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**Title:**

**Weed Classification by Active Shape Models**

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**Summary:**

The objective is to present a new method for classification of weed species by image processing based on active shape models. Young weed seedlings with up to four leaves and without mutual overlapping with other leaves are to be identified. A database containing image examples of more than 20 of the most important weed species in Danish agricultural fields has been established. The images have been used as training data for the construction of an active shape model for each species. On the basis of these models, an algorithm for identification of weed species in digital images has been developed. Preliminary results have shown that the performance rate (rate of correctly identified weed seedlings) of the algorithm is about 80% or more.

## 1. Introduction

It has been widely accepted that the use of herbicides within agriculture must be reduced in order to protect the environment and the resources of drinking water. One way to obtain such a reduction is to perform precision application of herbicides in the field, which means using the right mixtures and dose rates of herbicides at the right time and place, according to the distribution and growth stages of occurring weed species. The spraying technology and decision support systems for precision application of herbicides exist, and potentials for herbicide savings between 30 and 75% have been demonstrated (Heisel *et al.*, 1999). However, precision spraying presupposes that the distribution of different weed species has been mapped by counting of plants; a job which, until now, has mainly been done by way of time-consuming manual surveying. Though, some methods and systems for automatic identification and mapping of weed species by machine vision have been proposed (*e.g.* Manh *et al.*, 2001; Sökefeld *et al.*, 2000).

## 2. Objectives

The objective is to present a new method for classification of weed species by image processing based on active shape models. Young weed seedlings with up to four leaves and without mutual overlapping with other leaves are considered.

## 3. Method of approach

The project is a part of the large Danish project, *Autonomous Platform and Information system for registration of crops and weeds (API)*, see <http://www.cs.auc.dk/~api/>). The overall objective of the project is to develop and construct a small autonomous robotic vehicle for collection of information about weeds and crops in the field. The first job for the robot will be to acquire and process image information that can provide the basis for reliable weed maps. The images will be acquired in a grid pattern (*e.g.* a  $10 \times 10$  m grid), and by the use of geostatistical methods, weed maps for the weed species of interest will be produced.

The weed species were recognised by their shapes by use of active shape models (ASM) (Cootes *et al.*, 1994). The first step of this approach was to develop an ASM for each weed species from a set of representative training images. The next step was to develop software that could classify new unknown weed seedlings by comparing them with the weed models.

### 3.1. Image database

The training images for shape modelling were acquired in the field. Colour image scenes representing more than 20 of the most important weed species in Danish agricultural fields were collected in an image database (more than 20 examples of each species at early growth stages). Each image scene covers approx.  $150 \times 200$  mm with a resolution of about 10 pixels per mm. The images were taken vertically from above with a Canon Powershot G1 Digital Camera ( $2048 \times 1536$  pixels). To ensure diffuse illumination and a fixed camera height above the ground, the camera was mounted on top of a transparent plastic cylinder ( $\varnothing$  250 mm) covered with cloth.

From each image scene, one or more sub-images containing one weed seedling each were "cut out". As the ASM method requires grey-scale images (not colour images), the sub-images were subsequently converted to grey-scale images by the operation  $2 \times \text{green-red-blue}$  for each pixel (plus some appropriate scaling). This operation has

proven to greatly enhance the green vegetation in contrast to the background (Woebbecke *et al.*, 1995). The grey-scale sub-images and the associated species names were stored in a database and used as training images for the model building process.

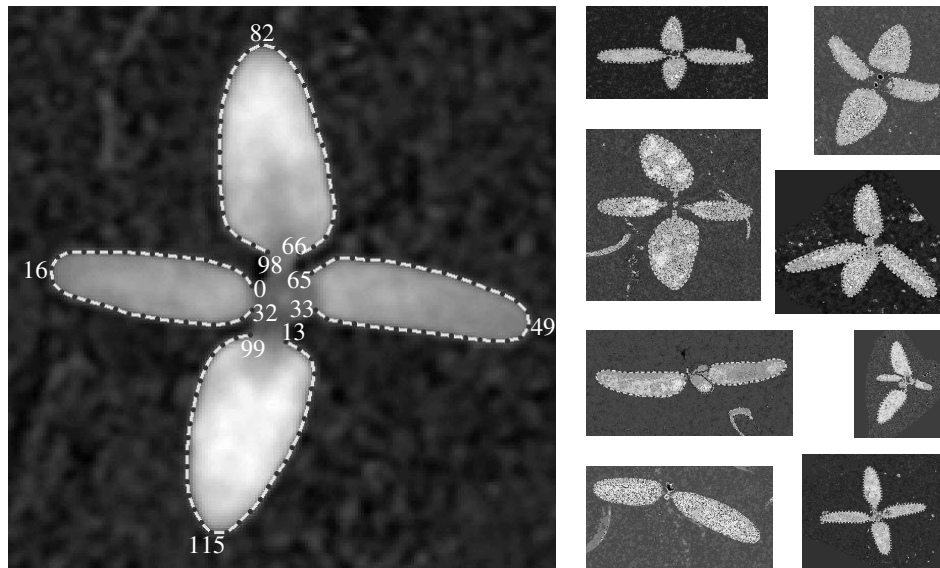
### 3.2. Modelling shapes of weed seedlings

