Computers and Electronics in Agriculture 74 (2010) 91–99

Contents lists available at ScienceDirect

Computers and Electronics in Agriculture

journal homepage: www.elsevier.com/locate/compag

Original paper

Early detection and classification of plant diseases with Support Vector Machines based on hyperspectral reflectance

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ARTICLE INFO

Article history:
Received 30 November 2009
Received in revised form 8 April 2010
Accepted 24 June 2010

Hyperspectral reflectance
Vegetation indices
Support Vector Machines
Automatic non-linear classification
Early detection
Cercospora beticola
Uromyces betae
Erysiphe betae
Sugar beet

ABSTRACT

Automatic methods for an early detection of plant diseases are vital for precision crop protection. The main contribution of this paper is a procedure for the early detection and differentiation of sugar beet diseases based on Support Vector Machines and spectral vegetation indices. The aim was (I) to discriminate diseased from non-diseased sugar beet leaves, (II) to differentiate between the diseases Cercospora leaf spot, leaf rust and powdery mildew, and (III) to identify diseases even before specific symptoms became visible. Hyperspectral data were recorded from healthy leaves and leaves inoculated with the pathogens *Cercospora beticola*, *Uromyces betae* or *Erysiphe betae* causing Cercospora leaf spot, sugar beet rust and powdery mildew, respectively for a period of 21 days after inoculation. Nine spectral vegetation indices, related to physiological parameters were used as features for an automatic classification. Early differentiation between healthy and inoculated plants as well as among specific diseases can be achieved by a Support Vector Machine with a radial basis function as kernel.

The discrimination between healthy sugar beet leaves and diseased leaves resulted in classification accuracies up to 97%. The multiple classification between healthy leaves and leaves with symptoms of the three diseases still achieved an accuracy higher than 86%. Furthermore the potential of presymptomatic detection of the plant diseases was demonstrated. Depending on the type and stage of disease the classification accuracy was between 65% and 90%.

1. Introduction

In the past different automatic classification methods have been used to classify remote sensing data and plant observations. Machine learning methods, such as artificial neural networks (ANNs), Decision Trees, K-means, *k* nearest neighbors, and Support Vector Machines (SVMs) have been applied in agricultural research (Mucherino et al., 2009). There is an extensive potential of automatic classification methods in site-specific weed detection (Gutiérrez et al., 2008; Karimi et al., 2006). Wang et al. (2008) predicted *Phytophthora infestans* infection on tomatoes by using ANNs, Camargo and Smith (2009) identified visual symptoms of cotton diseases using SVMs, Ferreiro-Armán et al. (2006) have discriminated between grape varieties from hyperspectral airborne data using SVMs. Furthermore, SVMs turned out as a powerful machine learning technique for general-purpose supervised prediction in biological research like, for example, in the classification of proteins (Park et al., 2005) or gene expression levels (Friedel et al., 2005), for yield prediction in agricultural sciences (Ruß et al., 2008; Ruß, 2009), environmental modeling or stress detection (Karimi et al., 2008) and in remote sensing for land cover classification (Waske and Benediktsson, 2007; Gonçalves et al., 2005) or change detection (He and Laptev, 2009; Nemmour and Chibani, 2006).

Support Vector Machine is a powerful classification method based on the statistical learning theory of Vapnik (1998). In general, classification algorithms aim at finding patterns in empirical data (training data or input data) with regard to label classes. The resulting classification model is used to make a prediction for new unlabeled data. In a sense, supervised learning concludes in finding a function *f* which fits the training data in the best way possible.

However, the identification of such a function is an ‘ill-posed problem’ since there is an infinite number of functions which describe the discrete data equally well. On the other hand, machine learning is mainly interested in predicting the class of unseen data, i.e. generalisation ability of the classifier, rather than fitting the training data. It is a basic insight of machine learning that the class of feasible functions *f* has to be restricted. In this respect the selection of the function class is a trade-off between a sufficiently modest complexity to achieve good generalisation and to avoid overfitting. Both issues are balanced by SVMs in an optimal way (Vapnik, 2000). SVMs separate two different classes through a hyperplane which

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doi:10.1016/j.compag.2010.06.009

is specified by its normal vector $\vec{w}$ and the bias b. By using a kernel function SVMs are also able to discriminate non-linear, which is required in the classification of plant diseases and especially the discrimination between healthy and diseased plants at early stages.

This study presents a procedure for an automatic classification of foliar sugar beet diseases with special focus on early detection. Foliar diseases are serious threats in sugar beet cultivation. The fungal pathogens *Cercospora beticola* (Sacc), *Erysiphe betae* (Vanha) Weltzien, and *Uromyces betae* (Persoon) Lev. causing Cercospora leaf spot, powdery mildew, and leaf rust, respectively, may induce losses in yield quantity and sugar yield; economic losses may reach up to US\$ 1500 ha^{-1} (Wolf and Verreet, 2002). Usually fungal leaf diseases are managed by cultural practices that reduce primary inoculums, planting resistant cultivars, and by applying fungicides (Steddom et al., 2005). Because of the high costs of chemical control and its ecologic impact, one aim of precision farming is to reduce and optimize pesticide applications. The detection and differentiation of several diseases at early stages of epidemics allow a more efficient application of agrochemicals (Hillnhuetter and Mahlein, 2008). But visual monitoring of diseases at early stages in the field is time-consuming and expensive (Steddom et al., 2005; Steiner et al., 2008). Hence, alternative evaluation methods are required. Optical methods like hyperspectral imaging and non-imaging sensors have proved to be useful tools in order to detect changes in plant vitality (Hatfield et al., 2008; West et al., 2003). A high potential of reflectance data in discriminating between healthy and diseased plants has been shown (Bravo et al., 2003; Delalieux et al., 2007; Carroll et al., 2008; Larsolle and Muhammed, 2007; Naidu et al., 2009; Steddom et al., 2003; Wang et al., 2008; Zhang et al., 2002). Spectral vegetation indices (VIs) related to specific physiological parameters have been exploited for the differentiation of healthy and diseased plants (Delalieux et al., 2009; Naidu et al., 2009; Graeff et al., 2006; Steddom et al., 2003, 2005). These VIs from remote sensing are not disease-specific, hence disease discrimination using a single VI is not feasible.

