

# 26\_JURNAL\_2023\_Majority Voting as Ensemble Classifier for Cervical Cancer Classification

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## Majority Voting as Ensemble Classifier for Cervical Cancer Classification

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### Abstract

Cervical cancer is one of the deadliest female cancers. Early identification of cervical cancer through pap smear cell image evaluation is one of the strategies to reduce cervical cancer cases. The classification methods that are often used are SVM, MLP, and K-NN. The weakness of the SVM method is that it is not efficient on large datasets. Meanwhile, in the MLP method, large amounts of data can increase complexity of each layer, thereby affecting the duration of the weighting process. Moreover, the K-NN method is not efficient for data with a large number of attributes. The ensemble method is one of the techniques to overcome the limitations of a single classification method. The ensemble classification method combines the performance of several classification methods. This study proposes an ensemble method with the majority voting that can be used in cervical cancer classification based on pap smear images in the Herlev dataset. Majority voting is used to integrate test results from the SVM, MLP, and KNN methods by looking at the majority results on the test data classification. The results of this study indicate that the accuracy results obtained in the ensemble method increased by 1.72% compared to the average accuracy value in SVM, MLP, and KNN. For sensitivity results, the results of the ensemble method were able to increase the sensitivity increase by 0.74% compared to the average of the three single classification methods. For specificity, the ensemble method can increase the specificity results by 3.4%. From the results of the study, it can be concluded that the ensemble method with the most votes is able to improve the classification performance of the single classification method in classifying cervical cancer abnormalities with pap smear images.

### Keywords

Cervical Cancer, Ensemble Methods, KNN, MLP, SVM

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## 1 INTRODUCTION

Cervical cancer is an abnormal proliferation of cells in the cervix (lower part of uterus/womb) used by the Human Papilloma Virus (Arbyn et al., 2020). The pap smear is a screening test for cervical cancer for women that determines whether or not there are alterations in uterine cells that are at risk of developing into cancer (Demirtas and Acikgoz, 2013). Observation of pap smear cells directly under a microscope requires high accuracy and error range in monitoring. The machine learning approach can be used to recognize cervical cancer in pap smear cells because machine learning has various classification methods. Using the machine learning classification method can help doctors diagnose cervical cancer earlier.

Several studies on cervical cancer classification have been conducted by Wu and Zhou (2017) using the Support Vector Machine (SVM) method and have an accuracy, sensitivity, and specificity of 90.18%, 94.33%, and 85.64% respectively. Ilyasu and Fatchah (2017) used the K-Nearest Neighbors (KNN)

method on the Herlev dataset to classify cervical cancer into two classes. This study produced poor accuracy, sensitivity, and specificity results, namely below 72%. In addition, Asadi et al. (2020) used the multi-layer perceptron (MLP) method with high accuracy, sensitivity, and specificity of 90.9%, 90%, and 91.5% respectively. The SVM, KNN, and MLP methods offer a number of advantages and drawbacks. The advantages of the SVM method include the ability to identify different hyperplanes by maximizing the distance between two different classes and having very good performance on data with two classes (Chen et al., 2020; Yadav and Thareja, 2019). Meanwhile, the weakness of the SVM method is that it is not efficient at working on large amounts of data (Zhang et al., 2018a). The advantages of the KNN method are its simplicity of calculation, relatively high accuracy for data with few labels, and suitability for non-linear situations (Taunk et al., 2019; Wang et al., 2020; Zhang et al., 2018b). The weakness of the KNN method is unable to handle data with a large number of features and is

necessary to choose the appropriate k parameters to achieve high accuracy (Campos et al., 2016; Lee and Styczynski, 2018). The advantage of MLP is suitable for numeric data types and is able to solve non-linear problems (Hemalatha and Rani, 2016; Hussain et al., 2020). Meanwhile, the weakness of MLP takes a very long time to train large amounts of data. Large amounts of data can increase the complexity of each MLP layer and result in a long weighting process (Joshuva et al., 2020; Pham et al., 2017).

