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Automatic leaf structure biometry: computer vision techniques and their applications in plant taxonomy

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AUTOMATIC LEAF STRUCTURE BIOMETRY: COMPUTER VISION TECHNIQUES AND THEIR APPLICATIONS IN PLANT TAXONOMY

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This paper proposes a new methodology to extract biometric features of plant leaf structures. Combining computer vision techniques and plant taxonomy protocols, these methods are capable of identifying plant species. The biometric measurements are concentrated in leaf internal forms, specifically in the veination system. The methodology was validated with real cases of plant taxonomy, and eleven species of passion fruit of the genus Passiflora were used. The features extracted from the leaves were applied to the neural network system to perform the classification of species. The results showed to be very accurate in correctly differentiating among species with 97% of success. The computer vision methods developed can be used to assist taxonomists to perform biometric measurements in plant leaf structures.

Keywords: Image analysis; biometry; plant taxonomy; morphometry; computer vision.

1. Introduction

In Botany, plant physiology and plant evolution, biometric methodology is used to extract and analyze the measurements of plant structures, thus supporting studies in plant biology phenomena.

Most of the current experiments carried out in plant biology still use traditional methods, in which biologists perform experiments based on manual and visual inspection. This approach, in addition to being a hard task for biologists, provides a limited vision of the problem. Adopting mathematical and computing techniques,

such as computer vision, image analysis, pattern recognition and artificial intelligence brings a new perspective to plant biology, making experimental procedures easier and more accurate, and also extracting a richer amount of information data, which can be studied more in depth.

This work presents a novel approach to perform biometric feature extractions in plant species. The methods were applied specifically to leaf venation system. To validate the developed methodology, techniques were used in real cases plant species biometry. Taking this into account, a set of 220 digital images of 11 plant species (20 samples per specie) were used.

This article is organized as follows: Sec. 2 describes the computer vision techniques developed to perform the leaf structure biometry. In Sec. 3, the experiments performed on real cases of leaf species are shown — the measurements extracted are used with an input of pattern recognition algorithms. Section 4 discusses the results obtained. Finally, Sec. 5 explains the conclusions concerning the developed techniques and their contributions.

2. Computer Techniques for Leaf Biometry

Nowadays, biometric features are essential in applications of pattern recognition, such as face and fingerprint identification, iris analysis, voice recognition, etc. In botany, biometric methods can be applied on two main leaf structures:

(1) Leaf outlines: A variety of information can be collected: width, height, center of mass, curvature, signatures, symmetry, complexity, among others.[2,12]
(2) Leaf veins: Measurements can be extracted such as: number of bifurcations, the angle in the ramifications, the length of the principal veins, etc.

This work is concentrated on developing computational methods for the second option. The information concerning the veins was defined by studies in plant species taxonomy protocols.[1,10,16] This was necessary to determine a set of features that were significant in terms of identifying species.

2.1. *Feature extraction in leaf vein structures*

The biometric features of leaf images were extracted by an *automatum* algorithm that navigates in the leaf venation system, which we called *Automatum Navigator*. Initially, the images were filtered to reduce noise (from digitalization) and the leaf venation system was segmented.

The complex task of leaf vein segmentation is carried out in four steps: (i) clarification (diafanization); (ii) filtering by anisotropic diffusion, (iii) adaptive thresholding, and (iv) thinning. In the first stage, the color pigmentation of the leaf is removed by chemical techniques. The second stage applies an anisotropic filter, proposed by Perona and Malik,[15] to ensure selective smoothing on the images of the leaves. The main characteristic of this filter is to reproduce smooth images

with strong outlines, as well as filter noises and discard details which are of little importance. The anisotropic filter was defined by an anisotropic diffusion (in the nonlinear scale-space), formulated in Eq. (1)[15]:

$$\begin{cases} \dfrac{\partial F_t(x,y)}{\partial t} = \nabla \cdot \left[g\left(\|\nabla F_t(x,y)\| \right) \nabla F_t(x,y) \right] \\ F_0(x,y) = f(x,y) \end{cases} \tag{1}$$

where $f(x,y)$ represents a two-dimensional image; $F_t(x,y)$ the scale-space of this image; $\|\nabla F_t(x,y)\|$ the gradient magnitude and g. The discrete representation of the analytic nonlinear anisotropic diffusion [Eq. (1)] is expressed as follows [Eq. (2)]:

$$I(s,t+1) = I(s,t) + \frac{\lambda}{|\eta_s|} \sum_{p \in \eta_s} g(|\nabla I_s, p(t)|) \nabla I_s, p(t). \tag{2}$$

The effective segmentation of the leaf veins (third stage) is achieved by the adaptive thresholding technique.[7,13] In this approach, the original image is divided into various subimages and then uses a different threshold to segment each subimage. The value of the threshold is based on approximating the subimage histogram using a weighted sum of probability densities with a normal distribution.[13] This adaptive technique was necessary because the results of the anisotropic filtering have high variations of grayscale intensity. Moreover, a singular threshold value (global) is ineffective in carrying out a satisfactory segmentation of the venation system. Figure 1 shows the necessary steps for the leaf venation system segmentation.

