
Recognition of crop leaf diseases based on multi-feature fusion and evolutionary algorithm optimisation

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Abstract: Crop leaf disease identification refers to automatically recognise crop leaf pictures suffering from disease, to determine the type of diseases, which is important for agricultural production. Much progress has been made in this field, but there are still many challenges. For example, there are not enough ideal schemes for either disease spot area segmentation or feature representation and matching. In order to meet these challenges, a new crop leaf disease recognition method was proposed in this paper. First, disease spot segmentation method combined ultra-green feature and threshold segmentation was presented. Then, feature representation scheme with multiple features was proposed, which combined colour, texture, and shape features. Finally, evolutionary algorithm was used to optimise similarity function for feature matching. Experimental results show that the scheme proposed in this paper can effectively improve recognition accuracy and has a certain practical value.

Keywords: crop leaf disease recognition; evolutionary algorithm; disease spot area segmentation; feature representation; feature matching.

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1 Introduction

With rapid development of computer vision related theories, research on target recognition using machine vision has been carried out widely. Crop leaf diseases recognition belongs to this research category. It refers to automatically recognise crop leaf pictures suffering from disease (Mohameth et al., 2020), to determine the type of crop disease.

Even lots of researches for crop leaf diseases recognition has been made, but there are still many challenges. The first is segmentation of disease spot area. Accurate separation of crop leaf spots from whole image can lay a good foundation for subsequent feature representation and matching. The second is feature representation. Images were taken in natural environment, which may be affected by lighting and shooting angle, resulting in poor robustness of extracted features. Finally, a good and universal similarity measurement method can be directly applied to crop leaf diseases recognition is needed for feature matching.

In order to solve above problems, a new recognition scheme of crop leaf diseases was proposed in this paper. Super green features combined with threshold segmentation were used to segment disease spot area. Multiple feature representation scheme was proposed, which combined colour, texture and shape features. Similarity measure function was designed for feature matching, and evolutionary algorithm was adopted for function optimisation.

The rest of this paper is organised as follows. Relevant literature of crop leaf disease recognition is described in Section 2. Section 3 details the whole approach proposed in this paper. In Section 4, several experimental results and comparative analyses are presented. And finally, Section 5 discusses conclusions and future perspectives.

2 Related work

According to existing research results, crop leaf disease recognition mainly includes three problems: foreground extraction, feature representation, and feature matching.

2.1 Foreground extraction

Foreground extraction is to separate disease spot area from background for subsequent feature representation and matching. Research about foreground extraction is very extensive, and it is also hot but difficult problem in image processing field. Most of existing methods can be applied to crop leaf diseases recognition, such as simple threshold segmentation method and edge detection method, complex

fuzzy clustering method and mathematical morphology method.

Threshold segmentation method (Peng et al., 2011) was early applied to crop diseases recognition for foreground extraction. It classifies the grey level of image pixels according to different thresholds, and pixels of same kind are regarded as same whole. Traditional threshold segmentation method uses RGB histogram to represent shape, position and other features. It often fails to obtain ideal effect. Some researchers analysed and improved it (Camargo, 2009; Pujari et al., 2015) and replaced traditional RGB histogram with optimal or local threshold method to represent shape feature histogram. Threshold segmentation method could be simple and efficient, if we know how to choose the threshold. When it is used in crop leaf disease images, the grey histogram of two areas (foreground and background) will be obviously different in colour and texture, so the threshold can be selected according to this.

Edge detection method (Canny, 1986) separates foreground and background by detecting edge information. It has been widely used in separation of leaf spots for rice, barley and other crops (Baum et al., 2011). Edge detection method is simple and easy to operate. When it is applied to crop leaf disease images, the edge's grey value of disease spot area usually changes significantly, so it can generally achieve relatively ideal separation effect. However, its efficiency is limited by edge detection operator, and its robustness is not guaranteed.

Fuzzy clustering method (Yang, 1993) is unsupervised learning method. It specifies that membership of each pixel to be processed is fuzzy. In recent years, it has been widely used in segmentation of maize, cucumber and other crops (Zhang et al., 2017b). As membership function is main component of fuzzy clustering algorithm, it can model ambiguity and uncertainty existing in the image, which is just in line with fuzzy and uncertain characteristics of most crop leaf disease images, so it might achieve good results. However, this method needs large amount of computation and is sensitive to noise interference.

Mathematical morphology method (Beucher, 1990) uses structural elements with specific forms to extract similar shapes in images, and there are also relevant application cases in foreground extraction of crop leaf disease recognition (Casady, 1996). It can simulate image shape information well, but sensitive to boundary noise and segmentation accuracy is usually low.

In addition to these traditional methods mentioned above, some new model theories are also widely used in foreground extraction of crop leaf disease images. For example, random field segmentation model (Lai et al., 2010) for maize, level set model (Zhou et al., 2015) for

cucumber, and multi-example graph model (Hu et al., 2012) for wheat.

Although most of the background extraction methods can be applied to the segmentation of crop leaf disease image spots, but due to particular shooting environment and influence of various complex backgrounds, it is an extremely difficult task to efficiently segment background and disease spots. It is necessary to find new segmentation algorithms, or improve traditional methods to obtain optimal solution scheme.