The ASM techniques were originally applied to image problems in the medical domain, *e.g.* for modelling and measuring *vertebrae* in the spine for *osteoporosis* diagnosis. However, ASM represents a general modelling technique that is applicable to all kinds of shapes exhibiting a certain degree of stochastic variation (Cootes *et al.*, 1994). An ASM consists of a flexible shape template, describing how the object shapes can vary.

In this project, the modelling and identification of weed seedlings was done by means of Matlab<sup>®</sup> 6 (Release 12; MathWorks, 2000) together with the Active Shape Model Toolkit (Visual Automation Ltd., 1998). The ASM Toolkit provides a library of basic Matlab functions for modelling and recognition of structures and shapes in digital images.

To build an ASM, the shape of each of the training objects must be represented by a set of points. For the weed seedlings, the points were placed on the boundaries of the leaves (an open contour for each leaf). In each training image, 132 points were placed on the leaf boundaries (Fig. 1).

The points were labelled with numbers from 0 to 131. The placement and labelling of points were important, as each point was to represent the same part of the seedling from one training example to another. For example, one of the cotyledons should always be represented by points numbered 0-32, with three of the points placed at key positions: points zero and 32 placed at the beginning of the leaf near the stem, and point 16 at the tip of the leaf. Several species had some characteristic incisions at the true leaves, which could also be used as identifiable key positions. The points between the key positions were spaced evenly along the leaf boundaries.



**Figure 1.** Placement of labelled points on the leaf boundaries of some examples of white goosefoot (*Chenopodium album*).

The co-ordinates of the points were stored and analysed statistically, species by species, to extract characteristic shape variations of seedlings within the same species. Before the real analysis of shape variations could take place, it was necessary to align the set of training shapes. The alignment was achieved by scaling, rotating and translating the training shapes so that they corresponded as closely as possible with each other. The alignment was performed in a way that minimised the sum of squared distances between equivalent points on different training shapes.

The analysis of the variation in shape across the  $N$  aligned training shapes from a given species was based on a principal component analysis, as described by Cootes *et al.*, (1994). Each of the aligned training shapes gave rise to a vector describing the  $n$  boundary points:

$$\mathbf{x}_i = (x_{i,0}, y_{i,0}, x_{i,1}, y_{i,1}, \dots, x_{i,n-1}, y_{i,n-1})^T, \quad i = 1, \dots, N$$

where  $(x_{i,j}, y_{i,j})$  is the  $j^{\text{th}}$  point of the  $i^{\text{th}}$  shape. The mean shape,  $\bar{\mathbf{x}}$ , is calculated as

$$\bar{\mathbf{x}} = \frac{1}{N} \sum_{i=1}^N \mathbf{x}_i$$

The modes of variations, *i.e.* the ways in which the points of the shape tend to move together, can be found by applying a principal component analysis to the deviations,  $\Delta \mathbf{x}_i = \mathbf{x}_i - \bar{\mathbf{x}}$  ( $i = 1, \dots, N$ ), from the mean. From these deviations, the  $2n$  by  $2n$  covariance matrix can be calculated:

$$\mathbf{S} = \frac{1}{N} \sum_{i=1}^N \Delta \mathbf{x}_i \Delta \mathbf{x}_i^T$$

The modes of variation of the point of the shape can be described by the  $2n$  unit eigenvectors,  $\mathbf{p}_1, \dots, \mathbf{p}_{2n}$ , of  $\mathbf{S}$ . The eigenvectors are defined by

$$\mathbf{S} \mathbf{p}_k = \lambda_k \mathbf{p}_k \quad \text{and} \quad \mathbf{p}_k^T \mathbf{p}_k = 1 \quad (k = 1, \dots, 2n)$$

where  $\lambda_1, \dots, \lambda_{2n}$  are the corresponding  $2n$  eigenvalues of  $\mathbf{S}$  ( $\lambda_1 \geq \lambda_2 \geq \dots \geq \lambda_{2n}$ ).