When the segmentation process is finished, a thinning algorithm was applied to the leaf image. Thinning is a process that reduces a shape into a simplified version, called a skeleton.[9,11] The skeleton form detains the essential features of the original shape. The thinning algorithm, applied to the leaf venation, decreases the noises of the segmentation process. Therefore, the leaf image is ready to perform the biometric measurement feature extraction.

2.2. *Automatum navigator algorithm*

The next stage determines (automatically) the starting point in the leaf venation system. For this, all the pixels of the image are scanned. This search can be made in two-ways: from top to bottom (from left to right) or from bottom to top (from right to left).[3] This method is similar to contour extraction (or following) algorithms.[6] The first pixel discovered is defined as the starting point.

Having the starting point determined, the algorithm is initiated. The main idea of the method is to visit all points (pixel) of the vein structure, collecting morphological information of the pixel. Considering a binary image, where the background pixels are 0 (zero) and the foreground pixels are 1 (one), and a structure of interest (leaf veins) has one pixel of width, each pixel of interest can be classified following their criteria: (i) bifurcation; (ii) extreme point and (iii) intermediary.

The bifurcation pixel determines the beginning of the new ramifications inside the leaf vein structure. In the vein structure, the bifurcations are responsible for the
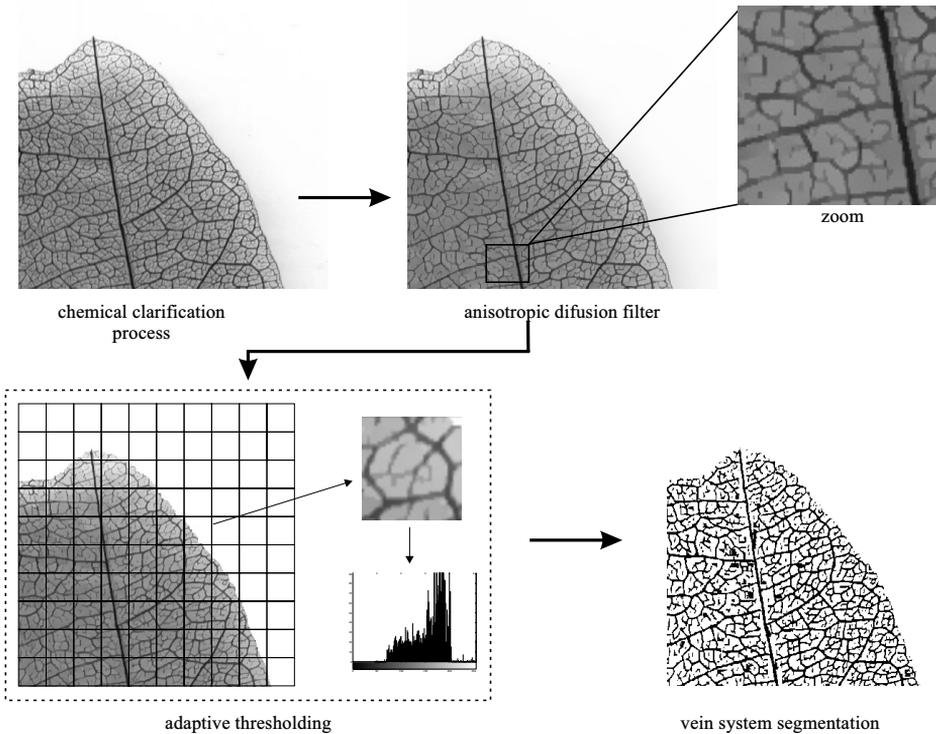
Fig. 1.   Leaf venation system segmentation by anisotropic diffusion and adaptive thresholding.

interconnection of the primary, secondary and tertiary venation systems. Figure 2 illustrates bifurcation pixels which are determined in the structure. Their definition is described as follows:

Definition 1. Let β be a binary image in which each pixel has up to eight adjacent neighbors. Pixel ρ is classified as a bifurcation when the number of transitions from 0 (zero) to 1 (one) is in the sequence: ρ_1, ρ_2, ρ_3, ρ_4, ρ_5, ρ_6, ρ_7, ρ_8 and ρ_1, is higher than 2. In other words, a pixel ρ is a bifurcation when $A(\rho) > 2$.