2.2 Feature representation

Colour, texture and local features are usually used in crop disease recognition.

Colour is most commonly used. Expression and extraction of colour are relatively intuitive, and execution efficiency is relatively high. However, images of crop leaf diseases taken in actual farmland environment are easily affected by factors such as illumination and shooting angle, which may change colour of the same disease image. Therefore, colour invariance processing is required. The study of colour invariance is not new. In early 1990s, Funt and Finlayson (1995) proposed a colour invariance descriptor called 'colour index', which solved colour change caused by illumination factors by taking the derivative of colour space. Many scholars extended and improved the algorithm (Van and Schmid, 2006). In recent years, it has attracted more attention involves all aspects of image processing. However, different applications have different requirements for colour invariance processing. Therefore, it is necessary to find a more robust processing method specifically for crop leaf diseases recognition.

Texture feature is also used in crop leaf diseases recognition. For example, difference method was used to extract texture features of tomato leaves lacking nutrient elements (Xu et al., 2002). Gray level co-occurrence matrix (GLCM) method was used to extract texture features of maize leaf disease spots (Liu et al., 2014). Texture feature has strong anti-interference ability and rotation invariance. However, texture feature extraction is usually time-consuming, so execution efficiency improving must be considered in practical application.

Shape feature is the usually used local feature for crop disease recognition. As early as 1995, Woebbecke et al. (1995b) had applied shape feature to weed recognition and used shape features such as perimeter, extension length, thickness and roundness of plant canopy to identify weed species. Since then, similar approaches have proliferated. For example, shape features of wheat spore images are extracted to identify common wheat smut (Chesmore et al., 2003), and shape features of wheat leaves are represented by moment invariant theory to identify common wheat leaf diseases (Wu et al., 2015). Relatively speaking, extraction of shape features is simple and easy to operate, so it is relatively common in early studies. However, due to imperfection of corresponding mathematical model, shape information expressed may deviate from direct observation of human beings, so effectiveness will be affected.

In addition, multi-feature fusion is also a common feature representation scheme, which can achieve better recognition effect. For example, colour, texture and geometric features are extracted to identify citrus diseases (Sharif et al., 2018). Colour and texture features are integrated to identify a variety of plant diseases (Chaki et al., 2018).

2.3 Feature matching

Various classification and recognition algorithms were mainly used on feature matching for crop leaf disease recognition to determine the types of diseases. Most of the early algorithms rely on visual intuitiveness, and the effect is poor. For example, genetic algorithm (Sasaki et al., 1999) was used to identify cucumber leaf diseases. With the development of research, more and more methods have been used, such as neural network, support vector machine (SVM) and so on.

Neural network method (Nigrin, 2001) uses decision function obtained by learning to classify and recognise images. This method has strong anti-noise ability and better classification accuracy, so it has been used in many cases, such as cotton (Gassoumi et al., 2000) and soybean (Han et al., 2017). However, it is computationally intensive and usually requires a mass of training samples, which restricts its application in classification and recognition.

SVM method (Adankon and Cheriet, 2002) is derived from relevant statistical theories. It builds an optimal classification surface in sample space to maximise interval of different categories, and classifies recognition targets. Compare with neural network, SVM can obtain better classification effect in fewer samples cases, so it is more suitable for crop leaf disease recognition. For example, SVM based on balanced decision tree was applied to wheat leaf diseases recognition (An et al., 2014), and the effect was remarkable. There are some defects of SVM, its performance mainly depends on construction of kernel function and speed of training sample, so, the result will be greatly reduced if these two aspects deviate.

Multi-method fusion feature matching scheme are also used in crop leaf disease recognition. For example, neural network is integrated with SVM (Sammany and Medhat, 2007). In addition, new methods and theories continue to emerge and have been applied in crop leaf disease recognition, such as the application of hyperspectral image analysis technology for tomato leaf early blight recognition (Xie et al., 2015).

3 The approach

A new crop leaf diseases recognition method was proposed in this paper. Super green feature combined with threshold segmentation were used to segment disease spot area. Multi-feature representation scheme was proposed as well, which combined colour, texture and shape features. Similarity measure function was designed for feature matching, and

evolutionary algorithm was adopted to optimise the function.

3.1 Segmentation of leaf disease spot area

In this paper, super green feature and traditional threshold segmentation method were combined for segmentation of leaf disease spot area. A brief introduction of these two problems was given in Sections 3.1.1 and 3.1.2, and Section 3.1.3 is the specific implementation ideas.

