}^n |Z_{(xi)} - \bar{Z}|^2}{\sum_{i=1}^n |Z_{(xi)} - \bar{Z}|^2} \quad [2]$$

Where $Z(X_i)$ is the measured value at a sampling plot i , $Z(x_i)$ is the estimated value, and $\bar{Z}$ is the overall mean of the measured sampling plots. A value of 1 indicates a perfect prediction, while a value of 0 describes no significant agreement, and negative values indicate that the predictions are less reliable than if one had used the sample mean instead (Schloeder et al. 2001).

2.5 Application of models

In order to extrapolate the predicted species richness of the sampling plots to the entire area of the six LUUs the model had to be applied accordingly. Lichen species richness for each pixel of the six test sites was calculated implementing the explanatory variables for the final models in a moving window approach (in our case a moving circle). The sum of values within a 56 m radius circle was calculated for each pixel of the selected explanatory variable (see fig. 4) using GIS operations. Then pixel-wise calculation of species richness for all lichens, lichens on trees, on rocks and on soil was performed using the four corresponding model equations (with their coefficients) as given in the section model development. The results are maps of predicted number of lichen species for each pixel in the entire six LUUs (see fig. 5).

3. RESULTS

The best results of the models and the combination of explanatory variables retained in each model are given in table 2. The quality of the models (r model) ranges between 0.59 for lichens on soil and 0.79 for lichens on trees. Predictive power, with a correlation coefficient (r reference) ranging between 0.48 and 0.79 and G ranging between 0.63 and 0.37, are obtained. In general, species richness is slightly underestimated for sampling plots with high species richness and overestimated for sampling plots with low species richness. A total of 29 variables correlated with the number of lichen species but only seven were used for the final models.

<i>Models</i>	<i>Lichen total</i>	<i>Trees</i>	<i>Rocks</i>	<i>Soil</i>
<i>Goodness of fit (r model)</i>	0.68	0.79	0.61	0.58
<i>Predictive power (r reference)</i>	0.58	0.79	0.54	0.48
<i>MAE (model)</i>	7.84	6.65	8.77	1.01
<i>95% Quantile of error (model)</i>	21.35	15.82	20.11	3.57
<i>Bias (model)</i>	+1.09	+1.52	+3.26	+0.46
<i>G</i>	0.52	0.63	0.37	0.40

Table 2. Means of 100 runs for validation of the four models of the species richness for all lichens, on trees, rocks soil

Fig. 5 shows the maps of the predicted number of species for all lichens in LUU1 (low intensively use) and LUU6 (high intensively use). Areas with low numbers of species are mapped gray whereas areas with high numbers of species are white.

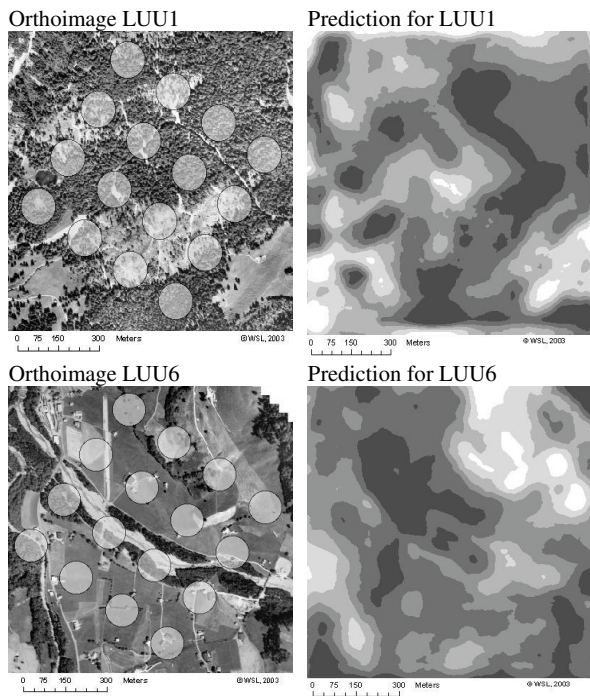


Figure 5. Maps of predicted species richness for all lichens for LUU1 and LUU6 with their corresponding CIR orthoimages

Our approach in distinguishing between 1st and 2nd level explanatory variables allowed us to assess their contribution to the corresponding model. This was an important step for the development of the final models and helped us to drop the variables that contribute less to the model. Particularly the use of simple spectral and textural information values of the CIR orthoimages which is linked to spectral reflection and spatial heterogeneity of the vegetation cover, respectively, produced best results. The implementation of additional 2nd level explanatory variables in fact improved model accuracy again – with the exception for lichens on trees. For this model best accuracy (r model of 0.79 and G 0.63) was produced with the single use of $\text{variance}_{\text{nir}}$ and its quadratic term whereas the implementation of additional explanatory variables slightly deteriorated the model's accuracy. In this case the number of species is directly related to a high heterogeneous vegetation

cover such as forest borders and forest itself. The nine land cover types extracted for this study are based on what was supposed to be detectable in CIR orthoimages, and what was regarded to be of importance for the lichen diversity. The main advantage of the application of an object-oriented image classification method is that it allowed us to define land cover types according to the needs of lichen experts. Thus land cover classification applied in this study in combination with image segmentation methods was an important step in the development of the models. The main disadvantage was the relatively high complexity and required amount of time of object-oriented image classification methods.

4. CONCLUSION

This study reveals that the application of homogenous and reproducible land cover information derived from remotely sensed data as basis for the model is adequate. The accuracies (r reference) obtained for both model lichens on trees (0.79) and for all lichens (0.58) can be regarded as good for the application purposes by lichenologists.

The crucial question is how we can improve our models for lichen species richness? In this study we were confronted with several problems concerning ecological modelling. According to Leathwick et al. (1996) a model used for biodiversity assessment should also be general, which means applicable in other regions or different times. Furthermore, according to Fielding and Bell (1997) the lack of validation and uncertainty assessment of models remains a serious issue in ecological modelling. Finally, according to Austin and Gaywood (1994) a model used for biodiversity assessment should not only be precise but also be ecologically sensible, meaningful and interpretable. Meeting all the suggested requirements turns out to be nearly impossible in our case. E.g. the particular model developed here has been applied only for six test sites. Thus, the resulting variables of the presented linear models may be used for calculating species richness in neighboring regions of the Entlebuch with similar vegetation cover and landscape structures. Applying the model to other regions is a well-known problem (Iverson and Prasad 1998).

There are four points to remember: First, linear regression models can be used to predict lichen diversity, but strongly depend on the sampling design of the lichen relevés. Thus the distribution of the lichen data should be analyzed further. Second, possible hotspots were calculated and may help in reducing field surveys and could be useful for possible conservation efforts. The resulting explanatory variables of the presented linear models may be used for calculating species richness in neighboring regions with similar landscape structures. Third, we can confirm that the application of homogenous and reproducible land cover information derived from high resolution remote sensing data as basis for the model is very adequate. This means that not so well-known areas can still serve as a basis for building the methods. Fourth, explanatory variables can be rapidly derived from high resolution remote sensing data and distinguishing between 1st and 2nd level of detail proved to be a good method for the development of the models.

This method cannot replace lichen surveys altogether, but it can be used to target focused lichen forays in the future. Finally, it should be noted that this method cannot produce any information on lichen species abundance, dynamics, or viabilities; it only indicates the potential presence or absence of species.

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