The extreme point concept can be understood as the last pixel of the structure ramification. In the leaf veins, they represent the end of a ramification. Figure 4 presents the extreme point of a structure and it can be defined as:

Definition 2. Let ρ be a foreground pixel, the neighbor number of ρ, denoted as $\mathbb{B}(\rho)$ are all adjacent pixels with values different from zero. If the neighbor number of ρ is equal to one, in other words $\mathbb{B}(\rho) = 1$, then ρ is classified as an extreme point (or terminal).

The intermediate pixel can easily be understood as all points that do not belong to class 1 (bifurcation) and class 2 (extreme points). Given the defined criteria, the
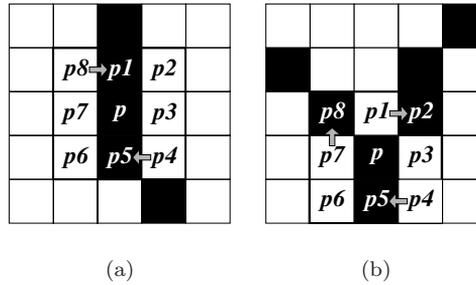
(a)   (b)

Fig. 2.   Determination of bifurcation pixels in structure: (a) pixel ρ is not a bifurcation $A(\rho) \leq 2$; (b) pixel ρ is a bifurcation $A(\rho) > 2$.

algorithm initiates an exploration process of the leaf vein structure. While the algorithm explores the leaf structure, it labels the visited pixels that do to not generate loops. The starting point for the method is the initial coordinate (x, y) determined by the sweeping process. Then, the algorithm explores the leaf vein structure as presented in Algorithm 1.

The algorithm is able to treat the special cases by the morphological situation found during navigation (line 6). These cases are identified by consulting the number

---

Algorithm 1. Leaf Vein Structure Exploration

```
1    void LeafExploration(){
2         while all the pixels of the structure were not visited{
3              signalize pixel p as visited
4              for all neighbors of current pixel
5                     if current pixel was not visited, add to stack
6              switch(special cases){
7                case 1: Stack elements = 1
8                  Move to next neighbor and sign it as visited
9                     if current pixel is an extreme point
10                       Add to extreme point vector
11               case 2: Stack elements > 1
12                 if current pixel is not a bifurcation
13                      Move to next neighbor and sign it as visited
14                    else
15                      Add to bifurcation vector
16
17                    for all elements in stack
18                      Recursive call: LeafExploration ()
19               case 3: Stack elements = 0
20                    All elements of the structure already visited
21              }
22         }
23    }
```

of stack elements. If pixel ρ_i is a neighbor of a current pixel and was still not visited, this pixel must be added to the stack.

When a number of stack elements is equal to 1 (one), it means that the current pixel has only one single neighbor (line 7). In this case, the current pixel is moved to its only neighbor, and marked as visited. However, the new current pixel can be classified as an extreme point, if it is true and the pixel is stored in an extreme point vector.

Another situation that can occur is special case 2, where the number of stack elements is greater than 1 (one) (line 11). In this case, the current pixel has more than one single neighbor. Thus, if the current pixel is not a bifurcation $A(\rho) \leq 2$, the algorithm must determine between two, or more pixels, which the next current pixel is. Nevertheless, if the current pixel is a bifurcation $A(\rho) > 2$, the algorithm inserts this pixel into a bifurcation vector. Moreover, for all elements of the stack, that are neighbors of the current pixel, a new instance (recursive) of the algorithm is initiated. This call makes the algorithm explore all the ramifications of the structure.

Finally, the last special case occurs when the stack is empty (line 19). This means that all pixels of the structure (leaf vein) have already been visited. This is the stop criteria of the algorithm.

2.3. *Biometric features extraction*

The computer algorithm is able to collect several measurements of the venation structure, and biometric information can be extracted. Using this computational method, three groups of features are extracted from the structure: (i) distances; (ii) length; and (iii) angles.

In the first category, the distance biometric features are based on distances between determined points of the vein structure. Taking this into account, the vectors of the bifurcations and extreme points, collected during the exploration of the structure, are used. In this case, the following features can be extracted: number of bifurcations; average distance among all bifurcations; standard deviation of distance among all bifurcations; variance of distance among bifurcations; greater distance among bifurcations; average distance/standard deviation/variance between all bifurcations and the origin point (petiole), etc. Figure 3 illustrates the result of the algorithm in the determination process of bifurcations and extreme points of the leaf vein structure.

