Rice disease classification based on leaf image using multilevel Support Vector Machine (SVM)

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Abstract. Plant disease is one of many factors that decrease the quality and quantity value of agriculture, especially rice plants. Automatic technology based on digital image processing is being developed to overcome this problem. Support Vector Machine (SVM) is one of the most used classifications and detection methods. SVM has been developed into multi SVM by combining several binary SVMs to classify more than two classes. In the proposed system, we use one of the multi SVM strategy, namely One Vs. All. The accuracy of classification reaches 86.10% using linear kernel. It has a higher value of accuracy than using polynomial and RBF kernel function. The scenario for the number of the dataset used is 70% for the training set and 30% for the testing set from a whole 240 images.

1. Introduction

Rice is the majority in Indonesian people's lives, and it is currently experiencing a decrease in the amount of yield production. Indonesia has productive land for farming, especially rice. Data from Badan Pusat Statistik (BPS) in 2018 said Indonesia's rice field area has decreased from 7.75 million hectares to 7.1 million hectares [1]. More than 95% of Indonesia's population consumes rice or is subsequently processed into the rice as a daily staple food [2]. Plant disease is one factor that causes a reduction in the quality and quantity of agricultural products.

Condition's inspection of diseased rice plants was previously carried out conventionally using human labor by checking conditions in fields directly. However, as technology develops, human labor has been replaced by automatic data collection using some image data that can be processed with modern algorithms. In some previous studies, the detection and classification of rice leaf disease have been carried out with various methods. Classification of rice plant diseases by feature extraction of Gray Level Co-occurrence Matrix (GLCM) with four angle intervals has been carried out [3]. Santanu Padhikar [4] has researched the classification process of rice plant diseases based on morphological changes from plants affected by brown spot and blast disease.

One classification method that is often used is the Support Vector Machine (SVM). In previous studies, multilevel SVM applied for wall-following robot navigation data [5] classification. This study using a One-against-one strategy to classify than increase the accuracy and computation complexity so it can improve robot intelligence in wall-following robot navigation data. Other studies have been conducted [6]. This research explains that a one-against-all strategy is more widely used by establishing N binary classifier for N class classification.

In this paper, we investigate the performance of a multilevel SVM classifier using the one-against-all strategy for rice plant disease classification. We set some scenarios to get the best model of a
multilevel SVM classifier. The scenario consists of the use of kernel function and comparison of the data number.

2. Methods

The classification process consists of several stages: image acquisition, image pre-processing, image segmentation, feature extraction, and classification stages. In the classification, the stage is divided into two parts, namely training and testing. Figure 1 displays a block diagram of the whole process of rice diseases classification using multilevel Support Vector Machine.

2.1. Pre-processing

The first input of the entire classification process is the image of diseased rice leaves blight, brown spots, and blast. Leaf image used in the form of a single leaf of rice. In the pre-processing stage, the input image will go through the resize stage, contrast adjustment, and color space transformation.

The first step of the pre-processing stage changes image size based on the desired scale. It means resize the original image into a new image that has a smaller size but on the same scale. It aims at time efficiency. The next step is image adjustment by contrast improvement. It aims to increase image intensity so it can bring out differences for each color scale. The third step is the color space transformation. It means to change color space of image from RGB color space to $L^*a^*b^*$ color space. It aims to get information at $a^*$ and $b^*$ color space because $a^*$ represent color intense in green, red color coordinates, and $b^*$ represent in yellow, blue color coordinates, this factor ease data clustering, and image segmentation process. So the output of this stage is the image in $L^*a^*b^*$ color space.

2.2. Image Segmentation using Fuzzy C-Means (FCM)

The segmentation process is dividing an image into some part based on differences. It aims to distinguish between background and foreground. FCM is introduced by Dunn (1973) and by Bezdek (1981) as the most used method for pattern recognition [7]. Data grouping in FCM is determined based on membership degree, and the value is between 0 until 1. FCM is a fuzzy clustering method allowing a
piece of data belongs to two or more clusters. FCM produces optimal partition by minimizing weight in a group of the objective function:

\[ P_t = \sum_{i=1}^{n} \sum_{k=1}^{c} \left( \frac{1}{m} \sum_{j=1}^{m} (x_{ij} - v_{kj})^2 \right) \left( \mu_{ik} \right)^w \]  

(1)

2.3. Image Extraction

The feature extraction process is carried out to obtain the characteristic value of the object. Characteristics of each disease are different, so the feature extraction takes out the shape, color, and texture feature as feature extraction variables.

2.3.1. Color Feature Extraction

The different color of the infected area with healthy leaf color is a good feature for pattern recognition. Each color space (R, G, and B) stores color information in one of the main color components [8]. Color extraction is obtained by calculating the average pixel value in the image using equation:

\[ \text{mean} = \frac{1}{M \times N} \sum_{i=1}^{N} \sum_{j=1}^{M} p(i, j) \]  

(2)

where \( p(i, j) \) is pixel value for \( i, j \) coordinate, \( M \) is image length, and \( N \) is image width.

