RAPID RECOGNITION OF TOMATO'S DISEASE STAGES BASED ON THE KERNEL MUTUAL SUBSPACE METHOD

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Research**

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HIGHLIGHTS

- A low time complexity and high accuracy recognition method of tomato's disease stages was proposed.
- Small number of disease image samples can support a stable and high accuracy method with less computation time and less memory cost.
- Provided a solution to establish a real-time and low energy consumption disease recognize system.

ABSTRACT. Disease stages recognition of tomato is important for the timely diagnosis and prevention of tomato diseases. In this article, the color and texture features were extracted, and the kernel mutual subspace method (KMSM) was introduced to establish a rapid Tomato's disease stage recognition method. Firstly, the color and textural features were extracted from tomato leaf and mapped to a high-dimensional space using a Gaussian kernel function. Secondly, a nonlinear disease feature subspace was established by applying principal component analysis (PCA) based on the mapped high-dimensional space. Finally, disease stages are recognized by calculating the canonical angles between the testing subspace and reference sub-spaces. To validate recognition rate of the proposed method, we conducted 10-fold cross-validation for experiments using the tomato disease sets contained in PlantVillage and artificial intelligence (AI) Challenger 2018 datasets. Also compared with the support vector machine (SVM) and VGG 16 methods, the results show that, accuracy of those three evaluated methods on the PlantVillage datasets are 99.34%, 89.2%, and 97%, respectively; and accuracy on the AI Challenger 2018 datasets are 98.66%, 71.14%, and 73.93%, respectively. Moreover, average training and recognition time of the proposed method is 0.1496 and 0.008 s, respectively, which is faster than SVM and VGG16 methods. In conclusion, the proposed method can be carried out in real-time recognition intelligent equipment which requires less memory space, less computation time, and with higher recognition rate, and low energy consumption.

Keywords. Color and textural feature, High dimensional feature space, Kernel mutual subspace method, Tomato's disease stages recognition,.

Tomatoes are a widely planted vegetable throughout the world, with the decreased quality and yield, the economic profit of is impacted by untimely diseases (Barbedo and Arnal, 2016; Kumar and Vani, 2019; Liu and Wang, 2020; Luna-Benoso et al., 2021). There are all kinds of tomato leaf diseases, such as tomato yellow leaf curl disease and powdery mildew, it's difficult to make a distinction (Juan et al., 2010; Mabvakure et al., 2016; Canizares et al., 2015). In a traditional agricultural production process, different stages of tomatoes disease are judged by experience or experts, which often leads to misdiagnosis. Besides, extensive experience is required for tomato disease stage judgement, and supports precision pesticide spray ap-

plication with high demand skills. Due to fast spread of diseases, the best control period for tomato diseases is short (Fuentes et al., 2018; Karthik et al., 2020). By means of computer-vision technology, tomato leaf spot features are extracted and identified automatically (Rangarajan et al., 2018; Tm et al., 2018), subjectivity of the diagnosis and dependence on experts are eliminated, and the diseases are identified in a timely and accurate approach. Precise pesticide spraying can control diseases and pests, but they also greatly reduce the dosage of pesticides and reduce environmental pollution. Plant diseases usually come with different symptoms, such as color change, shapes and texture change, which can be extracted and utilized by computer version (Deng et al., 2016; Everton et al., 2017 Hassanien et al., 2017; Pantazi et al., 2019; Kasinathan and Uyyala, 2021). In recent years, the research on the application of machine learning and deep learning methods in disease identification has made great progress and achievement, such as the support vector machine (Deng et al., 2016; Hassanien et al., 2017; Kasinathan and Uyyala, 2021), K-NN (Deng et al.,

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Table 1. Summary of proposed models and accuracy in disease recognition.

Author	Classifiers	Features Extraction/ Training Mechanism	Accuracy of the Model	Merit	Demerits
Conventional Methods					
Luna-Benoso et al. (2021)	Three classifiers (MLP, K-NN, SVM) are used to decide the output by means of a decision rule.	GLCM Gray Level Co-occurrence Matrix (GLCM) and Color moments.	86.45% (Healthy leaves and diseased leaves), 97.39% (type of diseases).	High accuracy with the type of disease.	Low accuracy on healthy and diseased.
Pantazi et al. (2019)	One Class Classifier.	Local Binary Patterns (LBPs).	95%	High generalization behavior.	Has not been extended to crop status detection.
Deng et al. (2016)	C-SVC.	Texture and histogram of the color space (gray and HSI)	91.93%	Low cost and low computational complexity.	Lower accuracy of classification.
Hassanien et al. (2017)	KNN	Moth-Flame Optimization and rough set (MFORSFS)	91.5%	Robustness and faster convergence.	Low accuracy.
Kasinathan and Uyyala (2021)	Base classifiers and ensemble classifiers were applied to decide the output by majority voting. Base classifiers: Naive Bayes (NB), SVM, KNN and MLP; Ensemble classifiers: Random forest (RF), Bagging and XGBoost.	The combination of texture, color, shape, HOG and GIST.	High classification and identification of insects.	Accuracy is improved by majority voting with ensemble classifiers.	NIL
CNN-based Methods					
Liu and Wang (2020)	MobileNet V2-YOLOV3.	Mixed training and transfer learning.	93.24% (F1), 91.32% (AP), 86.98% (IOU).	Achieved a good balance between accuracy and real-time detection.	Accuracy is reduced.
Kumar and Vani (2019)	1. LeNet; 2. VGGNet; 3. ResNet50; 4. Xception.	Training from scratch	99.25% (fine tuned VGGNet).	High accuracy	Consumes much time and requires high end hardware configuration.
Fuentes et al. (2018)	1. FRCNN; 2. Refinement Filter Bank.	Training from scratch.	96.25% (Mean AP).	High accuracy.	The processing stage takes much time.
Rangarajan et al. (2018)	1. AlexNet; 2. VGG16.	Pre-trained; Fine tuning.	97.29% (VGG16), 97.49% (AlexNet).	High accuracy on AlexNet.	The number of images significantly affected the performance of the models.