The second category is responsible for collecting measurements related to the length. In this case, information concerning the path covered by the leaf exploration algorithm was used. Some measures that can be extracted are: the leaf venation system area (in pixels); number of ramifications; average length of ramifications; standard deviation of length of the ramifications; length of primary vein, etc. Important information produced in the second category is the primary ramification path (or the primary vein). The primary vein is a ramification from the base (petiole) to the top of the leaf. This structure is essential for the species taxonomy.[16]
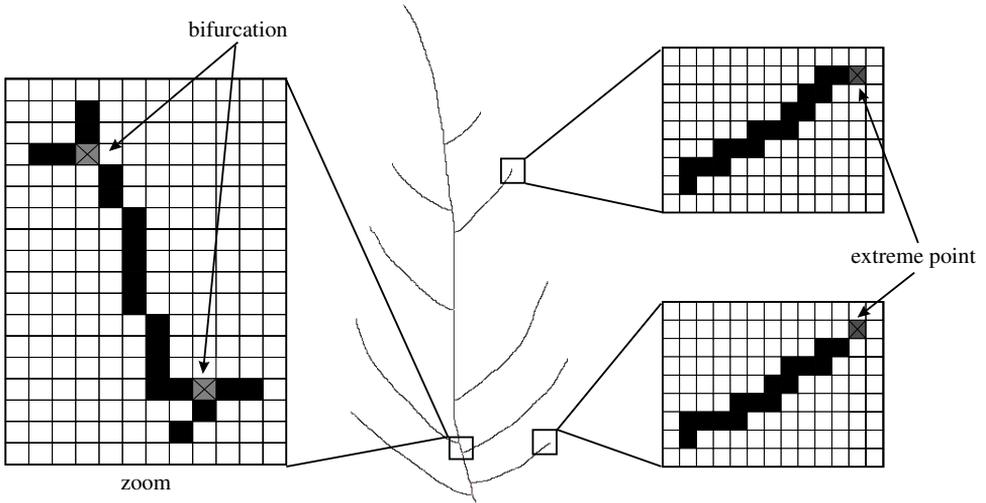
Fig. 3. Result of leaf structure feature extraction algorithm: determination of bifurcations and extreme points in the leaf vein structure.
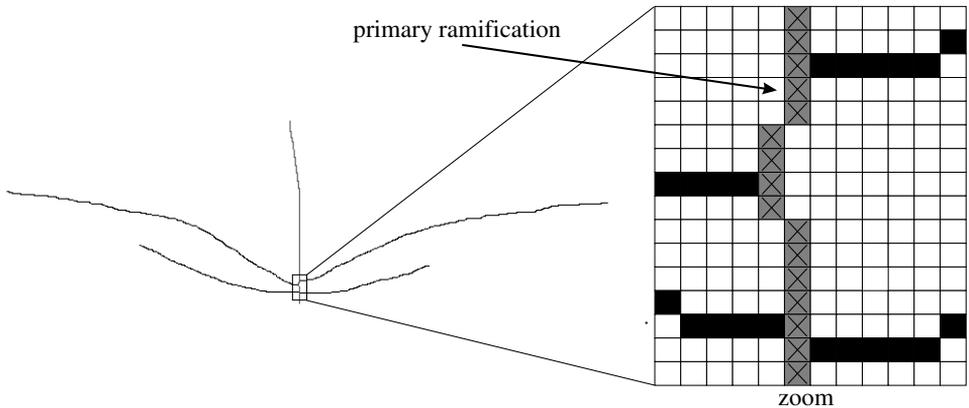

Fig. 4. Primary ramification extracted by the leaf exploration algorithm.

Figure 4 presents the result of the algorithm to determine the primary ramification of the leaf vein system.

In the third group of measurements the angles formed between the ramifications (of the veins) are extracted. These data can be collected for all ramifications (global analysis) or from a specific ramification (local analysis).

The extraction of angles is performed as follows: (i) define the root ramification pixel $P1$ ($A(P1) > 2$); (ii) create the list of neighbors of $P1$; (iii) for each neighbor ten pixels are navigated away from $P1$ and determines pixels $P2$ and $P3$. Vector **u** is defined by pixels $P1$ and $P2$, and vector **v** is formed by pixels $P1$ and $P3$. If
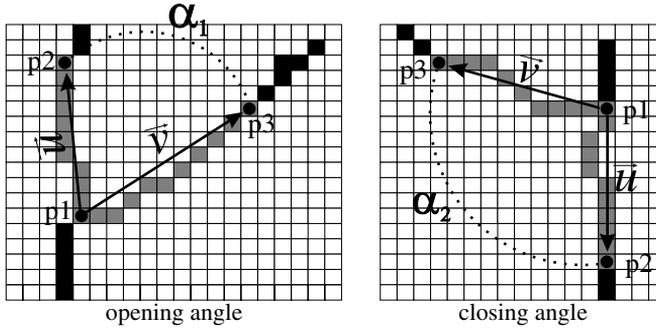
Fig. 5.   Angles between the ramifications collected by the algorithm; opening angle α_1; closing angle α_2.

the y-coordinate of $P2$ is greater than the y-coordinate of $P1$ ($P2_y > P1_y$) then an opening angle α_1 is extracted; however if $P2_y < P1_y$ a closing angle α_2 is extracted; Fig. 5 illustrates the angles (opening and closing) calculated by the leaf exploration algorithm. With the angle values, some statistical data can be collected such as the average of opening/closing angles; the standard deviation, etc.