2.3.2. Texture Feature Extraction

Haralick first developed a gray Level Co-occurrence Matrix (GLCM) in 1973 [9]. Texture feature extraction often uses GLCM. GLCM obtained by calculating the probability of neighborhood relationship between two pixels at a certain distance and orientation [3]. It built the coocurance matrix \( M \times N \) based on the desired distance \( (d) \) and angle \( (\theta) \). The distance is determined by pixel and angle is determined by 0°, 45°, 90°, or 135°. GLCM feature calculated by:

- Energy

\[ \text{energy} = \sum_{i=1}^{N} \sum_{j=1}^{M} p(i, j)^2 \]  

(3)

- Entropy

\[ \text{entropy} = \sum_{i=1}^{N} \sum_{j=1}^{M} p(i, j) * \log p(i, j) \]  

(4)

- Homogeneity

\[ \text{homogeneity} = \sum_{i=1}^{N} \sum_{j=1}^{M} \frac{p(i, j)}{1 + |i - j|} \]  

(5)

- Contrast

\[ \text{contrast} = \sum_{i=1}^{N} \sum_{j=1}^{M} |i - j|^2 p(i, j) \]  

(6)

- Correlation
\[ \text{correlation} = \sum_{j=1}^{N} \sum_{i=1}^{M} \frac{(i - \mu_i)(j - \mu_j)p(i,j)}{\sigma_i^2 \sigma_j^2} \]  

\[ e = \sqrt{1 - \frac{b^2}{a^2}} \]

2.3.3. Shape Feature Extraction
The shape features are built by calculating the center of the object (centroid), eccentricity, and measuring the axis length. The shape characteristics used are eccentricity and centroid. To calculate eccentricity use equation:

2.4. Disease Classification
Support Vector Machine (SVM) is a binary classification method. It means to classify data into two classes by finding the best hyperplane, as shown in Figure 2. Best hyperplane means one of the biggest margins between two support vectors.

For the multiclass problem, SVM developed into multilevel SVM, especially one-against-all strategy. It evaluates all classifier pairs by inducing \( k \) binary classifier, where \( k \) is the number of classes. The one-against-all architecture shown in Figure 3.

The input data is denoted as \( l(x_1, y_1), \ldots, (x_1, y_l) \) where \( x_i \in R^d, i = 1, 2, \ldots, l \) and target that denoted as \( y_i \in \{1, 2, \ldots, k\} \). It builds optimization for Equation(9) using slack variable \( \xi_i (\xi_i \geq 0) \) or often called soft margin hyperplane.
\[
\min_{w^m, b^m, \xi^m} \frac{1}{2} |w^m|^Tw^m + C \left( \sum_{i=1}^{l} \xi^m_i \right) 
\]

with constrains

\[
(w^m)^T \varphi(x_m) + b^m \geq 1 - \xi^m_i \text{ for } y_i = m, \\
(w^m)^T \varphi(x_m) + b^m \geq -1 + \xi^m_i \text{ for } y_i \neq m, \\
\xi^m_i \geq 0, i = 1, 2, ..., l
\]

Mapped function \( \varphi(x) \) will map input data to a new vector space with higher dimensional using Equation (10)

\[
K(x_i, x_j) = \varphi(x_i), \varphi(x_j) 
\]

It will simplify the classification process with complex data. It means data has many attributes to classify. In this study, the types of kernel functions used are linear, RBF, and polynomial. Following is the equation of each of these kernel functions.

- Linear kernel

\[
K(x_i, x) = x_i^T x
\]

- RBF kernel

\[
K(x_i, x) = (\gamma x_i^T x + r)^p, \gamma > 0
\]

- Polynomial kernel

\[
K(x_i, x) = \exp(-\gamma |x_i - x|^2), \gamma > 0
\]

The multilevel SVM process is used in the training and testing process, as shown in Figure 1. The training process is used to find the best classifier model, where inside it, there are alpha values and other variables. The classifier model is built based on training data.

3. Experiments Design

This paper is classifying the disease into three classes, i.e., blast, blight, and brown spot, as shown in Figure 4. Each disease has its characteristic, but for blast and brown spot almost have in common.

![Figure 4. Image of each disease (a) Blight, (b) Blast, and (c) Brown Spot](image)

Input data are diseased leaf rice images that performance as a feature matrix by going through processes before the classification stage. A total of 240 images consists of 40 blight, 100 brown spots, and 100 blasts. The label or class target consists of three diseases, then denoted as label vector. This disease types showed different feature visuality. This fact is used to determine what feature attribute in the classification stage.
The training and testing process is carried out five times with the data used being random, as shown in Table 1. Average of 5 randomizations will determine the appropriate classification model for rice disease classification cases.