A classification problem that uses only one classification method is known as a single classification method. The single classification method has the disadvantage of not having alternative choices to improve performance on the classification results. The ensemble method is one technique to overcome the limitations of a single classification method (Wang and Srinivasan, 2017). The ensemble method is an approach to combine the performance of a single classification method to make the classifier have better performance results (Ferrari and Bacciu, 2021). There are many techniques in the Ensemble Method, namely Majority Voting, Weighted Average, and Ranking (Araque et al., 2017). The advantages of the Majority Voting technique include the ease of implementing a single classification technique and its easy operation by involving the selection of the majority class from each class prediction produced by a single classification method (Raza, 2019). Bora et al. (2017) applied Ensemble with the SVM, MLP, Random Forest, SVM, and KNN methods in the classification of Cervical Cancer with three classes, the results of applying the ensemble method increased accuracy by 9.52% of the average accuracy of six classifier methods. Chandra et al. (2021) combined the SVM, Decision Tree, K-NN, Naïve Bayes, and Artificial MLP to create an ensemble method for Covid-19 classification. The results indicated that with ensemble majority voting, the accuracy increased by 3.93%. Raza (2019) used ensemble and Chi-square methods to classify DDos attacks and was able to increase accuracy by 2.017% to 99.68%. Meanwhile, Karim and Neehal (2019) applied the ensemble method to classify cervical cancer at the University of Caracas with an accuracy of 98.12%.

This study applies the Ensemble Method with the Majority Voting technique in order to overcome the limitations of a single classification. The single classification methods in this study are SVM, MLP, and K-NN methods. There are two labels used, namely normal and abnormal. Each performance result of a single classification method will be measured based on the accuracy, sensitivity, and specificity of each method. The next step is the application of the ensemble method to the performance results of each single classification method by majority voting, namely determining the label of a data based on the most label choices in the test data from each single classification method. The results obtained from the ensemble method are also measured for accuracy, sensitivity, and specificity and then compared with the performance results from the single classification method to find out to what extent the ensemble method with the majority voting is able to improve the performance

results of SVM, MLP, and KNN.

## 2. EXPERIMENTAL SECTION

### 2.1 Materials

The data for this study were derived from the website <http://mde-lab.aegean.gr/index.php/downloads> via Herlev University's data bank, based on Jantzen et al. (2005). The dataset contains 917 images that have been extracted into a.csv file with 21 attributes.

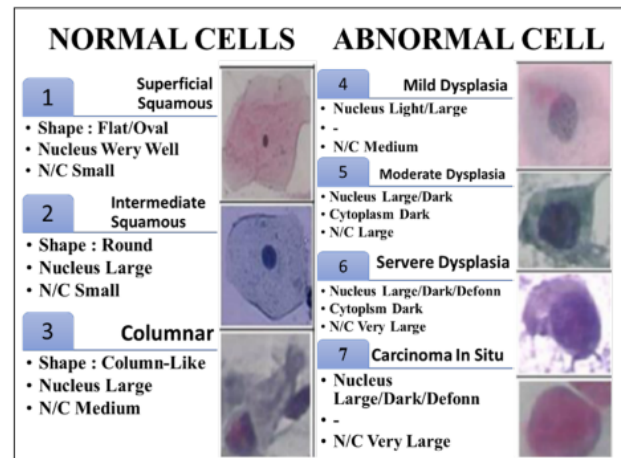


Figure 1. Pap Smear Cell Image from Herlev Dataset

Pathologists have observed cell properties such as cell color, nucleus size, cytoplasm, and cell area to determine the characteristics of Normal and Abnormal cells as shown in Figure 1. These characteristics are expressed as intensity and shape features. These characteristics present if cervical cells exhibit abnormal characteristics, as cells infected with Human Papilloma Virus (HPV), which can progress to cancer, exhibit certain biological alterations such as an expanded nucleus size and a darker nucleolus color than normal cells (Bora et al., 2017). The distribution of pap smear cell data is shown in Table 1.