The  $k^{\text{th}}$  principal component corresponding to the vector  $\mathbf{x}_i$  is defined as a weighted sum of the elements of this vector:

$$b_{i,k} = \mathbf{p}_k^T (\mathbf{x}_i - \bar{\mathbf{x}}), \quad i = 1, \dots, N, \quad k = 1, \dots, 2n$$

The principal components represent a linear independent decomposition of the variation of the training shapes. The first principal component, which is associated with the largest eigenvalue,  $\lambda_1$ , describes the largest part of the shape variation (the first mode of variation). In fact, the proportion of the total shape variance described by the  $k^{\text{th}}$  principal component is equal to the  $\lambda_k$ . Most of the variation can usually be represented by a small number of principal components, say  $t$  ( $t < 2n$ ). The value of  $t$  can, for instance, be chosen in such a way that the first  $t$  principal components explain a sufficiently large proportion (*e.g.* 99%) of the total variance,  $\lambda_T = \sum_k \lambda_k$ , of the shapes.

Any shape in the aligned training set can be approximated as a sum of the mean shape and a weighted sum of the first  $t$  eigenvectors:

$$\mathbf{x}_i \cong \bar{\mathbf{x}} + \mathbf{P}\mathbf{b}_i, \quad i = 1, \dots, N \quad (1)$$

where  $\mathbf{P} = (\mathbf{p}_1 \mathbf{p}_2 \dots \mathbf{p}_t)$  is a matrix of the first  $t$  eigenvectors, and  $\mathbf{b}_i = (b_{i,1} b_{i,2} \dots b_{i,t})^T$  is a vector of weights (principal components), which is calculated as

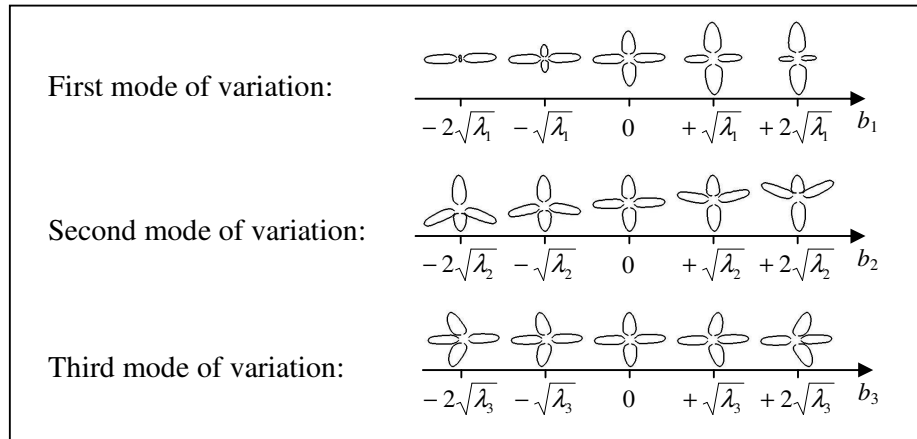
$$\mathbf{b}_i = \mathbf{P}^T (\mathbf{x}_i - \bar{\mathbf{x}}), \quad i = 1, \dots, N$$

Eqn. (1) permits generation of a new shape example by replacing  $\mathbf{b}_i$  by a new vector of weight values,  $\mathbf{b} = (b_1 b_2 \dots b_t)^T$ . Provided that the weights are not too far from zero, the new synthetic example will be similar to those in the training set, as the change in shape will be determined by the modes of variation represented by the training shapes. Suitable limits for the weight vector,  $\mathbf{b}$ , are derived by examining the distributions of the weight values to generate the training set. If Gaussian distributions are assumed, the set of weights can be chosen, so that the Mahalanobis distance,  $D_m^2$ , from the mean shape is less than a suitable value,  $D_{\max}^2$ :

$$D_m^2 = \sum_{h=1}^t \left( \frac{b_h^2}{\lambda_h} \right) \leq D_{\max}^2$$

Figure 2 illustrates the three first modes of variation for white goosefoot (*Chenopodium album*), as found by analysing examples like those given in Figure 1. The variation around the mean model shape is shown by varying  $b_1$ ,  $b_2$  and  $b_3$  one by one ( $D_{\max} = 2$ ) while keeping the other  $b$ -weights at zero.