3.1.1 Threshold segmentation

Threshold segmentation method is shown in formula (1). Where t is the threshold, and $g(x, y)$ is the grey value of pixel point (x, y) . $C(x, y)$ is a binary function that has a value of 0 or 1. The grey value of each pixel is compared with threshold value t . If it is greater than t , the value of function C is 1; otherwise, it is 0. In this way, all pixels are divided into two categories to achieve the purpose of image segmentation.

$$C(x, y) = \begin{cases} 1 & g(x, y) > t \\ 0 & g(x, y) \leq t \end{cases} \quad (1)$$

The key in threshold segmentation method is how to determine the threshold. There are many method, such as histogram method (Tan and Isa, 2011), optimal method (Guo and Wang, 2005), and maximum inter-class variance method (Liang and Wei, 2010), etc. Histogram method requires grey histogram of the image with obvious double peak. Optimal threshold method requires the probability density of greyscale images distribute normally. But the actual image may not have these characteristics. Comparatively, maximum inter-class variance method does not have many restrictions, calculation process is not very complicated, and it is more suitable for practical applications. Therefore, it is selected in this paper, which is briefly introduced below.

Maximum inter-class variance method uses optimal threshold to determine the segmentation threshold, which is a widely used method. The grey level of image can be divided into m class, assuming that there are n_i pixels in the first class i and N is the total number of pixels in the image, then N can be expressed as $N = \sum_{i=1}^m n_i$. P_i is the grey level probability of first class i , it can be expressed as $P_i = n_i/N$. The overall average greyscale of the image can be expressed as $\mu = \sum_{i=1}^m i \times P_i$.

Assuming the selected threshold value is k , and the goal is to find the best value of k as segmentation threshold. For separation of foreground and background, images will be divided into two categories according to grey level, which are assumed to be C_1 and C_2 . $C_1 = \{1, 2, \dots, k\}$, $C_2 = \{k+1, k+2, \dots, m\}$. $\mu(k)$ is the average grey level of class C_1 , and N_1 is total number of pixels in class C_1 , $\mu(k) = \sum_{i=1}^k i \times P_i$, $N_1 = \sum_{i=1}^k n_i$. The average grey level of

class C_2 is $\mu - \mu(k)$, and total number of pixels contained is $N - N_1$. Assuming the proportion of the image formed by pixels in class C_1 to total image is $\omega(k)$, then in class C_2 is $1 - \omega(k)$. Thus, by homogenising these two classes, $\mu_1 = \mu(k)/\omega(k)$, $\mu_2 = [\mu - \mu(k)]/[1 - \omega(k)]$ the overall average grey level can be re expressed as $\mu = \mu_1\omega_1 + \mu_2\omega_2$.

From above verification, the maximum inter-class variance as shown in formula (2) can be obtained, and be further reduced to formula (3).

$$\sigma(k) = \omega_1 (\mu - \mu_1)^2 + \omega_2 (\mu - \mu_2)^2 = \omega_1\omega_2 (\mu_1 - \mu_2)^2 \quad (2)$$

$$\sigma(k) = (\mu \times \omega(k) - \mu(k))^2 / (\omega(k) \times (1 - \omega(k))) \quad (3)$$

3.1.2 Super green feature

Super green feature is an interesting concept (Woebbeke et al., 1995a). The purpose of original study was to identify weeds in farmland. After that, many researchers tried to apply it to image foreground extraction. Experimental studies have found that for images containing plant, colour value difference between foreground and background is huge. For example, G colour component is greater than R and B for green plants. According to this characteristic, the importance of G colour component can be enhanced, and foreground and background of pictures containing plants can be separated by extracting super green features. It is shown in formula (4). Type one with super green features, and type two with not. Foreground of plants can be separated from background such as soil by using this method.

$$f(x, y) = \begin{cases} 2G - R - B, & \text{if } (2G - R - B \geq 0) \\ 0, & \text{else} \end{cases} \quad (4)$$

Due to vast majority of plant leaves are green, and colour of disease spot area usually have great difference with healthy leaves, therefore, super green features was chosen for disease spot area segmentation in this paper.

3.1.3 Segmentation of leaf disease spot area with super green feature and threshold segmentation

Firstly, pixel points of original image are classified by super green feature. Then, threshold is determined by maximum inter-class variance method. Finally, image is segmented by threshold segmentation method. The specific steps are as follows.

- 1 All pixels in segmented image can be divided into two categories by using formula (4).
- 2 Two categories obtained in step (1) are used as class C_1 and C_2 for maximum inter-class variance method for determining threshold value.
- 3 According to C_1 and C_2 obtained in step (2), maximum inter-class variance method is used to obtain optimal threshold value for segmentation on original image (the image to be segmented without super green feature processing).

- 4 Threshold segmentation method is used to segment image with optimal threshold obtained in step (3) to obtain isolated disease spot area.

3.2 Feature extraction and representation

Multi-features fusion method is adopted in this paper, and colour, texture and shape features are chosen.

3.2.1 Colour feature

Colour is one of the most frequently used features in image recognition. However, it is very easily affected by external factors such as illumination and shooting angle change. To obtain robust and reliable colour features, colour invariance processing must be carried out. There are many methods for colour invariance processing. An iterative processing method based on diagonal model has been proposed in our published paper (Zhang et al., 2017a). Another method based on moment invariant is presented in this paper. As early as 1962, Hu (1962) applied the moment invariant theory to the study of pattern recognition. The following is a brief introduction to the moment invariant theory, and then the extraction method of colour invariant descriptor based on moment invariant and RG chromaticity space in this paper.