2016), ensemble learning (Fuentes et al., 2018; Rangarajan et al., 2018), and many other methods. Table 1 summarizes previous work and accuracy in disease recognition.

Studies achieve great recognition rates for plant diseases with the use of one or more classifiers. Most of the work shown in the table take advantage of a one-classifier model such as CNN, SVM, K-NN, and MLP among others; other work propose to carry out a model with multi-classifiers and decide the output through a decision rule or majority voting (Luna-Benoso et al., 2021; Kasinathan and Uyyala, 2021), which achieve better results than one-classifier model with the sacrifice of time. In this article, we proposed a one-classifier method which can achieve better accuracy than multi-classifiers model with less computation time.

Although the CNN-based method has achieved good results in plant disease detection as a robust method, there are still many constraints, including: (1) The system is complex and has a large amount of computation, which requires high

requirements on the operating platform and operating environment, and usually requires a GPU computing core; (2) A large number of high-resolution image are needed, and the time complexity of training and recognition is high, which cannot meet the standard of the real-time system at present.

On the other hand, compared with deep learning methods, the advantages of machine learning method are mainly reflected in the following aspects: (1) The requirement of running platform and running environment is not high, and the system could run in the conventional computer and terminal equipment; (2) Small sample data set could achieve high recognition accuracy, and the training time and recognition time are shorter, which could meet the standard of real-time system.

As the training and recognition process of KMSM model are not dependent on GPU, the low-configuration system could also practice real-time operation. At the same time, the model generates the principal component features of the recognized objects based on the image set, which is conducive

to the recognition of local shape differences. Therefore, in this article, we employed the KMSM to classify the different stages of tomato diseases (early stage and advanced stage) to realize the accurate and rapid recognition. So far, there are many researches for disease recognition, but few researches conducted for different stages disease detection, the early stage tomato disease reveals weak features and is challenging to identify. Accurate identification of diseases at early stage is critical for timely prevention, and further reduce productive losses.

The methodology is divided into three stages: Firstly, the low-dimensional color features of disease leaves are extracted, which including the color moment (CM), color coherence vector (CCV) and histogram of oriented gradient (HOG). Secondly, the kernel mutual subspace method (KMSM) is utilized to map the extracted features to a high-dimensional feature subspace and established a nonlinear tomato disease feature subspace. Finally, by calculating the minimum regular angle between the training and testing nonlinear feature subspace, disease can be recognized and classified into different stages (early stage and advanced stage). The model takes full advantage of the robustness of KMSM to the image shooting angle and illumination conditions, combined with the color and texture characteristics of tomato leaves, it can realize rapid and efficient tomato leaf disease identification, and small size disease image samples can support stable and high accuracy system, with less computational cost and storage requirement.

MATERIALS AND METHODS

DATASETS

Plant Village (Hughes and Salathe, 2015) is a disease type datasets that includes 10 types: tomato bacterial spot (TBS), tomato early blight (TEB), healthy tomato (TH), tomato late blight (TLB), tomato leaf mold (TLM), tomato septoria leaf spot blight (TSL), tomato spider mites two spots spider mite (TSM), tomato target spot bacteria (TTS), tomato mosaic virus (TMV) and tomato yellow leaf curl virus (TYV). All images in the datasets are taken under natural light conditions with simple backgrounds. Each picture contains only one tomato leaf, and the leaf is located at the center of the picture.