The first and most dominating mode corresponds to varying growth stages and accounts for 59% of the total shape variance in the training set. The second and third modes account for 17 and 10% of the total shape variance, respectively, and correspond to V-positions of the cotyledons and the two first true leaves, respectively.



**Figure 2.** Illustration of the first three modes of variation for white goosefoot (*Chenopodium album*).

### 3.3. Modelling grey-level appearance

The active shape model of a given weed species should be used for locating new examples of this species. For this purpose, not only the shape, but also the typical grey-level appearance near the edges of the leaves are important. This is accounted for by examining the grey levels in the region around each of the labelled model points. Since a given point represents a particular part of the seedling, the grey-level pattern about that point in images of different examples will often be similar.

For each point, a one-dimensional grey-level profile normal to the model curve (contour) passing through this point is considered. The profiles are characterised by their mean and by their variation to give a statistical description of the expected profiles about each point. The detailed calculation procedure has been presented by Cootes *et al.*, (1994).

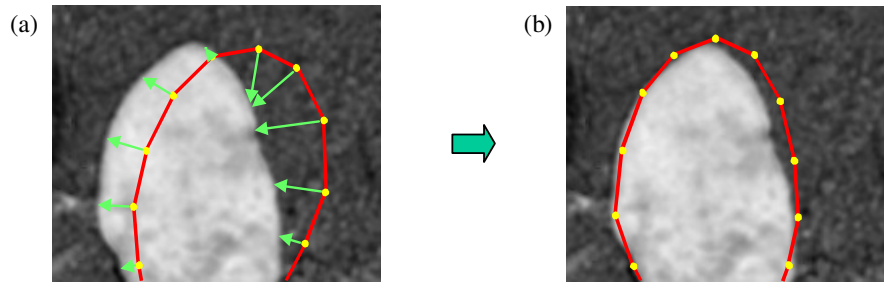
### 3.4. Seedling recognition in image scenes

On the basis of results from the ASM analysis, an algorithm for locating and identifying weed seedlings in image scenes was developed. In the first step of this algorithm, the image scene is searched for green objects, which are potential weed seedlings. Only objects having similar size as weed seedlings are selected for further processing.

In the second step, each of the selected objects is investigated to determine the weed species. This step involves an iterative search procedure in which each species model is refined gradually until the best fit to the object boundaries is obtained. Before the iterative procedure is started, a preliminary model alignment with respect to pose (position and orientation) and scale takes place. After that, the shape refining iterations are carried out by repeating the following three steps (see Fig. 3):

1. Compare the region of the image around each model point with the grey-level models to calculate the displacement of the point required to move it to a better location.
2. From these displacements calculate the optimal adjustments to the translation, rotation and scale and to the shape parameters (**b**-weights as defined above).
3. Update the model parameters and the point positions correspondingly (under the restrictions imposed on the shape by the  $t$  possible modes of variation in the model).

These three steps are repeated until the changes of the parameters between two successive iterations are sufficiently small. The result from fitting four different models to a white goosefoot seedling (*Chenopodium album*) appears from Fig. 4.



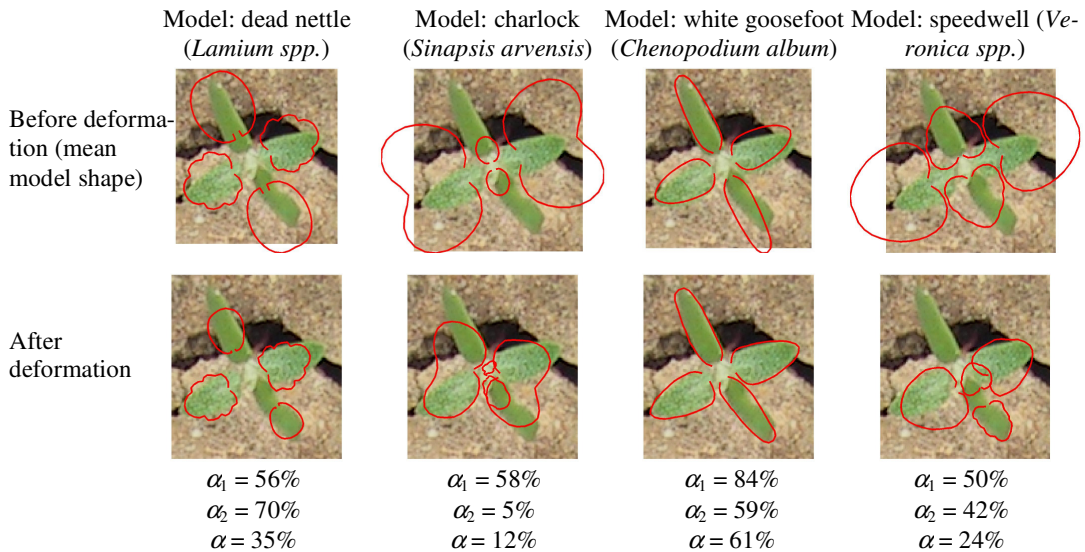
**Figure 3.** Illustration of a single iteration of the object search procedure used for active shape models (before (a) and after (b) moving the points). The green arrows indicate the desired displacements of the model points.