Assuming an image is I and expressed as function $I(x, y)$ of pixel point (x, y) , in the Cartesian coordinate system with x and y as axes, the definition of moment of order $U + V$ is shown in formula (5), according central moment is shown in formula (6), and centre distance after standardisation is shown in formula (7). Where (x_0, y_0) is the centre of gravity of image I .

$$M_{uv} = \sum_x \sum_y x^u y^v I(x, y) \quad (5)$$

$$U_{uv} = \sum_x \sum_y (x - x_0)^u (y - y_0)^v I(x, y) \quad (6)$$

$$V_{uv} = U_{uv} / M_{00}^p, p = \frac{u+v}{2} + 1 \quad (7)$$

In Hu's literature, seven invariant moments are constructed according to the normalised centre distance shown in Formula 7, which are used to describe the invariance of global shape features of images. On the basis of these studies, colour invariant moments used to describe colour invariance are given in combination with rg chromaticity space and moment invariant theory.

In rg chromaticity space, chromaticity histogram is used to improve traditional colour histogram. One colour channel of RGB is deselected and two left. For example, B is removed by using formula (8), but R and G are kept.

$$r = R / B, g = G / B \quad (8)$$

Compared with colour histogram, chromaticity histogram weakens the effect of shooting angle on image colour features to some extent.

If colour value of a pixel in one photography angle is (R, G, B) , and the other is $(\lambda R, \lambda G, \lambda B)$. According to

formula (8), in first case, $r = R/B$, $g = G/B$, and in second case, $r = \lambda R / \lambda B = R/B$, $g = \lambda G / \lambda B = G/B$. As you can see, the Chroma values are same in both cases. So, shooting angle problem has been solved in rg chromaticity space, and it is only necessary to address light change.

First, RGB colour space is converted to rg chromaticity space according to formula (8), and then the diagonal model shown in formula (9) can be given. If the colour descriptors obtained under two illumination conditions are (r_1, g_1) and (r_2, g_2) respectively, then $r_1 = \alpha r_2$, $g_1 = \beta g_2$. Define the colour moments of order $u + v$ of image I , as shown in formula (10). Where, $N(r, g)$ is a scale function, representing the proportion of number of pixel points with colour value of (r, g) to number in the whole image in rg chromaticity space.

$$\begin{bmatrix} r_1 \\ g_1 \end{bmatrix} = \begin{bmatrix} \alpha & 0 \\ 0 & \beta \end{bmatrix} \begin{bmatrix} r_2 \\ g_2 \end{bmatrix} \quad (9)$$

$$MC_{uv} = \sum_r \sum_g r^u g^v N(r, g) \quad (10)$$

In rg chromaticity space, it is assumed that colour moments under two different illumination conditions are $(MC_{uv})_1$ and $(MC_{uv})_2$ respectively, then it can be deduced from formula (9) and (10) that $(MC_{uv})_1$ and $(MC_{uv})_2$ are relative as shown in formula (11). Accordingly, the design moment invariants are shown in formula (12), α and β are eliminated to obtain colour invariant descriptor of the image.

$$(MC_{uv})_1 = \alpha^{u+1} \beta^{v+1} (MC_{uv})_2 \quad (11)$$

$$\sigma_{uv} = \frac{(MC_{00})^{\frac{u+v+2}{2}}}{(MC_{20})^{\frac{u+1}{2}} (MC_{02})^{\frac{v+1}{2}}} MC_{uv} \quad (12)$$

When constructing colour invariant descriptor based on invariant moment, in order to describe image more comprehensively and accurately and reduce the influence of noise at the same time, it is necessary to provide as much invariant moment as possible on premise of keeping sum of u and v relatively small. In this paper, a colour invariant descriptor composed of eight invariant moments is constructed to represent colour features. Show as formula (13).

$$\varphi = [\sigma_{01}, \sigma_{02}, \sigma_{10}, \sigma_{11}, \sigma_{12}, \sigma_{20}, \sigma_{21}, \sigma_{22}] \quad (13)$$

3.2.2 Texture feature

Texture feature describes the spatial distribution among pixels and can describe details of images. There are many excellent algorithms for texture feature extraction and representation, among them, the old grey level co-occurrence matrix method and the relatively young local binary pattern (LBP) has been widely used. On the basis of these two methods, a new texture feature extraction and representation method is proposed in this paper.

3.2.2.1 Gray level co-occurrence matrix

GLCM (Haralick et al., 1973) is a texture feature extraction method based on statistics, which is used to calculate the occurrence probability of a pair of pixels (x, y) with grey value m and n along the direction of θ and the distance between them is d , as shown in formula (14). Where, $\Delta x = d\cos\theta$, $\Delta y = d\sin\theta$, denotes the offset. The value of d is usually 1, 2, 3 or 4, and the value of θ is usually 0° , 45° , 90° or 135° . For example, $d = 1$, $\theta = 0^\circ$, means counting the number of occurrences of various forms of pixel pairs formed by a pixel and its left and right neighbourhood pixels.