For precision plant protection new disease detection methods must facilitate an automatic classification of the diseases. Data mining techniques, the process of extracting important and useful information from a large set of data (Mucherino et al., 2009; Wu et al., 2008b), seems to solve this complex agricultural problem. Different techniques have been proposed for mining data in terms of disease detection. Bravo et al. (2003) investigated the difference in spectral reflectance between healthy and rust diseased wheat plants. Using a quadratic discriminating model based on the reflectance of the most discriminating four wavebands determined by analysis of covariance (ANCOVA) *F*-test, they correctly classified diseased and healthy spectra with a classification accuracy of 96%. In a next step they used the neural network Self-Organizing Maps (SOM) successfully to discriminate between healthy plants, nitrogen deficiency, and rust diseased wheat plants in field (Moshou et al., 2006). Wang et al. (2008) spectrally predict late blight infections on tomatoes based on artificial neural networks (ANNs).

Because plant diseases are often associated with specific physiological and visual modifications of their host plants, we applied a method based on the combination of various VIs derived from hyperspectral data and used SVMs to fully exploit their combined information. As a consequence of learning with SVMs several advantages arise. First the function class for the classification model may be arbitrarily complex thus providing the flexibility for difficult classification tasks. A radial basis function (RBF) is parametrized by a simple parameter σ which controls the smoothness of the decision boundary, and therefore the handling is manageable. Reflecting the expectation that some of the training and test samples have been given a wrong label a second parameter C controls the penalisation of this kind of error. In summary, learning with SVMs amounts to find adequate parameters for C and σ.

The objectives of this study were (I) to discriminate diseased from non-diseased sugar beet leaves, (II) to differentiate between the diseases Cercospora leaf spot, leaf rust and powdery mildew, and (III) to identify diseases even before specific symptoms became visible. This study has shown that combined VIs, together with SVMs using an appropriate radial basic function are able to discriminate between the foliar diseases Cercospora leaf spot, sugar beet rust, powdery mildew and healthy plants and as well as between the plant diseases themselves. Furthermore latent infection could be predicted.

2. Materials and methods

2.1. Plant cultivation

Greenhouse experiments were conducted to assess spectral characteristics of sugar beet leaves under controlled conditions. Sugar beet plants (cv. Pauletta, KWS GmbH, Einbeck, Germany) were grown in a commercial substrate (Klasmann-Deilmann GmbH, Germany) in plastic pots (⌀ 13 cm) at 23/20 °C (day/night), 60% relative humidity (RH) and a photoperiod of 16 h. Plants were watered as necessary and fertilized weekly with 100 ml of a 0.2% solution of Poly Crescal (Aglukon GmbH, Düsseldorf, Germany).

2.2. Pathogens

For each treatment, 15 plants were inoculated with the pathogens at growth stage (GS) 14 (= four leaves fully developed). As healthy control 15 plants were kept non-inoculated at 23/20 °C and 60 ± 10% RH. *Cercospora beticola* was inoculated by spraying a spore suspension (4×10^4 conidia ml^{-1}) onto the leaves using a hand sprayer. Subsequently, the plants were covered with plastic bags to realize 100% RH at 25/20 °C for 48 h. Suspensions of *Uromyces betae* (4×10^4 urediniospores ml^{-1}), were sprayed onto the leaves before covering the plants with plastic bags and incubating them for 48 h at 19/16 °C. For further incubation the plants inoculated with *C. beticola* and *U. betae* were transferred to 23/20 °C and 60 ± 10% RH. Plants heavily infested with powdery mildew were used as inoculum source of *Erysiphe betae*. Healthy plants were inoculated in a chamber where a ventilator ran for 25 s to distribute *E. betae* conidia evenly on their leaves. Plants were left over night and afterwards transferred to 23/20 °C, however, separated from the other plants.

2.3. Data recording

Spectral reflectance was measured using a handheld non-imaging spectroradiometer (ASD FieldSpec Pro FR spectrometer, Analytic Spectral Devices, Boulder, USA) with a plant probe foreoptic and a leaf clip holder. The spectral range was from 400 nm to 1050 nm with a spectral resolution of 1.4 nm. The contact probe foreoptic has a 10 mm field of view and an integrated 100 W halogen lamp. Instrument optimization and reflectance calibration were performed prior to sample acquisition; the average of 25 dark current measurements was calibrated to the average of 25 barium sulphate white reference (Spectralon, Labsphere, North Sutton, NH, USA) measurements. Because of the internal light source the integration time was adjusted to 17 ms per scan constantly. Final reflectance spectra were obtained by determining the ratios of data acquired for a sample to data acquired for the white reflectance standard. Each sample scan represented an average of 25 reflectance spectra. In addition, a SPAD-502 chlorophyll meter (Minolta Camera Ltd., Osaka, Japan) was used to measure the leaf greenness as an indicator of the chlorophyll content.

Data from inoculated and non-inoculated leaves were recorded daily till 21 days after inoculation. For each treatment, spectra from

Table 1
Vegetation indices and equations used in this study (R = hyperspectral reflectance). These eight VIs and the SPAD-value are used as features for classification.