AI Challenger 2018 (Singkek sci-tech, 2020) (<https://challenger.ai/competition/pdr2018>) is a disease stage datasets that includes nine groups of diseases with general (early) and serious (advanced) stages, and one tomato mosaic virus and one healthy class. The image collection method is the same as that in PlantVillage. After pre-processing the datasets of tomato diseases with 14 categories was extracted from AI Challenger 2018, includes:

- healthy tomato (TH),
- tomato early blight fungus general (TEBg), tomato early blight fungus serious (TEBs),
- tomato late blight water mold general (TLBg), tomato late blight water mold serious (TLBs),
- tomato leaf mold fungus general (TLMg), tomato leaf mold fungus serious (TLMs),
- tomato Septoria leaf spot fungus general (TSLg), tomato Septoria leaf spot fungus serious (TSLs),

- tomato spider mite damage general (TSMg), tomato spider mite damage serious (TSMs),
- tomato yellow leaf curl virus general (TYVg), tomato yellow leaf curl virus serious (TYVs),
- tomato mosaic virus (TMV).

COLOR AND TEXTURE FEATURE EXTRACTION

As leaf diseases often show changes in the colors, shapes and textures, which are widely utilized for plant disease classify. The color features extracted in this article include the RGB color moments (CM) (Stricker and Orengo, 1995) and the color coherence vector (CCV) (Pass et al., 1997). The textural features extracted in this article are using the histogram of oriented gradients (HOG) (Dalal and Triggs, 2005).

Color Feature Extraction

At different disease stage, the disease leaf and spots on it may express different colors; usually leaf spot with an advanced stage disease express darker color. Figure 1 shows TEBg - tomato early blight fungus (general-early stage and serious-advanced stage) images in AI Challenger 2018. At the early stage of TEBg, small black spots appeared on the leaves and gradually expand to concentric ring spots with yellow or light green halos around; at the late stage of TEBs, irregular round or oval spots of dark brown accompanied by gray black mold. It can be found that, the color feature is acute to distinguish the disease types and stages, which can utilize color feature for early detection of tomato diseases.

The color moment (CM) was proposed by Stricker and Orengo (1995), was verified as an effective color feature. This method uses the concept of the moment in linear algebra to express the color distribution in an image with its moment. Because the color information is mainly distributed in low orders, the first-order color moment (average), the second-order color moment (variance) and the third-order color moment (skewness) are sufficient to describe the color distribution of one image. The mathematical definition is as follows (Stricker and Orengo, 1995) :

$$\mu_i = \frac{1}{N} \sum_{j=1}^N p_{i,j} \quad (1)$$

Figure 1. (a) Tomato early blight fungus general and (b) tomato early blight fungus serial.

$$\sigma_i = \left(\frac{1}{N} \sum_{j=1}^N (p_{i,j} - \mu_i)^2 \right)^{\frac{1}{2}} \quad (2)$$

$$s_i = \left(\frac{1}{N} \sum_{j=1}^N (p_{i,j} - \mu_i)^3 \right)^{\frac{1}{3}} \quad (3)$$

where N is the number of pixels P in the image, P_{ij} are the i -th color component of the j -th pixel of the color image, μ_i is the first-order color moment, σ_i is the second moment of color; s_i is the third moment of color. The advantage of this method is that it does not require color space quantization, and low dimension of feature vector.

The color coherence vector (CCV) is a more complex color histogram that contains the spatial information of the color distribution to overcome disadvantage of CM model where the color histogram cannot express the spatial position of the image color. It classifies each pixel into coherence pixels or incoherence pixels. The color coherence vector (CCV) formula of image is as follows (Pass et al., 1997):

$$\langle (a_1, b_1), \dots, (a_n, b_n) \rangle \quad (4)$$

where (a_i, b_i) is the coherence vector pair of the corresponding cluster. In this article, the aggregation threshold is 1 and the quantization level is 50.

Texture Feature Extraction

The histogram of oriented gradients (HOG) was proposed by the French researcher DALAL in CVPR in 2005. The HOG is a feature descriptor in image processing for image textures. Compared with other feature description methods, the HOG feature has many advantages for disease classify. First, the HOG is operated on the local grid element of image, it maintains good invariance to the geometric and optical deformation. Second, fine directional sampling and

strong local optical normalization are conducted by coarse spatial sampling, the sparse and small angular variance during acquisition process can be absorbed and classification results is improved. Its main idea is that the edge or contour of an image has a large gradient change. Therefore, the gradient direction histogram of the local area of the image is calculated to generate features. The edge or contour information of a leaf disease is described by the gradient of the pixel points (x, y) in the image:

$$G_x(x, y) = H(x+1, y) - H(x-1, y) \quad (5)$$

$$G_y(x, y) = H(x, y+1) - H(x, y-1) \quad (6)$$

The formulas $G_x(x, y)$, $G_y(x, y)$, and $H(x, y)$, respectively, represent the horizontal gradient, vertical gradient and image value of pixel (x, y) in the input image. The gradient amplitude and direction at pixels (x, y) are calculated as:

$$G(x, y) = \sqrt{G_x(x, y)^2 + G_y(x, y)^2} \quad (7)$$

$$\alpha(x, y) = \tan^{-1} \left(\frac{G_y(x, y)}{G_x(x, y)} \right) \quad (8)$$

In this article, the process of hog feature extraction is illustrated as follows: the sample image is divided into many cells of 64×64 pixel, and the gradient direction is divided into 9 intervals (bins) on average. In each cell, histogram statistics are calculated for the gradient direction of all pixels in each direction interval, and a 9-dimensional feature vector is obtained. Each 4 adjacent cells form a block, and the feature vectors in a block are connected to obtain 36-dimensional feature vectors. The sample image is scanned with blocks, and the scanning step is one cell. Finally, the features of all blocks are concatenated to obtain the image features.