The angles between ramifications (opening and closing) are determined with vector notation. Thus, for each bifurcation of the venation system two vectors are considered (Fig. 5). The angle between them is defined in Eq. (3):

$$\cos\alpha = \frac{\mathbf{u} \cdot \mathbf{v}}{\|\mathbf{u}\|\,\|\mathbf{v}\|}, \quad 0 \le \alpha \le \pi. \tag{3}$$

The information collected in the three groups of characteristics (distance, length and angle) form a set of 42 features used for plant leaf taxonomy. These data will be used as input information for a pattern recognition method to perform the species classification.

3. Experiments

The potential of the developed methods was proved by experiments with real cases of plant leaf identification. A set of 220 samples of 11 species were used in the experiments. This set contains wild species of passion fruit of the genus *Passiflora* (scientific name is *Passifloraceae*).[14] The samples were cultivated in the Escola Superior de Agronomia Luiz de Queiros (ESALq-USP). Figure 6 shows a sample of each species of the genus Passiflora used in the experiments.

The images of the leaves were acquired using a commercial scanner with a 300-dpi resolution. The leaf images were normalized for size, as the objective was to identity the plants by taking into consideration only the biometric features (only the venation system was considered). A Pentium IV computer (2.0 GHz and 512 Mb of RAM) was used to develop and execute the procedures for image processing, which were written in Borland Delphi and SCiLab environments.
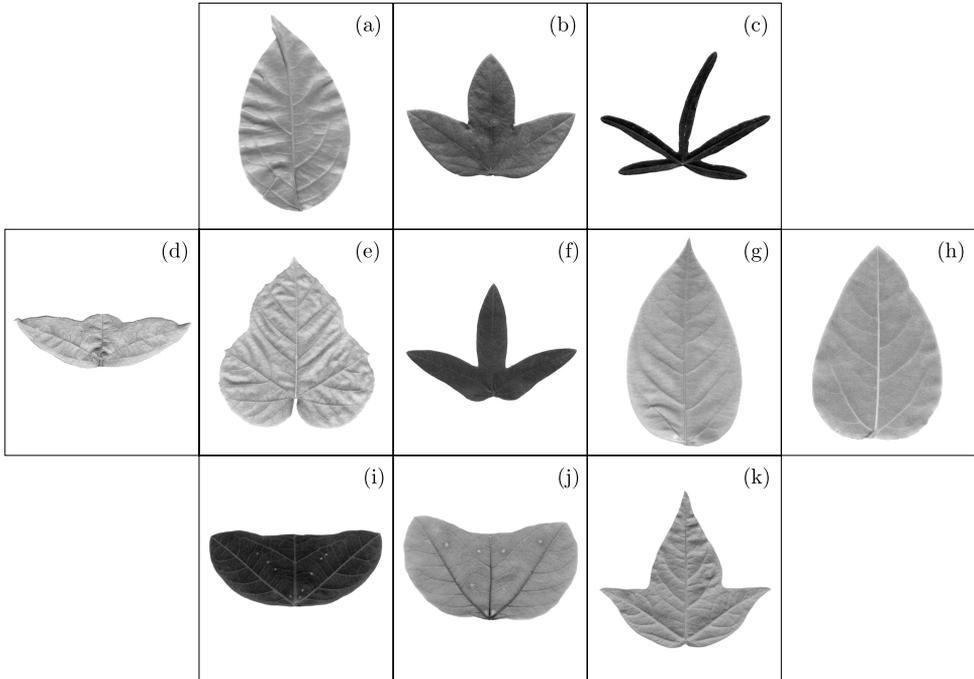
Fig. 6.   Species of *Passiflora* used in this study. The scientifc names of *Passiflora* species are: (a) *Passiflora alata*; (b) *P. amethystina*; (c) *P. caerulea*; (d) *P. coriacea*; (e) *P. foetida*; (f) *P. gilbertii*; (g) *P. maliformis*; (h) *P. miersii*; (i) *P. organensis*; (j) *P. pohlii*; and (k) *P. suberosa*.

The experiments using a set of *Passiflora* samples were divided into three main steps: (i) processing; (ii) biometric feature extraction; (iii) pattern recognition (neural networks).

In the processing step, all samples were segmented and the leaf venation system was extracted. The computer processing time for this stage is approximately four seconds (by sample). Figure 7 presents the 11 samples of leaf species after the processing step to segment the veins.

The pattern recognition stage identifies the leaf species using the features extracted by the biometric computational algorithm. For this, the pattern recognition technique used was artificial neural networks (ANN). This method was inspired by biological neurons.[8] The main characteristics of an artificial neural network are: (i) ability to learn nonlinear complex relations of input/output; (ii) sequential training of procedures and (iii) adaptation of the ANN in accordance with the entrance data.