$$P(m, n, d, \theta) = \{(x, y), (x + \Delta x, y + \Delta y)\} \quad (14)$$

3.2.2.2 Local binary pattern

LBP (Ojala et al., 2002) represents image texture information through local comparison of neighbourhood pixels. The basic idea of the algorithm is as follows: firstly, a pixel C is selected as the centre point, and its grey value is assumed to be g_c and a window of $n*n$ is defined. For all neighbourhood points i in the window, grey value is assumed to be g_i , g_c and g_i is compared, if $g_i \geq g_c$, this point is encoded as 1, otherwise 0, by now a string of binary code is obtained, which is the LBP value of central point c . The calculation method of LBP is shown in formula (15). Where m represents number of pixels contained in neighbourhood, n represents size of the window, and $f()$ is shown in formula (16). Gray image can be transformed into LBP image after LBP value of each point is calculated. Texture features will be obtained according to specific situation of LBP image statistics.

$$LBP_{m,n} = \sum_{i=1}^m 2^{i-1} \times f(g_i - g_c) \quad (15)$$

$$f(x) = \begin{cases} 1, & x \geq 0 \\ 0, & x < 0 \end{cases} \quad (16)$$

3.2.2.3 Texture feature descriptor based on fusion of GLCM and LBP

GLCM is based on statistics, it is difficult to describe the texture structure, while LBP is structure-based method, which can describe microstructure well, but it is difficult to reflect the macrostructure. In order to learn from each other and give full play to their respective advantages, a texture feature description method based on fusion of GLCM and LBP is proposed in this paper.

Firstly, grey image is converted to LBP image, and then GLCM is used for statistics on LBP image. In this way, the statistics show position relationship between local texture structures, thus showing a macroscopic structure with larger scale. It is named LBP-GLCM, and its definition is shown in formula (17).

$$LBP-GLCM = P'(m', n', d, \theta) = \{(x, y), (x + \Delta x, y + \Delta y)\} \quad (17)$$

where (x, y) , d , θ and Δx , Δy have the same meaning as formula (14). However, m' and n' are no longer the grey-scale values of pixels. They are mode change values of LBP values in θ direction instead, which are represented by LBPM with a value range of 1 to 5. Assuming that two neighbourhood points of pixel X in θ direction are X_i and X_j , and corresponding LBP values of these points are respectively denoted as Lx , Lx_i and Lx_j , then pseudocode for calculation process of LBPM value of X in θ direction is as follows:

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if ( $Lx == Lx_i$  &&  $Lx == Lx_j$ )  $LBPM^\theta = 1$ ;
else if ( $Lx < Lx_i$  &&  $Lx < Lx_j$ )  $LBPM^\theta = 2$ ;
    if ( $Lx < Lx_i$  &&  $Lx > Lx_j$ )  $LBPM^\theta = 3$ ;
    if ( $Lx > Lx_i$  &&  $Lx > Lx_j$ )  $LBPM^\theta = 4$ ;
    if ( $Lx > Lx_i$  &&  $Lx < Lx_j$ )  $LBPM^\theta = 5$ ;

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End

In practical application, window size of $3*3$ is selected, d is 1, and θ is 0° , 45° , 90° and 135° .

After LBPM values of all pixel points are calculated, each LBPM mode pair can be normalised by formula (18). Where N_x and N_y represent length and width of the image, and $f()$ is shown in formula (19).

$$H(m', n') = \sum_{x=2}^{N_x-1} \sum_{y=2}^{N_y-1} f(LBPM(x, y), LBPM(x + \Delta x, y + \Delta y), m', n') \quad (18)$$

$$f(a, b, c, d) = \begin{cases} 1, & \text{if } (a == b, c == d) \\ 0, & \text{else} \end{cases} \quad (19)$$

3.2.3 Shape feature

For many crop leaf diseases, there are some special shapes that can be used to distinguish types. Therefore, shape features also play an important role in crop leaf diseases identification.

3.2.3.1 Shape feature extraction

Firstly, contour tracking method was used to find the contour of lesion area. Then, pixel method was used to calculate the perimeter and area. Finally, circularity and rectangularity and other needed features can be calculated according to perimeter and area.

The idea of contour tracking method (Sharma et al., 2013) is as follows: binary image of the edge is obtained through edge detection algorithm. Assume 1 represents edge point, searching from top to bottom and left to right, take the first 1-value point encountered as starting point of contour, name it M , and record its position. Eight neighbourhood points of M are found in certain order (counterclockwise or clockwise) to determine next edge point. This process continues until the next edge point is M , indicating that a circle has been searched and whole contour has been found.

After finding contour of spot area, perimeter and area of lesion area can be obtained by using pixel method. Number of pixels on contour was calculated to represent perimeter, and number of pixels inside contour was calculated to represent area. Other features such as circularity and rectangularity can be calculated too. For example, $c = 4\pi S / L^2$ represents circularity, and $q = S / (w \times h)$ represents rectangularity. Where, L is perimeter, S is area, w is length, and h is width of the lesion area respectively.

In order to avoid the phenomenon of edge breaking, previously detected edges need to be compensated during contour tracking to extract a complete edge contour.