### 2.2 Data Normalization

At this stage, the cervical cancer data is normalized so that the intensity value in each data does not have a range that is too far away so that the data remains consistent. The normalization data used in this stage is mini normalization, as defined by Equation (1) (Desiani et al., 2022):

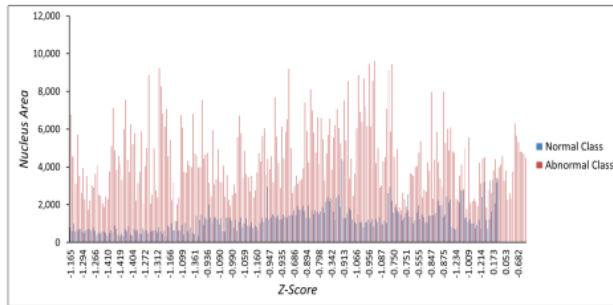
$$x' = \frac{x - \text{mean}}{\text{standard deviation}} \quad (1)$$

Where,  $x'$  is the new value that will be utilized as the classification's data. The dataset has a different type for each attribute, so it needs to be normalization. The results of data normalization using Z-Score standart with the Weka application can be seen in Figure 2 and 3. Figure 2 and Figure 3 show the interval

**Table 1.** Distribution of 917 Pap Smear Cells

| Class | Category | Cell Type                                    | Subtotal Cell | Total Cell |
|-------|----------|--|---------------|------------|
| 1     | Normal   | Superficial squamous epithelial              | 74            | 242        |
| 2     | Normal   | Intermediate squamous epithelial             | 70            |            |
| 3     | Normal   | Columnar epithelial                          | 98            |            |
| 4     | Abnormal | Mild squamous nonkeratinizing dysplasia      | 182           |            |
| 5     | Abnormal | Moderate squamous non-keratinizing dysplasia | 146           |            |
| 6     | Abnormal | Severe squamous non-keratinizing dysplasia   | 197           |            |
| 7     | Abnormal | Squamous cell carcinoma in situ intermediate | 150           |            |

graphs between normal and abnormal of nucleus area attribute and cytoplasm attribute.



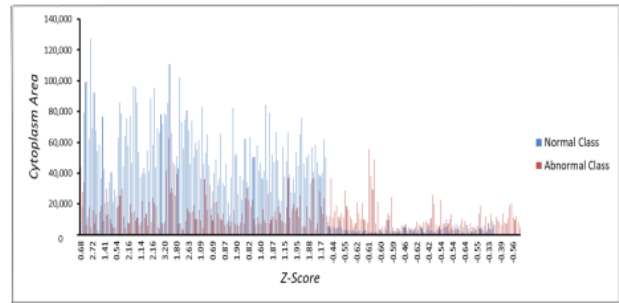
**Figure 2.** Interval Data Nucleus Area after Normalization

**2.3 K-Fold Cross Validation**

In the next step, the data is divided using the K-Fold Cross-Validation technique. K-Fold cross-validation chooses an arbitrary value of K to divide how much training data and test data are needed. The Herlev dataset has 917 pap smear image data, so the k chosen is 10, which means the data is divided into 10 groups and used alternately were 9 groups are training data and 1 is the other group as testing data so that the total training is carried out 10 times.

