

Plant Species Recognition Method Based on Wavelet Transform

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ABSTRACT

A new plant species recognition method is presented based on Wavelet Transform (WT) and Genetic Algorithm (GA). In the method, the feature vector of plant species is extracted by multi-distinguish analysis of WT and GA, and plant species is recognized by Support Vector Machines (SVM). This method is different from the traditional method of correlation matching recognition plant species. First, the stored space reduces greatly because recognition model is used to replace the store of plant species leaf image template. Thus this method reduces stored memory greatly. Second real-time is ensured in the process of plant species recognition by using SVM. The experiments on a public leaf image database are performed and the experiment results show the feasibility and effectiveness of the proposed method.

Keywords - Genetic Algorithm (GA); Wavelet Transform (WT); Plant leaf image; Plant species Recognition

I. INTRODUCTION

The plant species classification and identification is a basic research for the botanical research and agricultural production. It is also very significant for the classification of plant species groups, study of the

genetic relationships among plants and clarification of the law of plant system's evolution [1-2]. The early study about the classification and identification of plant species mainly used the morphology, but this way had a lot of defects because of the following reasons, work capacity, low efficiency and the difficulty to guarantee the objectivity of the data [3]. Thus it affected the accuracy of the classification. So it is a reasonable method by using leaf image processing and pattern recognition techniques to make up the deficiency of plant species recognition ability. This point can be performed just through computers and other image acquiring facilities.

Leaf shape provides rich information for classification. Some typical terms of leaf shape are shown in Fig.1A. Different shape and texture have different botany descriptor. For example, the kind Hastate can be described as triangular with basal lobes and obcordate is hearted-shaped, stem at point. But, it is a challenging research, because plant leaves are quite irregular, and there is large intra-class difference between the same species leaf images, as shown in Fig.1B. It is difficult to accurately describe their shapes compared with the industrial work pieces, and some between-species leaves are different from each other [1-4].

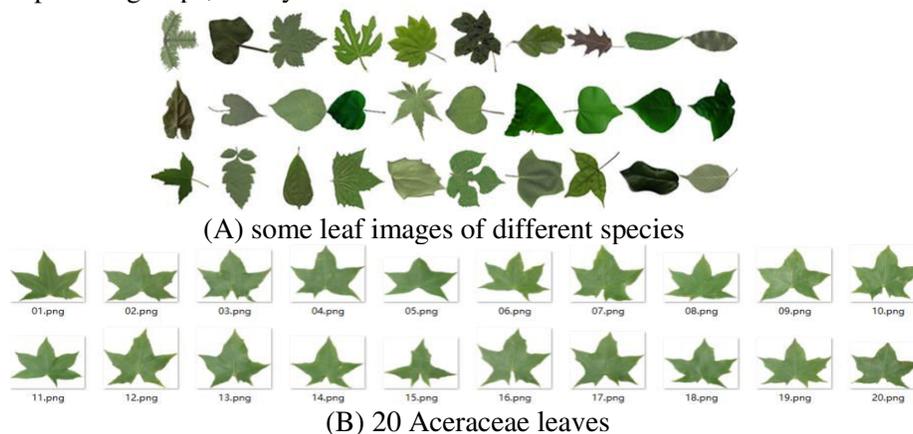


Fig.1 some plant leaf image samples

Many plant species recognition methods have been proposed recently [5-8]. Zhang et al. [9] proposed a modified orthogonal discriminant projection for leaf classification, and they proposed a semi-supervised locally discriminant projection for leaf classification and

recognition [10]. Wang et al. proposed a classification of plant leaf images with complicated background. Ahmad et al. [11] proposed a corn leaves classification by machine. Hong et al. [12] proposed several machine learning techniques for ontology-based leaf classification. Ye et al. [13] proposed a computerized plant species

recognition system. All above methods validated that the computer-aided plant classification methods are needed to extracted useful features to classify leaf automatically. Motivated by the recent progress and success of plant species recognition, a new method of plant species recognition is proposed based on WT and GA.