Index	Equation	Related to	Reference
Normalized difference vegetation index	$NDVI = \frac{R_{800}-R_{670}}{R_{800}+R_{670}}$	Biomass, leaf area	Rouse et al. (1974)
Simple ratio	$SR = \frac{R_{800}}{R_{670}}$	Biomass, leaf area	Birth and McVey (1968)
Structure insensitive vegetation index	$SIPI = \frac{R_{800}-R_{445}}{R_{800}+R_{680}}$	Ratio carotinoids/chlorrphyll a	Penuelas et al. (1995)
Pigments specific simple ratio	$PSSRa = \frac{R_{800}}{R_{680}}$	Chlorophyll (a/b) content	Blackburn (1998)
	$PSSRb = \frac{R_{800}}{R_{635}}$		
Anthocyanin reflectance index	$ARI = \left(\frac{1}{R_{550}}\right) - \left(\frac{1}{R_{700}}\right)$	Anthocyanin	Gitelson et al. (2001)
Red edge position	$REP = 700 + \frac{40\cdot(R_{RE}-R_{700})}{(R_{740}-R_{700})}$	Inflection point red edge	Guyot and Baret (1988)
	$R_{RE} = \frac{R_{670}+R_{780}}{2}$		
Modified chlorophyll absorption integral	$mCAI = \frac{(R_{545}+R_{752})}{2}\cdot(752-545) - \left(\sum_{R_{545}}^{R_{752}} R \cdot 1.423\right)$	Chlorophyll content	Laudien et al. (2003)

the adaxial surface of the two youngest, fully developed leaves of 15 plants were taken ($n = 30$). RGB images of the leaves were additionally taken. Disease severity of each pathogen was evaluated daily and classified according to Wolf and Verreet (2002). Experiments were repeated twice.

2.4. Spectral vegetation indices

In order to evaluate the suitability of VIs to identify and discriminate among foliar diseases, VIs related to different physiological parameters were calculated (Table 1). Correlation and regression analyses between VIs and disease severity were conducted for each disease (Mahlein et al., 2010).

Relationships between disease severity and VI values were determined by Pearson's correlation coefficient using the Superior Performing System SPSS 17.0 (SPSS Inc., Chicago, IL, USA).

2.5. Classification

In classification generally supervised and unsupervised learning methods are distinguished. Clustering is the most prominent method of unsupervised learning. There are several cluster analysis methods available, viz. DB-SCAN (Ester et al., 1997), K-Means, X-Means (Pelleg and Moore, 2000) or SVM-Clustering (Ben-Hur et al., 2001). In our study we intentionally focused on supervised learning methods, viz. Decision Trees, ANNs and SVMs. Supervised learning needs labeled training samples to learn a model which enables the classifier to predict the class of unseen pattern. For these three classification methods, eight VIs (Table 1) and the SPAD-value were used as features.

2.5.1. Decision Trees

Learning with Decision Trees is one of the most popular and widely used methods for inductive inference. This techniques have their roots in an algorithm which was proposed and refined on by Quinlan (1993). The basic data structure is a tree where the nodes represent features and the edges represent decisions in favor of a (range of) value(s) of the latter. The root and every interior node contains a decision criterion for that feature which has the best chance to reduce the entropy of the respective sample set. Entropy reduction is achieved by splitting the sample set in two or more subsets. This procedure is applied recursively until a given threshold for the minimal entropy is reached. In the case of numeric data, a split value which maximizes entropy reduction is calculated (Mitchell, 1998). After the split into two parts based on the feature with the highest relevance, the next feature which splits the data optimally is determined. Since always one feature is considered at a time, a stepwise axis-parallel boundary is formed in the domain of real numbers. Following a path from the root to a leaf node the Decision Tree corresponds to a rule based classifier.

2.5.2. Artificial neural networks

Artificial neural networks have been inspired by the research on human brain. In the network each node represents a neuron and each link the way two neurons interact. The most popular kind of ANNs is the multilayer perceptron, in which neurons are organized in layers. Each neuron can receive input signals from neurons of the previous layer and send it output to neurons of the successive layer. Further, the activation value is computed as weighted sum of all received signals. The weights between the linked neuron can either increase or decrease the signal. In the simplest case a linear combination of basis functions, especially sigmoid functions, is used to process the activation value of each neuron. ANNs are discussed extensively in Bishop (2005).

2.5.3. Support Vector Machines

In this paragraph Support Vector Machines are discussed in more detail. The simple case of linear SVMs assumes that two classes are linear separable, i.e. their discriminant can be described by a linear function. Starting point is a training data set.

$$\left(\vec{x}_1, y_1\right), \quad \left(\vec{x}_2, y_2\right), \ldots, \left(\vec{x}_n, y_n\right). \tag{1}$$

where $\vec{x}$ denotes a vector with m features $x_1, \ldots, x_m$ and $y_k = 1$ if $\vec{x}_k$ belongs to label class one and $y_k = -1$ if $\vec{x}_k$ was in label class two. Different labels define different classes. In our case the two classes correspond to were healthy sugar beet leaves and leaves inoculated with the different pathogens, respectively. The dot product, which is defined by the formula $\left\langle \vec{\omega}, \vec{x} \right\rangle = \omega_1 x_1 + \omega_2 x_2 + \cdots + \omega_m x_m$, intuitively specifies the distance (in an m-dimensional Euclidean space). This is used as similarity measure. The basic idea behind SVMs is to separate the two different classes through a hyperplane which is specified by its normal vector $\vec{\omega}$ and the bias b. The hyperplane can be given as

$$\left\langle \vec{\omega}, \vec{x} \right\rangle + b = 0 \quad \text{where} \quad \vec{\omega} \in \mathbb{R}^m,\ b \in \mathbb{R}. \tag{2}$$

This yields the corresponding decision function

$$f\left(\vec{x}\right) = \operatorname{sgn}\left(\left\langle \vec{\omega}, \vec{x} \right\rangle + b\right). \tag{3}$$

The sign of $f\left(\vec{x}\right)$ depends on the side of the hyperplane where the sample lies. As Vapnik (1998) shows the optimal separating hyperplane is the one which maximizes the distance between the hyperplane and the nearest points of both classes (called margin) and results in the best prediction for unseen data. The samples with minimal distance to the hyperplane are called Support Vectors (SV) and only they define the hyperplane. Thereby the separation is