Figure 2. Textural features (HOG) of tomato leaf diseases.

Figure 2 shows the HOG of general and serious tomato leaf diseases images in AI Challenger 2018. In figure 2, the HOG features as an array of rose plots, each rose plot shows the distribution of edge directions within a cell, the distribution is visualized by a set of directed lines whose lengths are scaled to indicate the contribution made by the gradients in that particular direction, the line directions are fixed to the bin centers of the orientation histogram and are between 0 and 360 stages measured counterclockwise from the positive X axis. In figure 2, each leaf image was divided into 16 cells, the distribution of edge directions are different in 16 cells of each image. It could find that HOGs can be clearly distinguished for different edges and outlines of leaves.

KMSM RECOGNITION MODEL

The kernel mutual subspace method (KMSM) (Wolf and Shashua, 2003; Marukatat, 2016) is an appearance-based method for classifying set of images or modes. As feature patterns usually have highly nonlinear structure, the nonlinear classification problem of multiple pattern sets is required to conquer. The KMSM is a nonlinear classifier extension from the mutual subspace method (MSM) (Oja, 1983; Maeda and Watanabe, 1985) by introducing kernel equation, with potential to solve the nonlinear classification problem.

The MSM is a well-known method for object recognition based on image sets, used widely for solving various pattern recognition problems, whose input subspace was generated from a set of input patterns as a class (Watanabe, 1973). It classifies an input pattern vector into several classes, based on the minimum distance or angle between the input pattern vector in each class subspace, where a class subspace corresponds to the distribution of pattern vectors of the class in high dimensional vector space (Fukui and Yamaguchi, 2015). The relationship between two sub-spaces is strictly defined by the multiple canonical angles (Chatelin et al., 2012), which is an extension of the angle between two vectors. Therefore, in the MSM method, the structural similarity between the distributions of the image patterns is measured by the canonical angles θ between two the eigenvectors P registered as a dictionary and the eigenvectors Q obtained from the input data (fig. 3).

Figure 3. MSM classification model.

In the m-dimensional feature subspace, a d_p -dimensional linear input subspace P and a d_q -dimensional linear reference subspace Q are given. The definition of the canonical angles

$\{0 \leq \theta_1, \dots, \theta_{m_p} \leq \frac{\pi}{2}\}$ between P and Q is (Maeda and Watanabe, 1985):

$$\cos(\theta_k) = \max_{u \in P} \max_{v \in Q} u^T v \quad (9)$$

where $u_i^T u_i = v_i^T v_i = 1$, $u_i^T u_j = 0$, $v_i^T v_j = 0$, $i \neq j$, $i = 1 \sim d_p$, and $i = j \sim d_q$, and d is the dimensional of the subspace for recognition. u_i and v_i represent the i -th dimensional orthogonal basis vectors of sub-spaces P and Q , respectively. These orthogonal basis vectors are the eigenvectors of covariance matrix $\sum_{i=1}^l x_i x_i^T$, which can be calculated using the l -learning pattern $\{x\}$ of each class.

In the subspace method, a subspace with d -dimensional vectors is selected according to a criterion such as the cumulative contribution rate from the eigenvectors, which are obtained by using principal component analysis (PCA) on the entered images (Fukui and Yamaguchi, 2015; Yamaguchi et al., 1998; Scholkopf et al., 1998), which is a powerful technique for extracting structure from possibly high-dimensional data sets (Schölkopf et al., 1998). It is readily performed by solving an eigenvalue problem or using iterative algorithms that estimate principal components. It is often the case that a small number of principal components is sufficient to account for most of the structure in the data, for the eigenvector with largest eigenvalue captures the most variation among training vectors, and eigenvector with smallest eigenvalue has least variation. These principal components characterize how the images data are distributed. For instance, the principal components would be the variance along the x - and y -axis for image set that are Gaussian distributed in 2D space. Figures 4 and 5 show the top 20 principal component feature maps in each training datasets of tomato late blight water mold (general and serious) with

Figure 4. The first 20 principal components of TLBg in the training data.

Figure 5. The first 20 principal components of TLBs in the training data.

225 training images in a 2D space. The components are ordered by their importance from top-left to bottom-right. We see that the first few components seem to primarily indicate lighting conditions, the remaining components pull out certain identifying features: shapes, textures, edge, etc.