II. RELATED WORKS

A. Wavelet Transform (WT)

WT is applied to several fields including computer vision, image processing, and geophysics, plant species tracking and target recognition [14-15]. The wavelet coefficients of data $x(t)$ are inner products of the data with the $\psi_{j,k}(t)$'s,

$$c_{jk} = \int x(t)\psi_{j,k}^*(t)dt \quad (1)$$

where $\psi(t)$ is wavelet 'basic functions' $\psi_{j,k}(t)$ is

$$\psi_{j,k}(t) = 2^{-\frac{j}{2}}\psi(2^{-j}t - k) \quad (2)$$

The WT decomposes a data into a set of bases for time–frequency analysis. This decomposition creates an opportunity for implementing distributed data mining where features are extracted from different wavelet coefficients and served as feature vectors for applications. Using Mallat algorithm to complete the wavelet transform of data on J level and get wavelet coefficients. Some statistical characteristics from wavelet coefficients are calculated as follow

Average:

$$AVG_j = \frac{1}{2^j} \sum_k c_{jk} \quad (3)$$

Absolute average:

$$AVG_j = \frac{1}{2^j} \sum_k |c_{jk}| \quad (4)$$

Wavelet coefficient sum of squares:

$$E_j = \frac{1}{2^j} \sum_k c_{jk}^2 \quad (5)$$

Willison range:

$$WAMP_j = \sum_k \text{sgn}(|c_{jk} - c_{jk+1}|) \quad (6)$$

Number of past zeros:

$$ZC_j = \sum_k \text{sgn}((c_{jk} - \mathcal{G}_j)(c_{jk+1} - \mathcal{G}_j)) \quad (7)$$

Divide width average frequency:

$$F_j = \frac{\sum_k F_{jk} P_{jk}}{\sum_k F_{jk}} \quad (8)$$

where j is level, c_{jk} is j -level wavelet coefficients, \mathcal{G}_j is threshold, F_{jk} and is frequency for power spectrum.

The effective features subset of target can be extracted,

$$F = \{AVG_1, AVG_{2,L}, AVG_J, AV_1, AV_{2,L}, AV_J, E_1, E_{2,L}, E_J, WAMP_1, WAMP_{2,L}, WAMP_J, ZC_1, ZC_{2,L}, ZC_J, F_1, F_{2,L}, F_J\} \quad (9)$$

B. Wavelet Genetic Algorithm (GA)

GA is a method for solving both constrained and unconstrained optimization problems based on a natural selection process that mimics biological evolution [16]. GA is an optimization procedure that operates in binary search spaces (the search space consists of binary strings). A point in the search space is represented by a finite sequence of 0s and 1s, called a chromosome. The algorithm repeatedly modifies a population of individual solutions. A population of candidate solutions is maintained at iteration of the evolution. Each chromosome consists of linearly arranged genes which are represented by binary strings. Three basic operations, namely, reproduction, crossover, and mutation, are adopted in the evolution to generate new offspring [17]. Those chromosomes which have higher fitness values are given more chances to 'reproduce' by the processes of crossover and mutation. The function of crossover is to mate two parental chromosomes to produce a pair of offspring chromosomes. In particular, if a chromosome is represented by a binary string, crossover can be implemented by randomly choosing a point, called the crossover point, at which two chromosomes exchange their parts to create two new chromosomes. Mutation randomly perturbs the bits of a single parent to create a child [18]. This procedure can increase the diversity of the population. Mutations can be performed by flipping randomly one or more bits in chromosomes. At each step, GA randomly selects individuals from the current population and uses them as parents to produce the children for the next generation. Over successive generations, the population "evolves" toward an optimal solution.

When solving a problem by GA, first a proper representation and fitness measure must be designed. Fitness value defines the relative strength of a chromosome to the others, and the optimality of the solution to the problem [18]. It is evaluated by the chromosome structure and a positive value is resulted. A large fitness value means the chromosome is strong. The measurement will consider the criterion of total cost of the system, fulfillment lead time, and the equality of utilization ratio. Devising the termination criterion should be the next step [19]. The termination criterion usually allows at most some predefined number of

iterations and verifies whether an acceptable solution has been found.

C. Support Vector Machine

A Support Vector Machine (SVM) is a supervised learning model [2] and multi-classification SVM operational details are in [35]. The proposed FZM classification model uses multi-SVM along with Radial Basis kernel function (RBF). There is no direct implementation for multi-classification but the classifiers performs one versus all based technique to eventually separate all the data classes. Thus 4 SVM models are created, one for each class and probability scores are used for prediction.

III. PLANT SPECIES RECOGNITION

$6 \times J$ recognition features as described earlier are extracted by Eqs.(3)-(8) from each leaf image. There are $26 \times J$ possible combinations of these features. The features are selected and reduced by GA. SVM classifier is applied to plant species recognition. An adaptive GA is implemented to automatically adapt the parameters such as crossover rate and mutation rate based on the performance of GA. In implementing GA [17], if the fitness value of the best individual is not improved for three or five generations in a row, GA will automatically raise the mutation rate to increase the diversity of the population. Also, elitism mechanism is adopted in the case of the best individual (set of features selected) is copied from generation to generation when performing reproduction [18].

The steps of plant species recognition method are shown as follows,

Step1: Extract the $6 \times J$ recognition features by Eqs.(3)-(8) from leaf image, and sort as in Eq.(9).