One of the families more often used in ANN for classification is the feed-forward networks, which includes the multilayer perceptron (MLP). The MLP model, or Multi Layer Perceptron, has at least three layers: the input layer which is initially the feature vector; (ii) one or more hidden layers; and (iii) the output layer — in this
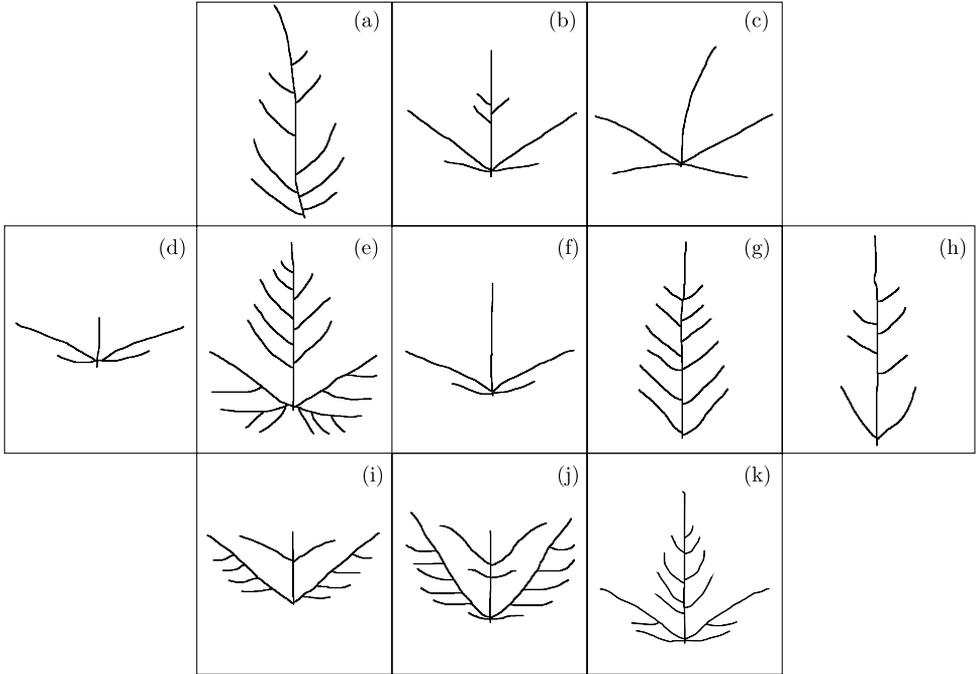
Fig. 7. Venation system of the samples of genus Passiflora used in the experiments: (a) *Passiflora alata*; (b) *P. amethystina*; (c) *P. caerulea*; (d) *P. coriacea*; (e) *P. foetida*; (f) *P. gilbertii*; (g) *P. maliformis*; (h) *P. miersii*; (i) *P. organensis*; (j) *P. pohlii*; and (k) *P. suberosa*

layer the learning results of the ANN are presented. The artificial neural networks of MLP are commonly applied to nonlinear separable problems.[8] Figure 8 illustrates an ANN (MLP), with an input layer $(x1, x2, x3, \ldots, xn)$ which represents the input patterns for the network; a hidden layer and an output layer $(y1, y2, \ldots, yn)$ represent the knowledge and the results reached for the ANN, respectively.

Diverse algorithms can be found in the literature to train the neural networks of MLP, however the most known is back-propagation.[5] This algorithm uses desired information from input/output to adjust the weights of the network by a mechanism of error correction. In back-propagation, the training occurs in two stages, called backward and forward. The forward phase is used to define the output of the ANN from the input patterns. The backward phase uses the desired output and the supplied output to update the weights of its connections.[8] The performance and the efficiency of the ANN can be measured by the error ratio. This calculation is based on the difference between the result reached for the algorithm and the result expected. One of the metrics which is more commonly used is the Mean Square Error — MSE.[8] Equation (4) defines the Mean Square Error.

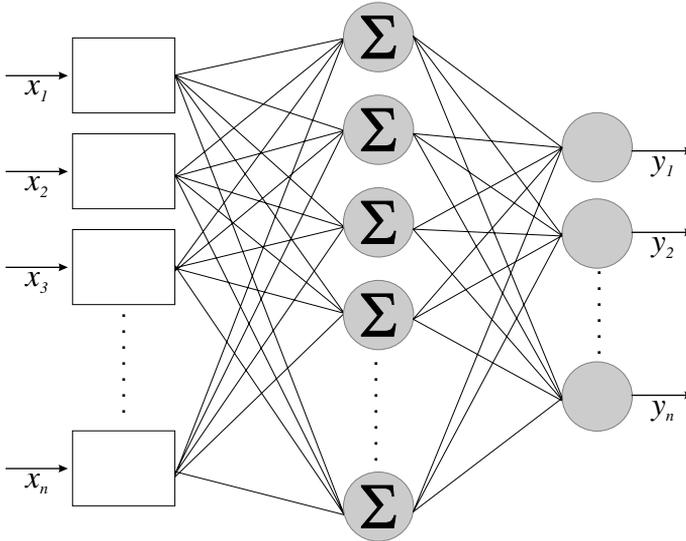$$\text{mse} = \frac{1}{2} \sum_j (t_j^{(p)} - y_j^{(p)})^2 \tag{4}$$