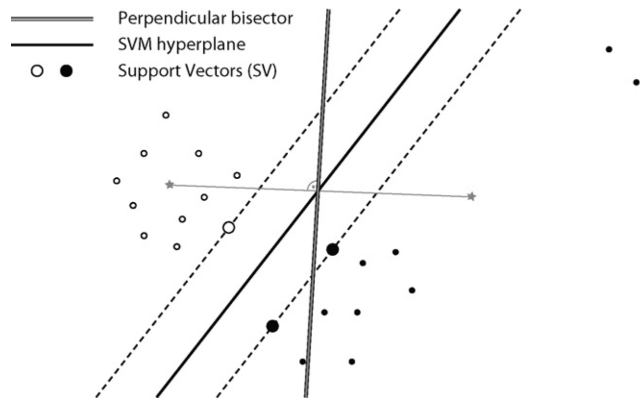

Fig. 1. Comparison of separating two classes. The perpendicular bisector of the line segment connecting the respective centroids (asterisk) of the two classes, obviously differs from the hyperplane with maximal margin constructed by SVMs. The maximal margin hyperplane is more robust against outliers.

robust against outliers — in contrast to the well-known Fisher discriminant which calculates a separating hyperplane based on the centroids of both classes (Fig. 1).

It is assumed that both classes are linearly separable. The specification of a hyperplane by ω and b is unique up to a factor λ. By requiring the scaling of ω and b to be such that the closest point(s) to the hyperplane satisfy $\left|\left\langle \vec{\omega}, \vec{x}_i \right\rangle + b\right| = 1$ the canonical form of a hyperplane is obtained. Accordingly the norm of the normal vector ω is equal to the inverse of the distance, of the closest sample(s) of both classes to the hyperplane. Hence, the optimal separating hyperplane with maximal margin can be formulated as the following quadratic optimization problem:

$$\min_{\vec{\omega} \in \mathbb{R}^m, b \in \mathbb{R}} \quad \tau(\vec{\omega}) = \frac{1}{2}\left|\vec{\omega}\right|^2 \tag{4}$$

$$\text{subject to} \quad y_i \cdot \left(\left\langle \vec{\omega}, \vec{x} \right\rangle + b\right) \geq 1 \quad \forall\, i = 1, \ldots, n. \tag{5}$$

The constraint (5) ensures that $f\left(\vec{x}_i\right)$ yields +1 for $y_i \in \left\{+1\right\}$ and -1 for $y_i \in \left\{-1\right\}$ so that the two classes are separated correctly.

Chapelle (2007) showed that already the primal optimization problem (4) can efficiently be solved, but it is often advisable to solve the dual maximization problem (Boyd and Vandenberghe, 2004). Using the Karush Kuhn Tucker conditions and introducing Lagrange multipliers α_i, ω and b are eliminated (Schölkopf and Smola, 2002).

$$\max_{\alpha \in \mathbb{R}^n} \quad W(\vec{\alpha}) = \sum_{i=1}^{n} \alpha_i - \frac{1}{2}\sum_{i,j=1}^{n} \alpha_i \alpha_j y_i y_j \left\langle \vec{x}_i, \vec{x}_j \right\rangle \tag{6}$$

$$\text{subject to} \quad \alpha_i \geq 0 \quad \forall\, i = 1, \ldots, n \tag{7}$$

$$\text{and} \quad \sum_{i=1}^{n} \alpha_i y_i = 0. \tag{8}$$

The optimal solution of (6) only depends on the $\alpha_i \neq 0$ (SV). All other $\vec{x}_i$ which are no SV become zero and have no influence on the construction of the optimal hyperplane which is given by

$$\vec{\omega}^* = \sum_{i=1}^{n} \alpha_i y_i \vec{x}_i \tag{9}$$

$$b^* = -\frac{1}{2}\left\langle \vec{\omega}^*, \vec{x}_a + \vec{x}_b \right\rangle, \tag{10}$$

where $\vec{x}_a \in \left\{+1\right\}$ and $\vec{x}_b \in \left\{-1\right\}$ are any support vectors of both classes. The decision function is then

$$f(\vec{x}) = \operatorname{sgn}\left(\left\langle \vec{\omega}^*, \vec{x} \right\rangle + b^*\right) \tag{11}$$

So far the discussion has been restricted to linear separation. However, in general data will not be linear separable. For this reason a kernel function is introduced to enable an efficient computation (Boser, 1992; Hofmann et al., 2008). It contains an implicit mapping in the feature space without explicitly computing the mapping Φ. The 'kernel trick' can be applied since all feature vectors only occurred in dot products (4), (10), (11) (Schölkopf et al., 1998). Accordingly, the dot product $\left\langle \vec{x}, \vec{x}_i \right\rangle$ as measure of similarity can be substituted by a kernel

$$k\left(\vec{x}, \vec{x}_i\right) = \left(\Phi\left(\vec{x}\right) \cdot \Phi\left(\vec{x}_i\right)\right). \tag{12}$$

One kernel commonly used in practice is the radial basis function (RBF) kernel, i.e.

$$k\left(\vec{x}, \vec{x}_i\right) = \exp\left(\frac{-\left|\vec{x} - \vec{x}_i\right|^2}{2\sigma^2}\right), \tag{13}$$

where the parameter σ controls the smoothness of the decision boundary in the feature space. In our case, this kernel was used to differentiate between healthy and inoculated sugar beet leaves.

Beyond specifying non-linear discriminants by RBF kernels, another generalisation has been proposed which replaces hard margins by soft margins. This way allows to handle noise and prelabeling errors, which often occur in practice. Slack-variables ξ_i are used to relax the hard-margin constraint (Cortes and Vapnik, 1995). The condition in (5) changes to

$$y_i\left(\left\langle \vec{\omega}, \vec{x} \right\rangle + b\right) \geq 1 - \xi_i, \quad \xi_i \geq 0, \quad \forall\, i = 1, \ldots, n \tag{14}$$

so that some classification errors which depend on ξ_i are allowed. In conclusion the quadratic optimization problem (4) converts to

$$\min_{\vec{\omega} \in \mathbb{R}^m, b \in \mathbb{R}} \quad \tau\left(\vec{\omega}, \xi_i\right) = \frac{1}{2}\left|\vec{\omega}\right|^2 + C\sum_{i=1}^{n} \xi_i, \tag{15}$$

with the regularisation parameter $C \geq 0$. A larger C penalizes a wrong classification more strongly.