- Step 1 According to traditional contour tracking algorithm, first contour point M is found as current contour point.
- Step 2 The found contour points are marked to prevent repeated. Find eight neighbourhood points of current contour point P in counterclockwise direction, and record all unmarked points with value 1: $v = \{v_1, v_2, \dots, v_n\}$.
- Step 3 If $n = 1$, it means that there is only one point in set v , and then it is the new current contour point, and return to step 2. Otherwise, go to step 4.
- Step 4 If $n > 1$, it indicates that there is more than one point in set v . The point closest to the direction of current contour point is selected as new current contour point, and return to step 2. Otherwise, go to Step 5.
- Step 5 If n 's value in step 3 and step 4 is not valid, it means that set v is empty, that is, no points meet conditions have been found. In this case, it will be re-judged, if all points with value 1 have been marked, the algorithm is ended. Otherwise, it means that the edge is broken and compensation is needed. Go to step 6.
- Step 6 For current contour point P , find the pixel points in its vertical direction, calculate a reference quantity, such as gradient, according to original image, take the pixel point of peak value as new current contour point, and return to step 2.

3.2.3.2 Shape feature selection

There are many available shape features, such as circumference, area, circularity, rectangularity, eccentricity and so on. In face of specific application problems, there is no unified standard for choosing appropriate shape features, but selection is mostly based on characteristics of the problem. If the problem is clearly biased towards certain shape feature, then this feature can be selected directly. For example, in later experiments of this paper, it was found through large number of experimental studies that for some common diseases, difference in circularity of leaf spots was obvious. In this case, selection of circularity as the shape feature was very helpful to distinguish different diseases.

3.3 Feature matching

Design of similarity measurement criterion is the key problem for feature matching. Design a distance function, and use it to calculate the similarity between matched samples to judge whether they are the same. Because multiple features representation scheme is adopted in this paper, corresponding matching scheme also need to be considered. Therefore, two kinds of distance functions are designed for measure single and fused feature respectively.

3.3.1 Distance function for single feature

Quadratic function is treated as the distance function. It is a generalised form of Mahalanobis distance function, which comes from quadratic polynomial function defined in mathematics. Its general form is shown in formula (20). Where, X and Y represent feature vectors of images to be matched, A is autocorrelation matrix, B is cross-correlation matrix, W reflects first-order relationship between feature vectors to be matched, and e is the offset.

$$F(X, Y) = X^T A X + Y^T A Y + X^T B X + Y^T B Y + W^T X + W^T Y + e \quad (20)$$

From the definition of quadratic function, it can be known that $X^T A X + Y^T A Y$ describes autocorrelation between samples, while $X^T B X + Y^T B Y$ describes mutual correlation, and there are W describing first-order relationship and e for adjustment, so it's a better function to describe similarity between samples.

3.3.2 Distance function for multiple features

Multi-feature fusion distance function is shown in formula (21). Where, X and Y is matching samples, $F_1()$, $F_2()$, $F_3()$ respectively represent distance for colour, texture and shape features. ∂ , β and γ are corresponding weight vectors.

$$D(X, Y) = \partial F_1(X, Y) + \beta F_2(X, Y) + \gamma F_3(X, Y) \quad (21)$$

In this paper, learning distance function of multi-feature fusion is no longer limited to ensure calculated distance of truly matched sample pair must be less than others, but to make it become one of M minimum distances, and try to maximise this probability event. In this way, the first M samples sorted according to similarity can be presented as reference objects for users to judge, and automatic matching can be combined with manual intervention.

3.3.3 Determine parameters of distance function based on evolutionary algorithm

Parameters of these two distance functions need to be obtained by learning. Because there is not enough prior knowledge, evolutionary algorithm (Cai et al., 2021; Zhang et al., 2022) is adopted to do this work through iterative optimisation (Wang et al., 2020, 2021).

1 Population initialisation

In order to make distribute initial population uniformly in whole solution space, mapping function shown in formula (22) is adopted in this paper. Where, ∂ takes experience value 0.4. Initial population is denoted by $P^0 = (P_1^0, P_2^0, \dots, P_n^0)$. For formula (20), $P_i^0 = (A, B, W, e)$, $P_1^0 = (-I, I, 0, 0)$, $P_i^0 (2 \leq i \leq n)$ is calculated by formula (22). For formula (21), $P_i^0 = (\partial, \beta, \gamma)$, the values of ∂ , β and γ are all floating point numbers in the interval of (0, 1), and the values satisfy $\partial + \beta + \gamma = 1$.

$$\tau_{n+1} = \begin{cases} \tau_n / \partial & 0 < \tau_n \leq \partial \\ (1 - \tau_n) / (1 - \partial) & 0 < \tau_n < 1 \end{cases} \quad (22)$$

2 Determine fitness function

For formula (20), fitness function is shown in formula (23). Where, R represents the set of related sample pairs, and S represents unrelated sample pairs. α and β are regulating parameters to prevent overfitting in iteration process. An empirical value should be given according to specific sample, such as $\alpha = 0.000001$, $\beta = 0.5$. $\|A\|$ is the norm of matrix A (two-norm or F-norm). The goal of evolution is to minimise this fitness function.