The MSM performs well in pattern recognition, which has been utilized to compare small variations in the training data and recognition target data, and this results in a powerful recognition technique in the condition that the data distribution can be linearly approximated, when multiple data can be taken as target image inputs. To solve this problem, Wolf and Shashua (2003) proposed the kernel mutual subspace method (KMSM). In the KMSM, PCA is applied to the high-dimensional space F to generate a nonlinear subspace that contains the nonlinear distribution of each set of image patterns. The input pattern is mapped to a high-dimensional (in some cases infinite) feature space via nonlinear mapping. Therefore, the KMSM uses the Karenina-Loeve (KL) expansion namely PCA to perform the MSM on the nonlinear subspace generated by the mapping pattern $\{\phi(x)\}$. This is a suitable method to solve the nonlinear clas-

sification problem of multiple groups of patterns. The theoretical basis of the KMSM is kernel principal component analysis (KPCA), as shown in figure 6. KPCA is a nonlinear extension of principal component analysis that can mine the nonlinear information from datasets.

The nonlinear function ϕ maps the pattern $x = (x_1, \dots, x_n)^T$ of the n -dimensional input space Γ to the f -dimensional feature space $F : \phi : R^n \rightarrow R^f, x \rightarrow \phi(x)$. To analyze the principal components of the mapped pattern, it is necessary to calculate the inner product $(\phi(x), \phi(y))$ between the function values. However, this kind of calculation is challenging because the dimension f of the feature space may be very high or even infinite. If the nonlinear mapping defined by the kernel function $k(x,y)$ satisfies the Mercer condition, then the inner product $(\phi(x), \phi(y))$ can be calculated by the inner product $(x \cdot y)$, this is called the “kernel technique.”

In general, the Gaussian kernel function, which maps the samples to a higher dimensional space non-linearly, is the best choice (Sakano et al., 2010; Zhang et al., 2018). The linear kernel function is a special case of the Gaussian kernel function for linear separation. Compared with the polynomial kernel function, the Gaussian kernel function needs to determine fewer parameters. The phenotype of the sigma kernel function is very similar to that of the Gaussian kernel function with certain parameters, thus this article adopts the Gaussian kernel function, which is as follows:

$$K_{ij} = \exp \left(-\frac{\bar{x}_i - \bar{x}_j^2}{\sigma^2} \right) \quad (10)$$

where $\bar{x}_i$ and $\bar{x}_j$ are the sample image vectors, and σ is the radius of the Gaussian kernel function.

RESEARCH DESIGN FOR COLOR TEXTURE BASED KMSM METHOD

The color texture based KMSM research approach involves two components: the learning phase and the recognition phase (fig.7). In the subspace method, multiple images were required for testing, and we noted that ten images were optimal for use in this application.

The learning phase involved three stages: First, the processed training images of each class $C \in \{1, \dots, N\}$ were input to the system. Second, for each class, the color and texture feature matrix was calculated by extracting from each image. Finally, the KPCA was applied to the color texture feature matrix generated in the second step, establishing a nonlinear subspace as a reference subspace for each class.

The recognition phase included four stages: First, all of the collected testing images of $I_j \in \{1, \dots, J\}$ were input into the system, and each I had features $\{f_1, \dots, f_n\}$. Second, test matrix MI was generated by extracting color and texture feature from f_i . Then, KPCA was applied to establish the nonlinear subspace for testing the subspace for each testing set. Finally, the canonical angles between the current testing subspace and each reference subspace were calculated. The current testing image set was assigned to the class with whom it shared the smallest canonical angles, which indicated that it had the high test similarity when referenced to the training datasets.

Figure 6. KMSM classification model.

Figure 7. Flowchart of the KMSM classification model.

EXPERIMENT AND RESULT ANALYSIS

EXPERIMENTAL ENVIRONMENT

In the experiment, the tomato diseases datasets in PlantVillage datasets and AI Challenger 2018 datasets were used to validate the effectiveness of the proposed color texture KMSM model, experiments were conducted for both disease types recognition and stages of disease recognition. The evaluation was based on the computation time, the recognition rate, and the recall and F1 value. The 10-fold cross-validation was applied to evaluate the proposed model performance, the original sample is randomly partitioned into 10 equal size sub-samples $S = \{S_i\}$, $i=1, \dots, 10$. Of the 10 sub-samples, a single sub-sample is retained as the validation data for testing the model, and the remaining 9 sub-samples as training data. The cross-validation process is then repeated 10 times, the 10 results from the folds can then be averaged to produce a single estimation.

For the setting of the experiments, the image features extracted in this article include the following: the color moment feature (CM, length:9), the color coherence vector (CCV, length:100), and the texture HOG feature (HOG, length:324). Then combined them into a 433×1 column vector CM+CCV+HOG as the color texture feature vector of each image.

In this research, the experimental platform is a PC with an Intel (R) core (TM) i7-7700 CPU @ 3.60 GHz and 8.0 GB of RAM.

TOMATO DISEASE TYPES RECOGNITION

The PlantVillage datasets of tomato diseases includes nine kinds of tomato diseases and one kind of healthy leaf. One thousand images were selected for each class of tomato disease datasets for a total of 10000 images (1000 images $\times$ 10 classes).