Learning an optimal SVM classifier with RBF kernel for the identification of sugar beet diseases is structured as follows. After deducing the vegetation indices out of the original spectral signature the relevance of the indices may be checked. There are several methods to determine the relevance of features, but their detailed discussion is beyond the scope of this paper. In our case it turned out to be appropriate to use all features. In order to specify the best radial basis function and to find an appropriate factor for penalizing classification errors, the parameter C and σ have to be optimized. In this respect, we applied an grid-based approach as recommended by Hsu et al. (2008). Afterwards the classification result of this model is evaluated by cross-validation (see Section 2.7).

2.6. Multi-class classification

Several methods are available to extend dichotomous classifiers such as SVMs for multi-class classification effectively. In this study Chang and Lin's library for SVMs (LIBSVM) has been used for classification (Chang and Lin, 2001). Here the 'one against one' approach (Knerr et al., 1990) is applied. The classifier is constructed for $k(k-1)/2$ times, where k is the number of classes. Each one is trained with data of two classes. The classification decision is based on a majority vote of the class assignments. If classes have identical votes, the one with the smallest index is selected.

Table 2
Important measures in a statistical classification task.

	Condition (e.g. disease detection)		
	True (inoculated leaf)	**False** (healthy leaf)	
Test result	No. of true positive (TP)	No. of false positive (FP)	Pos. predictive value (Precision) ($TP(TP+FP)$)
	No. of false negative (FN)	No. of true negative (TN)	Neg. predictive value ($TN(TN+FN)$)
	Sensitivity (Recall) $\frac{TP}{TP+FN}$	**Specificity** $\frac{TN}{TN+FP}$	**Accuracy** $\frac{TP+TN}{TP+FP+TN+FN}$

2.7. Evaluation

In general training samples and test samples have to be separated to evaluate the learned model. However, using only half of the data for learning may not be enough to detect all patterns. To realise an optimal utilisation of all information in the training data the model learned was evaluated by cross-validation. The cross-validation splits all examples into a defined number of groups S, out of which $S-1$ are applied to learn a model and the remaining one is used for evaluation. This approach was repeated for all possible choices of evaluation groups. The performance resulted from the average of all possibilities. Frequently 10 groups were chosen. Important performance measures are described in Table 2. Specificity gives the proportion of the correctly classified healthy leaves of all classified healthy leaves. Sensitivity (Recall) gives the proportion of correctly classified inoculated sugar beet leaves in relation to all classified inoculated leaves. The accuracy is given by the average of sensitivity and specificity.

3. Results

3.1. Disease development

Non-inoculated plants stayed healthy over the experiment period. Inoculated plants were first colonized without symptoms, after a latency period typical symptoms appeared. The development of diseases and the symptoms varied significantly for the three pathogens (Fig. 2). Small chloroses were the first symptoms of Cercospora leaf spot. After 6–8 days of incubation, these spots became necrotic and the characteristic red margin of the spots became visible. Fourteen days after inoculation the spots coalesced and formed large necrotic areas. First chloroses due to *Uromyces betae* became visible 9 days after inoculation (dai). At later stages, rust spores ruptured the epidermis and amber uredinia became visible on the upper and lower side of leaves. Symptoms of powdery mildew firstly appeared 5 dai. Small colonies visible on the upper side of leaves in the beginning rapidly expanded and after 14 dai the white, fluffy mycelium covered the total leaf surface.

3.2. Dichotomous classification between healthy leaves and leaves with disease symptoms

In a first dichotomous approach SVMs were used for the differentiation between the two classes, non-inoculated, healthy leaves and leaves inoculated with one of the three leaf pathogens. VIs calculated from characteristic reflectance spectra (Fig. 3) and the SPAD-value were used for classification.

The results showed that the specificity of the classification was always lower than the sensitivity. The classification error range was 7% to almost 3% (Table 3). In comparison with the classification results of Decision Trees and ANNs the classification error of SVMs was always lower.

The classification accuracy increased with increasing disease severity (Fig. 4). Differences in the number of leaves in the disease class give additional information on the reliability of classification results. With only 1–2% diseased leaf area, the classification accuracy was about 65% for all diseases. The accuracy of differentiating between healthy leaves and leaves with Cercospora leaf spot symptoms rapidly increased with a disease severity of 3–5%. When more than 10% of the leaf area was covered by leaf spots, the classification accuracy reached 100% (Fig. 4).

The accuracy of detecting sugar beet rust and powdery mildew symptoms increased less rapidly. At sugar beet rust disease severity stages of 6–9% the classification accuracy was about 95%. Leaves with powdery mildew could be differentiated from healthy leaves