$$\begin{aligned} Fit = & - \left[\frac{1}{|R|} \sum_{(X,Y) \in R} \log[G(X, Y)] \right. \\ & \left. + \frac{1}{|S|} \sum_{(X,Y) \in S} \log[1 - G(X, Y)] \right] \\ & + \frac{\alpha}{2} (\|A\|^2 + \|B\|^2) + \frac{\beta}{2} \|W\|^2 \end{aligned} \quad (23)$$

For formula (21), fitness function is shown in formula (24). Where, N represents number of samples participating in training. R represents the set of related sample pairs, and S represents unrelated sample pairs. $Num(x)$ is a counting function, representing the number of events in which x condition is true. $T(x)$ is a Boolean function, which means that if x condition is true; the result is 1, and otherwise 0. The goal of evolution is to maximise this fitness function.

$$Fit = \frac{1}{N} \sum T(Num((D(X, Y)_{(X,Y) \in R} < D(X, Y)_{(X,Y) \in S}) < M)) \quad (24)$$

3 Selection

The fitness value of each individual in current population was calculated, and M individuals with high fitness were selected to enter the subsequent cross-mutation process.

4 Variation

Individuals are randomly selected to carry out variation operation according to a certain probability. The definition of variation probability PM is shown in formula (25). Where Fit_{\max} and Fit_{\min} represent the highest and lowest fitness respectively, and $Fit(P_i)$ represents fitness value of individual P_i . Variation operation was carried out according to formula (26).

Where, P represents the individual before variation, P_{new} represents the individual after variation and δ is a random number with a value range of $[-1, 1]$. If the newly created individual is superior to the current one, the original individual is replaced with the new one.

$$PM = \frac{1 - e^{-2} \left[(Fit_{\max} - Fit(P_i)) / (Fit_{\max} - Fit_{\min}) \right]}{1 + e^{-2} \left[(Fit_{\max} - Fit(P_i)) / (Fit_{\max} - Fit_{\min}) \right]} \quad (25)$$

$$P_{new} = \begin{cases} P(1 - \delta^2) + \delta^2, & \delta > 0 \\ P(1 - \delta^2), & \delta \leq 0 \end{cases} \quad (26)$$

5 Crossover

Two individuals are randomly selected for cross crossover operation according to crossover probability. Crossover probability is $PC = 1 - PM$, and crossover operation is performed according to formula (27). Where, P_i and P_j are individuals selected for crossover, P_{i-new} and P_{j-new} are new individuals after crossover, and c and c' are random numbers with a value range of $[0, 1]$. If the newly created individual is superior to the current one, the original individual is replaced with the new one.

$$\begin{aligned} P_{i-new} &= c \times P_i + (1 - c) \times P_j \\ P_{j-new} &= c' \times P_j + (1 - c') \times P_i \end{aligned} \quad (27)$$

- 6 Repeat operations of steps (3) to (5) for new population, and judge whether it has reached specified termination conditions, such as fitness value of the optimal individual has been less than a certain critical value. If yes, move to next step, otherwise, continue to repeat operations (3) to (5).
- 7 Individual ranked the first in finally obtained population was regarded as the optimal individual to obtain final values of parameters.

4 Experimental results

In this section, relevant experiments will be presented. Firstly, test data set was briefly introduced. Then, evaluating standard is presented. Finally, a comparative experiment was carried out on the algorithm proposed in this paper from three aspects, and the corresponding experimental results and analysis were given.

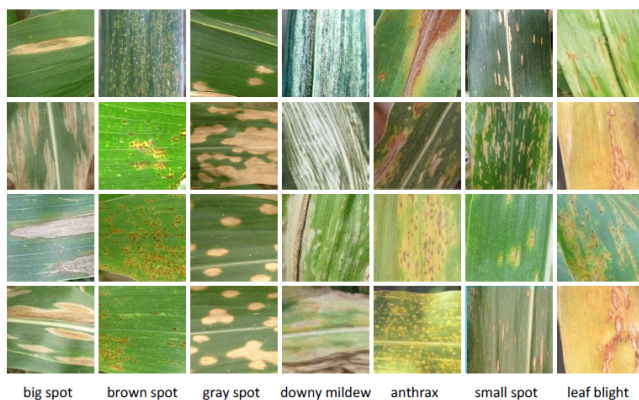
4.1 Test dataset and evaluation method

At present, PlantVillage (Hughes and Salathe, 2015) is the only open data set in the field of crop leaf disease identification, whose data are mainly derived from plant disease leaves in laboratory environment, under different plant species, disease categories, disease degrees and other conditions. However, it is relatively chaotic and noisy and not convenient to use. Therefore, a temporary test dataset is established in this paper, which takes corn as research object. Image sources mainly include Internet and field

photography. Leaf disease spot images of seven common maize diseases were collected in the dataset (big spot, brown spot, grey spot, small spot, downy mildew, anthrax and leaf blight). Number of images varies for each type of lesion, and generally around 200. Figure 1 is an example of some of the images in the test dataset.

Recognition accuracy is commonly used evaluation standard for crop leaf diseases recognition. The same experiment is repeated several times, suppose that after n experiments, number of success is m , then recognition accuracy can be expressed as $p = m/n$. In order to ensure effectiveness of the results, above steps could be repeated to obtain average recognition accuracy.