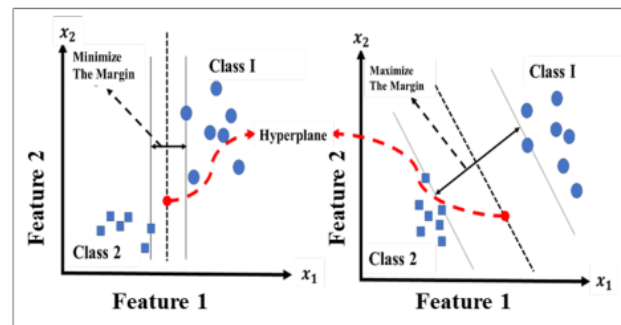
**2.4 SVM Method**

The SVM method is a machine learning system that employs a hypothetical space in the form of linear functions in a high-dimensional feature space and is trained using an optimization-based learning theory. The selection of the appropriate kernel function is critical and vital, as the kernel function determines the



**Figure 3.** Interval Data Cytoplasm Area after Normalization

feature space in which the classifier function will be searched. The SVM concept is to identify a hyperplane that divides data sets linearly into two classes (Ilyasu and Faticah, 2017). To put it simply, the SVM concept is to discover the best hyperplane that acts as a separator between two classes in the input space (Ilyasu and Faticah, 2017). SVM linear classification is employed on data that can be separated linearly. Linearly separable data indicates the number of distinct hyperplanes that can be used to classify data (Figure 4).



**Figure 4.** SVM Hyperplane Concept

Figure 4 presents data from members of class 1 and class 2. Hyperplanes are denoted by dotted lines in Figure 4, while the margins show the distance between hyperplanes and data closest to the hyperplane in each class. The hyperplane with the highest margin is considered the optimal hyperplane (Schohn and Cohn, 2000). SVM divides the dataset into 2 classes. The first class is labeled -1, while the other classes are labeled +1. The hyperplane function is given in Equation (2) (Schohn and Cohn, 2000).

$$D(\vec{w}) = \vec{w}_i \vec{x}_i + b \tag{2}$$

$\vec{w}$  is a vector of dimension  $m$  that represents a vector line perpendicular to the hyperplane line,  $b$  represents the bias, and  $i=1,2,3,\dots,l$  represents the number of data. Inequality (3) can be used to express the data  $\vec{w}_i$  belonging to the class (-1) (Schohn and Cohn, 2000):

$$\vec{w}_l \vec{x}_l + b \leq -1 \tag{3}$$

Meanwhile, the class (+1) follows the inequality (4).

$$\vec{w}_l \vec{x}_l + b \geq +1 \tag{4}$$

Class separation is accomplished by taking into account inequalities (5).

$$y_i(\vec{w}_l \vec{x}_l + b) \geq 1 \quad i = 1, 2, \dots, l \tag{5}$$

Additionally, the hyperplane becomes a decision function as seen in Equation (6):

$$f(x) = \sum_{i=1}^n y_i(\vec{w}_l \vec{x}_l + b) \geq 1 \tag{6}$$

Equation (7) is used to determine the final forecast results.

$$\text{class} = \text{sign}(f(x)) \tag{7}$$

**2.5 MLP Method**

The MLP method is a method with a machine learning technique that mimics how human neural networks work. Learning in this method is carried out by updating the backpropagation periodically. MLP stages and work can be seen in Figure 5.

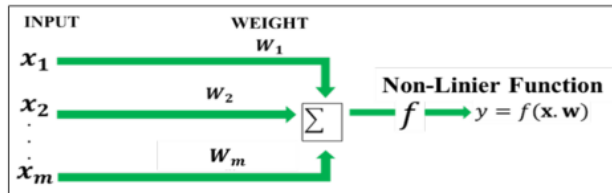


Figure 5. Mathematical Model of Artificial Neural Network

The mathematical notation in Figure 5 can be written in Equation (8) (Lawal and Idris, 2020):

$$y = f(x_1w_1 + x_2w_2 + \dots + x_mw_m) \text{ or } y = f(x, w) \tag{8}$$

where  $f$  is a non-linear function or activation function.