Step2: Initialize a population of chromosomes (solutions) in $6 \times J$ 0s~ $6 \times J$ 1s. Each feature is represented as a bit in the GA, where 0 express the corresponding feature is not selected, while 1 the corresponding feature is selected.

Step3: Evaluate each chromosome value in the population. The plant species recognition rate is regarded as the fitness function.

Step4: Create new chromosomes by mating current chromosomes and apply mutation and recombination when the parent chromosomes mate.

Step5: Delete members of the population to make room for the new chromosomes.

Step6: Evaluate the new chromosomes, and insert them into the population.

Step7: If a stopping criterion is satisfied, then stop and output the best chromosome (solution); otherwise, go to Step 4.

Step8: Plant species is recognized by the extracted features through SVM.

IV. EXPERIMENTAL RESULT and ANALYSIS

The Swedish leaf dataset which contains isolated leaf from 15 different Swedish tree species, with 75 leaves per species [21]. Note that the original Swedish leaf images contain footstalks, which are not suitable characteristics for robust leaf shape recognition, since the length and orientation of those footstalks may heavily depend on the collection process [10]. Though this petiole might provide some discriminate information between different classes, we could regard them as some kind of noises and cut them off to construct another dataset, named Swedish leaf dataset processed. Fig.3B shows some representative examples and Fig.3A contains the same images which are not processed. We test those algorithms on this new dataset and the results reveal something important. We compare the proposed method with two methods: Recognizing plant species by leaf shapes (LF)[22], HOG-Based Approach for Leaf Classification (HOG) [23].



(A) Original leaf images



(B) Segmented leaf images

Fig.3. Leaf images from the Swedish leaf data set, one image per species. (a) The original Swedish leaf dataset. (b) Swedish leaf dataset processed, the leaf petiole on images are erased.

Resize: The leaf images are all of different sizes having different number of pixels. So, in order to get accurate results, image resizing has an important role. All the collected images are resized to 64×64 pixels which make them square in shape and of same size. Moreover, the computation process is also fast as the size is decreased.

Conversion: Conversion of images from RGB scale to gray scale is also necessary as it increases speed of processing, decreases code complexity and gray images can be easily visualized.

Normalization: The images of plant leaves are captured in different sizes and from different distances. The size may change because of illumination variations. Such changes in the images will influence the plant disease recognition results. So, it is necessary to compensate for such changes or deformations for achieving more accurate results.

In the experiments, GA-based feature selection framework, the nearest neighbor classifier is adopted to classify the training plant species data and the resulting error rate is used as the feedback into the feature selection algorithm [19]. The size of the population is 100, the initial crossover rate is 0.8 and the initial mutation rate is 0.01. If the fitness value of the best individual is not improved for three generations in a row, GA increases the mutation rate by 0.02. In order to reduce the training time, we set an error rate threshold 1. The GA stops when either the error rate of the best set of features selected is below the specified threshold 1 or the mutation rate is increased above 0.09.

First, we extract the WT features by WT. Then we select and reduce the dimension of features to 50 by GA, this dimension reduction process significantly improves the performance of each detector (by 5%-10% at accuracy rate). After feature extraction, SVM is used for the final classification. To quantify detector, performance accuracy rate is calculated each time, it is defined as follows:

$$Accu_rate = \frac{R_num}{T_num} \quad (10)$$

where R_num is the right sample number detected and T_num is the total sample number tested.

We randomly split the dataset into two parts which are used for training and the second part is kept for testing. For comparison, we choose 25 samples per species for training samples the same as [8] in Swedish dataset each time. In the ICL leaf dataset, we first choose 15 training samples per species and the second experiments 29 training samples. This procedure is repeated for 100 times [22]. The recognition accuracy per class is reported over all independent experiments, where the accuracy per class is the percentage of the successful recognitions of each class relative to the number of leaves from the corresponding class. The recognition rate is 99.35%. To show the effectiveness of the proposed method, the results of two comparing methods are also shown in Table 1.

Method	LF	HOG	Our
Recognition rate	91.32	93.25	94.31

From Table 1, it is found that the proposed method performs better.

V. CONCLUSION

In this work, an efficient algorithm for plant species recognition based on WT and GA was presented. The algorithm in our experiments can extract the 6×J useful classifying features in the plant species sequences by WT. The 6×J features are selected by GA. SVM classifier is adopted to recognize the plant species. Experimental results have demonstrated the effectiveness of the proposed algorithm on Swedish leaf dataset. Although we have obtain an encouraging results on the database, more research on a more realistic plant species database is still required before plant species recognition can be used for human identification in actual environment.

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