Fig. 8.   Multi Layer Perceptron (MLP) structure: input layer; hidden layer and output layer.

where j represents the neurons of the output layer, t is the output obtained and y the desired output of the neural network.

In the experiments, the artificial neural networks were fundamental in evaluating the biometric methods. Using the ANN, the potential of extracted features could be observed. Moreover, the process of analysis and feature extraction of the leaves would not be complete without the classification of these forms (samples) in classes (species).

3.1. *Results*

The Passiflora species are distributed between 220 samples of 11 different species. The leaf venation systems were previously segmented and 42 biometric features were extracted.

The collected biometric information was used with input for the pattern recognition method — artificial neural networks. The ANN was trained using the back-propagation algorithm, with a topology of: $42x20x11$ (42 neurons in the input layer; 20 neurons in the hidden layer and 11 neuron in the output layer). The parameter adopted for training was of 0.1, for 5000 epochs in the training phase. The results of correct/incorrect classification of the network were estimated by the f cross-validation method known as k-fold cross-validation. The dataset (220 samples) was divided into k mutually exclusive partitions, for $k = 10$. For each iteration, one of the k partitions was used for testing purposes and the others $k - 1$ were used in training.

On average, the network was capable of classifying 97% of the species correctly. The results can be visualized by the confusion matrix. In this type of matrix, the

Table 1.   Classification results of neural networks for 42 biometric features of the leaf venation system.

	a	b	c	d	e	f	g	h	i	j	k	%A	%E
a	19	0	0	0	0	0	0	0	0	0	0	100%	0%
b	0	19	0	0	0	0	0	0	0	0	0	100%	0%
c	0	0	19	0	0	1	0	0	0	0	1	90%	10%
d	0	0	0	20	0	0	0	0	0	0	0	100%	0%
e	0	0	0	0	20	0	0	0	0	0	0	100%	0%
f	0	0	1	0	0	19	0	0	0	0	0	95%	5%
g	1	0	0	0	0	0	20	0	0	0	0	95%	5%
h	0	0	0	0	0	0	0	20	1	0	0	95%	5%
i	0	1	0	0	0	0	0	0	19	0	0	95%	5%
j	0	0	0	0	0	0	0	0	0	20	0	100%	0%
k	0	0	0	0	0	0	0	0	0	0	19	100%	0%
											μ	97%	3%

number of correct predictions for each class is represented along the main diagonal line. In the other positions of the matrix the incorrect classified cases (incorrect predictions) are represented. Table 1 presents the results of experiments. These data are obtained from the output results of the ANN for all $k = 10$ partitions. The elements $a, b, c, d, \ldots, k$ represent the 11 species of *Passiflora* (see Fig. 6). The columns %A and %E describe the percentages of correct and incorrect classification.

Table 2 shows the results obtained from the ANN in each one of k partitions. The correct/incorrect ratios are related, as well as the estimates of the MSE error during the training and the test phase. The average error ratio and the standard deviation during the training are: 0.00967 and 0.01452. For the test, the average error/standard deviations are: 0.00231 and 0.00530.

The biometric features of the Passiflora species were also evaluated by a statistical classifier. The method is referred to as the nearest-mean or Bayes minimum-distance classifier.[6] This classifier is based on traditional offline training and the

Table 2.   Evaluation of the neural network results in each one of $k = 10$ partitions of the data set (220 samples).

k	%A	%E	Training MSE	Test MSE
1	95%	5%	0.01735	0.01735
2	100%	0%	0.00069	0.00097
3	100%	0%	0.00134	0.00096
4	86%	14%	0.04800	0.00017
5	95%	5%	0.00613	0.00027
6	100%	0%	0.00108	0.00099
7	100%	0%	0.01005	0.00099
8	100%	0%	0.00229	0.00097
9	100%	0%	0.00085	0.00039
10	95%	5%	0.00889	0.00004
μ	97%	3%	0.00967	0.00231

Table 3. Nearest-mean classifier results with biometric features of Passiflora species.