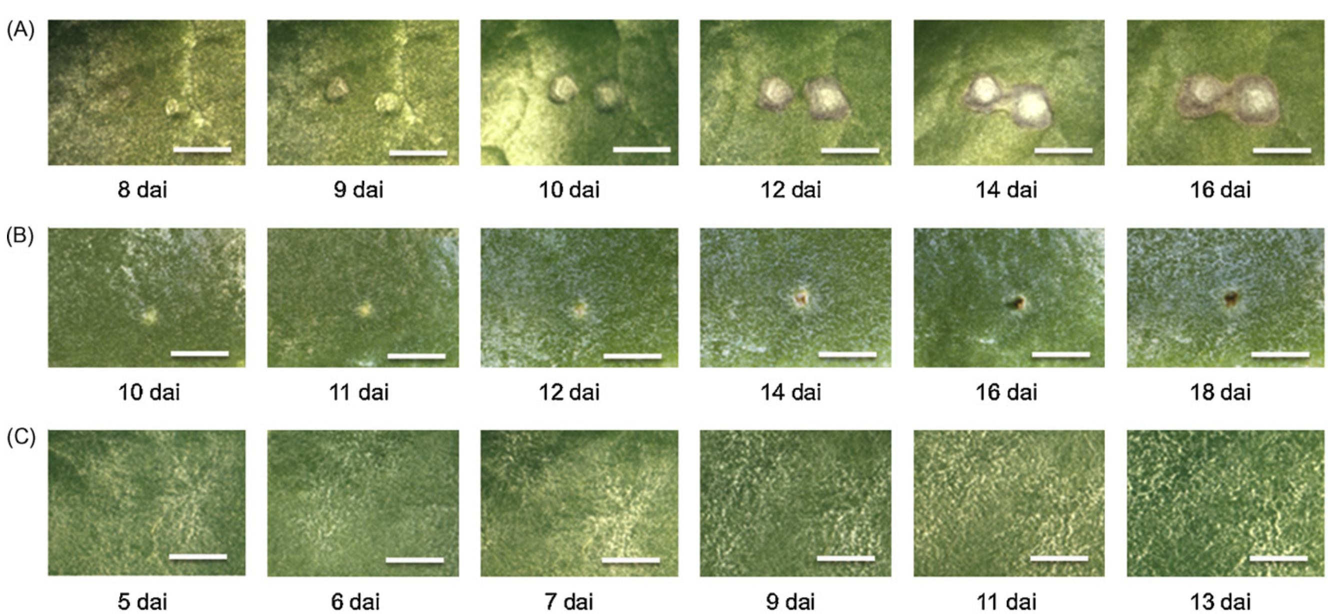

Fig. 2. Development of disease specific symptoms of three diseases on sugar beet leaves; Cercospora leaf spot (A), sugar beet rust (B), and powdery mildew (C) (dai = days after inoculation; bar = 4 mm).

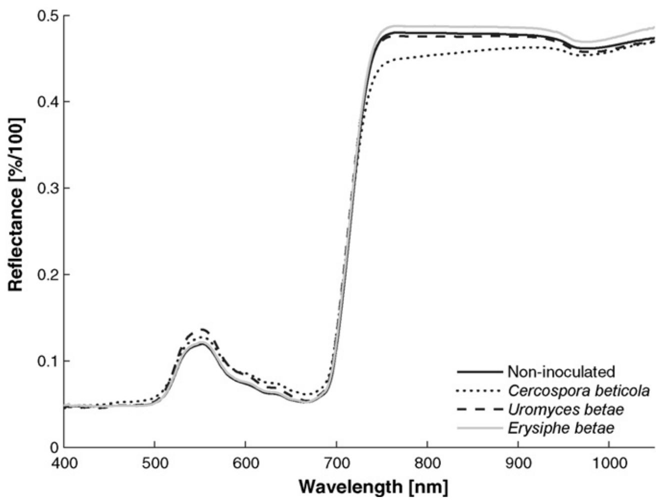

Fig. 3. Spectral signatures of the non-inoculated sugar beet leaves and sugar beet leaves inoculated with the different pathogens. The showed reflectance spectra are the mean of all sugar beet leaves with diseases severity under 10%, respectively.

Table 3
Results of the dichotomous classification based on spectral vegetation indices. Comparison between the three different classification methods Decison Tree, ANNs and SVMs.

Leaf disease	Classification error [%]		
	Accuracy	Specificity (healthy leaves)	Sensitivity (diseased leaves)
Decision Trees			
Cercospora leaf spot	4.67	1.15	8.52
Sugar beet rust	7.15	4.76	9.86
Powdery mildew	13.18	5.59	21.51
ANNs			
Cercospora leaf spot	3.64	3.02	4.32
Sugar beet rust	4.30	2.38	6.49
Powdery mildew	8.41	11.67	4.84
SVMs			
Cercospora leaf spot	2.88	1.35	4.55
Sugar beet rust	3.73	3.21	4.32
Powdery mildew	6.92	5.29	8.71

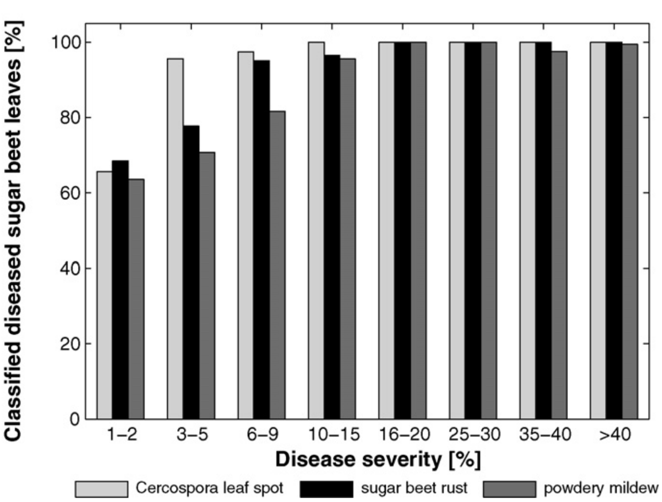

Fig. 4. Classification results of non-inoculated sugar beet leaves and sugar beet leaves inoculated with the different pathogens depending to disease severity.