Figure 8 shows the experiment results by using the proposed method on the PlantVillage, which include three parts: the average results of the 10-fold cross-validation for each class, the best accuracy with sub-samples S_6 and the average accuracy for all 10 categories AC. The results AC showed that the average recognition rate of the 10-fold cross-validation is 98.5%, and the average recognition rate of the best accuracy with sub-samples S_6 is 99.34%, the precision is 99.26%, the recall is 99.23%, the F1 score is 99.25%, see as table 2. Figure 9 shows the confusion matrices of with testing sub-samples S_6 , it shows that a tomato bacterial spot (TBS) was recognized as tomato target spot bacteria (TTS) once, and tomato leaf mold (TLM) was mistakenly recognized as a healthy tomato (TH) four times and tomato late blight (TLB) once.

Figure 8. Comparison of the recognition rate between the validation set and sub-sample S_6 in PlantVillage.

	TBS	TEB	TH	TLB	TLM	TSL	TSM	TTS	TMV	TYV
TBS	90 (98.9%)	0	0	0	0	0	0	1	0	0
TEB	0	91 (100%)	0	0	0	0	0	0	0	0
TH	0	0	91 (100%)	0	0	0	0	0	0	0
TLB	0	0	0	91 (100%)	0	0	0	0	0	0
TLM	0	0	4	1	86 (94.5%)	0	0	0	0	0
TSL	0	0	0	0	0	91 (100%)	0	0	0	0
TSM	0	0	0	0	0	0	91 (100%)	0	0	0
TTS	0	0	0	0	0	0	0	91 (100%)	0	0
TMV	0	0	0	0	0	0	0	0	91 (100%)	0
TYV	0	0	0	0	0	0	0	0	0	91 (100%)

Figure 9. Confusion matrix of the sub-sample S_6 on PlantVillage using the proposed method.

Table 2. The recognition results on sub-sample S_6 in PlantVillage using the proposed method.

The Proposed Method	Accuracy (%)	Precision (%)	Recall (%)	F1 Score (%)
PlantVillage S_6	99.34	99.26	99.23	99.25

STAGES OF TOMATO DISEASE RECOGNITION

In this experiment, the AI Challenger 2018 tomato disease datasets was used, through preprocessing, 6 groups (general and serious) of tomato diseases, 1 tomato mosaic virus group and 1 healthy tomato group were selected for a total of 14 categories: TH, TEBg, TEBs, TLBg, TLBs, TLMg, TLMs, TSLg, TSLs, TSMg, TSMs, TYVg, TYVs, TMV. For the processed datasets, 250 disease pictures were selected for each category, forming a total of 3500 tomato disease images (250 images×14 classes).

Figure 10 shows the experiment results by applying the proposed method on the AI Challenger 2018. The results also include three parts: the average results of the 10-fold cross-validation for each class, the best accuracy with sub-samples S_{10} and the average accuracy for all 14 categories AC. The results of AC show that the average recognition rate of 10-fold cross-validation is 96.1%, and the average recognition rate of the best accuracy with subsamples S_{10} is

98.66%, the precision is 98.87%, the recall is 91.51%, the F1 score is 95.05% (table 3). In the test set sub-samples S_{10} , only tomato late blight had a slightly lower recognition rate, and the recognition rates of the other 13 categories were 100%. Figure 11 shows the confusion matrixes of the best accuracy with sub-samples S_{10} , the results that tomato late blight general was mistaken as serious three times, compare to 224 testing images, this mistaken can be accepted, and as the mistaken happen in one disease classes, the characteristics of the disease spots were relatively similar.

COMPARISON WITH DIFFERENT MODELS

Our model is evaluated by comparing with the SVM and VGG16 networks on the PlantVillage and AI Challenger 2018 datasets, and the comparison results are shown in tables 3 and 4, which show the input pattern, model parameters, recognition rate, model training time and average testing time of each model. In this comparative experiment, there are two input patterns for the KMSM model and SVM model to verify the superiority of the color texture feature extracted in this article: pattern one is a 10×10 grayscale image, and pattern two is the color texture feature CM + CCV + HOG. The input pattern of the VGG16 model is a $224 \times 224 \times 3$ RGB image.

According to the experimental results on the PlantVillage datasets in table 4, the recognition rate 99.34% of color texture feature + KMSM is the highest among those three models; while the recognition rate of grayscale image + KMSM 97% is the same as that of VGG16; and the recognition rate 89.2% of color texture feature + SVM is better than that of grayscale image + SVM. The results show that the three classification models have great recognition abilities for tomato disease type datasets. Among these methods, the proposed method has the best performance, and the proposed color texture feature performed well. Regarding the training time, the grayscale image + KMSM model is the quickest, which is 0.369 s; and that of the color texture KMSM model is 0.637 s. Both of these two models are far quicker than the SVM and VGG16. In terms of the average testing time, the color texture feature +KMSM model is 0.04 s, which is still quicker than that of VGG16.