Since there are only  $t$  ( $< 2n$ ) modes of variation available in the model, while the required displacements of the points represents  $2n$  degrees of freedom, the final model can only be an approximation to the object shape.

When a model search has been carried out for all weed species searched for, only one step remains, namely the classification step. In this step each object is classified according to the species model that gives the best fit to the object boundary. The assessment of the degree of fit for a given species model is based on a combined criterion that takes two aspects (sub-criteria) into account:

- How well the deformed model shape resembles the object shape, and
- How much the model needs to be deformed to achieve the best fit.

A model which fits the object very well and only requires a moderate deformation of the mean model shape will result in a high fit score. The resemblance between the model and the object (sub-criterion a.) can be measured as the ratio,  $\alpha_1$  ( $0 \leq \alpha_1 \leq 1$ ), of pixels covered both by the model *and* the object (intersection of sets) to the number of pixels covered by the model *and/or* the object (union of sets). The model coverage is defined as pixels within the four polygons made up by the leaf contours. The ratio will tend to one in case of close resemblance. To measure how close the deformed model is to the mean model shape (sub-criterion b.), one can use Hotelling's  $T^2$  test for two samples (Anderson, 1958) to test the hypothesis that the set of shape parameters is an outcome of the multivariate Gaussian distribution of shape parameters in the training set. The test will result in a significance level,  $\alpha_2$  ( $0 \leq \alpha_2 \leq 1$ ), and high values will indicate low degree of deformation. A combined criterion can be calculated as  $\alpha = \alpha_1^\phi \alpha_2^\theta$  ( $0 \leq \alpha \leq 1$ ,  $\phi > 0$ ,  $\theta > 0$ ). Preliminary investigations have indicated that the resemblance sub-criterion is more important than the deformation sub-criterion. In most cases  $\phi = 1.52$  together with  $\theta = 0.44$  seem to result in  $\alpha > 0.5$  if the model corresponds to the same weed species as the object (Fig. 4). The object is therefore classified according to the model that



**Figure 4.** Result from fitting four different models to a white goosefoot seedling (*Chenopodium album*).

results in the highest  $\alpha$ -value. However, if the  $\alpha$ -values for all of the models are less than 0.5, the object cannot be identified as one of the species represented by the models.

#### 4. Results and discussion

Until now, models for 12 weed species have been generated, and the weed identification procedure has been tested preliminarily for six weed species. However, the number of tests performed will not be sufficient to put forward accurate statements about the performance rate of the identification procedure (likelihood that a given weed seedling will be correctly identified), although preliminary results indicate that the rate of correctly identified weed seedlings is around 80% or more.

In comparison with other deformable models, *e.g.* snakes (Manh, 2001), one of the advantages of the ASM technique is that the models do not only take leaf shapes into account, but also the overall geometry of the seedlings. This aspect makes it easier to discriminate between species.

The model parameters associated with the ASM of a given weed species are sufficient for reconstruction of the shapes of real weed seedlings. Each parameter corresponds to a mode of shape or pose variation with an intuitively understandable interpretation, which may help assessing whether the model is sufficient to model the natural variation.

The algorithm for identification of weeds has not yet been designed and optimised for real-time use. Therefore, the speed of the process is still rather low (several seconds to identify a weed seedling when using a common Windows PC of today). However, the ASM Toolkit, which was used for this study is probably not the most speed efficient implementation of the ASM approach, one of the reasons being that the toolkit runs under Matlab. An alternative and probably faster C++ implementation of ASM and AAM (Active Appearance Models) has been developed at the Technical University of Denmark (see <http://www.imm.dtu.dk/~aam/>).

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