Figure 1 Some typical maize disease images in our test dataset (see online version for colours)



4.2 Display and analysis of experimental results

In the field of crop leaf disease recognition based on machine vision, it is difficult to find some classical open algorithms, which can be used for comparison. Therefore, experimental comparison of this paper is following two aspects.

Firstly, in order to show influence of different feature representation schemes on recognition results, four different feature representation schemes were compared, and they used unified feature matching scheme proposed in this paper. The first three are using colour, texture or shape individually, and the fourth is multi-feature fusion. For single-feature scheme, only quadratic distance function is required, while for multi-feature fusion scheme, the final fused distance function is required as well.

Then, in order to show influence of different feature matching schemes on recognition results, three different features matching schemes were compared. They are multi-feature fusion matching scheme proposed in this paper, Adaboost classification (Freund and Schapire, 1995) based scheme and SVM classifier (Joachims, 1998) based scheme. And they all used multi-feature fusion representation scheme.

Table 1 shows the comparison of recognition accuracy of different feature representation schemes. Among them, 'fusion' refers to multi-feature fusion scheme proposed in this paper. 'Colour' refers to only colour feature, and 'texture' and 'shape' are the same. For each feature

representation scheme, recognition accuracy of seven different maize diseases was given.

As can be seen from Table 1, 'fusion' has the highest recognition accuracy. 'Shape' rank second, while 'colour' and 'texture' are lower. This shows that, for seven common maize diseases listed in the table, simple colour and texture feature are not highly distinguishable, while shape feature is more advantageous. However, multi-feature fusion scheme can achieve the best recognition effect. It can also be seen that recognition accuracy of the same scheme varies greatly for different kinds of diseases. This phenomenon may have two reasons. One is that image features reflected by some diseases are not very obvious, leading to low distinguishable degree of extracted features. Second, data set is not big enough, which leads to unsatisfactory training results.

Table 2 shows recognition accuracy of different feature matching schemes. Among them, 'OurMethod' refers to multi-feature fusion scheme proposed in this paper, and the other two algorithms are SVM and Adaboost classifier, which are commonly used in image recognition.

It can be seen from Table 2, OurMethod has the highest recognition accuracy. SVM came in second, and Adaboost was a little lower. This indicates that it is meaningful to improve recognition accuracy by optimising weights of different features, so that different features make different contributions in matching.

Table 1 The recognition accuracy comparison of different feature representation schemes

	Recognition accuracy (%)			
	Big spot	Brown spot	Gray spot	Small spot
Colour	68.57	66.52	64.55	68.86
Texture	69.25	69.36	67.18	68.65
Shape	87.57	76.24	77.52	88.95
Fusion	90.78	78.56	80.35	91.02
	Downy mildew	Anthracnose	Leaf blight	
	Colour	64.25	63.55	60.58
Texture	65.14	66.82	61.63	
Shape	73.58	84.65	69.96	
Fusion	76.31	89.15	72.19	

Table 2 The recognition accuracy comparison of different feature matching schemes

	Recognition accuracy (%)			
	Big spot	Brown spot	Gray spot	Small spot
OurMethod	90.78	78.56	80.35	91.02
SVM	88.21	75.32	77.36	90.26
AdaBoost	83.54	71.68	72.53	88.57
	Downy mildew	Anthracnose	Leaf blight	
	OurMethod	76.31	89.15	72.19
SVM	72.38	86.34	70.65	
AdaBoost	73.69	83.97	70.08	

5 Conclusions

A multi-feature fusion recognition scheme of crop leaf diseases was proposed in this paper. First of all, method combining ultra-green feature and threshold segmentation was proposed for segmentation of leaf lesions. Then, multi-feature fusion representation scheme is presented, which integrates colour, texture and shape features. For colour features, colour invariant moment is given to describe colour invariance, which combines RG chromaticity space and moment invariant theory. For texture features, feature representation method combining grey level co-occurrence matrix and LBP is proposed. For shape features, basic algorithm of feature extraction, contour tracking algorithm is improved. Finally, feature matching scheme based on multi-feature fusion is presented. Two similarity measurement functions are learned by using evolutionary algorithm. One is used to measure similarity of various features, and the other is used to measure similarity of multiple features after fusion.

Method proposed in this paper is experimentally compared from two different angles by using recognition accuracy. One is to compare influence of different feature representation schemes on recognition effect, the other is different feature matching scheme. It can be seen from experimental results that multi-feature fusion scheme of crop disease recognition based on evolutionary algorithm proposed in this paper has good recognition accuracy and is an effective method.

Although the research work in this paper has a certain promotion effect on crop leaf diseases recognition, there are still some problems which need to be further improved. First of all, evolutionary algorithms need to be further studied and applied. Improve traditional evolutionary algorithm, and apply it reasonably to target optimisation of each link of image recognition, so that it can make a greater contribution to improving recognition accuracy. Secondly, it is necessary to build a test data set for crop leaf diseases recognition. At present, there is no good data set for crop leaf diseases recognition, which makes it very inconvenient to carry out relevant experiments.

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