The Sigmoid function is an activation function that is widely used in MLP, where the sum of the weight of the many inputs is entered into the activation function through the transfer function to produce an output. If the MLP consists of multiple layers, the inputs to each MLP layer are fed in a layered feed-forward topology (Desiani et al., 2021). The output of a hidden layer will be the input for the next hidden layer, the output of the hidden layer is entered into the next hidden layer, and

for each next layer the weights obtained are added separately. According to Lawal and Idris (2020), the mathematical model of a multilayer perceptron artificial neural network can be stated as Equation (9).

$$y_k = \sum_{j=1}^p w_{kj} \cdot f \left[ y_k + \sum_{j=1}^n x_i v_{ji} \right] + w_{k0} \tag{9}$$

**2.6 KNN Method**

The KNN method finds groupings of  $k$  objects in the training data that are most alike (similar) to the objects in the new data or data testing (Sinaga and Suwilo, 2020).

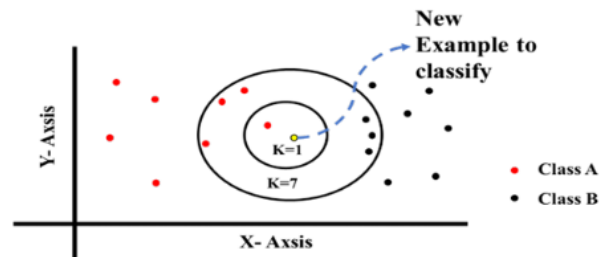


Figure 6. Illustration of the KNN Method

Figure 6 demonstrates the existence of a large number of data points classified into two classes, namely class A (red) and class B (black). For example, in Figure 6 there is new data (yellow color) that will be classified using the KNN method, so to predict the class an arbitrary  $k$  value is taken which indicates the number of nearest neighbors taken. In Figure 4 it can be seen that there are  $k=1$  and  $k=7$ .  $k=1$  means that new data is grouped based on similarity to one of the nearest neighbors while  $k=7$  means that data is grouped based on its 7 nearest neighbors. The proximity or similarity of neighbors is calculated using Euclidean Distance, which can be used in one dimension, two dimensions, or multi-dimensions. The Euclidean distance is identical to the calculation of the Pythagorean distance, except that the Euclidean distance has dimensions greater than two. Equation (10) shows the Euclidean formula for two dimensions and Equation (11) for more than two dimensions (Kataria and Singh, 2013):

$$\text{dis}(x, y) = \sqrt{(x_1 - y_1)^2 + (x_2 - y_2)^2} \tag{10}$$

$$\begin{aligned} \text{dis}(x, y) &= \sqrt{(x_1 - y_1)^2 + (x_2 - y_2)^2 + \dots + (x_n - y_n)^2} \\ &\equiv \sqrt{\sum_{i=1}^n (x_i - y_i)^2} \end{aligned} \tag{11}$$

Based on Figure 6, after calculating the Euclidean distance between the new data points (yellow) and other data points,

for  $k= 1$ , it results in the nearest neighbor (the data in red). It means that new data in yellow is included in the group labeled red. For  $k= 7$ , it can be seen that the closest neighbor to the yellow data is red data, and the new data can be grouped into data labeled red.

**2.7 Ensemble Methods**

The Ensemble method combines many single classifications to create new classifications that result in better performance (Dietterich, 2000). The ensemble method combines many single classifications with the aim of maximizing the performance of each classification in solving classification problems. This study uses majority voting, which involves selecting the majority class from a single classification group. Majority voting rules exist in three forms (Dey et al., 2018):

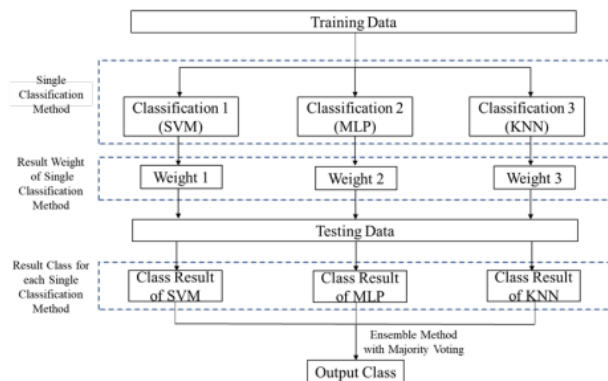
- a. Unanimous vote, in which all classifiers must agree with the prediction.
- b. A simple majority is voting that needs more than half of all results of single classification methods.
- c. Plurality or majority vote, namely voting is carried out based on where the highest number of votes exceeds 50%.