According to the experimental results on AI Challenger 2018 in table 5, the recognition rate of color texture feature

Figure 10. Comparison of the recognition rate between the validation set and sub-sample S_{10} on AI Challenger 2018.

	TH	TEBg	TEBs	TLBg	TLBs	TLMg	TLMs	TSLg	TSLs	TSMg	TSMs	TYVg	TYVs	TMV
TH	16 (100%)	0	0	0	0	0	0	0	0	0	0	0	0	0
TEBg	0	16 (100%)	0	0	0	0	0	0	0	0	0	0	0	0
TEBs	0	0	16 (100%)	0	0	0	0	0	0	0	0	0	0	0
TLBg	0	0	0	13 (81.2%)	3	0	0	0	0	0	0	0	0	0
TLBs	0	0	0	0	16 (100%)	0	0	0	0	0	0	0	0	0
TLMg	0	0	0	0	0	16 (100%)	0	0	0	0	0	0	0	0
TLMs	0	0	0	0	0	0	16 (100%)	0	0	0	0	0	0	0
TSLg	0	0	0	0	0	0	0	16 (100%)	0	0	0	0	0	0
TSLs	0	0	0	0	0	0	0	0	16 (100%)	0	0	0	0	0
TSMg	0	0	0	0	0	0	0	0	0	16 (100%)	0	0	0	0
TSMs	0	0	0	0	0	0	0	0	0	0	16 (100%)	0	0	0
TYVg	0	0	0	0	0	0	0	0	0	0	0	16 (100%)	0	0
TYVs	0	0	0	0	0	0	0	0	0	0	0	0	16 (100%)	0
TMV	0	0	0	0	0	0	0	0	0	0	0	0	0	16 (100%)

Figure 11. Confusion matrix of sub-sample S₁₀ on AI Challenger 2018 by using the proposed method.

Table 3. The recognition results on sub-sample S₁₀ in AI Challenger 2018 using the proposed method.

The Proposed Method	Accuracy (%)	Precision (%)	Recall (%)	F1 Score (%)
AI 2018 S ₁₀	98.66	98.87	91.51	95.05

+ KMSM is 98.66%, that of grayscale image + KMSM is 86.67%, that of the SVM is 71.14% and that of VGG16 is 73.93%, indicating that the SVM and VGG16 have poor recognition abilities on the stage of tomato disease data. In terms of the model training time, grayscale image + KMSM is the quickest; and the color texture feature + KMSM model takes 0.1496 s, which is also far quicker than the SVM and VGG16. In terms of the average testing time, the grayscale image + KMSM model in this article takes 0.0047 s, and the color texture feature + KMSM model takes 0.008 s, which can meet the requirements of real-time system.

Compared with the SVM and VGG16, the color texture feature + KMSM model has a better recognition rate for the type and stage of tomato diseases than the SVM and VGG16; furthermore, it occupies less memory space, has a shorter training recognition time, is more stable and has higher accuracy.

EXPERIMENT ON ARGUMENT IMAGES

To verify the ability of the proposed method on diseases identification, the argument images are utilized to simulate

Table 4. Comparison of different classification models on PlantVillage.

Recognition Model	Image Feature	Recognition Rate (%)	Training Time (s)	Average Test Time (s)
SVM	Grayscale 10×10	69.8	13.956	0.001
	CM+CCV+HOG	89.2	19.663	0.003
VGG16	224×224×3	97	62569	0.185
KMSM	Grayscale 10×10	97	0.369	0.0056
	CM+CCV+HOG	99.34	0.537	0.04

Table 5. Comparison of different classification models on AI Challenger 2018.

Recognition Model	Image Feature	Recognition Rate (%)	Training Time (s)	Average Test Time (s)
SVM	CM+CCV+HOG	71.14	3.4387	0.002
VGG16	224×224×3	73.93	39059	0.18
KMSM	Grayscale 10×10	86.6	0.078	0.0047
	CM+CCV+HOG	98.66	0.1496	0.008

the different camera angles and illumination condition. The experiment was verified based on AI Challenger 2018 Tomato Disease for disease stage identification. With the brightness adjustment and rotation of images, the argument images based on the S₁ was used for test-set.

The image brightness adjustment were conducted by adjust pixels value of: +20, +40, -20 and -40 for R, G, and B channels, respectively. The image rotation is set with small angle and large angle, where the small angle were defined as 1°, 2°, and 3°, and the large angle were defined as 90°, 180°, and 270°. Through the above image argument, the S₁ set was expanded to 3500 (25 images × 14 classes × 10 argument kinds), and the total number of training set images after the argument were 31500 images (225 images × 14 classes × 10 argument kinds).