**Table 1.** System testing scenario

| Scenario | Training Data (from 240 images) | Test Data (from 240 images) |
|----------|---------------------------------|-----------------------------|
| 1        | 80 %                            | 20 %                        |
| 2        | 70 %                            | 30 %                        |
| 3        | 60 %                            | 40 %                        |
| 4        | 50 %                            | 50 %                        |

This model performance will evaluate by a testing process based on accuracy, precision, and recall value, as shown below. Testing data is different data from training data. The classifier model is tested with training data separately for evaluating model performances. It should generate 100% of accuracy.

**Table 2.** Confusion matrix for calculate accuracy, precision, and recall value

| Real Value | TRUE | FALSE |
|------------|------|-------|
| Prediction | TP (True Positive) | FP (False Positive) |
| FALSE      | FN (False Negative) | TN (True Negative) |

\[
\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN}
\]

\[
\text{Precision} = \frac{TP_i}{TP_i + FP_i}
\]

\[
\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN}
\]

4. Result and Discussion

The pre-processing stage consists of image resize, contrast adjustment, and color space transformation. Image resize aim for speeding up the next processing time. After the scaling process, a morphological operation process is carried out to remove the background image. Continuing with the contrast adjustment with a contrast value limit of 10%.

![Figure 5](image.png)

Figure 5. Result of pre-processing (a) Resize (b) Morphology (c) Contrast adjustment (d) Color space transforming into L*a*b*

The pre-processing stage is ended by color space transformation and gets a*b* color space for the segmentation process. The result of the segmentation process is shown in Figure 6 (b) below.
In order to compare each value of disease feature horizontally, the result of the feature extraction process shown in Table 3.

Table 3. Feature extraction result using color, shape, and texture feature

| Feature          | Blight   | Brown   | Blast   |
|------------------|----------|---------|---------|
| Mean R           | 197.2505 | 113.1126| 118.9054|
| Mean G           | 152.3522 | 72.1064 | 79.70484|
| Mean B           | 77.23198 | 19.0366 | 27.3562 |
| Contrast         | 0.033664 | 0.001582| 0.002404|
| Correlation      | 0.984689 | 0.937334| 0.966822|
| Energy           | 0.898517 | 0.994139| 0.988409|
| Homogeneity      | 0.99743  | 0.999782| 0.99927 |
| Entropy          | 0.687943 | 0.046457| 0.092905|
| Centroid x       | 726.5486 | 242.4074| 983     |
| Centroid y       | 248.2528 | 551.7037| 2180    |
| Eccentricity     | 27.57214 | 4.975895| 1       |

Data above used in the classification process for training and testing. The next process is classification with a multilevel SVM one-against-all strategy. Performance analysis of the classification model is done by measuring accuracy, precision, and recall. At the feature extraction stage, matrix 240*11 containing information about the features or characteristics of each disease is produced. The feature data has previously been labeled manually according to the type of disease (blight, blast, and brown). The results of the analysis show that the best multilevel SVM classification model for the classification of rice plant diseases in leaf images is by linear kernel function with scenario 2.

Table 4. Accuracy of each kernel function

| Scenario | Accuracy (%) | Linear | Poly | RBF |
|----------|--------------|--------|------|-----|
| 1        | 81.56        | 47.08  | 72.92|
| 2        | 86.10        | 46.11  | 71.67|
| 3        | 80.97        | 43.33  | 66.88|
| 4        | 78.00        | 38.00  | 63.50|
| 1        | 80.83        | 44.58  | 69.17|
| 2        | 74.29        | 43.05  | 67.22|
| 3        | 64.17        | 46.88  | 65.83|
| 4        | 70.67        | 46.67  | 62.67|

Scenario Scaling

No Scaling
### Table 5. Computing Time of Kernel Function

| Scenario | Accurate (%) | Computing Time (s) |  |
|----------|--------------|--------------------|---|
|          |              | Training           | Testing                     |
| 1        | 81.56        | 8.55191            | 0.180972                    |
| 2        | 86.10        | 5.8527             | 0.130413                    |
| 3        | 80.97        | 4.68928            | 0.060691                    |
| 4        | 78.00        | 3.709239           | 0.015835                    |
| 1        | 80.83        | 10.35274           | 0.045616                    |
| 2        | 74.29        | 8.085996           | 0.016518                    |
| 3        | 64.17        | 6.839893           | 0.010026                    |
| 4        | 70.67        | 5.413888           | 0.008903                    |

#### 5. Conclusion

This research has been carried out the application of multilevel Support Vector Machine (SVM) algorithm for classification of rice plant diseases in leaf images. The classification system with multilevel SVM produces performance with an accuracy value of 86.51% for 70% of training data and 30% of test data from total data. The accuracy value is obtained by using a linear kernel in the SVM training process, and through the scaling process in the pre-image processing stage. The computation time is 143.8616 seconds for the process before classification, 5.8527 seconds for the training process, and 0.1304 seconds for the testing process.

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