Ensemble results through majority voting from single classification methods always improve performance predictions (Dey et al., 2018). The final class is predicted with class label  $\hat{y}$  via majority (plurality) voting of each classifier  $C_j(x)$  by Equation (12).

$$\hat{y} = \text{mode}\{C_1(x), C_2(x), \dots, C_j(x)\} \quad j = 1, 2, \dots, N \quad (12)$$

$j$  is the index for each class resulting from a single classifier and  $N$  is the number of single classifiers used.

1 An illustration of the Ensemble method in this study can be seen in Figure 7. In Figure 7 it can be seen that every single classifier selected based on the labels generated by each classifier in the test data. The last label in the test data is determined based on the results of majority voting in a single classifier.



**Figure 7.** Majority Voting Ensemble Method Process

In Figure 7, the training stage produces the weights used to classify the test data into the available classes. After each test data has been successfully classified into each class, an ensemble is carried out with majority voting to see which majority of the classes are selected for each test data. The selected majority class will be the final class decision for the test data.

**2.6 Evaluation**

A confusion matrix was used to evaluate the results of this study. Each result of SVM, MLP, and KNN methods is evaluated by a confusion matrix to determine performance based on accuracy, sensitivity, and specificity. In addition, the performance of the ensemble method is also evaluated based on accuracy, sensitivity, and specificity to find out how much influence the ensemble classification results obtained on the results of the three single classification methods SVM, MLP, and KNN.

**3. RESULT AND DISCUSSION**

**3.1 SVM Method**

The SVM method in this study uses a linear kernel because the data only consists of two normal and abnormal classes. performance results on data testing with the SVM method can be seen from the confusion matrix in Table 2.

**Table 2.** Confusion Matrix of SVM Method with Two Classes

|              |         | Confusion Matrix |              |
|--------------|---------|------------------|--------------|
|              |         | Normal (+)       | Abnormal (-) |
| Normal (+)   | TP= 193 | FP= 49           |              |
| Abnormal (-) | FN= 17  | TN= 658          |              |

Based on Table 2, the SVM method manages to get 92.80% accuracy. The sensitivity results are 91.90% for the normal class and 93.06% for the abnormal class. the specificity results obtained are 97.48% for normal and 79.75% for abnormal. These results show that SVM has a very good performance on the test data, but the specificity obtained for the abnormal class is still below 80% but the sensitivity is above 90%. The result shows that SVM works better in classifying data that is in the abnormal class than data that is not in the abnormal class.

**3.2 MLP Method**

In this study, the MLP method uses 3 layers, namely the input layer, 1 hidden layer, and the output layer. MLP performance results at the testing stage for the Cervical Cancer dataset with 2 Class Labels can be seen from the confusion matrix in Table 3.

The MLP method produces an accuracy of 93.78% and places it in very good testing data. The sensitivity results for each class are 87.75% for normal and 95.98% for abnormal. the specificity results for each class are 95.6% for normal and 88.84% for abnormal. These results indicate that MLP works very well in classifying pap smear cells. Unfortunately, MLP works very well in recognizing abnormal classes compared to

**Table 3.** Confusion Matrix of MLP Method with Two Classes on Cervical Cancer Classification

|              | Confusion Matrix |              |
|--------------|------------------|--------------|
|              | Normal (+)       | Abnormal (-) |
| Normal (+)   | 215              | 27           |
| Abnormal (-) | 30               | 645          |

normal class. it can be seen from the sensitivity results of the normal class which is lower than abnormal class, but the specificity results are the opposite.