Table 6 shows the comparison of performance using S₁ test-set at different rotation angles and table 7 shows the comparison of performance by increasing or decreasing of image pixels values in S₁ test-set. In the table, EER (Equal Error Rate) is the Equal Error Rate, by adjusting the threshold, the False Rejection Rate (FRR) is equal to the False Acceptance Rate (FAR). As could be seen from table 6, the model proposed in this article has strong robustness to angle adjustment, and the adjusted average accuracy is 97.77%, slightly lower than the original test image set. However, the average Recall and F1 values are higher than the original test

Table 6. Comparison of experimental results for different rotation of the sample S₁.

Testing Samples			Accuracy (%)	Precision (%)	EER	Recall (%)	F1 (%)
Rotation image	Small Angle	1°	97.77	98.30	0.0455	97.77	98.03
		2°	97.77	98.30	0.0313	97.77	98.03
		3°	97.77	98.30	0.0302	97.77	98.03
	Large Angle	90°	97.77	98.30	0.0402	97.77	98.03
		180°	97.77	98.30	0.0362	97.77	98.03
		270°	97.77	98.30	0.0361	97.77	98.03
	Average Value		97.77	98.3	0.037	97.77	98.03

Table 7. Comparison of experimental results for different brightness of the sample S₁.

Testing Samples			Accuracy (%)	Precision (%)	EER	Recall (%)	F1 (%)
Image after pixel value adjustment	Reduction value/pixels	20	95.09	97.09	0.0495	95.09	96.08
		40	100	100	0.0491	100	100
	Increase value/pixel	20	95.09	96.83	0.0755	95.09	95.95
		40	98.21	98.39	0.0223	98.21	98.3
	Average Value		97.1	98.08	0.049	97.1	97.58

data, and the ERR is lower than the original test image. In table 7, the average accuracy is 97.1%, the average precision is 98.08%, the average Recall is 97.1%, and the average F1 score is 97.58%. Compared with the image set before argument, the recognition rate is slightly lower than that of the test image set. However, both Recall and F1 were higher than the original test image set. On the whole, the adjustment of sample pixels had little effect on the recognition of disease stage, indicating the robustness of the method proposed in this article under different illumination and different shooting positions.

CONCLUSIONS AND FUTURE WORK

CONCLUSIONS

Rapid recognition of tomato disease stages is of great significance to the timely diagnosis and control of tomatoes. To recognize the stage of diseases in tomato, the Kernel Mutual Subspace Method (KMSM) is introduced in this study. The method maps the color feature and texture feature of tomato disease leaves to the high-dimensional feature space, generates a nonlinear subspace by applying principal component analysis on the generated high-dimensional feature space, and calculates the canonical angles between the generated spaces for recognition.

1. In this article, the KMSM is proposed for the fast and stable recognition of the stage of tomato diseases. Compared with the different classification models of the SVM and VGG16 on the PlantVillage and AI Challenger 2018 datasets, respectively, the experimental results show that the proposed method has the best recognition ability for the stage of tomato disease compared to those of the SVM and VGG16.
2. In the PlantVillage tomato disease type datasets, the recognition rate of color texture feature + KMSM is 99.34% and that of grayscale image + KMSM is 97%. In the AI Challenger 2018 stage of tomato disease datasets, the recognition rate of color texture feature + KMSM is 98.66% and that of grayscale image + KMSM is 86.6%, which shows that the color texture feature extracted in this article can distinguish different types and stages of diseases better.

3. In terms of the memory space and running time for the PlantVillage datasets, the training time of grayscale image + KMSM is 0.369 s, and the average testing time is 0.0056 s. The training time of color texture feature + KMSM is 0.537 s. The training times of both of these methods are far lower than those of SVM (19.66 s) and VGG16 (62569 s).
4. The experimental data only include 250 images in each category from the AI Challenger 2018 tomato disease stage datasets for a total of 3500 images (250 images per category × 14 categories). The research results show that the proposed method can use small samples to achieve efficient and high accuracy recognition, which overcomes the problem that large samples are difficult to obtain.
5. To verify the ability of the proposed method to identify diseases using the argument images to simulate the different camera angles and illumination condition. The average accuracy slightly lower, but the average Recall and F1 values are higher than the original test data after conducted the brightness adjustment and rotation of images, indicating that the method proposed in this article has strong robustness to different camera angles and illumination condition.

The proposed method does not require a complicated model parameter training process or tedious parameter setting steps. It has the advantages of small amounts of calculations, a high disease accuracy and better stability. It can play an important role in intelligent terminal applications that have strict requirements for real-time performance, storage space and energy consumption.

FUTURE WORK

Tomato disease stages identification is of great significance for timely diagnosis and control of tomato diseases. In order to identify the disease stage of tomato quickly and stably, a rapid and stable identification method of disease stage of tomato was proposed. However, after adjustment the angle and illumination of the original image, the average accuracy is lower than that of the original image set. This is because the number of test samples is multiplied after adjust-

ing the angle and illumination, which make the sample quality worse. Too large adjustment angle, too bright or too dark illumination condition would lead to the reduction of sample quality, so led to slight lower accuracy. In the future research, we will increase the diversity and number of training samples, and further improve the algorithm to improve the recognition rate.

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