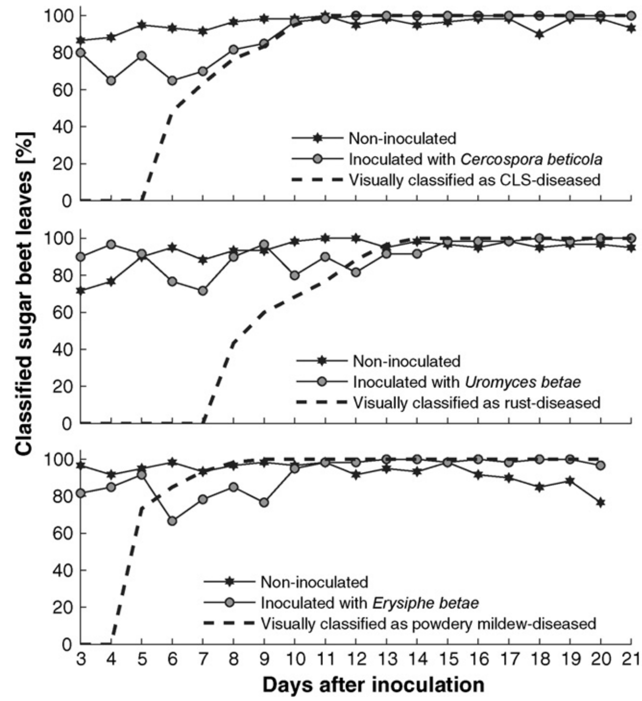

Fig. 5. Effect of incubation time on the results of SVM classification between healthy sugar beet leaves inoculated with *Cercospora beticola* (A), *Uromyces betae* (B) and *Erysiphe betae* (C), respectively.

with an accuracy of about 95% when 10–15% of the leaf area was covered with fluffy mycelium (Fig. 4).

3.3. Multi-class classification among healthy leaves and leaves with symptoms of three diseases

Table 4 summarises the results of the model learned which classified healthy sugar beet leaves and leaves diseased with Cercospora leaf spot, sugar beet rust and powdery mildew, respectively (multi-class classification). The overall classification accuracy was better than 86%, but the difference between the classes were low. The class recall of each class ranged between 84% and more than 92%. The class of healthy leaves was classified best. Classification difficulties occurred in separating between sugar beet rust and Cercospora leaf spot and also in the classification between powdery mildew and healthy sugar beet leaves.

3.4. Classification of healthy leaves and leaves inoculated with fungal pathogens at early stages of pathogenesis

For the differentiation between healthy sugar beet leaves and leaves inoculated with one of the different pathogens before specific disease symptoms became visible — VI data were used starting 3 dai. First symptoms of Cercospora leaf spot appeared 6 dai, rust 8 dai and powdery mildew 5 dai. Leaves inoculated with *C. beticola* were correctly classified by SVMs with an accuracy range from 65% to 80%, even before symptoms became visible (Fig. 5A). When specific symptoms occurred 6 dai, the classification accuracy steadily increased until 12 dai where it converged at 100%. Throughout the 21 days of the experiment, the classification accuracy of the automatic procedure was consistent to visually classified Cercospora leaf spot-infected leaves. The classification accuracy of healthy leaves was 3 dai almost 87% and reached >95% starting from 8 dai.

Although first symptoms of sugar beet rust appeared only 8 dai, a classification accuracy of 90% for *U. betae*-infected leaves was reached 3–5 dai (Fig. 5B). One day before first rust symp-

Table 4
Results of the Support Vector Machines multi-class classification based on spectral vegetation indices.

Prediction	Ground truth				*Class precision*
	Healthy	Cercospora leaf spot	Sugar beet rust	Powdery mildew	
Healthy	942	32	47	69	86.42%
Cercospora leaf spot	12	748	61	13	89.69%
Sugar beet rust	20	88	622	14	83.60%
Powdery mildew	46	12	10	834	92.46%
Class recall	92.35%	85.00%	84.05%	89.68%	*86.42%*

toms became visible, the sensitivity decreased to about 71% and increased again 15 dai to over 98%. The results of the automatic classification were inferior to the visual ratings only between days 12 and 14 after inoculation. Healthy sugar beet leaves were classified with an accuracy of 72% at early stages of leaf colonization by *U. betae*, but from 10 dai the classification accuracy was always greater than 95%.

Already 3 dai the classification accuracy of powdery mildew was above 80% and increased to almost 92% 5 dai (Fig. 5C). After the appearance of first visible colonies the classification rate decreased to under 70% 6 dai, subsequently increased again from 10 dai to 20 dai to over 95%. In contrast with the results for the leaves colonized by the other pathogens from 6 dai to 9 dai the visual classification of *E. betae*-infected leaves was superior (13–23%) to the automatic classification procedure. In the beginning of the experiment the classification rate of healthy leaves was above 91%; in the third week, however, it decreased to 77% 20 dai.

4. Discussion and conclusion

This article demonstrated the feasibility of presymptomatic identification of foliar sugar beet diseases. SVMs proved to be a powerful tool for automatic classification. The main advantages of SVMs go back to their generalisation ability which is achieved by using the maximum margin hyperplane for separation and the application of non-linear discriminant functions such as RBF kernels (Vapnik, 2000). In addition high performance in learning the best model, the comparison of the different classifiers shows that SVMs use the inherent information of the vegetation indices in an optimal way. Above, not only the identification of diseased leaves (dichotomous approach), but also the differentiation between distinct diseases (multi-class approach) can be realised. Comparing SVMs and ANNs both are discriminant methods without any assumption of a density distribution. There are important differences, however, which are important both from a theoretical and practical perspective. In order to find the best discriminant SVMs have to solve a quadratic optimization problem. Convexity of this problem ensures a unique, global solution. The applied techniques tend to converge rapidly thus providing good performance. In contrast, the optimization problem for ANNs is not convex, there are in general several local optima rather than a unique global solution, and good performance of the optimizer is not guaranteed (Suykens, 2002). Above, ANNs prone to overfitting by using empirical risk minimization, while SVMs use structural risk minimization for controlling the generalisation ability (Vapnik, 2000).