**3.3 KNN Method**

Parameter k is chosen randomly and repeatedly. the results of the confusion matrix for each k are calculated for the performance results. the best performance results were obtained for k= 3 with the confusion matrix as shown in Table 4. Table 4 represents the output of the KNN method training process on the Herlev Cervical Cancer Dataset with two classes for k= 3.

**Table 4.** Confusion Matrix of KNN-Method

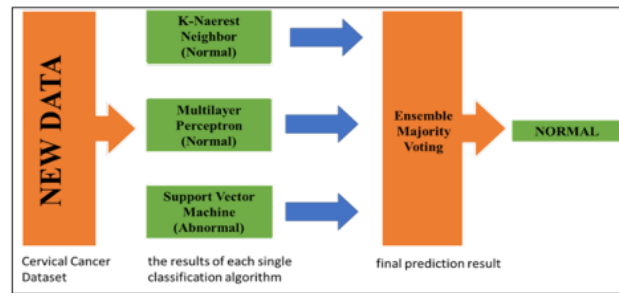
|              | Confusion Matrix |              |
|--------------|------------------|--------------|
|              | Normal (+)       | Abnormal (-) |
| Normal (+)   | 200              | 42           |
| Abnormal (-) | 33               | 642          |

Based on Table 4, KNN obtains an accuracy of 91.8%. The sensitivity results obtained are 85.83% for the normal class and 93.85% for the abnormal class. The results for the specificity of each class are 95.11% for the normal class and 82.64% for the abnormal class. The results show that KNN is able to classify pap smear cells for new data but it still needs to improve for sensitivity in the normal class and for specificity in the abnormal class.

**3.4 Ensemble Methods**

An illustration of how the ensemble method works are shown in Figure 8. In Figure 8 it can be seen that if new data should be classified, the data must be classified first using a single classification method. In Figure 8 it can be seen that the results of KNN and MLP classify the new data into the normal class, while SVM classifies the data into the abnormal class. From the results of the single classification methods, the data class is determined using the ensemble method by looking at the majority of the resulting classes. The majority of the resulting classes are normal classes, so the final decision for the new data is grouped into normal class.

The ensemble method only works on test data and does not work on training data, because the steps taken are to find the value or majority class from each result single classification method. In this study, the training and testing process for every single method was carried out using the k-fold-cross validation



**Figure 8.** Illustration Work of Ensemble Method Majority Voting on Cervical Cancer Classification

technique where k is selected 10. It means the total training and testing for a single classification was 10 times, thus the ensemble method with majority voting was also carried out 10 times on each testing result of a single classification. the total testing results of the Ensemble Method with majority voting can be seen in Table 5.

Based on Table 5, the Ensemble Method obtains an accuracy of 94.32%. The sensitivity results for each class are 91.7% for the normal class and 95.21% for the abnormal class. It shows that the level of accuracy between the information requested for each class and the answers given by the ensemble method with the majority is excellent for both classes. The specificity results for each class are 96.75% for normal and 86.36% for abnormal. These results show that the ensemble method has a good balance in classifying each class even though the specificity results in the abnormal class are still lower than the normal class but the results obtained are above 85%.

**Table 5.** Confusion Matrix of Ensemble Method for Cervical Cancer Classification on Herlev Dataset

|              | Confusion Matrix |              |
|--------------|------------------|--------------|
|              | Normal (+)       | Abnormal (-) |
| Normal (+)   | 193              | 49           |
| Abnormal (-) | 17               | 658          |

**Table 6.** The Comparison Performance Results of SVM, MLP, KNN, and Ensemble Method

| Method   | Accuracy | Sensitivity | Specificity |
|----------|----------|-------------|-------------|
| SVM      | 92.80%   | 92.48%      | 88.60%      |
| MLP      | 93.26%   | 91.85%      | 91.80%      |
| KNN      | 91.82%   | 88.85%      | 89.85%      |
| Ensemble | 94.32%   | 91.80%      | 93.45%      |