	a	b	c	d	e	f	g	h	i	j	k	%A	%E
a	83	0	0	0	0	0	15	2	0	0	0	83.00%	17.00%
b	0	99	0	0	0	0	0	0	0	0	1	99.00%	1.00%
c	0	0	99	0	0	1	0	0	0	0	0	99.00%	1.00%
d	0	0	0	98	0	2	0	0	0	0	0	98.00%	2.00%
e	0	0	0	0	100	0	0	0	0	0	0	100.00%	0.00%
f	0	0	4	1	0	95	0	0	0	0	0	95.00%	5.00%
g	1	0	0	0	0	0	98	0	0	0	1	98.00%	2.00%
h	0	0	0	0	0	0	0	100	0	0	0	100.00%	0.00%
i	0	0	0	0	0	0	0	0	99	1	0	99.00%	1.00%
j	0	0	0	0	0	0	0	0	5	95	0	95.00%	5.00%
k	0	0	0	0	0	0	0	0	0	0	100	100.00%	0.00%
											μ	96.91%	3.09%

online testing approach.[4] The classification was performed as follows: initially, the biometric features were normalized by the standard deviation. For each species, ten samples were randomly selected to compose the training set and ten to compose the testing set (this procedure was repeated ten times). The classifier is built by calculation of the cluster center for all Passiflora species of the training set. The next step was to classify the species of the testing set. The new species were determined by applying a minimum-distance criterion between each cluster center (of training set) and the extracted biometric features to determine the closest class. The metric adopted was the Euclidean distance.

The cluster centers are calculated by averaging all the biometric features of samples in the training set which belong to same class c. Let $\mathbf{X}_c^i$ the feature vector of samples i and k_c is the number of samples in class c, the cluster can be determined by Eq. (5).[6]

$$\mathbf{A}_c = \frac{1}{k_c} \sum_{i=0}^{k_c-1} \mathbf{X}_c^i. \tag{5}$$

If $\mathbf{X}_d$ is the feature vector of samples d, in the test set and $\mathbf{A}_i$ is the cluster vector of class i, $i \in [0, n_c - 1]$, with n_c being the number of classes, then d is the attributed class j ($j \in [0, n_c - 1]$) for which $|\mathbf{A}_i - \mathbf{X}_d|$ is the smallest.

The classifier results are indicated in Table 3. The Passilfora species are represented by $a, b, c, d, \ldots, k$ elements and the columns %A and %E describe the percentages of correct and incorrect classification. The experiments were repeated ten times with random selections of training and test set. On average, the classifier was able to distinguish 96.91% (± 0.0495) of species correctly.

4. Discussion

The experiments have described a computer vision methodology to extract biometric features to identify plant species. A set of 11 species of passion fruits of genus Passiflora were used (20 samples by specie). The genus showed a wide range of leaf

venation forms, but there were some pairs or groups of species whose biometric similarity made it difficult to identify them correctly.

The proposed methodology was able to collect 42 distinct features of the leaf venation system. The biometric analysis is important in plant taxonomy due to some morphological characters (such as sepal, petal, stipule, etc.) which are not available at all times of year. Furthermore, Passiflora is perhaps the most suitable taxon for testing the efficiency of this methodology.

The aim of experiments was to show the potentiality of 42 biometric features when identifying plant species. The extracted feature vectors (of each sample) were used as inputs in an artificial neural network, and a k-fold cross-validation was performed to estimate the correct/incorrect ratio of species classification.

The results are highly promising where the ANN was able to classify correctly 97% (±3.43776) of Passiflora species. Although the number of samples used to train the ANN was not large (some of the plant species used are rare), the k-fold cross-validation was applied to increase the experiments efficiency. Moreover, the results were validated by a nearest-mean statistical classifier. This classifier was able to distinguish properly 96.91% (±0.0495) of species. The results show a great potential of the extracted biometric feature in the taxonomy of plant species. Besides this, the developed methods can be used as a toolbox during the complex task of taxonomy.

The principal limitation of the proposed methodology is diafanization protocols. This chemical procedure is usually done by biologists, but has been necessary to develop tools to carry out the automatic clarification of the leaves.

5. Conclusion

Plant species taxonomy is a complex task mainly due to the high biodiversity of the species. The traditional taxonomy protocols are out-of-date and based on visual inspection (performed by botanists). In this context, the need arises for the development of computer vision methodologies to recognize and characterize species by the shape of their vegetative structures.

In this work, a novel approach to plant species identification was proposed. The methods performed the biometric feature extraction of the plant species. This biometrical analysis can help taxonomists in identifying the problem. A set of 42 biometric features of the leaf venation system are extracted and using an artificial neural network perform the classification of the species. To estimate the validity of the methodology, 11 species of passion fruit of genus Passiflora were used (20 samples per specie). The Passiflora species is a high diversity genus.

The results demonstrated a high potentiality of biometric features used in experiments. In a diversity group of 220 samples, the methodology was able to classify 97% (ANN) and 96.91% (nearest-mean) of the samples correctly. In addition, the results indicated the viability of computer vision techniques applied to the taxonomy of plant species.

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