Recently, there has been growing interest in exploring the potential of SVMs for early detection of plant diseases. In a recent publication Camargo and Smith (2009) used SVMs for the identification of visual symptoms of plant diseases based on RGB images. They extracted a set of features, like shape, texture or grey level, from segmented diseased regions of cotton leaves. Using all features they reached a classification accuracy of 90%. Whereas the differentiation between different plant diseases, especially at a very earlier stage before symptoms are visible, has not been considered until now. Wu et al. (2008a) recently showed that an early detection of *Botryis cinerea* on eggplant leaves is possible, even before symptoms appeared. Owing to the complexity of the original spectral data, principal component analysis was applied to reduce the numerous wavelengths to several principal components (PCs) in order to decrease the amount of calculation and improve the accuracy. These PCs were set as input variables of back-propagation neural networks. In contrast to Wu et al. (2008a), we achieved classification errors between barely 7% and under 3%, dependent on the plant disease, by using VIs, which contains combinations of individual wavelength. In Table 5 a comparison of the results, by using the first six PCs similar to Wu et al. (2008a), is presented. For each plant disease the classification error by using VIs as features is noticeably inferior (Table 5). In order to additionally improve the detection of the three above mentioned plant diseases one could try to find wavelengths or combination of wavelengths more specific for the given task.

Most VIs are based on only two or three specific wavelengths of the visible- and near infrared region of the reflection spectrum. These wavelengths are highly correlated to specific physiological plant parameters, like pigment content, biomass or vitality (Thenkabail et al., 2000). During pathogenesis and symptom development, plant pathogens are affecting these physiological parameters. Earlier studies successfully used VIs to discriminate between healthy and diseased plants. Derived from airborne hyperspectral imagery Carroll et al. (2008) have shown that a detection of European corn borer is possible. In literature the potential of leaf spectral reflectance changes and VIs for detecting leaf biotic stress of apple plants (Delalieux et al., 2009) or virus infected grapevines (Naidu et al., 2009) was investigated. Changes in reflectance of sugar beet plants caused by diseases are strongly correlated to the stage of pathogenesis and diseases severity (Steddom et al., 2005; Mahlein et al., 2009). All these researchers could deduce changes in plant health using VIs, but the detection of a specific disease using VIs was not feasible so far. As we know, this work has been the first study in literature using combinations of VIs to predict plant diseases in a very early stage. A combination of spec-

Table 5
Comparison of the results of the dichotomous classification based on spectral vegetation indices or principal components.

Leaf disease	Classification error [%]		
	Accuracy	Specificity (healthy leaves)	Sensitivity (diseased leaves)
SVMs (VIs)			
Cercospora leaf spot	2.88	1.35	4.55
Sugar beet rust	3.73	3.21	4.32
Powdery mildew	6.92	5.29	8.71
SVMs (PCs)			
Cercospora leaf spot	3.47	0.62	6.58
Sugar beet rust	9.34	1.90	17.96
Powdery mildew	14.26	4.51	24.95

tral vegetation indices, based on different wavelengths, describing different physiological parameters enhances the information content for an automatic classification and improves the classification accuracy.

By using combined VIs both, the feature combination and the number of features proves to be dependent on the specific plant diseases (Rumpf et al., 2009). For detection of Cercospora leaf spot only two VIs are necessary whereas three and more are needed to detect leaf rust or powdery mildew. Concerning an early detection of plant diseases before visible symptoms appeared the best classification accuracy is achieved by using the information of all nine VIs (Rumpf et al., 2009).

This study proved the feasibility of early detection of sugar beet leaves respectively inoculated with different pathogens by using SVMs. Inoculated leaves were already identified 3 days after inoculation. Even before characteristic symptoms are visible, several putative modifications in cellular leaf structure, for example changes in water content at infection sites, initiating cell death caused by fungal toxins or resistance reactions of plant tissue occur (Daub and Ehrenshaft, 2000; Jones and Dangl, 2006; Knogge, 1996). These modifications are associated with changes in spectral reflectance characteristics (Jacquemoud and Ustin, 2001). Comparative observations of the pathogenesis of the three foliar sugar beet pathogens suggested that the influence on spectral signatures depends on the intensity of physiological changes and on the extent of the symptoms (Mahlein et al., 2010), because physiological interactions between a fungal pathogen and a host plant vary depending on the pathogen (Glazebrook, 2005). Further investigations are necessary to describe these interactions for each pathogen in detail. The classification accuracy differs also between the pathogens. Difficulties emerge especially at early development stages of the characteristic symptoms. Slight variations can be accounted for the original source of the reflectance data. The reflectance curve, measured with a non-imaging sensor, is always the mean of the reflectance of healthy and diseased plant tissue. This results in a number of problems that are typical for such single point measurements (Scholten et al., 2005). Due to the very small size of sugar beet rust colonies (0.5–1.5 mm), a precise classification at early stages or in the case that only few pustules occur is very complex. Also a distinctive detection of powdery mildew at early stages is challenging. First powdery mildew symptoms are fluffy white mycelia covering the leaf surface. This fungal tissue on the leaf surface shifts the spectral signature like a dusty coat. It could be anticipated that imaging hyperspectral sensors can improve a hyperspectral disease detection through a better understanding of the pathogen host interactions (Chaerle and van der Straeten, 2001). With imaging sensor systems a pixel wise attribution of disease specific symptoms and tissue could be facilitated (Steiner et al., 2008).

In this study, our results showed that the SVMs method based on VIs has successfully been applied to identify leaves inoculated with *Cercospora beticola*, *Uromyces betae* or *Erysiphe betae*. One aim of our work has been to prove a simple disease detection technique which can easily be modified for online application in the field. Based on this results specific sensors for practical use may be developed in future. These sensors have to be robust, economically priced and user-friendly. By using the SVMs method based on VIs related to physiological parameters of plants, this procedure is even applicable to other plant–pathogen systems. In order to improve the early identification and discrimination of plant diseases on sugar beet leaves, machine learning techniques will be applied on the original hyperspectral data. In this context the focus will be the definition of optimal scanning positions in the whole reflection spectrum, and the development of specific indices for the detection of leaves that are inoculated with one of the three foliar sugar beet diseases.

Acknowledgement

This study has been conducted within the Research Training Group 722 'Information Techniques for Precision Crop Protection', funded by the German Research Foundation (DFG).

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