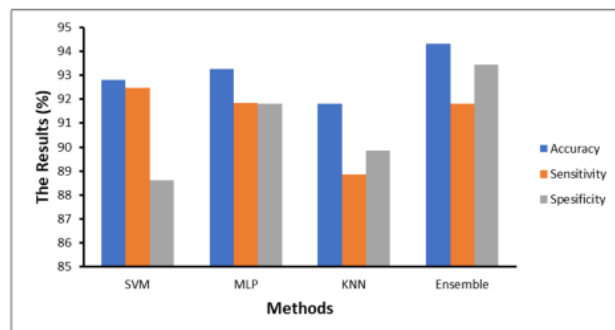
The comparison performance results of the ensemble method with majority voting and 3 single classification methods can be seen in Table 6. In Figure 9 it can be seen that the

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**Table 7.** The Comparison Results in The Proposed Method and Other Studies

| Method  | Class Labels | Performance Results |             |             |
|---|--------------|---------------------|-------------|-------------|
|   |              | Accuracy            | Sensitivity | Specificity |
| NN+PSO+Bagging (Zuama and Sobari, 2020)                                 | 2            | 64.56%              | -           | -           |
| MLP 3 Layer (Fekri-Ershad, 2019)  | 2            | 85,16%              | -           | -           |
| Feature Selection Bagging Ensemble and Random Forest (Win et al., 2019) | 2            | 97.83%              | -           | -           |
| Neural Network (Riana et al., 2018)                                     | 2            | 93.12%              | -           | -           |
| SVM (Amole and Osalusi, 2018)   | 2            | 90%                 | 67.3%       | 31.62%      |
| Ensemble Method (Bora et al., 2017)                                     | 2            | 93.75%              | -           | -           |
| Proposed Method   | 2            | 91.8%               | 91.8%       | 93.45%      |

ensemble method is able to improve the results of the accuracy and specificity of the results of a single classification. for sensitivity, the results from the ensemble method are still low compared to the results from SVM and MLP but the results given have a small difference, namely 0.68. In addition, the sensitivity and specificity results for each normal and abnormal class are more balanced than the results for single classification methods. To see how the ensemble method with majority voting has succeeded in increasing the performance of single classification methods, the results of this study are compared with several other studies. the results of the comparison with other studies can be seen in Table 7.



**Figure 9.** The Comparison Results of Ensemble Method Majority Voting with Single Classification Methods SVM, MLP, and KNN for Cervical Cancer Classification on Herlev Dataset

Based on Table 7, the highest accuracy result is 97.83% which is the result of a study by Win et al. (2019). Unfortunately, this study did not report sensitivity and specificity results. In addition, the results of the proposed method provide an accuracy of 94.32%, which is the second-highest accuracy result compared to other studies in Table 7. The results of sensitivity and specificity of the proposed method provide better results compared to the results of Amole and Osalusi (2018), which only reached 67.3% and 31.62% respectively. These results indicate that the majority voting ensemble method is an excel-

lent and novel method for the classification of cervical cancer based on pap smear cells into two classes, namely normal and abnormal.

#### 4. CONCLUSION

The Ensemble method with majority voting using 5-fold cross-validation with two classes produces the highest accuracy and specificity compared to the SVM, MLP, and KNN results. In addition, although the sensitivity results are lower than the average sensitivity results of the single classification methods, the sensitivity results of the ensemble method for each class are better than the results for each class of the single classification methods. Its results show that the ensemble method with the majority voting can improve performance and overcome the weaknesses of the performance results of the single classification method. The ensemble voting method gives very good performance results and can be used in the classification of cervical cancer abnormalities based on pap smear cells in two classes, namely normal and abnormal. for future work, this study can be focused on the classification of cervical cancer abnormalities that have more than 2 classes.

#### 5. ACKNOWLEDGMENT

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